

**Molecular characterization of South African *Ehrlichia ruminantium* field isolates
and development of a qPCR assay for the evaluation of a multivalent inactivated
vaccine**

Zinathi Dlamkile

04892519

**Submitted in partial fulfilment of the requirements for the degree
Doctor of Philosophy (Veterinary Tropical Diseases)**

in the

FACULTY OF VETERINARY SCIENCES

at the

UNIVERSITY OF PRETORIA

Study leader:

Prof L Neves

April 2023

Declaration

I hereby declare that this thesis which I submit for the degree Philosophiae Doctor at the Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, South Africa is my original research work and has not been submitted by me to any institution or University for the conferment of an award.



.....

Zinathi Dlamkile

...April 2023....

Date

Acknowledgements

I would like to express my heartfelt gratitude and appreciation to the following individuals, institutions and organizations for their dedication, service and impact they have made upon my life and career during the course this research;

First to God Almighty for giving me the life, courage, determination, and strength to pursue this research. Throughout this journey, God I have experienced your steadfast love that never ceases; your mercies never come to an end, they are new every morning; great is your faithfulness.

Prof Luis Neves (UP), you are a living definition of a mentor. Your outstanding commitment, patience, guidance, and support in the entire course of this study is unmatched. You have pushed me not only to be a better scientist but to believe and see value in myself. You have inspired me. May God keep you so that I can learn more from you.

To my Co-supervisor, Prof Darshana Morar-Leather (UP), your continued support throughout this study and my journey at University of Pretoria warms my heart. If it was not for you choosing me to be your NRF intern, I do not think I would have embarked on a PhD journey. Thank you for not giving up on me when I have given you reasons to. You are for “keeps”.

My Co-supervisors (ARC-OVI), Dr Helena Steyn, Dr Alri Pretorius, and Dr Junita Liebenberg, thank you for the expert advice, insights, and direction during the course of this research. It has been a privilege to drink from your wells of knowledge.

To Karen Ebersohn (UP), thank you for your time and patience during my training on maintenance of cell cultures. I have learned your orderly manner of working in the laboratory.

Dr Charles Byaruhanga (UP), thank you for your tireless support and assistance with sequence analysis and phylogenetics of the study.

To Dr Erika Faber (ARC-OVI), thank you for training me on RNA isolation and qPCR at ARC-OVI. Your drive and determination are admirable.

Mr Christopher Brandt (ARC-OVR) and Ms Andeliza Smit (UP), your support and assistance during sample collection and processing throughout the research is greatly appreciated.

Belgian Directorate General for Development Co-operation Framework FA4 (ITM/DECD) for financially supporting the sustenance my sustenance throughout the study.

To my funders, A Long-term EU Africa research and Innovation Partnership on food and nutrition security and sustainable Agriculture (LEAP-Agri) and Agricultural Sector Education Training Authority (AgriSETA), thank you for funding this research. Without you, this research would not have been possible.

To the staff and all postgraduate students of the Department of Veterinary Tropical Diseases, thank you for the conducive environment, the support and the laughter you have provided during the years of my stay at the Department.

My husband, Phumlani Dlamkile, the love of my life, my greatest cheerleader and prayer partner, thank you for choosing me every day. Doing life with you by my side is exciting. Given a chance in another lifetime, I would choose you again. Thank you for holding the fort when I travel for my field trips and making sure that our daughter, Lusanele is well taken care of.

My daughter Lusanele Dlamkile, my precious one whom I adore, a great blessing to my life, thank you for understanding when I have to travel and be away from you for some days.

To my parents Mr Wanda and Mrs Phumeza Lukanji, thank you for raising me to be the woman that I am today. Your great sacrifices have contributed to put me where I am today. Throughout my life you have loved and supported me, I thank God for you.

To my friends, Refilwe Bokaba and Nokuzola Faith Nkosi, thank you for readily availing your ears to listen to my frustrations and your words of encouragement were like air to the lungs.

To the people that supported me through prayers Apostle and Mrs Jezile, Sbongile Mhlanga thank you for covering me spiritually. I am grateful to God for you.

Table of Contents

Declaration	i
Acknowledgements.....	ii
List of abbreviations.....	ix
List of figures.....	xii
List of tables.....	xiv
Thesis Summary.....	1
Chapter 1.....	1
Introduction and Literature Review.....	1
1.1 Introduction.....	1
1.2 Historical background	2
1.3 Classification of <i>E. ruminantium</i>	2
1.4 Life cycle of <i>E. ruminantium</i>	3
1.5 Transmission.....	4
1.6 Distribution.....	5
1.7 Laboratory Diagnosis	6
1.8 Characterization of <i>E. ruminantium</i> strains.....	7
1.8.1 Small subunit (16S) ribosomal ribonucleic acid.....	8
1.8.2 pCS20	9
1.8.3 Major Antigenic Protein gene (<i>map1</i>).....	10
1.8.4 Multi Locus Sequence Typing (MLST).....	10
1.8.5 Other tools.....	11
1.9 <i>In vitro</i> propagation of <i>E. ruminantium</i>	12
1.9.1 <i>In vitro</i> propagation in tick cell lines.....	12
1.9.2 <i>In vitro</i> propagation in mammalian cell lines	13
1.9.3 Inoculum	14
1.9.4 Culture media.....	15
1.9.5 Propagation of <i>E. ruminantium</i> in cell cultures	16
1.9.6 Detection of <i>E. ruminantium</i> in cell cultures.....	17
1.10 Immune response to <i>E. ruminantium</i> and vaccine development.....	17
1.10.1 Inactivated vaccines	18
1.10.2 Attenuated vaccines	20

1.10.3 Recombinant vaccines	21
1.11 Justification.....	21
1.12 Aim and Objectives	22
1.13 References	24
Chapter 2.....	38
Characterization of <i>Ehrlichia ruminantium</i> from field <i>Amblyomma hebraeum</i> ticks collected from cattle in three South African provinces using Multi-Locus Sequence Typing.....	38
2.1 Abstract	38
2.2 Introduction.....	39
2.3 Ethical considerations	40
2.4 Materials and Methods	41
2.4.1 Study areas	41
2.4.2 Tick collection	41
2.4.3 DNA extraction.....	42
2.4.4 Detection of <i>E. ruminantium</i> using pCS20 qPCR.....	42
2.4.5 Characterization of <i>E. ruminantium</i> isolates using MLST	43
2.4.6 Sequences and phylogenetic analysis.....	45
2.4.7 Statistical analysis.....	45
2.5 Results	46
2.5.1 Tick collection	46
2.5.2 Detection and prevalence of <i>E. ruminantium</i> by pCS20 qPCR.....	46
2.5.3 Characterization of <i>E. ruminantium</i> isolates using MLST	49
2.6 Discussion.....	53
2.7 Conclusion	56
2.8 References	58
Chapter 3.....	62
<i>In vitro</i> culture of <i>Ehrlichia ruminantium</i> using tick salivary glands and gut.....	62
3.1 Abstract	62
3.2 Introduction.....	63
3.3 Materials and Methods	66
3.3.1 Culture medium	66
3.3.2 Inoculum preparation	66

3.3.3 Inoculum	66
3.3.4 Initiating <i>in vitro</i> culture of <i>E. ruminantium</i> using tick material	67
3.4 Results	68
3.5 Discussion.....	70
3.6 Conclusion	72
3.7 References	74
Chapter 4.....	78
Development of a reverse transcription quantitative real-time PCR assay for the evaluation of a multivalent inactivated vaccine.....	78
4.1 Abstract	78
4.2 Introduction.....	80
4.3 Materials and Methods	82
4.3.1 Selection of housekeeping genes as reference for a RT qPCR assay using RNA sequences obtained from sheep PBMC infected with <i>E. ruminantium</i>	82
4.3.2 Selection of immune markers using transcriptome sequence data.....	85
4.3.3 Validation of the housekeeping genes and immune markers selected for the RT-qPCR using RNA isolated from a current inactivated vaccine trial.....	87
4.4 Results	90
4.4.1 Identification of candidate housekeeping genes using transcriptome data.....	90
4.4.2 Selection of immune markers for protection.....	91
4.4.3 Animal trial.....	92
4.4.4 qPCR validation of housekeeping genes to use using total RNA samples collected during animal trial	93
4.4.5 Expression levels of the selected markers for protection using RT-qPCR with the validated housekeeping genes using RNA from the animal trial	96
4.5 Discussion.....	99
4.6 Conclusion	101
4.7 References	103
4.8 Supplementary data	106
Chapter 5.....	109
General Discussion, Recommendations and Conclusion.....	109
5.1 References	113
Appendices.....	115

Appendix 1 115
Appendix 2 143

List of abbreviations

16S rRNA	16S ribosomal ribonucleic acid
β	Beta
$^{\circ}\text{C}$	Degrees Celcius
δ	Delta
γ	Gamma
μg	Microgram
μl	Microliter
μM	Micromolar
ARC-OVR	Agricultural Research Council- Onderstepoort Veterinary Institute
BA	Bovine Aorta
bp	Basepairs
BHK	Baby hamster kidney
CO_2	Carbon dioxide
CyX	Cycloheximide
CPE	Cytopathic effect
D	Day
DALRRD	Department of Agriculture, Land Reform and Rural Development
DEPC	Diethyl pyrocarbonate
DNA	Deoxyribonucleic acid
EC	Eastern Cape
EDTA	Ethylenediaminetetraacetic acid
ELISA	Enzyme linked immunosorbent assay
FA	Freund's adjuvant

GP	Gauteng province
G	Group
IFAT	Indirect fluorescent antibody test
IFN	Interferon
IL-2R	Interleukin 2 receptor
KZN	KwaZulu-Natal
LP	Limpopo
MAFFT	Multiple Alignment, Fast Fourier Transform
MAP1	Major antigenic protein 1
MDBK	Madin Darby bovine kidney
MEGA	Molecular Evolutionary Genetics Analysis
ML	Maximum likelihood
MHC	Major histocompatibility complex
ML	Multi locus
MLST	Multi-Locus Sequence Typing
MLVA	Multi locus variable number tandem repeat analysis
MP	Mpumalanga
NCBI	National Center for Biotechnology Information
NK	Natural killer
NW	North West
PBMC	Peripheral blood mononuclear cells
PBS	Phosphate buffered saline
PC	Post challenge
PV	Post vaccination
REC	Research Ethics Committee

RFLP	Restriction fragment length polymorphism
RT qPCR	Reverse transcription quantitative real-time polymerase chain reaction
ST	Sequence Type
SPG	Sucrose Phosphate Glutamate
SNP	Single nucleotide polymorphism
US	United States
TNF	Tumor necrosis factor
UNG	Uracil-N-glycosylase
UP	University of Pretoria
UV	Ultra violet
V1	Variable1
VNTR	Variable number tandem repeat

List of figures

- Figure 1:** Distribution of some of African vectors of heartwater..... 6
- Figure 2.1:** Map of South Africa showing where sample collection areas (coloured dots) are situated in the provinces of Limpopo, Mpumalanga and KwaZulu-Natal..... .41
- Figure 2.2:** Amplification plot of *E. ruminantium* specific qPCR assay targeting the pCS20 gene fragment..... 47
- Figure 2.3:** Bar graph showing the occurrence of *E. ruminantium* in *A. hebraeum* ticks collected from cattle in the study areas..... 49
- Figure 2.4:** Phylogenetic tree showing relationship between *E. ruminantium* field isolates from three South African provinces and global reference isolates. The phylogenetic tree was constructed based on concatenated nucleotide sequences of housekeeping genes (*sodB*, *secY*, *lipB*, and *lipA* partial sequences), using MEGA7 and maximum likelihood method. Sequences from this study are shown in bold font. The numbers at the nodes represent bootstrap values and they are calculated from 100 replicates.....52
- Figure 2.5:** Phylogenetic tree showing relationship between *E. ruminantium* field isolates from three South African provinces and global reference isolates based on *secY* gene. Study isolate E29 from Cecelia dip tank KZN province circled in red clustered with the unique South African isolates. The numbers at the nodes represent bootstrap values and they are calculated from 100 replicates..... 56

Figure 3.1: Amplification plot of *E. ruminantium* positive ticks used for extracting salivary glands and gut for *E. ruminantium in vitro* culture..... 69

Figure 3.2 A, B & C: BPAE cells 19 days post inoculation with tick gut and salivary glands (A and B). Dark purple colonies that resemble elementary bodies of *E. ruminantium* were observed. C is the negative control cell culture inoculated with culture medium 19 days after inoculation. The dark purple colonies that resemble elementary bodies of *E. ruminantium* were not present.....70

Figure 4.1: Box-and-whisker plots indicating the range of normalized RPKM values in CLC of the selected candidate reference genes throughout *E. ruminantium* infection in sheep PBMC. Values of represent four biological replicates taken as averages of three technical replicates, taken at eight time points are given. The whiskers represent standard deviation of n samples (n = 24)..... 91

Figure 4.2: Markers selected that were upregulated in animals that survived heartwater challenge. This shows the heat map of markers that were upregulated at the post challenge time points (PC) but not during infection..... 92

Figure 4.3: Survival plot of animals in group 1, 2, 3, and 4..... 93

List of tables

Table 1: <i>Amblyomma</i> tick species proven to be experimental and natural vectors of heartwater.....	5
Table 2.1: Oligonucleotides used for pCS20 qPCR and housekeeping genes.....	44
Table 2.2: Occurrence of <i>E. ruminantium</i> in <i>A. hebraeum</i> ticks collected from cattle in the study areas.....	48
Table 2.3: Number of samples with percentage similarity identity with reference strains according to each housekeeping gene.....	50
Table 4.1: Summary of the candidate ovine housekeeping genes used in the RNA-seq analyses and evaluated in this study. The Gene symbol, Gene ID (the number allocated to the gene in the ovine genome sequence), Official name, Transcript variant (where applicable) and gene size are shown.....	83
Table 4.2: Selected housekeeping genes (not highlighted) and immune biomarkers (highlighted in blue).....	86
Table 4.3: Animal groups for animal trial.....	89
Table 4.4: Animal groups for the animal trial pooled for qPCR screening.....	94

Table 4.5: The ranking of the selected housekeeping genes..... 95

Table 4.6: $2^{-\Delta\Delta CT}$ to analyze the relative fold changes in gene expression of the immune markers of protection..... 98

Supplementary Table 4.1: Animal groups and pools and individual animals combined to make RNA pools at different time points to be tested for immune markers.....106

Supplementary Table 4.2: Sheep numbers with their RNA concentrations.....106

Supplementary Table 4.3: Volume of RNA for each sheep needed to make the pools..... 107

Supplementary Table 4.4: Volume of RNA, buffer and H₂O needed for making each pool.....108

Molecular characterization of South African *Ehrlichia ruminantium* field isolates and development of a qPCR assay for the evaluation of a multivalent inactivated vaccine

Candidate: Zinathi Dlamkile

Supervisor: Prof Luis Neves

Co-supervisors: Prof Darshana Morar-Leather, Dr Helena Steyn, Dr Alri Pretorius

Department: Veterinary Tropical Diseases

Degree: PhD Veterinary Tropical Diseases

Thesis Summary

Heartwater is one of the major tick-borne diseases of both domestic and some wild ruminants in Africa and some Caribbean islands. The disease is caused by *Ehrlichia ruminantium*, a member of the phylum Proteobacteria and order Rickettsiales. *Amblyomma* genus ticks transmit *E. ruminantium*. Heartwater is a cause for concern, it challenges livestock farmers from introducing high producing exotic breeds to upgrade local stock. The exotic breeds are highly susceptible to *E. ruminantium*, and the mortality rate of susceptible animals ranges from 20 to 90% depending on the animal's species, breed, and previous exposures. *Ehrlichia ruminantium* has diverse genotypes and immunogenicity caused by recombination that occurs between different isolates in the field. The diversity of *E. ruminantium* isolates render the commercially available vaccine ineffective against some virulent isolates. A development of an inactivated vaccine that can cross protect against virulent isolates is crucial. To develop an effective vaccine researchers must, isolate field *E. ruminantium* by *in vitro* culture system to provide the antigen required for the vaccine, characterize the isolates by genotyping to determine the

possibility of their use in an inactivated cocktail vaccine. Then, the vaccine can be developed and tested. This study was therefore carried out to characterize South African *E. ruminantium* field isolates by Multi-Locus Sequence Typing (MLST) and develop a reverse transcription quantitative real-time polymerase chain reaction assay for the evaluation of a multivalent inactivated vaccine.

A total of 1004 DNA samples were extracted from *Amblyomma hebraeum* ticks collected from cattle in Mpumalanga, Limpopo, and KwaZulu-Natal provinces of South Africa, and were tested for *E. ruminantium* by pCS20 Sol1 qPCR. The *E. ruminantium* positive samples were characterized by MLST using five housekeeping genes. Out of 1004 samples tested, overall *E. ruminantium* infection rate was 22% and provincially 19%, 22% and 27% in Mpumalanga, KwaZulu-Natal and Limpopo respectively. Sequencing of the housekeeping genes showed genetic variation in the sequenced regions and phylogenetic analysis revealed three main lineages, clade 1 made up of worldwide isolates (eastern, southern Africa, and Caribbean isolates); clade 2 comprised only West African isolates; and clade 3 consisted of the unique South African isolates, Omatjenne, Kümme2, and Riverside. MLST can clearly distinguish the South African genotypes from the distinct West African genotype. The genetic variation in the sequenced regions does not change the makeup and function of the protein encoded by the genes.

In vitro culture using gut and salivary glands from *E. ruminantium* positive field ticks as an inoculum was initiated. First attempt of *E. ruminantium in vitro* culture, 19 days post inoculation, the cultures were *E. ruminantium* negative and at 25 days the cultures were contaminated. The second attempt had to be discontinued due to national lockdown caused by the worldwide corona virus pandemic. There is *E. ruminantium* positive tick material stored at -80 °C and that can be used in future to initiate *in vitro* culture of *E. ruminantium*. *Ehrlichia ruminantium in vitro* culture from tick material must be optimized and is a possible alternative for isolating field *E. ruminantium* without the need of infecting an animal. Also, the optimization of the method would make it easier to sequence

genomes of *E. ruminantium* field isolates and fast track the development of an efficient vaccine.

Methods to determine success of a developed vaccine need to be developed. One of the assays the current study developed was a reverse transcription quantitative real-time PCR (RT qPCR) assay to evaluate a multivalent inactivated vaccine against heartwater. This method requires selection and validation of housekeeping genes to obtain reliable results in immune markers for protection. Most housekeeping genes commonly used for qPCR analyses were selected from previous studies and the sheep homologues were selected from GenBank. The housekeeping genes were validated using Ct mean, CV of RPKM values and CT values and the Δ Ct method to estimate the expression stability of each housekeeping gene. The genes were ranked for RT qPCR data normalization using an online tool, RefFinder. Immune markers for protection differentially expressed between surviving animals and animals that were treated (considered dead) were identified using RNA-seq data from a previous study.

The most suitable choice combination of housekeeping genes that showed the least expression variation throughout the experimental conditions is SDHA, RPL22, YWHAZ and GAPDH. The immune markers for protection were identified and were upregulated in animals that survived heartwater challenge: CD41–ITGA2B, CD156A-ADAM8, CXCR5, CD8B, CD5, GZMB-LIKE, IFN- γ and TGFB1. Based on the developed RT qPCR the immune markers for protection were differentially expressed throughout the experimental conditions. The upregulation of the identified immune markers for protection does not inform protective immunity against the disease.

In conclusion, the study revealed genetic diversity among *E. ruminantium* field isolates from *A. hebraeum* ticks in three provinces of South Africa. The RT qPCR assay developed to evaluate a multivalent inactivated vaccine against heartwater can be validated and

applied in further studies. Also, there is a need for alternative genotypic genes that reveal immunogenicity of isolates for identifying best vaccine isolates for the development of an effective vaccine against heartwater. Optimization of *E. ruminantium* *in vitro* culture using tick salivary gland and gut is important.

Chapter 1

Introduction and Literature Review

1.1 Introduction

Ehrlichia ruminantium, previously called *Cowdria ruminantium* causes heartwater disease in some wild and domestic ruminants (Cowdry, 1925). Ticks of the *Amblyomma* genus are responsible for transmitting the pathogen (Bezuidenhout, 1985). Heartwater occurs in different forms: peracute, acute, subacute, or chronic depending on the type and age of animal infected, how the animal was infected and pathogenicity of strain that infected the animal (Van de Pypekamp and Prozesky, 1987). Heartwater is typified by high fever, nervous signs, hydropericardium, hydrothorax, oedema of the lungs and brain (Allsopp, 2010).

Heartwater is fatal to susceptible animals with mortality rate of up to 90%. The susceptible rate varies depending on the type of animal and prior exposures (Mahan et al., 1992). Heartwater presents a major obstacle to livestock farmers from introducing high producing susceptible exotic breeds to upgrade local stock (Meltzer et al., 1996). According to Mukhebi et al. (1999) the disease is estimated to cost the Southern African Development Community an estimate of US\$ 47.6 million per year. Crucial losses caused by heartwater include the cost of antibiotics and acaracides used to treat animals and decreased produce by farmers (CABI, 2020). A safe and effective method to control heartwater could reduce the negative economic repercussion exerted by the disease on farmers.

1.2 Historical background

On the 17th of February 1838, Louis Trichardt noted in his diary that his sheep suffered a fatal death due to a disease locally called “nintas” three weeks after the tick infestation they acquired (Bezuidenhout, 1987a). In 1877 at the Cattle and Sheep Disease Commission in Grahamstown, John Webb described a disease "boschsickness" (heartwater) fatal in sheep in the Eastern Cape (Provost and Bezuidenhout, 1987). John Webb was certain the disease was first observed in the Eastern Cape immediately after William Bowker found a bont tick on a cow that came from Zululand in 1837 (Bezuidenhout, 2009b).

In 1898, Edington and Dixton separately demonstrated that heartwater can be transmitted by inoculating blood from an infected animal to healthy susceptible animals (Provost and Bezuidenhout, 1987). Even though no organisms could be observed in the blood or tissues of the infected animal, it was suggested that heartwater was caused by a living microorganism believed to be a filterable virus (Provost and Bezuidenhout, 1987). It was Lounsbury in 1900 who confirmed the vector of heartwater as the bont tick, *Amblyomma hebraeum* in South Africa (Cowdry, 1925). The breakthrough of Edington and Dixton allowed the possibility to replicate laboratory heartwater infection, making it easy to define the disease. Subsequently, Cowdry was able to prove that heartwater is caused by a pathogen and named it *Rickettsia ruminantium* (Cowdry, 1925). In 1947, the organism was classified to the genus *Cowdria*, and renamed after Cowdry and called *Cowdria ruminantium* (Bezuidenhout, 2009a).

1.3 Classification of *E. ruminantium*

The causal agent of heartwater is an obligate intracellular bacterium formerly called *Cowdria ruminantium*. The heartwater causing agent was previously classified as a member of the family Rickettsiaceae, order Rickettsiales, tribe Ehrlichieae and genus *Cowdria*. With the emergence of molecular phylogenetics the order Rickettsiales was

reorganised into two families, Rickettsiaceae and Anaplasmataceae causing different assignment of the genera in those families (Allsopp, 2010). The genotypic results of 16S rRNA genes, *groESL* and surface protein genes, assigned the heartwater agent to the family Anaplasmataceae, genus *Ehrlichia* (Dumler et al., 2001).

Phylum: Proteobacteria

Class: Alphaproteobacteria

Order: Rickettsiales

Family: Anaplasmataceae

Genus: *Ehrlichia*

Species: *Ehrlichia ruminantium*

1.4 Life cycle of *E. ruminantium*

Certain *Amblyomma* species can disseminate *E. ruminantium* transstadially. However, *E. ruminantium* can be passed on transovarially even though it is not frequent as proven by Bezuidenhout and Jacobsz (1986). *Ehrlichia ruminantium* divides by binary fission within intracytoplasmic vacuoles (Pienaar, 1970). In culture, the organism has different morphological forms that vary in particle size: large colonies of reticulate bodies, minute moderate bodies indicated by an electron-dense core and electron-dense elementary bodies (Jongejan et al., 1991). Subsequent to infected blood meal by a tick, the pathogen is first observed in the gut epithelial cells and salivary gland acini cells eventually become infected (Kocan and Bezuidenhout, 1987a). The predominant form of organism in both the gut and salivary glands is reticulate bodies. The heartwater agent can be found in tick haemocytes and malpighian tubules (Kocan et al., 1987b).

In vertebrate host the organism is transmitted via saliva when the tick is indulging on blood meal and by regurgitation of previous meal constituents. Initial development of organisms appears to take place in reticulo-endothelial cells (Cowdry, 1926). The infected reticulo-endothelial cells finally disrupt, and the organisms escape into the general circulation to occupy endothelial cells of various organs and tissues (Du Plessis, 1975). Apart from endothelial cells, *E. ruminantium* is detected in the brain, followed by the kidneys. However, the organisms were saturated in the lungs in mice infected with the Welgevonden strain (Prozesky and Du Plessis, 1985).

1.5 Transmission

Ehrlichia ruminantium is transmitted by members of the three-host life cycle tick of the *Amblyomma* genus. There are twelve species of *Amblyomma* species found to be able of disseminating *E. ruminantium* and are outlined in table 1.1. Among the *Amblyomma* species in Africa, *A. variegatum* is the most broadly widespread vector (Walker and Olwage, 1987). Bezuidenhout (1985) attributes Lounsbury as the first to prove that *A. hebraeum*, is the principal vector of heartwater in South Africa. Infections in *A. hebraeum* ticks are transmitted transstadially even though a report by Bezuidenhout and Jacobsz (1986) proved that transovarial transmission does occur. Infection acquired in the vector's juvenile stage can be spread by both young and adult stages, despite the host for the juvenile not being diseased (Bezuidenhout, 1987a). A reptile tick, *A. dissimile* has been shown to experimentally transmit *E. ruminantium*. However, its role is insignificant in transmitting heartwater among ruminants but potentially serve as a source in the reptile inhabitants (Jongejan, 1992).

Table 1.1: *Amblyomma* tick species proven to be experimental and natural vectors of heartwater.

<i>Amblyomma</i> spp	Mode of transmission
African	
<i>A. hebraeum</i>	I ^a , II ^b , III ^c
<i>A. variegatum</i>	I, II, III
<i>A. pomposum</i>	I, II
<i>A. gemma</i>	? ^d
<i>A. lepidum</i>	I, II
<i>A. tholloni</i>	I, II, III
<i>A. sparsum</i>	I
<i>A. astrion</i>	I, III
<i>A. cohaerens</i>	I, III
<i>A. marmoreum</i>	I, III
American	
<i>A. maculatum</i>	I, II, III
<i>A. cajennense</i>	I

^aI from larval to nymphal stage

^bII from nymphal to adult stage

^cIII from larval through nymphal to adult stage

^d? stage(s) not reported

Table is from Bezuidenhout (1987a) and Walker and Olwage (1987) with modification.

1.6 Distribution

Heartwater occurs in regions where ticks from the *Amblyomma* genus capable of transmitting the organism are present (Petney et al., 1987). In southern Africa, the main vector of heartwater is *A. hebraeum* (Bezuidenhout, 2009b). The endemic areas for the vector includes sub-Saharan Africa, Madagascar, Reunion, Mauritius, Zanzibar, the Comoros Islands, and Sao Tomé and three Caribbean islands: Guadeloupe, Marie-Galante, and Antigua (Spickler, 2015). Figure 1 shows the distribution of some *Amblyomma* spp. capable of transmitting heartwater in the continent of Africa (Pascucci

et al., 2007). The vector occurs in bush veld and low veld, therefore in South Africa it is endemic in six of the nine provinces: Limpopo, Mpumalanga, Kwa-Zulu Natal, Gauteng, Eastern Cape and North West Province (Purnell, 1984).

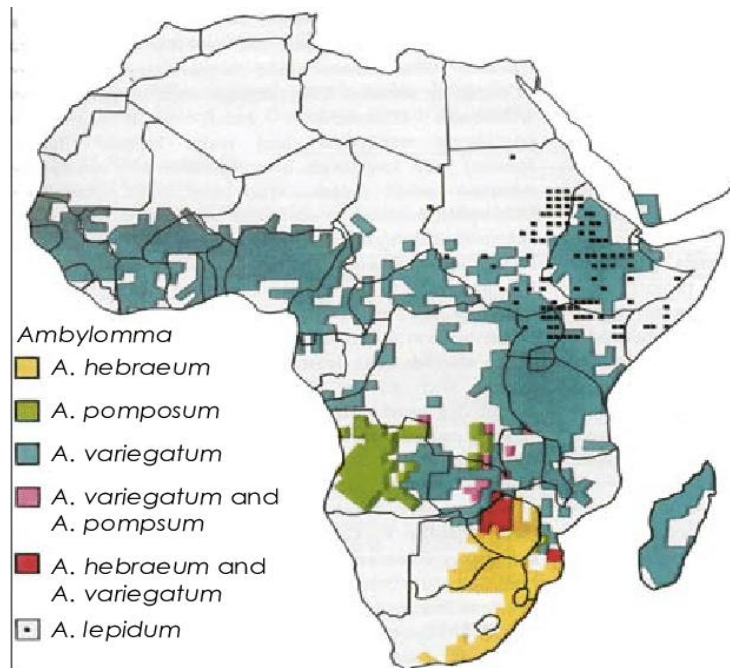


Figure 1: Distribution of some African vectors of heartwater (Pascucci et al., 2007).

1.7 Laboratory Diagnosis

The laboratory diagnosis of heartwater in live animals was filled with hurdles until the development of molecular techniques for detection of *E. ruminantium* infection. Laboratory diagnosis of heartwater was by a serological test called indirect fluorescent antibody test (IFAT). The IFAT target antigen was the Kümm stock in peritoneal macrophages in infected mice (Du Plessis and Malan, 1987a). The test cross reacted with *Ehrlichia* and *Anaplasma* spp causing error in result (Du Plessis and Malan, 1987b). Following IFAT, a competitive enzyme linked immunosorbent assay (ELISA) was developed using a monoclonal anti-major antigenic protein 1 (MAP1) antibody (Jongejan et al., 1991b). This test also gave false positive reactions with related *Ehrlichia* spp (Katz et al., 1996). To remedy the problem, the competitive ELISA was modified by making use of a partial fragment of MAP1 called MAP1B in an indirect ELISA (van Vliet et al., 1995).

There was improvement in the specificity of the test compared to previously developed serological tests. However, MAP1B ELISA cross reacted with *E. canis* and *E. chaffeensis* (Katz et al., 1996).

With the advent of molecular techniques, the problem of cross reaction was solved with the development of probes targeting the pCS20 region, the small subunit ribosomal RNA (16S RNA) gene, or the *map1* gene. The 16S rRNA has been extensively used as a taxonomic and phylogenetic tool for classifying microorganisms (Allsopp, 2010). The pCS20 region is best used for the detection of *E. ruminantium* while the *map1* is best used to provide immunotypic information about *E. ruminantium* isolates (Allsopp et al., 1998).

1.8 Characterization of *E. ruminantium* strains

Heartwater is a disease that affects the economy in sub-Saharan Africa, Madagascar, and some Caribbean islands (Mukhebi et al., 1999). The disease presents a great challenge to the improvement of livestock and productivity in the farming sector (Provost and Bezuidenhout, 1987). Heartwater is controlled by use of acaricide to control tick infestation, antibiotic therapy of cases showing symptoms of the disease, prophylactic use of antibiotics and immunization (Yunker, 1996). The commercially available vaccine is made by cryopreserving blood from an infected sheep with *E. ruminantium* strain Ball3 (Van der Merwe, 1987). The vaccine lacks ability to elicit protective immunity against all genotypes of *E. ruminantium*. The lack of cross protection is caused by the wide genetic and antigenic distinction of *E. ruminantium* strains in the field (Allsopp, 2010). Therefore, it is necessary to characterize strains of *E. ruminantium* to pave a path for development of a more efficient vaccine.

Different tools to characterize *E. ruminantium* strains have been developed and are mostly based on conserved regions. Markers that have been used to characterize *E.*

ruminantium strains include the small subunit (16S) ribosomal RNA, pCS20, *map1* and core function genes.

1.8.1 Small subunit (16S) ribosomal ribonucleic acid

The 16S ribosomal ribonucleic acid is a good marker for strain characterization because it is present in all pathogens, support precise comparative sequence alignments to be created and has species-specific variations (Collins et al., 2002). The 16S rRNA has been successfully used to characterize strains of *E. ruminantium* and closely related *Ehrlichia* species (Mahan, 1995a, Allsopp et al., 1999, Allsopp et al., 2007). There are eight known 16S genotypes of *E. ruminantium* that are intimately related to each other when compared to other *Ehrlichia* species. These are Mara 87/7, Pretoria North, Ball3, Welgevonden, Gardel, Senegal, Crystal Springs and Omatjenne (Collins et al., 2002).

Phenotypic behavior of heartwater isolates, in terms of their ability to elicit protective immunity against other isolates and establishment in culture vary. *Ehrlichia ruminantium* stocks having different phenotypes also reveal differences in their 16S rRNA genes (Allsopp, 2010). However, it has been demonstrated that the 16S rRNA gene is unable to discriminate between non-pathogenic from pathogenic isolates (Allsopp et al., 2003). The difference of the 16S rDNA sequences between the Senegal and Crystal Springs (Zimbabwe) isolates served as earliest proof of genetic diversity within the *Cowdria* genus (Dame et al., 1992, Van Vliet et al., 1992). Allsopp et al. (1997) targeted the highly variable V1 loop region of the 16S rRNA gene to characterize organisms associated with heartwater and two new *E. ruminantium* genotypes (*Ehrlichia* spp Ball3 (U03777), Omatjenne (U03776)) and one *Ehrlichia* sp. (Germishuys (U03776)) were determined. There is no *E. ruminantium* homologous sequence for Germishuys, instead a close relation to *Ehrlichia* 16S sequence similar to that of *E. canis* is observed. The Germishuys was isolated from a naturally tick challenged infected sheep and results of brain smear examination and pathology, revealed that the sheep seemed to be suffering from heartwater. The initial isolation of the Omatjenne genotype was by challenging a mouse

with a lysate of a *Hyalomma truncatum* tick collected from apparently healthy cattle that tested positive for heartwater in a farm free of heartwater in Namibia (Du Plessis, 1990). The Crystal Springs (Allsopp et al., 1997) and Mara87/7 (Allsopp et al., 1999) genotypes are predominantly found in heartwater rampant areas in South Africa, and the Omatjenne genotype is prevalent, both in and out of the heartwater rife areas (Allsopp et al., 1997).

Small-subunit rRNA molecules are structurally and functionally preserved amongst all living microorganisms and availed a practical initial way for phylogenetic categorization of organisms. However, 16S gene differences cannot be relied upon as an exclusive method for genotyping, therefore Wayne et al. (1987) suggested that before defining different genotypes, whole genomic DNA/DNA hybridization variables should be ascertained.

1.8.2 pCS20

Another DNA probe that has been utilized for *E. ruminantium* strain characterization is the pCS20 probe, a cloned piece of DNA. The first pCS20 probe was developed by Waghela et al. (1991) to identify *E. ruminantium* from *Amblyomma variegatum* ticks. The approximately 1300 bp fragment is specific for *E. ruminantium* and results in no cross reaction with other *Ehrlichia* species (Allsopp, 2010). When compared to other available probes for testing for positivity of *E. ruminantium*, the pCS20 is the most highly sensitive (Allsopp et al., 1999, Allsopp et al., 1998). The ability of the method to detect even the minute amount of pathogen was boosted by making new primers and probes (Van Heerden et al., 2004). With the new primers and probes it was possible to obtain sequences of the pCS20 region of fourteen different *E. ruminantium* isolates and revealed high conservation of the West African isolates compared to more variation amongst southern African isolates (Van Heerden et al., 2004). The probe has been extensively used for detection of *E. ruminantium* in domestic animals, ticks and wildlife species (Guo et al., 2019). The pCS20 probe is suggested as the probe of choice for initial screening of *E. ruminantium*. However, the probe fails to differentiate between the various *E.*

ruminantium genotypes (Allsopp et al., 2007) and cannot differentiate between virulent and avirulent isolates (Allsopp et al., 2003). It is advised that the 16S probes must be used if inter species phylogenetic information is required (Allsopp et al., 1999).

1.8.3 Major Antigenic Protein gene (*map1*)

Ehrlichia ruminantium expresses an immunodominant protein, major antigenic protein 1 (MAP1), located on the surface of the organism. This protein was used as a serodiagnostic tool of heartwater (van Vliet et al., 1995). The gene encoding this protein is designated *map1*. A subunit serological assay using recombinantly expressed MAP1 protein proved its ability to recognize *E. ruminantium* antibodies in sera from domestic ruminants that were exposed to several different *E. ruminantium* isolates. However, the test cross reacted with other *Ehrlichia* spp, limiting its use in serodiagnosis of heartwater (Reddy et al., 1996). Although the *map1* gene exhibit high degree of sequence polymorphisms between isolates, it does not provide any genotypic information (Allsopp et al., 1999). The *map1* gene is an unsuitable candidate for use as a typing marker to provide a phylogeographic correlation between *E. ruminantium* strains (Allsopp et al., 2001, Cangi et al., 2016).

1.8.4 Multi Locus Sequence Typing (MLST)

Multi Locus Sequence Typing (MLST) is a technique that investigate nucleotide sequence features from various conserved structural or functional genes known as housekeeping genes to obtain consolidated alleles defined as a sequence type (ST). These STs allows for differentiation of isolates and give precise distinction with enough resolution for pathogen characterization without the need of full-genome sequencing (Sullivan et al., 2005). MLST is an extensively used system to characterize pathogens molecularly (Maiden, 2006). Mayer et al. (2002) supports the use of MLST and says “MLST enables the genotypic characterization of isolates and the study of the global dispersion of some new variants of pathogens”. Additionally, the information deduced from MLST method is relevant to the application of evolutionary and population studies (Jolley et al., 2000). It is

believed that MLST lacks ambiguity, is portable, reproducible, has high differentiation abilities to distinguish isolates and can be automated (Sullivan et al., 2005).

The first MLST scheme for *E. ruminantium* based on eight different housekeeping genes (*gltA*, *groEL*, *lepA*, *lipA*, *lipB*, *secY*, *sodB* and *sucA*) was developed by Adakal et al. (2009). The same tool was used by Nakao et al. (2011) on a group of reference strains and field sample originating from different geographical areas. Based on studies of Nakao et al. (2011) and Adakal et al. (2010), *sodB* was the less variable gene between the investigated strains, conversely, the gene with many variable sites was *secY*. The MLST scheme was able to differentiate between closely related strains and a great level of genetic dissimilarity among the examined strains was observed. However, no notable relation was observed amongst genotypes and geographic origins. Though the phylogeography of *E. ruminantium* isolates is unclear, *E. ruminantium* isolates cluster into two major groups: Group1 (West Africa) and Group2 (worldwide) which encompasses West, East, and southern Africa, Indian Ocean, and Caribbean strains when using MLST (Nakao et al., 2011, Cangi et al., 2016).

1.8.5 Other tools

Additional tools that have been used to characterize *E. ruminantium* isolates include restriction fragment length polymorphism (RFLP) and multi locus (ML) variable number tandem repeat (VNTR) analysis (MLVA). RFLP entails DNA amplification with primers, PCR products are then digested with restriction enzymes and visualized by gel electrophoresis (Cheriyedath, 2019). Genotypic diversity within West African and southern Africa *E. ruminantium* isolates was revealed by the clustering of *map1* restriction profiles. de Villiers et al. (2000) used *SmaI* and *KspI* restriction enzymes on DNA and could not differentiate among the four West African isolates examined, Kerr Seringe, Senegal, Sankat 430 and Pokoase 417. Faburay et al. (2008) suggested that alternatively, the exact selected amplified gene, *map1* must be used rather than whole genomic DNA. Although the *map1* restriction profiles showed genotypic diversity, the

profile did not reveal any geographical clustering and clusters resulting from the RFLP method did not correspond with cross protection with other strains of *E. ruminantium* (Faburay et al., 2008).

A complete genome sequence of the Welgevonden isolate proved that *E. ruminantium* has many tandem repeated sequences (Collins et al., 2005). Multi locus variable number tandem repeat analysis assay is based on direct polymerase chain reaction (PCR) amplification of specific loci that are repeated elements (Yazdankhah and Lindstedt, 2007). The first development of MLVA based on VNTR structures, for the purpose of characterizing the heterogeneity of *E. ruminantium* was by Pilet et al. (2012). The tool revealed a great level of variables among the tested strains, with 10 different profiles out of 13 *E. ruminantium* strains. The VNTR profiles could not show any differences between virulent and attenuated strains.

1.9 *In vitro* propagation of *E. ruminantium*

E. ruminantium is an intracellular parasite dependent on a living host for survival and growth (Bell-Sakyi, 2004). Cultivation of *E. ruminantium* outside its host animal has resulted in the production of large quantities of relatively pure organisms, attenuation of the organism for use in immunization, preparation of antigen for serological tests and screening of chemotherapeutics (Jongejan et al., 1980a). Initial reports on *in vitro* propagation of *E. ruminantium* met with failure or limited success (Bezuidenhout et al., 1985). However successful isolation and propagation of *E. ruminantium* in endothelial cells (Bezuidenhout et al., 1985) and tick cells (Bell-Sakyi et al., 2000) have been reported.

1.9.1 *In vitro* propagation in tick cell lines

Isolation and cultivation of tick-borne pathogens in tick cell lines is an important tool to investigate the interactions between tick cells and disease-causing pathogens (Bell-Sakyi

et al., 2007). Currently there are 63 cell lines made from 18 ixodid and argasid tick species and one each from the sand fly *Lutzomyia longipalpis* and the biting midge *Culicoides sonorensis* in a biobank established by Bell-Sakyi et al. (2018).

The first successful attempt at short term propagation of *E. ruminantium* in primary cultures of tick cells from moulting nymphs of *A. hebraeum* and *A. variegatum* dates to 1974 (Bell-Sakyi, 2004). Continuous growth of the Gardel stock of *E. ruminantium* was established in *Ixodes scapularis* cell line IDE8 for over 500 days by Bell-Sakyi et al. (2000). Additionally, a *Rhipicephalus appendiculatus* cell line RAN/CTVM3 was infected with the Gardel stock of *E. ruminantium* that was initially cultured in *I. scapularis* cell line IDE8 (Bekker et al., 2002a). Bell-Sakyi et al. (2002) successfully tested the capacity of different tick cell lines from non-vector (*I. scapularis*, *I. ricinus*, *Boophilus decoloratus*, *B. microplus* and *R. appendiculatus*) tick species to support growth of *E. ruminantium*, proving that *E. ruminantium* can be propagated in cells from other tick genera. Also, the absence of the elementary bodies in tick cell culture, the infective stage of *E. ruminantium* in ruminants and endothelial cell cultures is an indication that *E. ruminantium* develops differently in vectors from ruminant host cells (Bell-Sakyi et al., 2000). Furthermore, *E. ruminantium* cultivated in ruminant host cell and vector cell cultures exhibit different pathogenicity and immunogenicity for animals they were tested on (Bell-Sakyi et al., 2002).

1.9.2 *In vitro* propagation in mammalian cell lines

Jongejan et al. (1980b) initiated primary kidney cell cultures derived from heartwater diseased goats. The goats were infected by intravenously injecting varying period old primary kidney cultures and the goats suffered from heartwater symptoms. Despite this success, Jongejan and authors could not detect *E. ruminantium* when the kidney cell cultures were Giemsa stained and the cultures were not pathogenic. Bezuidenhout et al. (1985) established the first successful cultivation of *E. ruminantium* by making use of bovine umbilical cord endothelial cells. Following the success of Bezuidenhout et al.

(1985), other authors used endothelial cells of different kinds of ruminants, and from varying anatomical areas to cultivate *E. ruminantium* and they are ovine pulmonary artery (Byrom et al., 1991), bovine endothelial cells isolated from brain microvasculature (Martinez et al., 1993, Totté et al., 1993). In addition, Smith et al. (1998) cultivated *E. ruminantium* in endothelial cells of three species of African wild mammals, sable antelope (*Hippotragus niger*), buffalo (*Syncerus caffer*) and eland (*Taurotragus oryx*) suggesting that *in vitro* cultivation of *E. ruminantium* is possible in these species and may be natural hosts of the organism. Furthermore, Logan et al. (1987) successfully established primary neutrophil culture of *E. ruminantium* that can be an alternate method to infect secondary cell lines.

1.9.3 Inoculum

The type of inoculum used to isolate and cultivate *E. ruminantium* plays a significant role in an *in vitro* culture system (Bezuidenhout et al., 1985). Different inoculums have been used in both the tick cell and mammalian cell culture systems. The inoculum used in the first successful continuous growth of *E. ruminantium* in tick cell line IDE8 was elementary bodies obtained from a supernatant of an infected bovine pulmonary endothelial cell culture (Bell-Sakyi et al., 2000). Other researchers used infected endothelial cells from various anatomical sites to infect tick cells (Bekker et al., 2002a, Bell-Sakyi et al., 2002). The possibility of using infected tick cells as an inoculum to infect other tick cell lines has been reported (Bell-Sakyi et al., 2002, Bell-Sakyi, 2004). It was only later, that *in vitro* isolation of *E. ruminantium* from sheep blood (leukocyte fraction of the blood) into tick cell (IDE8) cultures was reported (Zweygarth et al., 2008).

A stabilate prepared from *A. hebraeum* nymphae was used as an inoculum to inoculate a calf endothelial cell line (Bezuidenhout et al., 1985). Two years later, Bezuidenhout (1987b) used infected choroid plexus, freshly drawn heparinized blood, liver and spleen suspensions made from moribund mice to initiate cultures in endothelial cells. A heparin-derived plasma was successfully inoculated in bovine and ovine vascular endothelial

cells, proving that *E. ruminantium* is present in plasma of infected animals (Byrom et al., 1991).

Apart from the tick-derived stabilate prepared by Bezuidenhout et al. (1985), there is no literature on the use of tick material (gut and salivary glands) as an inoculum in isolation and growth of *E. ruminantium* in endothelial and tick cell *in vitro* culture systems.

1.9.4 Culture media

The base of culture medium used in cultivating *E. ruminantium* in tick cells is L-15 Leibovitz medium. Bell-Sakyi et al. (2000) supplemented the medium with 10% tryptose phosphate broth (TPB), 5% heat inactivated fetal calf serum, 0.1% bovine lipoprotein and 100 Units/ml penicillin and 100 µg/ml streptomycin as choice of antibiotics for the continuous growth of *E. ruminantium* in IDE8 cell line. Dulbecco's Modified Eagle's medium nutrient mixture Ham F-12 (DME/F-12) containing 15 mM HEPES and 1.2 g/l sodium bicarbonate used for infected and uninfected endothelial cell cultures can also be used for maintaining tick cells provided it is supplemented with the above mentioned nutrients (Zweygarth et al., 2008).

The first *in vitro* culture of *E. ruminantium* in an endothelial cell line was achieved using Eagle's medium containing 10% bovine serum, sodium benzylpenicillin, streptomycinsulphate and fungizone (Bezuidenhout et al., 1985). Other media that have been used include Glasgow minimal essential medium (GMEM) (Bezuidenhout, 1987b), Leibovitz L-15 supplemented with 0.45% glucose (Byrom and Yunker, 1990), Dulbecco's minimal essential medium (DMEM) and RPMI 1640 (Martinez et al., 1993). The media is supplemented with varying amounts of foetal bovine serum and tryptose phosphate broth (TPB). However, *E. ruminantium* has been successfully isolated *in vitro* using serum and TPB free medium supplemented with bovine lipoproteins and transferrin (Zweygarth et al., 1997).

1.9.5 Propagation of *E. ruminantium* in cell cultures

Endothelial cells inoculated with *E. ruminantium* are incubated at 37°C with 5% CO₂ and tick cells are incubated at 30 ± 2°C without CO₂ with weekly medium change (Bekker et al., 2002a). Post inoculation, the cultures are monitored for cytopathic effect (CPE) that occurs in a form of a line across the monolayer of endothelial cells (Byrom et al., 1991). When infected cells are observed under an inverted microscope, the line consists of spherical, refractile cells that have space in the middle where a portion of cells had detached. In contrast to endothelial cells, tick cells exhibit very little obvious CPE (Bell-Sakyi et al., 2000). The cytopathic effect is evident 3-14 days post inoculation depending on the type of inoculum used to infect the cells. Using tick stabilate as an inoculum, *E. ruminantium* colonies were first observed 11 days after inoculation and passaged after 4-7 days of visible CPE (Bezuidenhout, 1987b). When plasma of infected ruminants was used to infect bovine aorta and bovine pulmonary artery endothelial cells, *E. ruminantium* colonies were observed after 11-14 days (Byrom et al., 1991). However, when bovine brain capillary endothelial cells were inoculated with supernatant of infected bovine umbilical endothelial cells the CPE was detected in 7 days and was passaged 8 days after initial inoculation (Martinez et al., 1993).

Bell-Sakyi et al. (2000) observed *E. ruminantium* on day 21 post inoculation of an IDE8 cell line from a non-vector species infected with supernatant from infected bovine pulmonary artery endothelial cells. The first and second subcultures were carried on days 51 and 66 respectively and rickettsiae was detected within 12 and 9 days respectively after subculture. An *A. variegatum* cell line inoculated with supernatant from infected bovine pulmonary artery endothelial cells exhibited *E. ruminantium* infection after 9-10 weeks (Bell-Sakyi, 2004). *Ehrlichia ruminantium* infection was detected in 18 and 9 days when IDE8 cells were infected using leukocytes isolated from sheep inoculated with Ball3 and Welgevonden stocks of *E. ruminantium* respectively (Zweygarth et al., 2008).

Heavily infected cultures are harvested for sub-cultivation by means of trypsin (Bezuidenhout, 1987b) or cell scraper that can be either a Pasteur pipette curved at the narrow end (Zweygarth et al., 1997) or a sterile 21 gauge needle with a bent tip (Zweygarth and Josemans, 2001) to form a small hook. A 21-gauge needle is utilized to separate clumps and disintegrate the cells. The cell suspension is centrifuged (800 x g for 10 minutes) to separate the elementary bodies from the cells and the supernatant is distributed into culture flasks containing confluent monolayer of uninfected cells (Byrom and Yunker, 1990).

1.9.6 Detection of *E. ruminantium* in cell cultures

Cultures are observed for common well-being and development of *E. ruminantium* weekly by microscopic examination. Cultures showing CPE are sampled by removing a small portion of the cell monolayer with a sterile bent 21-gauge needle to make a smear on slide. The slide is air-dried, fixed using methanol, stained with Giemsa (Bezuidenhout, 1987b) or RapiDiff (Zweygarth and Josemans, 2003) or Leukostat (Byrom and Yunker, 1990) and examined for cytoplasmic inclusions (colonies) typical of *E. ruminantium*. The organisms appear as small and dark colonies and as they multiply the colonies become larger and less dense. Ultimately the colonies disrupt and give rise to individual elementary bodies (Byrom et al., 1991).

1.10 Immune response to *E. ruminantium* and vaccine development

Plotkin (2008) states that “cell mediated immune functions play a critical role in protection against intracellular infections, and in almost all diseases, CD4⁺ T cells are necessary to help B cell development”. Since *E. ruminantium* is a pathogen dependent on a cell for its survival, protective immunity to heartwater in vertebrate host is believed to be essentially cell mediated (Du Plessis et al., 1991) although *E. ruminantium* antibodies are detected (Mahan et al., 1995b) in serum and colostrum and are likely to play a role in immunity (Deem et al., 1996). Therefore, production of a heartwater vaccine that elicits a cellular immune response is important. In South Africa, the available method of vaccination

against heartwater is the “infection and treatment” method that involves intravenously inoculating sheep blood infected with Ball3 strain of *E. ruminantium* and subsequently treating with tetracycline (Oberem and Bezuidenhout, 1987). Although the vaccine has been useful in controlling the disease, it has its disadvantages. Alternative vaccines have been explored with inactivated, attenuated, and DNA vaccines receiving more attention.

1.10.1 Inactivated vaccines

Inactivated vaccines are vaccines that contain organisms that have been grown in cell culture and rendered non-viable before vaccination. Inactivated vaccines are mixed with an adjuvant, a medium that supplements an accurate immune response by an antigen when utilized in conjunction with specific vaccine antigens (Schmidt and Lenz, 2014). A number of adjuvants have been tested with an *E. ruminantium* antigen: Freund's adjuvant (FA) (Mahan et al., 1994), Montanide ISA50 (Martinez et al., 1996), and Quil A (Mahan et al., 1998). It was found that FA has inflammatory side-effects and is commercially not acceptable making it unsuitable for use in the field (Martinez et al., 1996). Montanide ISA50 is an adjuvant with acceptable safety, has comparable efficacy as FA and is the choice of adjuvant to formulate an inactivated vaccine in (Mahan et al., 1998).

Martinez et al. (1994) reported the first successful use of heartwater inactivated vaccine made from elementary bodies of *E. ruminantium* (Gardel strain) mixed with FA. The vaccine protected more than 50% of the immunized goats against a homologous intravenous challenge as opposed to 100% mortality of the negative control group. Mechanisms of immune resistance on the survivors were not determined but the authors hypothesized that the protection is T cell mediated. The hypothesis that immune response to *E. ruminantium* is T cell mediated was proved by Totté et al. (1997). Totté et al. (1997) observed *E. ruminantium* specific T cell cultures initiated from animals vaccinated with inactivated elementary bodies in FA and restimulated with *E. ruminantium* lysate to be 95-100% CD4⁺ T lymphocytes, major histocompatibility complex (MHC) class II restricted and produce interferon gamma (IFN- γ). Also, activation of CD8⁺ T cells to a reduced

degree compared to CD4⁺ T cells was observed from *E. ruminantium* stimulated peripheral blood mononuclear cells (PBMC) collected from goats immunized by an inactivated vaccine (Gunter et al., 2002, Esteves et al., 2004a). However, CD8⁺ T cells need the assistance of CD4⁺ T cells to express IFN- γ (Esteves et al., 2004b).

IFN- γ has been reported to suppress multiplication of *in vitro* *E. ruminantium* (Totté et al., 1993). Even though IFN- γ reduces growth of *E. ruminantium in vitro*, infected endothelial cells treated with IFN- γ fails to generate cell surface expression of MHC class II molecules (Totté et al., 1996). The core function of MHC class II molecule is antigen peptide presentation on the cell surface for recognition by antigen presenting cells to stimulate CD4⁺ T cells, causing the coordination and regulation of effector cells (Wieczorek et al., 2017). Therefore, if the immune cells fail to present the antigen, there will be no immune protection mounted to fight the infection. Totté et al. (1996) suggests that *E. ruminantium* produces inhibitory factors that minimizes the ability of endothelial cells to produce MHC class II molecules.

Additionally, PBMC from vaccinated goats with inactivated *E. ruminantium* in ISA adjuvant expresses increased interleukin 2 receptor (IL-2R) after antigenic recall *in vitro* (Gunter et al., 2002). Upon activation, IL-2R is momentarily indicated on T cells surface (Manning and Nakanishi, 1996). Binding of IL-2 to IL-2R activates the functions of IL-2 which include activation of the cytotoxic function of natural killer (NK) cells, T lymphocytes, monocytes, and enhance the secretion of IFN- γ as well as tumor necrosis factor-beta (TNF- β) (Skupin-Mrugalska, 2019).

More than one field isolate that has been tested and found to offer broad protection against virulent isolates can be included in an inactivated vaccine to improve the protective capability of the vaccine. Also, through the breakthrough of inactivated vaccines, antigens that elicit protective immune response have been determined; and

have made it possible for developing a subunit vaccine against the disease (Mahan et al., 1999).

1.10.2 Attenuated vaccines

Another type of vaccine that has received interest is the attenuated vaccine. An attenuated vaccine consists of live, whole pathogen particles with reduced virulence, causing no clinical disease but stimulate an immune response (Mak and Saunders, 2006). The possibility of using an attenuated heartwater vaccine was proven by Jongejan (1991a) using the Senegal isolate. This isolate was the first to be attenuated *in vitro* through passages on bovine umbilical endothelial cells (Jongejan, 1991a). The vaccine protected 100% of goats and sheep against a virulent homologous needle challenge. However, the protection levels were less satisfactory with a decrease to 75% when the same vaccine was tested against a natural field tick challenge (Faburay et al., 2007, Adakal et al., 2010). The Senegal strain has been found to attenuate faster than other *E. ruminantium* strains due the observed attenuator gene *ntrX* (Gordon et al., 2023). The attenuation in the Senegal strain take place by gene conversion, causing a 4 base pair deletion which is exclusivel to the Senegal strain. Collins et al. (2003) attenuated the virulent Welgevonden isolate through passages in a canine macrophage monocyte cell line DH82 and recorded a 100% protection against virulent homologous needle challenge. Since the cell line DH82 is cancerous, the Welgevonden isolate was re-adapted to grow in bovine endothelial cells and has been reported to provide cross protection against a needle challenge of Ball3, Gardel, Mara87/7, Kwanyanga and Blaauwkrans isolates (Zweygarth et al., 2005). However, the attenuated Welgevonden vaccine is yet to be tested against a natural field tick challenge. With all the effort directed in heartwater attenuated vaccines, there is no study that reports the cellular immune response conferred by attenuated vaccines.

1.10.3 Recombinant vaccines

The reports of inactivated *E. ruminantium* organisms to stimulate an immune response suggested that live organism is not a requirement for a vaccine to confer protective immunity. Therefore, presenting a possibility for the development of defined recombinant antigens as vaccines. Recombinant vaccines are proteins or DNA recombinants capable of stimulating an immune response, that are inserted into bacterial or mammalian cells, and express the antigen in these cells (Mukkeed, 2022). Recombinant vaccines are affordable to manufacture; eliminate the need of cold chain storage and can be utilized to halt an outbreak in areas where a disease is not endemic (Allsopp, 2015).

Recombinant vaccines made from DNA recombinants has been investigated and shown to offer protective immunity (Nyika et al., 1998, Pretorius et al., 2007, Tshilwane et al., 2019). Splenocytes from mice immunized with the *map1* gene vaccine proliferated in response to *E. ruminantium* antigen and secreted IFN- γ and IL-2. The protective capacity of the DNA vaccine was improved by protein boost against a homologous challenge and significantly protected the mice (Nyika et al., 2002). Pretorius et al. (2007) tested four *E. ruminantium* open reading frames as a DNA vaccine and the vaccine protected the sheep against a homologous needle challenge.

Proteins of *E. ruminantium* as possible vaccine components have been investigated. Sebatjane et al. (2010) investigated proteins of the five open reading frames different from those investigated by Pretorius et al. (2007) for potential use as vaccine. Liebenberg et al. (2012) identified *E. ruminantium* proteins that stimulate responses mediated by CD4⁺ T cells and have been found to be protective. Thema et al. (2016) found that secreted proteins induce a Th1 immune response which characterizes the *E. ruminantium* protective immune response.

1.11 Justification

E. ruminantium causes heartwater in cattle, sheep, goats and some wild ruminants Raliniaina et al. (2010). According to World Organization for Animal Health, heartwater is

a notifiable disease and is one of the major causes of livestock loss in sub-Saharan Africa (Steyn, 2022). Heartwater is an obstacle to livestock farmers who want to introduce high yielding breeds to their farms to upgrade their breed due to their susceptibility to the infection with 20-90% mortality (Allsopp, 2015). *Ehrlichia ruminantium* has diverse immunogenicity with recombination occurring between different genotypes giving rise to new strains in the field (Allsopp, 2010). The diverse immunogenicity of *E. ruminantium* has proved to be a challenge for the development of new vaccines against heartwater. The “infection and treatment” vaccination technique currently in use in South Africa is laborious as daily monitoring of rectal temperature of the animal after vaccination is mandatory, the necessary use of antibiotics after immunization, the mandatory intravenous injection of the vaccine by a trained personnel, the necessity to keep a cold chain for the distribution of the vaccine posing a challenge for rural area farmers who do not have such facilities; and it does not cross protect against all virulent strains. Development of a more practical vaccine against heartwater is important for the future control of the disease. An inactivated multivalent cocktail vaccine may offer cross protection against virulent *E. ruminantium* field isolates (EU-funded MuVHA [Multivalent inactivated Vaccine against Heartwater in Africa]). Also, a clear understanding of the immune markers of protection against the agent is an important requirement for the achievement of this goal. Therefore, there is a need for characterization of new isolates and be tested as a multivalent inactivated cocktail vaccine for protection against virulent genotypes of *E. ruminantium* in the field.

1.12 Aim and Objectives

The aim of the study is to characterise new *E. ruminantium* field isolates and develop a reverse transcription quantitative real-time PCR assay (RT qPCR) for the evaluation of a multivalent inactivated vaccine. The aim will be achieved through the following objectives:

- Collection of *A. hebraeum* ticks from cattle
- Isolate and characterize *E. ruminantium* from *A. hebraeum* ticks using MLST

- Initiate *E. ruminantium* *in vitro* culture using tick salivary glands and gut
- Develop a RT qPCR for the evaluation of a multivalent inactivated vaccine

1.13 References

- ADAKAL, H., GAVOTTE, L., STACHURSKI, F., KONKOBO, M., HENRI, H., ZOUNGRANA, S., HUBER, K., VACHIERY, N., MARTINEZ, D., MORAND, S. & FRUTOS, R. 2010. Clonal origin of emerging populations of *Ehrlichia ruminantium* in Burkina Faso. *Infection, Genetics and Evolution*, 10, 903-912.
- ADAKAL, H., MEYER, D. F., CARASCO-LACOMBE, C., PINARELLO, V., ALLÈGRE, F., HUBER, K., STACHURSKI, F., MORAND, S., MARTINEZ, D., LEFRANÇOIS, T., VACHIERY, N. & FRUTOS, R. 2009. MLST scheme of *Ehrlichia ruminantium*: Genomic stasis and recombination in strains from Burkina-Faso. *Infection, Genetics and Evolution*, 9, 1320-1328.
- ALLSOPP, B. A. 2010. Natural history of *Ehrlichia ruminantium*. *Veterinary Parasitology*, 167, 123-135.
- ALLSOPP, B. A. 2015. Heartwater-*Ehrlichia ruminantium* infection. *Revue Scientifique et Technique*, 34, 557-568.
- ALLSOPP, M. T., HATTINGH, C. M., VOGEL, S. W. & ALLSOPP, B. A. 1998. Comparative evaluation of 16S, map1 and pCS20 probes for the detection of *Cowdria* and *Ehrlichia* species in ticks. *Annals of the New York Academy of Sciences*, 849, 78-84.
- ALLSOPP, M. T., HATTINGH, C. M., VOGEL, S. W. & ALLSOPP, B. A. 1999. Evaluation of 16S, map1 and pCS20 probes for detection of *Cowdria* and *Ehrlichia* species. *Epidemiology and Infection*, 122, 323-8.
- ALLSOPP, M. T. E. P., DORFLING, C. M., MAILLARD, J. C., BENSALD, A., HAYDON, D. T., VAN HEERDEN, H. & ALLSOPP, B. A. 2001. *Ehrlichia ruminantium* Major Antigenic Protein Gene (map1) Variants Are Not Geographically Constrained and Show No Evidence of Having Evolved under Positive Selection Pressure. *Journal of Clinical Microbiology*, 39, 4200-4203.
- ALLSOPP, M. T. E. P., VAN HEERDEN, H., STEYN, H. C. & ALLSOPP, B. A. 2003. Phylogenetic Relationships among *Ehrlichia ruminantium* Isolates. *Annals of the New York Academy of Sciences*, 990, 685-691.

- ALLSOPP, M. T. E. P., VAN STRIJP, M. F., FABER, E., JOSEMANS, A. I. & ALLSOPP, B. A. 2007. *Ehrlichia ruminantium* variants which do not cause heartwater found in South Africa. *Veterinary Microbiology*, 120, 158-166.
- ALLSOPP, M. T. E. P., VISSER, E. S., DU PLESSIS, J. L., VOGEL, S. W. & ALLSOPP, B. A. 1997. Different organisms associated with heartwater as shown by analysis of 16S ribosomal RNA gene sequences. *Veterinary Parasitology*, 71, 283-300.
- BEKKER, C. P., BELL-SAKYI, L., PAXTON, E. A., MARTINEZ, D., BENSAID, A. & JONGEJAN, F. 2002a. Transcriptional analysis of the major antigenic protein 1 multigene family of *Cowdria ruminantium*. *Gene*, 285, 193-201.
- BELL-SAKYI, L. 2004. *Ehrlichia ruminantium* grows in cell lines from four ixodid tick genera. *Journal of Comparative Pathology*, 130, 285-93.
- BELL-SAKYI, L., DARBY, A., BAYLIS, M. & MAKEPEACE, B. L. 2018. The Tick Cell Biobank: A global resource for *in vitro* research on ticks, other arthropods and the pathogens they transmit. *Ticks and Tick-Borne Diseases*, 9, 1364-1371.
- BELL-SAKYI, L., PAXTON, E., WRIGHT, P. & SUMPTION, K. 2002. Immunogenicity of *Ehrlichia ruminantium* grown in tick cell lines. *Experimental and Applied Acarology*, 28, 177-85.
- BELL-SAKYI, L., PAXTON, E. A., MUNDERLOH, U. G. & SUMPTION, K. J. 2000. Growth of *Cowdria ruminantium*, the causative agent of heartwater, in a tick cell line. *Journal of Clinical Microbiology*, 38, 1238-40.
- BELL-SAKYI, L., ZWEYGARTH, E., BLOUIN, E. F., GOULD, E. A. & JONGEJAN, F. 2007. Tick cell lines: tools for tick and tick-borne disease research. *Trends in Parasitology*, 23, 450-7.
- BEZUIDENHOUT, J. D. 1985. The epizootiology and control of heartwater and other tick-borne diseases of cattle in South Africa. *Onderstepoort Journal of Veterinary Research*, 52, 211-4.
- BEZUIDENHOUT, J. D. 1987a. Natural transmission of heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 349-51.
- BEZUIDENHOUT, J. D. 1987b. The present state of *Cowdria ruminantium* cultivation in cell lines. *Onderstepoort Journal of Veterinary Research*, 54, 205-10.

- BEZUIDENHOUT, J. D. 2009a. Heartwater: An abridged historical account. *Journal of the South African Veterinary Association*, 80, 208-209.
- BEZUIDENHOUT, J. D. 2009b. Heartwater: an abridged historical account. *Journal of the South African Veterinary Association*, 80, 208-9.
- BEZUIDENHOUT, J. D. & JACOBSZ, C. J. 1986. Proof of transovarial transmission of *Cowdria ruminantium* by *Amblyomma herbraeum*. *Onderstepoort Journal of Veterinary Research*, 53, 31-4.
- BEZUIDENHOUT, J. D., PATERSON, C. L. & BARNARD, B. J. 1985. *In vitro* cultivation of *Cowdria ruminantium*. *Onderstepoort Journal of Veterinary Research*, 52, 113-20.
- BYROM, B. & YUNKER, C. E. 1990. Improved culture conditions for *Cowdria ruminantium* (Rickettsiales), the agent of heartwater disease of domestic ruminants. *Cytotechnology*, 4, 285-90.
- BYROM, B., YUNKER, C. E., DONOVAN, P. L. & SMITH, G. E. 1991. *In vitro* isolation of *Cowdria ruminantium* from plasma of infected ruminants. *Veterinary Microbiology*, 26, 263-8.
- CABI. 2020. *Heartwater* [Online]. Available: <https://www.cabi.org/isc/datasheet/87241> [Accessed 02/06 2020].
- CANGI, N., GORDON, J. L., BOURNEZ, L., PINARELLO, V., APRELON, R., HUBER, K., LEFRANÇOIS, T., NEVES, L., MEYER, D. F. & VACHIÉRY, N. 2016. Recombination Is a Major Driving Force of Genetic Diversity in the Anaplasmataceae *Ehrlichia ruminantium*. *Frontiers in Cellular and Infection Microbiology*, 6.
- CHERIYEDATH, S. 2019. *Restriction Fragment Length Polymorphism (RFLP) Technique* [Online]. Available: [/www.news-medical.net/life-sciences/Restriction-Fragment-Length-Polymorphism-\(RFLP\)-Technique.aspx](http://www.news-medical.net/life-sciences/Restriction-Fragment-Length-Polymorphism-(RFLP)-Technique.aspx) [Accessed 10 /10/2019].
- COLLINS, N. E., ALLSOPP, M. T. E. P. & ALLSOPP, B. A. 2002. Molecular diagnosis of theileriosis and heartwater in bovines in Africa. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 96, S217-S224.
- COLLINS, N. E., LIEBENBERG, J., DE VILLIERS, E. P., BRAYTON, K. A., LOUW, E., PRETORIUS, A., FABER, F. E., VAN HEERDEN, H., JOSEMANS, A., VAN

- KLEEF, M., STEYN, H. C., VAN STRIJP, M. F., ZWEYGARTH, E., JONGEJAN, F., MAILLARD, J. C., BERTHIER, D., BOTHA, M., JOUBERT, F., CORTON, C. H., THOMSON, N. R., ALLSOPP, M. T. & ALLSOPP, B. A. 2005. The genome of the heartwater agent *Ehrlichia ruminantium* contains multiple tandem repeats of actively variable copy number. *Proc Natl Acad Sci U S A*, 102, 838-43.
- COLLINS, N. E., PRETORIUS, A., VAN KLEEF, M., BRAYTON, K. A., ZWEYGARTH, E. & ALLSOPP, B. A. 2003. Development of Improved Vaccines for Heartwater. *Annals of the New York Academy of Sciences*, 990, 474-484.
- COWDRY, E. V. 1925. Studies on the etiology of heartwater : I. Observation of a *Rickettsia*, *Rickettsia ruminantium* (N. SP.), in the tissues of infected animals. *Journal of Experimental Medicine*, 42, 231-52.
- COWDRY, E. V. 1926. Studies on the etiology of heartwater: III. The multiplication of *Rickettsia ruminantium* within the endothelial cells of infected animals and their discharge into circulation. *Journal of Experimental Medicine*, 44, 803-14.
- DAME, J. B., MAHAN, S. M. & YOWELL, C. A. 1992. Phylogenetic Relationship of *Cowdria ruminantium*, Agent of Heartwater, to *Anaplasma marginale* and Other Members of the Order Rickettsiales Determined on the Basis of 16S rRNA Sequence†. *International Journal of Systematic and Evolutionary Microbiology*, 42, 270-274.
- DE VILLIERS, E. P., BRAYTON, K. A., ZWEYGARTH, E. & ALLSOPP, B. A. 2000. Macrorestriction fragment profiles reveal genetic variation of *Cowdria ruminantium* isolates. *Journal of Clinical Microbiology*, 38, 1967-70.
- DEEM, S. L., NORVAL, R. A. I., DONACHIE, P. L. & MAHAN, S. M. 1996. Demonstration of vertical transmission of *Cowdria ruminantium*, the causative agent of heartwater, from cows to their calves. *Veterinary Parasitology*, 61, 119-132.
- DU PLESSIS, J. L. 1975. Electron microscopy of *Cowdria ruminantium* infected reticulo-endothelial cells of the mammalian host. *Onderstepoort Journal of Veterinary Research*, 42, 1-13.
- DU PLESSIS, J. L. 1990. Increased pathogenicity of an *Ehrlichia*-like agent after passage through *Amblyomma hebraeum*: a preliminary report. *Onderstepoort Journal of Veterinary Research*, 57, 233-7.

- DU PLESSIS, J. L., BERCHE, P. & VAN GAS, L. 1991. T cell-mediated immunity to *Cowdria ruminantium* in mice: the protective role of Lyt-2+ T cells. *Onderstepoort Journal of Veterinary Research*, 58, 171-9.
- DU PLESSIS, J. L. & MALAN, L. 1987a. The application of the indirect fluorescent antibody test in research on heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 319-25.
- DU PLESSIS, J. L. & MALAN, L. 1987b. Problems with the interpretation of epidemiological data in heartwater: a study on 23 farms. *Onderstepoort Journal of Veterinary Research*, 54, 427-33.
- DUMLER, J. S., BARBET, A. F., BEKKER, C. P., DASCH, G. A., PALMER, G. H., RAY, S. C., RIKIHISA, Y. & RURANGIRWA, F. R. 2001. Reorganization of genera in the families Rickettsiaceae and Anaplasmataceae in the order Rickettsiales: unification of some species of *Ehrlichia* with *Anaplasma*, *Cowdria* with *Ehrlichia* and *Ehrlichia* with *Neorickettsia*, descriptions of six new species combinations and designation of *Ehrlichia equi* and 'HGE agent' as subjective synonyms of *Ehrlichia phagocytophila*. *International Journal of Systematic and Evolutionary Microbiology*, 51, 2145-2165.
- ESTEVEZ, I., VACHIÉRY, N., MARTINEZ, D. & TOTTE, P. 2004a. Analysis of *Ehrlichia ruminantium*-specific T1/T2 responses during vaccination with a protective killed vaccine and challenge of goats. *Parasite Immunology*, 26, 95-103.
- ESTEVEZ, I., WALRAVENS, K., VACHIÉRY, N., MARTINEZ, D., LETESSON, J.-J. & TOTTE, P. 2004b. Protective killed *Ehrlichia ruminantium* vaccine elicits IFN- γ responses by CD4+ and CD8+ T lymphocytes in goats. *Veterinary Immunology and Immunopathology*, 98, 49-57.
- FABURAY, B., GEYSEN, D., CEESAY, A., MARCELINO, I., ALVES, P. M., TAOUFIK, A., POSTIGO, M., BELL-SAKYI, L. & JONGEJAN, F. 2007. Immunisation of sheep against heartwater in The Gambia using inactivated and attenuated *Ehrlichia ruminantium* vaccines. *Vaccine*, 25, 7939-7947.
- FABURAY, B., JONGEJAN, F., TAOUFIK, A., CEESAY, A. & GEYSEN, D. 2008. Genetic diversity of *Ehrlichia ruminantium* in *Amblyomma variegatum* ticks and small

- ruminants in The Gambia determined by restriction fragment profile analysis. *Veterinary Microbiology*, 126, 189-199.
- GORDON, J. L., OLIVA CHAVEZ, A. S., MARTINEZ, D., VACHIERY, N. & MEYER, D. F. 2023. Possible biased virulence attenuation in the Senegal strain of *Ehrlichia ruminantium* by *ntrX* gene conversion from an inverted segmental duplication. *PLOS ONE*, 18, e0266234.
- GUNTER, N., ESTEVES, I., KANDASSAMY, Y., MARTINEZ, D., BENSALD, A., VAN KLEEF, M., DU PLESSIS, D. & TOTTE, P. 2002. *Cowdria ruminantium* antigens of around 15 kDa are potent inducers of IFN-gamma. *Annals of the New York Academy of Sciences*, 969, 135-40.
- GUO, H., ADJOU MOUMOUNI, P. F., THEKISOE, O., GAO, Y., LIU, M., LI, J., GALON, E. M., EFSTRATIOU, A., WANG, G., JIRAPATTHARASATE, C., RINGO, A. E., MTSHALI, K., INOUE, N., SUZUKI, H. & XUAN, X. 2019. Genetic characterization of tick-borne pathogens in ticks infesting cattle and sheep from three South African provinces. *Ticks and Tick-borne Diseases*, 10, 875-882.
- JOLLEY, K. A., KALMUSOVA, J., FEIL, E. J., GUPTA, S., MUSILEK, M., KRIZ, P. & MAIDEN, M. C. J. 2000. Carried Meningococci in the Czech Republic: a Diverse Recombining Population. *Journal of Clinical Microbiology*, 38, 4492-4498.
- JONGEJAN, F. 1991a. Protective immunity to heartwater (*Cowdria ruminantium* infection) is acquired after vaccination with *in vitro*-attenuated rickettsiae. *Infection and Immunity*, 59, 729-31.
- JONGEJAN, F. 1992. Experimental transmission of *Cowdria ruminantium* (Rickettsiales) by the American reptile tick *Amblyomma dissimile* Koch, 1844. *Experimental and Applied Acarology*, 15, 117-21.
- JONGEJAN, F., THIELEMANS, M. J. C., DE GROOT, M., VAN KOOTEN, P. J. S. & VAN DER ZEIJST, B. A. M. 1991b. Competitive enzyme-linked immunosorbent assay for heartwater using monoclonal antibodies to a *Cowdria ruminantium*-specific 32-kilodalton protein. *Veterinary Microbiology*, 28, 199-211.
- JONGEJAN, F., VAN WINKELHOFF, A. J. & UILENBERG, G. 1980a. *Cowdria ruminantium* (Rickettsiales) in primary goat kidney cell cultures. *Research in Veterinary Science*, 29, 392-3.

- JONGEJAN, F., VAN WLNKELHOFF, A. J. & ULLENBERG, G. 1980b. *Cowdria ruminantium* (Rickettsiales) in primary goat kidney cell cultures. *Research in Veterinary Science*, 29, 392-393.
- JONGEJAN, F., ZANDBERGEN, T. A., VAN DE WIEL, P. A., DE GROOT, M. & UILENBERG, G. 1991. The tick-borne rickettsia *Cowdria ruminantium* has a Chlamydia-like developmental cycle. *Onderstepoort Journal of Veterinary Research*, 58, 227-37.
- KATZ, J. B., BARBET, A. F., MAHAN, S. M., KUMBULA, D., LOCKHART, J. M., KEEL, M. K., DAWSON, J. E., OLSON, J. G. & EWING, S. A. 1996. A recombinant antigen from the heartwater agent (*Cowdria ruminantium*) reactive with antibodies in some southeastern United States white-tailed deer (*Odocoileus virginianus*), but not cattle, sera. *Journal of Wildlife Diseases*, 32, 424-30.
- KOCAN, K. M. & BEZUIDENHOUT, J. D. 1987a. Morphology and development of *Cowdria ruminantium* in *Amblyomma* ticks. *Onderstepoort Journal of Veterinary Research*, 54, 177-82.
- KOCAN, K. M., BEZUIDENHOUT, J. D. & HART, A. 1987b. Ultrastructural features of *Cowdria ruminantium* in midgut epithelial cells and salivary glands of nymphal *Amblyomma hebraeum*. *Onderstepoort Journal of Veterinary Research*, 54, 87-92.
- LIEBENBERG, J., PRETORIUS, A., FABERA, F. E., COLLINS, N. E., ALLSOPP, B. A. & VAN KLEEF, M. 2012. Identification of *Ehrlichia ruminantium* proteins that activate cellular immune responses using a reverse vaccinology strategy. *Veterinary Immunology and Immunopathology*, 145, 340-349.
- LOGAN, L. L., WHYARD, T. C., QUINTERO, J. C. & MEBUS, C. A. 1987. The development of *Cowdria ruminantium* in neutrophils. *Onderstepoort Journal of Veterinary Research*, 54, 197-204.
- MAHAN, S. M. 1995a. Review of the molecular biology of *Cowdria ruminantium*. *Veterinary Parasitology*, 57, 51-56.
- MAHAN, S. M., ALLSOPP, B., KOCAN, K. M., PALMER, G. H. & F., J. 1999. Vaccine strategies for *Cowdria ruminantium* infections and their application to other ehrlichial infections. *Parasitology Today*, 15, 290-294.

- MAHAN, S. M., ANDREW, H. R., TEBELE, N., BURRIDGE, M. J. & BARBET, A. F. 1995b. Immunisation of sheep against heartwater with inactivated *Cowdria ruminantium*. *Research in Veterinary Science*, 58, 46-9.
- MAHAN, S. M., KUMBULA, D., BURRIDGE, M. J. & BARBET, A. F. 1998. The inactivated *Cowdria ruminantium* vaccine for heartwater protects against heterologous strains and against laboratory and field tick challenge. *Vaccine*, 16, 1203-1211.
- MAHAN, S. M., SMITH, G. E. & BYROM, B. 1994. Concanavalin A-stimulated bovine T-cell supernatants inhibit growth of *Cowdria ruminantium* in bovine endothelial cells in vitro. *Infection and Immunity*, 62, 747-750.
- MAHAN, S. M., WAGHELA, S. D., MCGUIRE, T. C., RURANGIRWA, F. R., WASSINK, L. A. & BARBET, A. F. 1992. A cloned DNA probe for *Cowdria ruminantium* hybridizes with eight heartwater strains and detects infected sheep. *Journal of Clinical Microbiology*, 30, 981-986.
- MAIDEN, M. C. J. 2006. Multilocus Sequence Typing of Bacteria. *Annual Review of Microbiology*, 60, 561-588.
- MAK, T. W. & SAUNDERS, M. E. 2006. Introduction to the Immune Response. In: MAK, T. W. & SAUNDERS, M. E. (eds.) *The Immune Response*. Burlington: Academic Press.
- MANNING, M. J. & NAKANISHI, T. 1996. The Specific Immune System: Cellular Defenses. In: IWAMA, G. & NAKANISHI, T. (eds.) *Fish Physiology*. Academic Press.
- MARTINEZ, D., MAILLARD, J. C., COISNE, S., SHEIKBOUDOU, C. & BENSALD, A. 1994. Protection of goats against heartwater acquired by immunisation with inactivated elementary bodies of *Cowdria ruminantium*. *Veterinary Immunology and Immunopathology*, 41, 153-163.
- MARTINEZ, D., PEREZ, J. M., SHEIKBOUDOU, C., DEBUS, A. & BENSALD, A. 1996. Comparative efficacy of Freund's and Montanide ISA50 adjuvants for the immunisation of goats against heartwater with inactivated *Cowdria ruminantium*. *Veterinary Parasitology*, 67, 175-84.

- MARTINEZ, D., SHEIKBOUDOU, C., COURAUD, P. O. & BENSAID, A. 1993. In vitro infection of bovine brain endothelial cells by *Cowdria ruminantium*. *Research in Veterinary Science*, 55, 258-260.
- MAYER, L. W., REEVES, M. W., AL-HAMDAN, N., SACCHI, C. T., TAHA, M.-K., AJELLO, G. W., SCHMINK, S. E., NOBLE, C. A., TONDELLA, M. L. C., WHITNEY, A. M., AL-MAZROU, Y., AL-JEFRI, M., MISHKHIS, A., SABBAN, S., CAUGANT, D. A., LINGAPPA, J., ROSENSTEIN, N. E. & POPOVIC, T. 2002. Outbreak of W135 Meningococcal Disease in 2000: Not Emergence of a New W135 Strain but Clonal Expansion within the Electrophoretic Type-37 Complex. *The Journal of Infectious Diseases*, 185, 1596-1605.
- MELTZER, M. I., PERRY, B. D. & DONACHIE, P. L. 1996. Mortality percentages related to heartwater and the economic impact of heartwater disease on large-scale commercial farms in Zimbabwe. *Preventive Veterinary Medicine*, 26, 187-199.
- MUKHEBI, A. W., CHAMBOKO, T., O'CALLAGHAN, C. J., PETER, T. F., KRUSKA, R. L., MEDLEY, G. F., MAHAN, S. M. & PERRY, B. D. 1999. An assessment of the economic impact of heartwater (*Cowdria ruminantium* infection) and its control in Zimbabwe. *Preventative Veterinary Medicine*, 39, 173-89.
- MUKKEED, M. 2022. Applications and Challenges of Recombinant Vaccines. *Journal of Vaccines & Vaccination*, S17.
- NAKAO, R., MAGONA, J. W., ZHOU, L., JONGEJAN, F. & SUGIMOTO, C. 2011. Multi-locus sequence typing of *Ehrlichia ruminantium* strains from geographically diverse origins and collected in *Amblyomma variegatum* from Uganda. *Parasites & Vectors*, 4, 137.
- NYIKA, A., BARBET, A. F., BURRIDGE, M. J. & MAHAN, S. M. 2002. DNA vaccination with *map1* gene followed by protein boost augments protection against challenge with *Cowdria ruminantium*, the agent of heartwater. *Vaccine*, 20, 1215-1225.
- NYIKA, A., MAHAN, S. M., BURRIDGE, M. J., MCGUIRE, T. C., RURANGIRWA, F. & BARBET, A. F. 1998. A DNA vaccine protects mice against the rickettsial agent *Cowdria ruminantium*. *Parasite Immunology*, 20, 111-9.
- OBEREM, P. T. & BEZUIDENHOUT, J. D. 1987. The production of heartwater vaccine. *Onderstepoort Journal of Veterinary Research*, 54, 485-8.

- PASCUCCI, I., CONTE, A. & SCACCHIA, M. 2007. Use of geographic information systems to identify areas at risk of introducing *Amblyomma variegatum* and *A. hebraeum* to Italy. *Veterinaria italiana*, 43, 655-61.
- PETNEY, T. N., HORAK, I. G. & REHAV, Y. 1987. The ecology of the African vectors of heartwater, with particular reference to *Amblyomma hebraeum* and *Amblyomma variegatum*. *Onderstepoort Journal of Veterinary Research*, 54, 381-95.
- PIENAAR, J. G. 1970. Electron microscopy of *Cowdria (Rickettsia) ruminantium* (Cowdry, 1926) in the endothelial cells of the vertebrate host. *Onderstepoort Journal of Veterinary Research*, 37, 67-78.
- PILET, H., VACHIÉRY, N., BERRICH, M., BOUCHOUICHA, R., DURAND, B., PRUNEAU, L., PINARELLO, V., SALDANA, A., CARASCO-LACOMBE, C., LEFRANÇOIS, T., MEYER, D. F., MARTINEZ, D., BOULOUIS, H.-J. & HADDAD, N. 2012. A new typing technique for the Rickettsiales *Ehrlichia ruminantium*: Multiple-locus variable number tandem repeat analysis. *Journal of Microbiological Methods*, 88, 205-211.
- PLOTKIN, S. A. 2008. Vaccines: correlates of vaccine-induced immunity. *Clinical Infectious Diseases*, 47, 401-9.
- PRETORIUS, A., COLLINS, N. E., STEYN, H. C., VAN STRIJP, F., VAN KLEEF, M. & ALLSOPP, B. A. 2007. Protection against heartwater by DNA immunisation with four *Ehrlichia ruminantium* open reading frames. *Vaccine*, 25, 2316-24.
- PROVOST, A. & BEZUIDENHOUT, J. D. 1987. The historical background and global importance of heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 165-9.
- PROZESKY, L. & DU PLESSIS, J. L. 1985. The pathology of heartwater. I. A study of mice infected with the Welgevonden strain of *Cowdria ruminantium*. *Onderstepoort Journal of Veterinary Research*, 52, 71-9.
- PURNELL, R. E. 1984. Control of heartwater in cattle in Southern Africa using terramycin/LA. *Preventive Veterinary Medicine*, 2, 239-254.
- RALINIAINA, M., MEYER, D. F., PINARELLO, V., SHEIKBOUDOU, C., EMBOULÉ, L., KANDASSAMY, Y., ADAKAL, H., STACHURSKI, F., MARTINEZ, D.,

- LEFRANÇOIS, T. & VACHIÉRY, N. 2010. Mining the genetic diversity of *Ehrlichia ruminantium* using map genes family. *Veterinary Parasitology*, 167, 187-195.
- REDDY, G. R., SULSONA, C. R., HARRISON, R. H., MAHAN, S. M., BURRIDGE, M. J. & BARBET, A. F. 1996. Sequence heterogeneity of the major antigenic protein 1 genes from *Cowdria ruminantium* isolates from different geographical areas. *Clinical and Diagnostic Laboratory Immunology*, 3, 417-422.
- SCHMIDT, R. & LENZ, L. L. 2014. Chapter 13 - Adjuvants Targeting the DNA Sensing Pathways – Cyclic-di-GMP and other Cyclic-Dinucleotides. *In: ISHII, K. J. & TANG, C. K. (eds.) Biological DNA Sensor*. Amsterdam: Academic Press.
- SEBATJANE, S. I., PRETORIUS, A., LIEBENBERG, J., STEYN, H. & VAN KLEEF, M. 2010. In vitro and in vivo evaluation of five low molecular weight proteins of *Ehrlichia ruminantium* as potential vaccine components. *Veterinary Immunology and Immunopathology*, 137, 217-25.
- SKUPIN-MRUGALSKA, P. 2019. Chapter 6 - Liposome-Based Drug Delivery for Lung Cancer. *In: KESHARWANI, P. (ed.) Nanotechnology-Based Targeted Drug Delivery Systems for Lung Cancer*. Academic Press.
- SMITH, G. E., ANDERSON, E. C., BURRIDGE, M. J., PETER, T. F. & MAHAN, S. M. 1998. Growth of *Cowdria ruminantium* in tissue culture endothelial cell lines from wild African mammals. *Journal of Wildlife Diseases*, 34, 297-304.
- SPICKLER, A. R. 2015. *Heartwater* [Online]. Available: <http://www.cfsph.iastate.edu/DiseaseInfo/factsheets.php> [Accessed 2022].
- STEYN, H. 2022. *Heartwater*, CABI International.
- SULLIVAN, C. B., DIGGLE, M. A. & CLARKE, S. C. 2005. Multilocus sequence typing. *Molecular Biotechnology*, 29, 245.
- THEMA, N., PRETORIUS, A., TSHILWANE, S. I., LIEBENBERG, J., STEYN, H. & VAN KLEEF, M. 2016. Cellular immune responses induced *in vitro* by *Ehrlichia ruminantium* secreted proteins and identification of vaccine candidate peptides. *Onderstepoort Journal of Veterinary Research*, 83, 1-11.
- TOTTÉ, P., BLANKAERT, D., ZILIMWABAGABO, P. & WÉRENNE, J. 1993. Inhibition of *Cowdria ruminantium* infectious yield by interferons alpha and gamma in

- endothelial cells. *Revue D'élevage et de Médecine Vétérinaire Des Pays Tropicaux*, 189-94.
- TOTTÉ, P., MCKEEVER, D., MARTINEZ, D. & BENSALD, A. 1997. Analysis of T-cell responses in cattle immunized against heartwater by vaccination with killed elementary bodies of *Cowdria ruminantium*. *Infection and Immunity*, 65, 236-41.
- TOTTÉ, P., VACHIERY, N., MARTINEZ, D., TRAP, I., BALLINGALL, K. T., MACHUGH, N. D., BENSALD, A. & WÉRENNE, J. 1996. Recombinant bovine interferon gamma inhibits the growth of *Cowdria ruminantium* but fails to induce major histocompatibility complex class II following infection of endothelial cells. *Veterinary Immunology and Immunopathology*, 53, 61-71.
- TSHILWANE, S. I., THEMA, N., STEYN, H. C., VAN KLEEF, M. & PRETORIUS, A. 2019. A multi-epitope DNA vaccine co-administered with monophosphoryl lipid A adjuvant provides protection against tick transmitted *Ehrlichia ruminantium* in sheep. *Vaccine*, 37, 4354-4363.
- VAN DE PYPEKAMP, H. E. & PROZESKY, L. 1987. Heartwater. An overview of the clinical signs, susceptibility and differential diagnoses of the disease in domestic ruminants. *Onderstepoort Journal of Veterinary Research*, 54, 263-6.
- VAN DER MERWE, L. 1987. The infection and treatment method of vaccination against heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 489-91.
- VAN HEERDEN, H., STEYN, H. C., ALLSOPP, M. T. E. P., ZWEYGARTH, E., JOSEMANS, A. I. & ALLSOPP, B. A. 2004. Characterization of the pCS20 region of different *Ehrlichia ruminantium* isolates. *Veterinary Microbiology*, 101, 279-291.
- VAN VLIET, A. H., VAN DER ZEIJST, B. A., CAMUS, E., MAHAN, S. M., MARTINEZ, D. & JONGEJAN, F. 1995. Use of a specific immunogenic region on the *Cowdria ruminantium* MAP1 protein in a serological assay. *Journal of Clinical Microbiology*, 33, 2405-2410.
- VAN VLIET, A. H. M., JONGEJAN, F. & VAN DER ZEIJST, B. A. M. 1992. Phylogenetic Position of *Cowdria ruminantium* (Rickettsiales) Determined by Analysis of Amplified 16S Ribosomal DNA Sequences. *International Journal of Systematic and Evolutionary Microbiology*, 42, 494-498.

- WAGHELA, S. D., RURANGIRWA, F. R., MAHAN, S. M., YUNKER, C. E., CRAWFORD, T. B., BARBET, A. F., BURRIDGE, M. J. & MCGUIRE, T. C. 1991. A cloned DNA probe identifies *Cowdria ruminantium* in *Amblyomma variegatum* ticks. *Journal of Clinical Microbiology*, 29, 2571-2577.
- WALKER, J. B. & OLWAGE, A. 1987. The tick vectors of *Cowdria ruminantium* (Ixodoidea, Ixodidae, genus *Amblyomma*) and their distribution. *Onderstepoort Journal of Veterinary Research*, 54, 353-79.
- WAYNE, L. G., BRENNER, D. J., COLWELL, R. R., GRIMONT, P. A., KRICHEVSKY, M., MOORE, L. H., MOORE, W. E. C., MURRAY, R. G. E., STACKEBRANDT, E., STARR, M. P. & TRUPER, H. G. 1987. Report of the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics. *International Journal of Systematic Bacteriology* 37, 463-464.
- WIECZOREK, M., ABUALROUS, E. T., STICHT, J., ÁLVARO-BENITO, M., STOLZENBERG, S., NOÉ, F. & FREUND, C. 2017. Major Histocompatibility Complex (MHC) Class I and MHC Class II Proteins: Conformational Plasticity in Antigen Presentation. *Frontiers in Immunology*, 8.
- YAZDANKHAH, S. P. & LINDSTEDT, B.-A. 2007. Variable Number Tandem Repeat Typing of Bacteria. In: BERGMAN, N. H. (ed.) *Comparative Genomics*. Totowa, NJ: Humana Press.
- YUNKER, C. E. 1996. Heartwater in sheep and goats: a review. *Onderstepoort Journal of Veterinary Research*, 63, 159-70.
- ZWEYGARTH, E. & JOSEMANS, A. I. 2001. Continuous *in vitro* propagation of *Cowdria ruminantium* (Welgevonden stock) in a canine macrophage-monocyte cell line. *Onderstepoort Journal of Veterinary Research*, 68, 155-7.
- ZWEYGARTH, E. & JOSEMANS, A. I. 2003. *In vitro* infection by *Ehrlichia ruminantium* of baby hamster kidney (BHK), Chinese hamster ovary (CHO-K1) and Madin Darby bovine kidney (MDBK) cells. *Onderstepoort Journal of Veterinary Research*, 70, 165-8.
- ZWEYGARTH, E., JOSEMANS, A. I. & STEYN, H. C. 2008. *In vitro* isolation of *Ehrlichia ruminantium* from ovine blood into *Ixodes scapularis* (IDE8) cell cultures. *Onderstepoort Journal of Veterinary Research*, 75, 121-6.

- ZWEYGARTH, E., JOSEMANS, A. I., VAN STRIJP, M. F., LOPEZ-REBOLLAR, L., VAN KLEEF, M. & ALLSOPP, B. A. 2005. An attenuated *Ehrlichia ruminantium* (Welgevonden stock) vaccine protects small ruminants against virulent heartwater challenge. *Vaccine*, 23, 1695-1702.
- ZWEYGARTH, E., VOGEL, S. W., JOSEMANS, A. I. & HORN, E. 1997. *In vitro* isolation and cultivation of *Cowdria ruminantium* under serum-free culture conditions. *Research in Veterinary Science*, 63, 161-4.

Chapter 2

Characterization of *Ehrlichia ruminantium* from field *Amblyomma hebraeum* ticks collected from cattle in three South African provinces using Multi-Locus Sequence Typing

2.1 Abstract

Heartwater is one of the major tick-borne diseases of both domestic and some wild ruminants in Africa and some Caribbean islands. The disease is caused by *Ehrlichia ruminantium*, a member of the class Alphaproteobacteria and order Rickettsiales. The diversity of *E. ruminantium* isolates render the commercially available vaccine ineffective against some virulent isolates. To better understand the *E. ruminantium* genotypes circulating in South Africa, a total of 1004 *A. hebraeum* tick DNA samples from cattle in three South African provinces were tested by pCS20 Sol1 qPCR and characterized by Multi-Locus Sequence Typing (MLST) using five housekeeping genes. Out of 1004 samples tested, 222 (22%) were positive for *E. ruminantium*. The occurrence of *E. ruminantium* in the Mpumalanga, KwaZulu-Natal and Limpopo provinces was 19%, 22% and 27%, respectively. The *E. ruminantium* positive samples were screened for five housekeeping genes and sequenced. From the five housekeeping genes investigated, *lipB* and *sodB* were the most conserved. Phylogenetic analysis revealed three main lineages: clade 1 made up of worldwide isolates (eastern, southern Africa, and Caribbean isolates); clade 2 comprised only West Africa isolates; and clade 3 consisted of the unique South African isolates, Omatjenne, Küm2, and Riverside. Genetic variation in the sequenced regions was observed in the form of single nucleotide polymorphisms (SNPs). These variations did not alter the function of the proteins encoded by the housekeeping genes. Using MLST to characterize *E. ruminantium* field isolates reveals genetic diversity and allows the South African genotypes to be clearly distinguished from the distinct West African isolates.

Key words

Ehrlichia ruminantium, heartwater, characterisation, pCS20, MLST, phylogenetic, PCR

2.2 Introduction

Ehrlichia ruminantium, previously called *Cowdria ruminantium* is the causative agent of heartwater in some wild and domestic ruminants (Bezuidenhout, 2009). Heartwater occurs in regions where ticks from the *Amblyomma* genus capable of transmitting the organism are present (Petney et al., 1987). In South Africa, *E. ruminantium* is transmitted by *A. hebraeum* and in sub Saharan Africa, Indian ocean islands and the Caribbean predominantly by *A. variegatum* (Walker and Olwage, 1987). Heartwater is endemic in six of the nine provinces of South Africa: Limpopo (LP), Mpumalanga (MP), KwaZulu-Natal (KZN), Gauteng (G), Eastern Cape (EC) and North West Province (NW) (Purnell, 1984). Livestock farmers interested in introducing high producing susceptible exotic breeds to upgrade local stock are hindered by heartwater as mortality rate of susceptible animals ranges from 20 to 90% (Mahan et al., 1992).

Currently there is no efficient vaccine against heartwater, the commercially available vaccine in South Africa consists of sheep blood infected with the Ball3 strain and employs the “infection and treatment” vaccination method (Van der Merwe, 1987). However, the Ball3 vaccine does not cross protect against all virulent and field isolates. The limited cross protection is a result of high genetic diversity caused by recombination of *E. ruminantium* giving rise to new isolates (Cangi et al., 2016). A prerequisite to develop effective control strategies of heartwater is the comprehension of genetic diversity of *E. ruminantium* strains. Different methods of genotyping *E. ruminantium* have been investigated and are mostly based on conserved molecular markers. Allsopp et al. (2003) used the genes *groESL*, citrate synthase (*gltA*), 16S rRNA and pCS20 (a cloned DNA fragment containing two partial reading frames) to phylogenetically characterize *E. ruminantium* isolates. The sequences of *groESL*, *gltA* and pCS20 revealed SNPs spread throughout the sequenced regions (Allsopp et al., 2003). In addition to the above

mentioned markers, Allsopp and Allsopp (2007) used the functional genes (*rnc*, *ctaG*, *ftsZ*, *nuoB* and *sodB*) to characterize *E. ruminantium* isolates from different geographic origins. Isolates from southern and eastern Africa grouped together while isolates from western Africa and one from southern Africa clustered together revealing a great genetic variability between southern and eastern African *E. ruminantium* isolates.

Multi Locus Sequence Typing (MLST) is a technique broadly used for molecular characterization of pathogens (Maiden, 2006). Adakal et al. (2009) developed a MLST scheme for *E. ruminantium* using eight housekeeping genes (*gltA*, *groEL*, *lepA*, *lipA*, *lipB*, *secY*, *sodB* and *sucA*). The same technique was used by Nakao et al. (2011) on various reference strains and field samples from different geographic origins. Based on both studies, *sodB* was the most conserved gene between the strains investigated, conversely, the gene with many variable sites was *secY*. The MLST scheme was able to differentiate among closely related strains and significant level of genetic variations among the examined strains was observed. *Ehrlichia ruminantium* isolates cluster into two main groups: Group1 (West Africa) and Group2 (worldwide) which is represented by West, East, and southern Africa, Indian Ocean, and Caribbean strains when using this method (Nakao et al., 2011, Cangi et al., 2016). The aim of the study is to characterize *E. ruminantium* field isolates currently circulating in three South African provinces using MLST.

2.3 Ethical considerations

The study was approved by the research ethics committee and part of the study that involves animals was performed in accordance with the stipulation of the Animal Ethics Committee at the University of Pretoria, Faculty of Veterinary Science (research ethical clearance and animal ethical clearance number: REC205-19). Permission to conduct the study in terms of Section 20 of the Animal Diseases Act, 1984 (Act No. 35 of 1984) was granted by Department of Agriculture, Land Reform and Rural Development (DALRRD) (reference number 12/11/1/1/6).

2.4 Materials and Methods

2.4.1 Study areas

Sample collection areas are shown in Figure 2.1 DNA extracted from ticks collected in MP in Utha and Welverdiend dip tanks was obtained from Mazhetese et al. (2022). Ticks were collected from cattle in Moddergat and Geodere-S dip tanks in MP. In LP, ticks were collected from cattle in Koedoeskop dip tank, Motlhabane Colchester 3 animal camp and a commercial farm in Groblersdal. In KZN, ticks were collected from cattle at the following dip tanks: Cecelia, Uthukela and Mpungamhlophe.

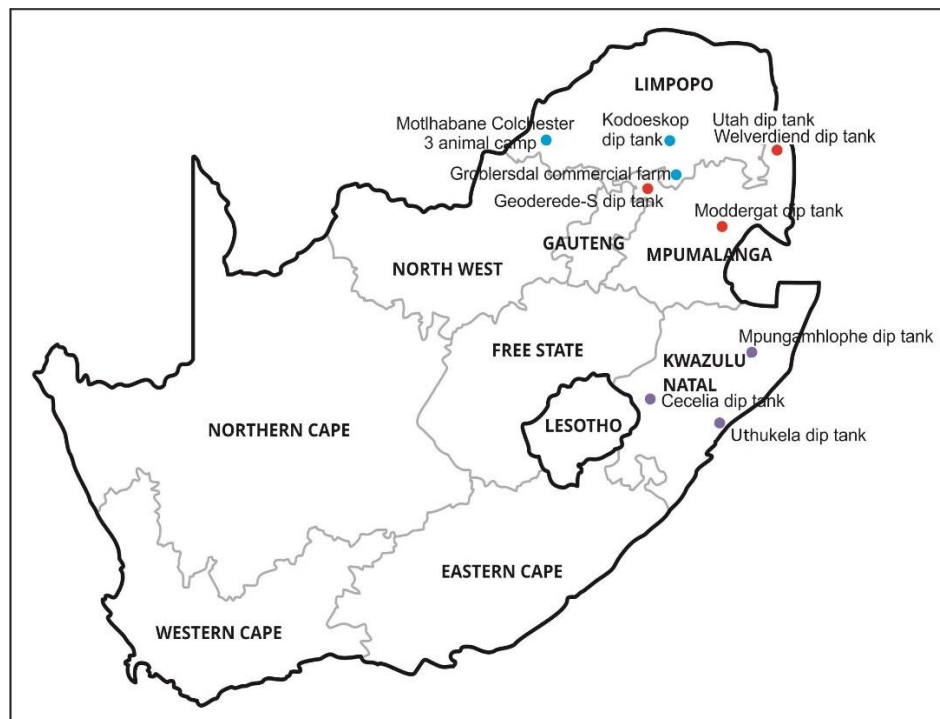


Figure 2.1: Map of South Africa showing where sample collection areas (coloured dots) are situated in the provinces of Limpopo, Mpumalanga and KwaZulu-Natal.

2.4.2 Tick collection

Tick sampling was carried out between October 2020 and January 2022 where rainfall was expected to increase and tick population to have been abundant. *Amblyomma*

hebraeum ticks were handpicked from cattle with permission from the cattle owners at dip tanks. About 3-5 adult ticks were handpicked from each animal and the minimum number of cattle sampled per collection site was 20. Collected ticks were kept alive in a humid environment and transported to the Research and Training laboratories, Department of Veterinary Tropical Diseases, University of Pretoria adhering to the biosafety rules and regulations stipulated by the Section 20 permit (DALRRD). Using a stereo microscope the ticks were identified based on entomological keys by Walker et al. (2003). Microscopy was done to correctly identify *A. hebraeum* ticks to be tested.

2.4.3 DNA extraction

Individual ticks were washed with 70% ethanol, rinsed with distilled water then air dried in a laminar flow. DNA was extracted from two legs of a tick using Qiagen DNeasy Blood and Tissue kit according to the manufacturer's instructions. Two legs were cut off close enough to the body of the tick to get the hemolymph from the tick and cut into small pieces in 180 µl lysis buffer (ATL). The rest of the tick was kept alive for gut and salivary glands extraction and preserved in sucrose phosphate glutamate buffer for possible culturing (see chapter 3 methods section 3.3.2) for vaccine development and genome sequencing if the tick is positive for *E. ruminantium*. The proteinase K digestion was carried out at 56 °C overnight. The genomic DNA was eluted from the column with 100 µl elution buffer. The DNA was kept at -20°C for further analysis.

2.4.4 Detection of *E. ruminantium* using pCS20 qPCR

Detection of *E. ruminantium* was performed by targeting a conserved genomic DNA fragment known as the pCS20 region using the TaqMan real time polymerase chain reaction (qPCR) previously described by Cangi et al. (2017). Each reaction was performed in a final volume of 25 µl containing 2 µl DNA as template, a final concentration 0.25 µM each primer (pCS20 Sol1 Forward and pCS20 Sol1 Reverse in Table 2.1), 0.2 µM probe (Sol1 TM probe in table 2.1) and TaqMan Universal PCR MasterMix 1X. Thermal cycling consisted of 1 cycle of uracil-N-glycosylase (UNG) incubation at 50 °C for 2 minutes and 1 cycle of AmpliTaq Gold pre-activation at 95 °C for 10 minutes. This

was then followed by 40 cycles of denaturing at 95 °C for 15 seconds and annealing at 55 °C for 1 minute and kept at 4 °C.

2.4.5 Characterization of *E. ruminantium* isolates using MLST

MLST was conducted on pCS20 qPCR positive samples using the housekeeping genes *lipA*, *lipB*, *secY*, *sodB*, *sucA* to characterize *E. ruminantium* field samples (Cangi et al., 2016). Each housekeeping gene was amplified using conventional PCR with the primers listed in table 2.1. PCR amplification was performed in a 20 µl reaction with 1X Phusion Flash High Fidelity PCR Master Mix (Thermo Fisher Scientific, Lithuania), 2.5 µl template DNA and 0.5 µM final concentration of each primer (each primer set with its annealing temperature is indicated in table 2.1). The PCR program consisted of 94 °C for 3 minutes; followed by 40 cycles of denaturing at 94 °C for 50 seconds, primer annealing (see temperature in table 2.1) for 50 seconds and extension at 72 °C for 50 seconds, followed by a final extension of 72 °C for 10 minutes. The PCR products were run on a 1.5% agarose gel stained with ethidium bromide and visualised with UV light illumination and photography. The PCR products were sequenced at Inqaba Biotec using Sanger sequencing.

Table 2.1: Oligonucleotides used for pCS20 qPCR and PCR amplification of housekeeping genes.

Primers/Probe	Sequence 5'- 3'	Annealing temperature °C	Product size (bp)
pCS20 Sol1F	ACAAATCTGGYCCAGATCAC	55	280
pCS20 Sol1 R	CAGCTTTCTGTTCAGCTAGT		
Sol1 TM probe	6-FAM- ATCAATTCACATGAAACATTA CATGCAACTGG-BHQ1		
lipA F	GGATCCTCATGAGCCTCAAA	62	430
lipA R	CTGCCGACCTTAAATCATCCA TA		
lipB F	TGGAAGATTGAATCCTTACCT G	59	452
lipB R	CCATGATATGTTATCCATTTT C		
secY F	CCAGGCATTAATCCAGATGT	61	690
secY R	GCGGAACATATGTAGATGCA GT		
sodB F	TGCCAGAACTGCCTTATCAA	61	507
sodB R	AAGCGTGTGCCATACATCC		
sucA F	TGAAAGGCTTTGGCTACAGG	59	566
sucA R	CCTGACCAATTACAGCAGCA		

2.4.6 Sequences and phylogenetic analysis

Sequences obtained from the housekeeping genes were processed using CLC Genomics Workbench version 7.5.1 (CLC Bio, Boston, MA, USA). The homologous sequences of the five genes were identified in the genome sequences available from NCBI (<https://www.ncbi.nlm.nih.gov/genome/microbes/>): Welgevonden (NC_005295.2/CR767821.1), Gardel (NC_006831.1/CR925677.1), Blaauwkrans (CP063043), Grootvallei (CP040120), Kwanyanga (CP040119), Mara87/7 (CP040118), Nonile (CP040117), Springbokfontein1 (CP040116), Springbokfontein2 (CP040115), Springbokfontein4 (CP040114), Springbokfontein5 (CP040113), Springbokfontein6 (CP040112), Springbokfontein7 (CP040111), Um Banein (CP063044), Crystal Springs (BDDK01000001 to BDDK01000034), Senegal (NZ_MQUJ00000000.1), Sankat 430 (BDDN01000001 to BDDN01000183), Küm2 (CP033456), Omatjenne (CP033455), and Riverside (CP033454), as well as the incomplete genome sequence of Ball3 (personal data, property of Dr Junita Liebenberg).

Alignments of sequences from the housekeeping genes were created using the Multiple Alignment, Fast Fourier Transform (MAFFT) [version 7] program (Kato and Standley, 2013) and subsequently modified using BioEdit (version 7.2.5) (Hall, 1999). A phylogenetic tree was constructed using concatenated nucleotide sequences of the housekeeping genes, *sodB*, *secY*, *lipB*, and *lipA* partial sequences, using the maximum likelihood (ML) method in MEGA7. The credibility for the internal branches was evaluated using bootstrapping (100 bootstrap replicates) (Felsenstein, 1985). Phylogenetic trees were constructed using MEGA7 and edited on Paint Tool for Windows 10.0.

2.4.7 Statistical analysis

Distributional patterns for the occurrence of *E. ruminantium* were described for each province and for study areas within each province. We determined how provinces and study areas differed in their occurrence using the non-parametric Kruskal-Wallis test. The

provinces and study areas were the independent variables while the occurrence served as the dependent variable. To measure the difference between the various provinces and study areas within the provinces, a post hoc test (Tukey's Honest Significant Difference) was performed at a significance level of 5% ($P < 0.05$). All statistical analyses were performed in R Console version 3.2.1.

2.5 Results

2.5.1 Tick collection

The collected ticks were verified to be *A. hebraeum*. A total of 1004 DNA samples were extracted from *A. hebraeum* ticks collected from cattle in MP, LP and KZN provinces of South Africa, and were tested for *E. ruminantium*.

2.5.2 Detection and prevalence of *E. ruminantium* by pCS20 qPCR

The number of ticks collected in each locality and that of pCS20 positive ticks are shown in table 2.2. *Ehrlichia ruminantium* DNA was successfully amplified from 222/1004 ticks of *A. hebraeum* using the pCS20 Sol1 qPCR assay that amplifies a 280 bp gene fragment of all *E. ruminantium* (Figure 2.2). Occurrence of *E. ruminantium* was 19%, 22% and 27% in ticks collected in MP, KZN and LP provinces respectively. The overall *E. ruminantium* infection rate in ticks collected in the three *E. ruminantium* endemic provinces of South Africa was 22%. The positivity rate was the highest in samples collected in Moddergat dip tank followed by Motlhabane Colchester animal camp (43% and 34% respectively).

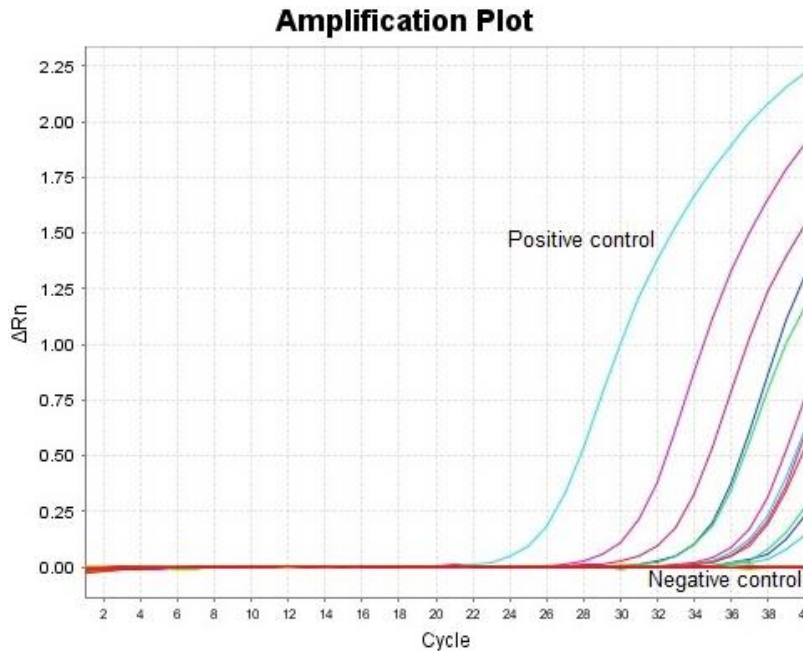


Figure 2.2: Amplification plot of *E. ruminantium* specific qPCR assay targeting the pCS20 gene fragment.

Comparing all the provinces together, the Kruskal-Wallis test showed that even though MP had the highest occurrence, this was not significant ($p > 0.0946$). Also, the post hoc test across the provinces showed no significant difference (Figure 2.3). Pairwise comparison across the study areas showed significant differences between all the study areas in MP ($P < 0.005$), study areas within LP province ($p < 0.005$), but no significant differences between the study areas in the KZN Province ($p > 0.005$; Figure 2.3).

Table 2.2: Occurrence of *E. ruminantium* in *A. hebraeum* ticks collected from cattle in the study areas.

Sample collection areas	Samples processed (n)	Number (%) pCS20 qPCR positive
Mpumalanga		
Utha	100	8 (8%)
Welverdiend	150	20 (13%)
Moddergat	58	25 (43%)
Geoderede-S	87	22 (25%)
Total	395	75 (19%)
Limpopo		
Groblersdal	28	4 (14%)
Koedoeskop	102	23 (23%)
Motlhabane Colchester	136	46 (34%)
Total	266	73 (27%)
KwaZulu-Natal		
Cecelia	140	31 (22%)
Uthukela	83	19 (23%)
Mpungamhlophe	120	24 (20%)
Total	343	74 (22%)

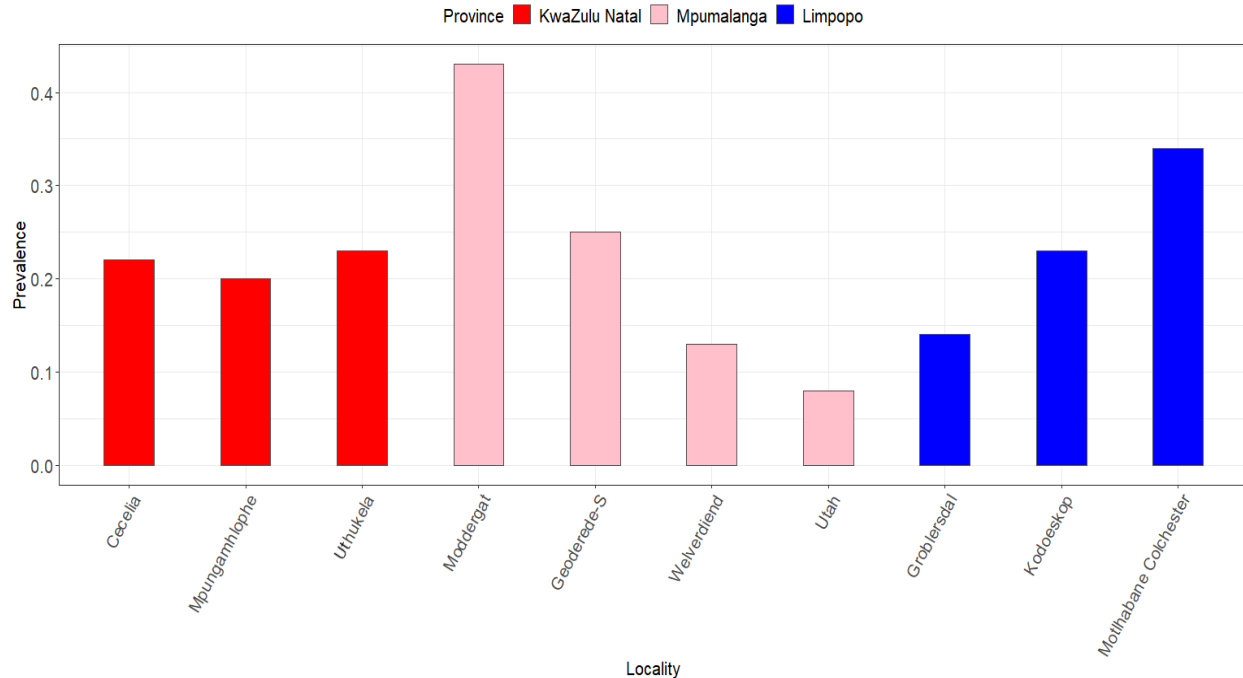


Figure 2.3: Bar graph showing the occurrence of *E. ruminantium* in *A. hebraeum* ticks collected from cattle in the study areas.

2.5.3 Characterization of *E. ruminantium* isolates using MLST

All the 222 pCS20 positive samples were tested for the five housekeeping genes (*lipA*, *lipB*, *secY*, *sodB*, *sucA*) to characterize the *E. ruminantium* field isolates. For some samples, amplification was not successful for all the MLST genes, which limited the possibility of obtaining sequences for all loci of all samples and some samples had multiple unspecific amplification. A total of 524 amplicons (all loci) were sent for sequencing: *lipA* = 133; *lipB* = 109; *sodB* = 125; *secY* = 98; *sucA* = 59. Out of the 28 samples from Utah and Welverdiend dip tanks, 14 allowed for the successful amplification all the housekeeping genes, with *sodB* amplicons available in 27 samples.

All the amplicons of samples for which the housekeeping genes were amplified were sequenced (Inqaba Biotechnical Industries (Pty) Ltd) and found to be 99.4-100% identical to selected reference genes: Ball3, Nonile, Kwanyanga, Mara87-7, Grootvallei,

Welgevonden, Crystal Springs, Kiswani, Omatjenne, Kümm2, Riverside Springbokfontein 1; 2; 4; 5; 6; 7 for each gene (see table 2.3) (Altschul et al., 1990). Out of the 133 *lipA* amplicons sent for sequencing 15 samples could not meet standard requirements for Sanger sequencing. Some samples had bad sequences and could not be analyzed further: *lipA* =19, *sodB* = 2, *secY* = 8 and *sucA* = 17. Since the identity of some samples were the same, a small number of sequences was included in the construction of the phylogenetic tree.

Table 2.3: Number of samples with percentage similarity identity with reference strains according to each housekeeping gene.

Gene	No of samples	% Similarity	Reference isolates
<i>lipA</i>	23	100	SBF1, SBF4, Ball3
	17	100	Crystal Springs, Mara87-7, SBF2
	15	99.7	Nonile, SBF1, SBF4, Ball3
	5	99.7	Grootvallei, SBF6, SBF7
	40	99.5	Kwanyanga
<i>lipB</i>	52	100	Kwanyanga, Nonile, SBF1, Ball3
	24	100	Mara87-7, SBF2, SBF5
	28	100	Grootvallei, SBF4, SBF6, SBF7
	6	100	Sao Tome
	1	99.8	Kwanyanga, Mara87-7, SBF2
	1	99.7	Mara87-7, SBF2, SBF5
<i>sodB</i>	50	100	Grootvallei, Nonile, SBF1
	36	100	Mara87-7, SBF2
	37	100	Kwanyanga, Blaauwkrans

Gene	No of samples	% Similarity	Reference isolates
<i>secY</i>	39	100	Grootvallei, SBF4, SBF6
	12	100	Nonile, SBF1, Ball3
	27	100	Kwanyanga, Mara87-7, SBF2
	2	99.8	Grootvallei, SBF4, SBF6
	1	99.8	Omatjenne, Kümm2, Riverside
	1	99.8	Nonile, SBF1, Ball3
	1	99.8	Kwanyanga, Mara87-7, SBF2
	4	99.6	Grootvallei, Nonile, SBF1
	3	99.6	Grootvallei, Kwanyanga, Mara87-7
<i>sucA</i>	12	100	CHIP026MH1
	8	100	Kwanyanga
	8	100	Grootvallei, SBF4, SBF6
	8	100	Nonile, SBF1, Kiswani
	3	99.8	Grootvallei, SBF1, SBF6
	3	99.8	Nonile, SBF1, Kiswani

A consistent pattern of SNPs extending throughout the sequenced genes was observed for all genes. Using concatenated nucleotide sequences of housekeeping genes, *sodB*, *secY*, *lipB*, and *lipA*, a MLST phylogenetic tree was constructed using only samples that successfully amplified all the four genes. The alignment of the concatenated sequences used to construct the tree is shown in Appendix 1. The *sucA* gene was only successfully amplified in a small portion of the samples and was excluded from the MLST analysis. Phylogenetic tree topology showed three clades: clade 1 (southern and East African and Caribbean isolates), clade 2 (West African isolates) and clade 3 (unique South African isolates: Omatjenne, Kümm2, and Riverside). It was observed that some samples were not identical to any of the reference isolates (samples blocked in red in Figure 2.4). However, they were all found to belong to the southern and East African/worldwide clade

(clade 1). No province-specific grouping was found among the analysed field strains, suggesting that similar isolates are found all over South Africa.

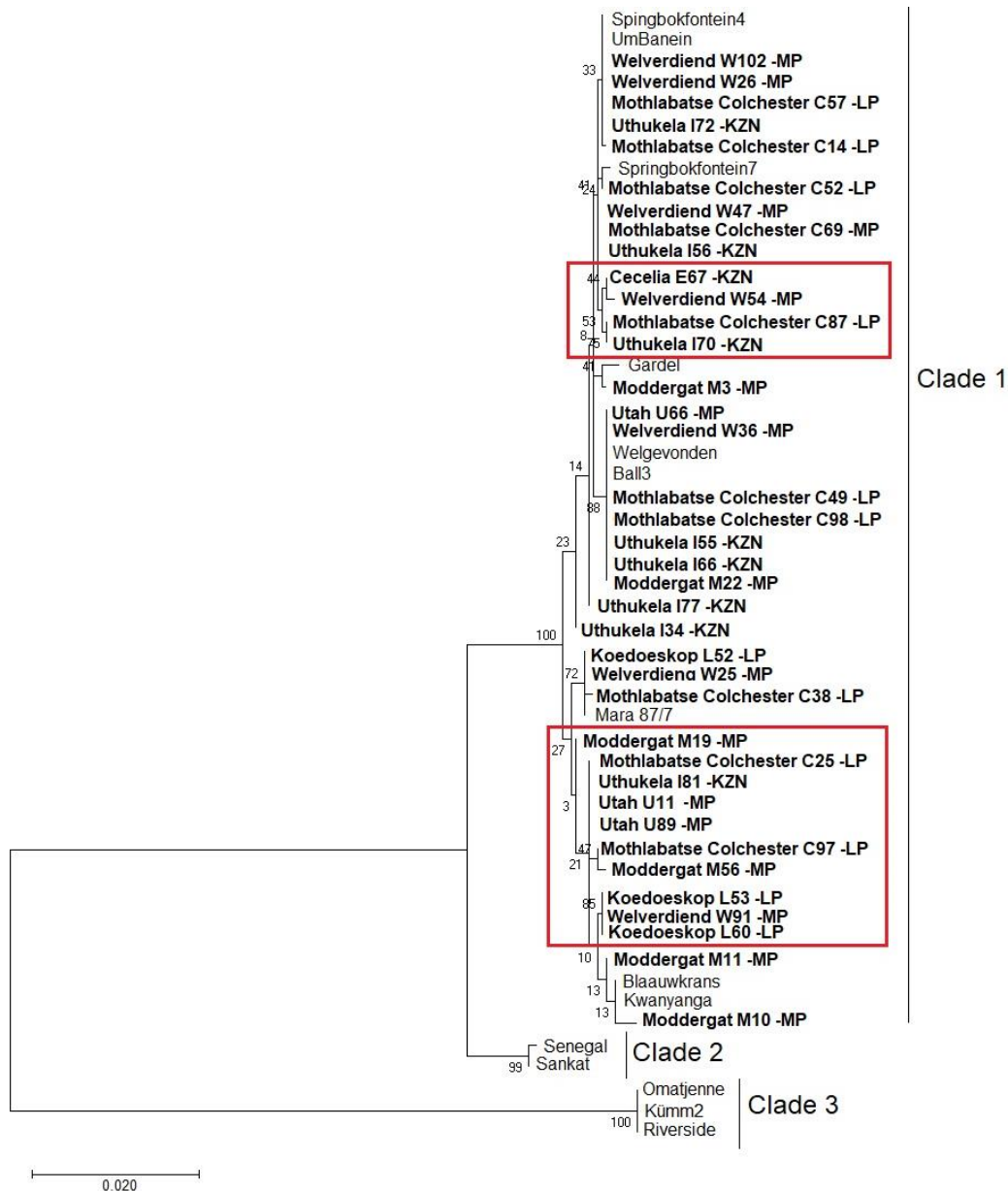


Figure 2.4: Phylogenetic tree showing relationship between *E. ruminantium* field isolates from three South African provinces and global reference isolates. The phylogenetic tree was constructed based on concatenated nucleotide sequences of housekeeping genes (*sodB*, *secY*, *lipB*, and *lipA* partial sequences), using MEGA7 and maximum likelihood method. Sequences from this study are shown in bold font. Bootstrap values are

represented as the numbers shown at the nodes and they were calculated from 100 replicates.

2.6 Discussion

Heartwater, caused by *E. ruminantium* is one of the major causes of livestock loss in sub-Saharan Africa with mortalities up to 90% (Allsopp, 2015). The high genetic diversity of *E. ruminantium* is a hindrance to the development of an efficient vaccine (Cangi et al., 2016). Understanding the genotypic characteristics of *E. ruminantium* isolates currently circulating is a prerequisite to developing an efficient vaccine.

In this study, we screened *A. hebraeum* ticks obtained from cattle in three provinces of South Africa to characterize circulating *E. ruminantium* isolates. The overall occurrence of *E. ruminantium* in the three South African provinces is 23% which is higher than Cameroon, Benin and Mozambique (6.6%, 6% and 15%) respectively; (Esemu et al., 2018, Guo et al., 2018, Matos et al., 2019). All the above mentioned authors used the nested pCS20 PCR to detect *E. ruminantium*. Mtshali et al. (2015) reported the infection rate of *A. hebraeum* ticks collected in KZN to be slightly over 25%, which is similar to the 22% reported in the current study. Mtshali et al. (2015) used the loop-mediated isothermal amplification (LAMP) assay to test *E. ruminantium* infection in *A. hebraeum* ticks. Guo et al. (2019) did not detect any *E. ruminantium* from *A. hebraeum* ticks collected in Msinga Mountainview dip tank, an area that is surrounded by the three sample collection areas of our study in KZN. However, in the current study, the overall occurrence of *E. ruminantium* in sample collection sites in KZN was 22%. A possible explanation for the discrepancy in these findings might be that Guo et al. (2019) may have missed low parasitaemia positive ticks as they used conventional nested pCS20 PCR, which is less specific and less sensitive than pCS20 Sol1 qPCR (Cangi et al., 2017), which was used in our study.

Altogether, there was genetic variation in the five analyzed housekeeping genes among the *E. ruminantium* field isolates. The topology of the phylogenetic tree had three *E. ruminantium* clades; clade 1 consisting of isolates from the current study; southern and East African and Caribbean (Gardel); clade 2 with exclusively West African isolates and clade 3 with the unique South African isolates. The most conserved genes were *lipB* and *sodB* as all the analysed isolates were 100% identical to previously known *E. ruminantium* isolates. The *sodB* gene was also highly conserved in *E. ruminantium* isolates obtained from *A. variegatum* samples in Burkina Faso (Adakal et al., 2010) and Uganda (Nakao et al., 2011), and it has been suggested that *sodB* might be a promising target for a molecular diagnostic test to identify *E. ruminantium* (Nakao et al., 2011). Adakal et al. (2010) found *lipB* to have the most polymorphic sites out of the genes used in our study, however, the current study found *lipB* to be one of the most conserved genes.

Study isolate E29 from *Cecelia* dip tank, KZN was observed to be 99.8% identical to *E. ruminantium* isolates, Omatjenne, Küm2 and Riverside, and grouped with the same isolates for *secY* gene (circled red in Figure 2.5). The same phylogenetic tree topology of the three isolates (Omatjenne, Küm2 and Riverside) grouping together was observed by Steyn and Pretorius (2020) and Liebenberg et al. (2020). Omatjenne genotype was isolated from a *Hyalomma truncatum* female tick collected from cattle in the heartwater free Otjiwarongo district of Namibia and contributed to the heartwater seropositivity of cattle in the area. Initially, the isolate was apathogenic until it was passaged through three generations of *A. hebraeum* and caused a disease similar to heartwater in sheep (Du Plessis, 1990). The same Omatjenne genotype was detected in blood from healthy sheep in LP, South Africa, which was seropositive for heartwater (Allsopp et al., 1997). In our study Küm2 clustered with Omatjenne implying they are indeed closely related and concur with the findings of Zweygarth et al. (2002).

Küm2 isolate is a component of the Küm isolate and has an exact 16S rDNA genotype of Omatjenne isolate (Zweygarth et al., 2002). The isolate was obtained from naturally

infected goats in Rust de Winter, an area bordering LP and northern Gauteng provinces in South Africa (Du Plessis, 1981). The Riverside isolate was obtained from the blood of a sick Angora goat in one of the heartwater endemic areas in South Africa, in the EC province in a farm called Riverside situated in Makhanda (formerly known as Grahamstown) (Steyn and Pretorius, 2020).

Omatjenne, Kümm2 and Riverside genotypes can be initiated *in vitro* in the tick cell line IDE8, but not on bovine endothelial cells (Liebenberg et al., 2020) and they lack certain open reading frames which are present in other *E. ruminantium* isolates (Allsopp et al., 2003). Liebenberg et al. (2020) found variations in the membrane protein families of Omatjenne, Kümm2 and Riverside which may play a critical role in their ability to be propagated in other cells. Study isolate E29 may exhibit these unique genotypic characteristics since it is closely related to the three isolates. These genotypes were previously found in the EC (Steyn and Pretorius, 2020) and borders of LP and northern Gauteng provinces (Du Plessis, 1981) in South Africa. In our study, the unique genotype was observed in KZN. The movement of animals from one province to another, allowed by trade, may have played a role in disseminating the unique genotype provincially or some isolates have evolved.

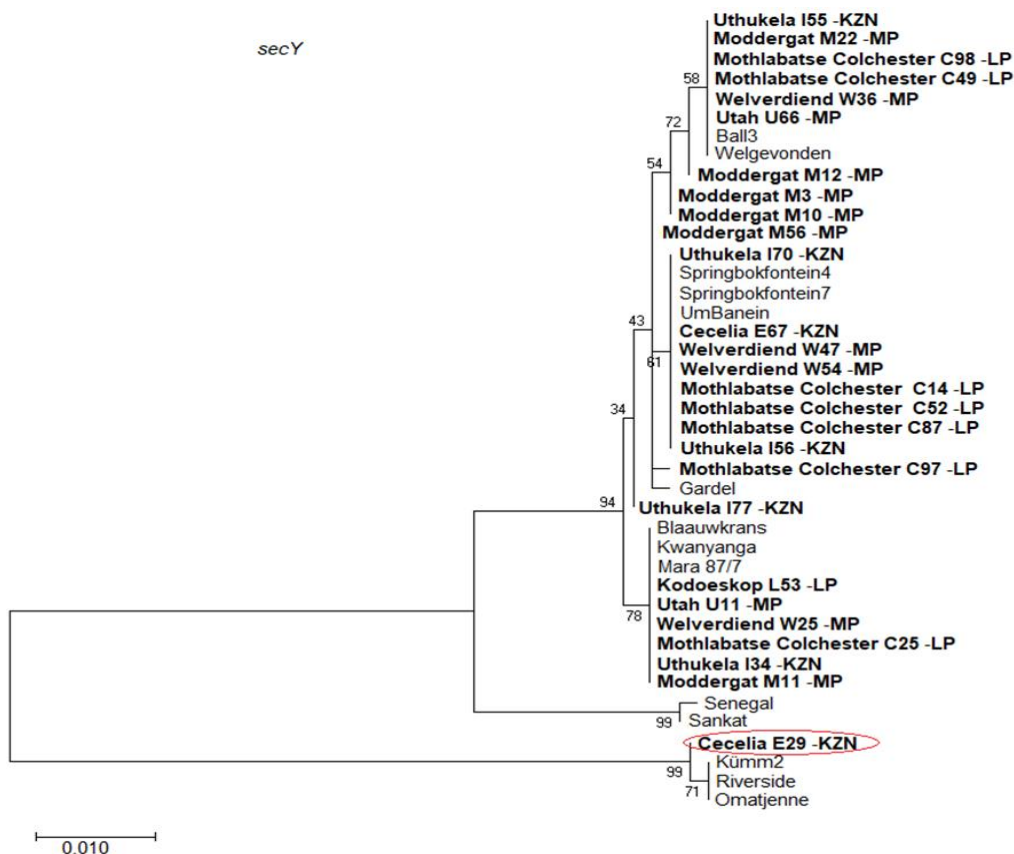


Figure 2.5: Phylogenetic tree showing relationship between *E. ruminantium* field isolates from three South African provinces and global reference isolates based on *secY* gene. Study isolate E29 from Cecelia dip tank KZN province circled in red clustered with the unique South African isolates. The numbers at the nodes represents bootstrap values that were calculated from 100 replicates.

2.7 Conclusion

Using the MLST scheme to characterise *E. ruminantium* isolates reveals genetic diversity, SNPs throughout the sequenced regions, and three main lineages. The SNPs do not change the makeup and function of the protein encoded by the genes. The three main lineages, one made up of the worldwide isolates, the other comprising of only West African isolates and the last one consisting of the unique South African isolates remains throughout the years despite the occurrence of recombination or evolution of isolates in the field. Since there are many genotypes at any location at any given time, especially in

southern Africa, there is a need for regular surveillance to understand the driving force of cross protection or lack thereof between *E. ruminantium* isolates. MLST can clearly distinguish the South African genotypes from the distinct West African genotype and to the best of our knowledge this is a first report of using a panel of housekeeping genes to characterize *E. ruminantium* field isolates from ticks in three South African provinces.

2.8 References

- ADAKAL, H., GAVOTTE, L., STACHURSKI, F., KONKOBO, M., HENRI, H., ZOUNGRANA, S., HUBER, K., VACHIERY, N., MARTINEZ, D., MORAND, S. & FRUTOS, R. 2010. Clonal origin of emerging populations of *Ehrlichia ruminantium* in Burkina Faso. *Infection, Genetics and Evolution*, 10, 903-912.
- ADAKAL, H., MEYER, D. F., CARASCO-LACOMBE, C., PINARELLO, V., ALLÈGRE, F., HUBER, K., STACHURSKI, F., MORAND, S., MARTINEZ, D., LEFRANÇOIS, T., VACHIERY, N. & FRUTOS, R. 2009. MLST scheme of *Ehrlichia ruminantium*: Genomic stasis and recombination in strains from Burkina-Faso. *Infection, Genetics and Evolution*, 9, 1320-1328.
- ALLSOPP, B. A. 2015. Heartwater-*Ehrlichia ruminantium* infection. *Revue Scientifique et Technique*, 34, 557-568.
- ALLSOPP, M. T. E. P. & ALLSOPP, B. A. 2007. Extensive genetic recombination occurs in the field between different genotypes of *Ehrlichia ruminantium*. *Veterinary Microbiology*, 124, 58-65.
- ALLSOPP, M. T. E. P., VAN HEERDEN, H., STEYN, H. C. & ALLSOPP, B. A. 2003. Phylogenetic Relationships among *Ehrlichia ruminantium* Isolates. *Annals of the New York Academy of Sciences*, 990, 685-691.
- ALLSOPP, M. T. E. P., VISSER, E. S., DU PLESSIS, J. L., VOGEL, S. W. & ALLSOPP, B. A. 1997. Different organisms associated with heartwater as shown by analysis of 16S ribosomal RNA gene sequences. *Veterinary Parasitology*, 71, 283-300.
- ALTSCHUL, S. F., GISH, W., MILLER, W., MYERS, E. W. & LIPMAN, D. J. 1990. Basic local alignment search tool. *Journal of Molecular Biology*, 215, 403-10.
- BEZUIDENHOUT, J. D. 2009. Heartwater: an abridged historical account. *Journal of the South African Veterinary Association*, 80, 208-9.
- CANGI, N., GORDON, J. L., BOURNEZ, L., PINARELLO, V., APRELON, R., HUBER, K., LEFRANÇOIS, T., NEVES, L., MEYER, D. F. & VACHIÉRY, N. 2016. Recombination Is a Major Driving Force of Genetic Diversity in the Anaplasmataceae *Ehrlichia ruminantium*. *Frontiers in Cellular and Infection Microbiology*, 6.

- CANGI, N., PINARELLO, V., BOURNEZ, L., LEFRANÇOIS, T., ALBINA, E., NEVES, L. & VACHIÉRY, N. 2017. Efficient high-throughput molecular method to detect *Ehrlichia ruminantium* in ticks. *Parasites & Vectors*, 10, 566.
- DU PLESSIS, J. L. 1981. *Mice infected with a Cowdria ruminantium-like agent as a model in the study of heartwater*. D.V.Sc. thesis, University of Pretoria.
- DU PLESSIS, J. L. 1990. Increased pathogenicity of an Ehrlichia-like agent after passage through *Amblyomma hebraeum*: a preliminary report. *Onderstepoort Journal of Veterinary Research*, 57, 233-7.
- ESEMU, S. N., NDIP, R. N. & NDIP, L. M. 2018. Detection of *Ehrlichia ruminantium* infection in cattle in Cameroon. *BioMed Central Research Notes*, 11, 388.
- FELSENSTEIN, J. 1985. Confidence limits on phylogenies: An approach using the bootstrap. *Evolution*, 39, 783-791.
- GUO, H., ADJOU MOUMOUNI, P. F., THEKISOE, O., GAO, Y., LIU, M., LI, J., GALON, E. M., EFSTRATIOU, A., WANG, G., JIRAPATTHARASATE, C., RINGO, A. E., MTSHALI, K., INOUE, N., SUZUKI, H. & XUAN, X. 2019. Genetic characterization of tick-borne pathogens in ticks infesting cattle and sheep from three South African provinces. *Ticks and Tick-borne Diseases*, 10, 875-882.
- GUO, H., YIN, C., GALON, E. M., DU, J., GAO, Y., ADJOU MOUMOUNI, P. F., LIU, M., EFSTRATIOU, A., LEE, S.-H., LI, J., RINGO, A. E., WANG, G., LI, Y., TUMWEBAZE, M. A. & XUAN, X. 2018. Molecular survey and characterization of *Theileria annulata* and *Ehrlichia ruminantium* in cattle from Northwest China. *Parasitology International*, 67, 679-683.
- HALL, T. A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, 41, 95-98.
- KATOH, K. & STANDLEY, D. M. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution*, 30, 772-780.
- LIEBENBERG, J., STEYN, H. C., JOSEMANS, A. I., FABER, E. & ZWEYGARTH, E. 2020. In vitro propagation and genome sequencing of three 'atypical' *Ehrlichia ruminantium* isolates. *Onderstepoort Journal of Veterinary Research*, 87, 1-14.

- MAHAN, S. M., WAGHELA, S. D., MCGUIRE, T. C., RURANGIRWA, F. R., WASSINK, L. A. & BARBET, A. F. 1992. A cloned DNA probe for *Cowdria ruminantium* hybridizes with eight heartwater strains and detects infected sheep. *Journal of Clinical Microbiology*, 30, 981-986.
- MAIDEN, M. C. J. 2006. Multilocus Sequence Typing of Bacteria. *Annual Review of Microbiology*, 60, 561-588.
- MATOS, C. A., GONÇALVES, L. R., DE SOUZA RAMOS, I. A., MENDES, N. S., ZANATTO, D. C. S., ANDRÉ, M. R. & MACHADO, R. Z. 2019. Molecular detection and characterization of *Ehrlichia ruminantium* from cattle in Mozambique. *Acta Tropica*, 191, 198-203.
- MAZHETESE, E., LUKANJI, Z., BYARUHANGA, C., NEVES, L. & MORAR-LEATHER, D. 2022. Rickettsia africae infection rates and transovarial transmission in *Amblyomma hebraeum* ticks in Mnisi, Bushbuckridge, South Africa. *Experimental and Applied Acarology*, 86, 407-418.
- MTSHALI, K., KHUMALO, Z. T. H., NAKAO, R., GRAB, D. J., SUGIMOTO, C. & THEKISOE, O. M. M. 2015. Molecular detection of zoonotic tick-borne pathogens from ticks collected from ruminants in four South African provinces. *Journal of Veterinary Medical Science*, 77, 1573-1579.
- NAKAO, R., MAGONA, J. W., ZHOU, L., JONGEJAN, F. & SUGIMOTO, C. 2011. Multilocus sequence typing of *Ehrlichia ruminantium* strains from geographically diverse origins and collected in *Amblyomma variegatum* from Uganda. *Parasites & Vectors*, 4, 137.
- PETNEY, T. N., HORAK, I. G. & RECHAV, Y. 1987. The ecology of the African vectors of heartwater, with particular reference to *Amblyomma hebraeum* and *Amblyomma variegatum*. *Onderstepoort Journal of Veterinary Research*, 54, 381-95.
- PURNELL, R. E. 1984. Control of heartwater in cattle in Southern Africa using terramycin/LA. *Preventive Veterinary Medicine*, 2, 239-254.
- STEYN, H. C. & PRETORIUS, A. 2020. Genetic diversity of *Ehrlichia ruminantium* field strains from selected farms in South Africa. *Onderstepoort Journal of Veterinary Research*, 87.

- VAN DER MERWE, L. 1987. The infection and treatment method of vaccination against heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 489-91.
- WALKER, A., BOUATTOUR, A., CAMICAS, J. L., ESTRADA-PEÑA, A., HORAK, I., LATIF, A., PEGRAM, R. G. & PRESTON, P. M. 2003. Ticks of Domestic Animals in Africa: a guide to identification of species.
- WALKER, J. B. & OLWAGE, A. 1987. The tick vectors of *Cowdria ruminantium* (Ixodoidea, Ixodidae, genus *Amblyomma*) and their distribution. *Onderstepoort Journal of Veterinary Research*, 54, 353-79.
- ZWEYGARTH, E., JOSEMANS, A. I., VAN STRIJP, M. F., VAN HEERDEN, H., ALLSOPP, M. T. & ALLSOPP, B. A. 2002. The Kümme isolate of *Ehrlichia ruminantium*: in vitro isolation, propagation and characterization. *Onderstepoort Journal of Veterinary Research*, 69, 147-53.

Chapter 3

***In vitro* culture of *Ehrlichia ruminantium* using tick salivary glands and gut**

3.1 Abstract

Ehrlichia ruminantium causes heartwater, an infectious, non-contagious disease in some domestic and wild ruminants. Heartwater disease is controlled by vigorous use of acaricides and live blood vaccine. The blood vaccine offers limited protection against some virulent *E. ruminantium* isolates and highlights the need for development of effective vaccines. The antigen used in an inactivated vaccine development is obtained by *in vitro* culture of *E. ruminantium*. The conventional method of propagating *E. ruminantium in vitro* employs *E. ruminantium* blood stabilate which is obtained by infecting a blood donor animal. There is a need for developing an alternative method of propagating *E. ruminantium in vitro* without the requirement of a blood donor animal. Therefore, this study is aimed at initiating *in vitro* culture of *E. ruminantium* using salivary glands and gut from *E. ruminantium* positive field ticks. Salivary glands and gut were extracted from *E. ruminantium* positive ticks and preserved in sucrose phosphate glutamate buffer. Confluent monolayer of bovine aorta endothelial cells in a 6-well cell culture plate was inoculated with the tick material and incubated at 37°C with 5% CO₂. The cell cultures were examined for cytopathic effect using inverted microscope and were examined for *E. ruminantium* by quick staining with Rapi-Diff II stain Rapid and tested by pCS20 Sol1 qPCR 19 days post inoculation. Microscopic examination from the cell culture plate showed no cytopathic effect. Dark purple colonies like *E. ruminantium* elementary were observed after staining. However, the cell cultures were *E. ruminantium* negative by pCS20 Sol1 qPCR. The cell cultures had microbial contamination 23 days post inoculation. A second attempt to initiate *E. ruminantium in vitro* culture was cut short due to the South African lockdown caused by the worldwide corona virus pandemic. *Ehrlichia ruminantium in vitro* culture from tick material could be a better alternative for isolating various *E. ruminantium* genotypes circulating in the field without the need of infecting an

animal. Therefore, there is a need to optimize this cell culture system and its optimization could provide an easier way for creating a biobank of *E. ruminantium* isolates that could be used for development of efficient heartwater vaccines.

Key words

Ehrlichia ruminantium, tick salivary glands, gut, *in vitro*, optimization, heartwater

3.2 Introduction

Ehrlichia ruminantium is a pathogen that causes heartwater, an infectious, non-contagious disease of cattle, sheep, goats, and some wild ruminants such as the springbok (Oberem and Bezuidenhout, 1987). *Amblyomma* genus ticks are responsible for disseminating heartwater and in southern Africa it is *A. hebraeum* and *A. variegatum* that transmit the disease (Bezuidenhout, 2009). Infected susceptible animals suffer from high fever and central nervous signs that leads to death within a few hours or days (Allsopp, 2010). Heartwater is prevalent in regions where the tick vector capable of transmitting the pathogen is present. The endemic areas includes sub-Saharan Africa, Madagascar, Reunion, Mauritius, Zanzibar, the Comoros Islands, and Sao Tomé and three Caribbean islands: Guadeloupe, Marie-Galante, and Antigua (Spickler, 2015).

Incubation of heartwater is about 10 to 30 days post infectious tick bite and in most cases an instant increase in body temperature presents as an initial symptom (Kocan and Bezuidenhout, 1987a). The multiplication of the parasite is at its peak during the febrile reaction when the temperature of the animal reaches 40°C. Infected animals suffer from fever, heavy breathing, loss of appetite, diarrhoea, repeated blinking of the eyes, hypersensitivity to touch and once recumbent they exhibit pedalling movements (Allsopp, 2010). Autopsy reveal hydrothorax and hydro-pericardium with oedema in the lungs.

Tetracycline antibiotics have been found to be efficient when administered immediately after the rise in body temperature (Van Amstel, 1987). Vaccination is one of the strategies

used to fight against heartwater. The commercially available vaccine in South Africa consists of sheep blood infected with the live Ball3 isolate and employs the “infection and treatment” vaccination method (Van der Merwe, 1987). However, the Ball3 vaccine does not cross-protect against all isolates due to high genetic diversity of *E. ruminantium* that give rise to new isolates (Cangi et al., 2016).

Etiological studies of heartwater suggest that *E. ruminantium* parasitizes endothelial cells and is confined in the endothelial cells of the smaller blood vessels throughout the body (Cowdry, 1925). The parasite accumulates as large densely packed masses which are spherical that grow within vacuole-like cytoplasmic spaces filled with a clear fluid in a single endothelial cell (Cowdry, 1926). Bezuidenhout et al. (1985) reported the first successful *E. ruminantium in vitro* culture system where a calf endothelial cell line known as E₅ was irradiated or chemically treated and inoculated with tick-derived stabilate, prepared from *Amblyomma hebraeum* nymphae. Subsequent successful continuous culture of various *E. ruminantium* isolates has been achieved using endothelial cells of several animal species and from varying anatomical sites (Jongejan et al., 1991b, Martinez et al., 1993, Totté et al., 1993, Smith et al., 1998).

In vitro culture of *E. ruminantium* in other cells could be achieved, including leukocytes (Logan et al., 1987). However, the culture system is not suitable for continuous *in vitro* culture as Logan et al. (1987) was able to maintain the cultures for only 5 days and the collection of host cells is laborious. Zweygarth and Josemans (2003), successfully propagated *E. ruminantium in vitro* in non-endothelial cells including: baby hamster kidney (BHK), Chinese hamster ovary (CHO-K1) and Madin Darby bovine kidney (MDBK) cells. However, the cell lines required treatment of cycloheximide (CyX) for regular growth. Bezuidenhout (1987) observed that Vero, lamb foetal kidney and Mouse L-cells do not support *in vitro* growth of *E. ruminantium*.

E. ruminantium is transmitted by members of Ixodidae family with *A. hebraeum* being the predominant vector in the southern Africa region and *A. variegatum* in other parts of Africa (Bezuidenhout, 2009). In the tick vector, *E. ruminantium* is found in midgut and salivary glands (Cowdry, 1925b). Bell-Sakyi et al. (2000) successfully propagated *E. ruminantium* in *Ixodes scapularis* tick cell line IDE8 by infecting the cells with Gardel isolate from bovine pulmonary artery endothelial cells. Propagation of *E. ruminantium* is not only achieved in vector tick cells but is also possible in cell lines from non-vector (*Ixodes scapularis*, *I. ricinus*, *Boophilus decoloratus*, *B. microplus* and *Rhipicephalus appendiculatus*) tick species (Bell-Sakyi et al., 2002). There are 63 cell lines obtained from 18 ixodid and argasid tick species and one from sand fly and biting midge in the tick cell biobank with various geographic origins (Bell-Sakyi et al., 2018). Out of the 63 tick cell lines available, *E. ruminantium* can be propagated successfully in 10 cell lines from 4 ixodid tick genera (Bekker et al., 2002a, Bell-Sakyi, 2004, Bekker et al., 2005, Postigo et al., 2008, Zweygarth et al., 2008).

When using tick cells to propagate *E. ruminantium*, the choice of inoculum has been infected tick cell lines and infected endothelial cells (Bell-Sakyi, 2004) and leukocyte fraction of blood of infected sheep (Zweygarth et al., 2008). The use of leukocytes to inoculate tick cells was reported by Munderloh et al. (1999) for the purpose of isolating and propagating the human granulocytic ehrlichiosis agent. Use of tick organs to isolate and propagate various potential pathogenic tick-borne microorganisms on tick cell lines has been reported (Palomar et al., 2019).

Culture inoculums from ticks are currently prepared by first feeding an infected tick on a naive animal, once the animal develops fever blood is collected that is used for propagation. Ethical requirements for the use and infection of host animals have impacted on the feasibility of using this method, and it would be an advantage if the use of animals is eliminated. Therefore, there is a need for the optimization of *in vitro* isolation method of *E. ruminantium* directly from ticks to allow for field isolate collection and ultimately will assist in whole genome sequencing of *E. ruminantium* strains circulating in the field.

Successful optimization of *in vitro* cell cultures initiated directly from ticks could lead to extensive research that could provide genotypic and phenotypic information that informs isolates with best immunogenicity and broad protective capacity against various *E. ruminantium* isolates. Also, such an *in vitro* culture system will provide enough antigen for vaccine development. Hence the aim of the study is to initiate *E. ruminantium in vitro* culture using tick salivary glands and gut.

3.3 Materials and Methods

3.3.1 Culture medium

Infected and uninfected cells were grown in Dulbecco's modified eagle's medium/Ham's nutrient mixture: F12 containing L-glutamine, 15 mM HEPES and sodium bicarbonate (DME/F-12). The medium was supplemented with 10% heat inactivated fetal bovine serum and 100 IU penicillin and 100 µg/ml streptomycin.

3.3.2 Inoculum preparation

Ticks were disinfected with 70% ethanol, rinsed twice with sterile water, and allowed to dry on sterile filter paper. The ticks were tested by pCS20 Sol1 qPCR for *E. ruminantium* positivity (see methods in chapter 2 section 2.4.4 for detection of *E. ruminantium* using pCS20 Sol1 qPCR) by testing the tick DNA extracted from two legs of the tick cut close enough to the body to get the hemolymph (see methods in chapter 2 section 2.4.3 for DNA extraction).

3.3.3 Inoculum

In a laminar flow, under a microscope, the *E. ruminantium* positive tick was put in sterile petri dish containing sucrose phosphate glutamate buffer. Tick gut and salivary glands were extracted by removing the dorsal integument and cutting round the midline with a scalpel. The gut and salivary glands were removed and rinsed once in sucrose phosphate

glutamate buffer. The gut and salivary glands were homogenized in a 2 ml Precelly lysing tube containing culture medium using Precelly homogenizer program 1 once (centrifuge at 6800 x g for 90 seconds). The gut and salivary gland suspension was centrifuged at slow speed (2000 x g) for 10 minutes and the supernatant was used as the inoculum. Some *E. ruminantium* positive tick gut and salivary glands were preserved in sucrose phosphate glutamate buffer and stored at -80°C for later attempts at initiating *E. ruminantium in vitro* culture.

3.3.4 Initiating *in vitro* culture of *E. ruminantium* using tick material

Approximately 0.2 ml supernatant was used to inoculate a confluent monolayer of bovine aorta endothelial cells in a 6-well cell culture plate. Another confluent monolayer of bovine aorta endothelial cells was inoculated with culture medium and served as negative control. Both cultures were incubated at 37°C with 5% CO₂ in a slow rocking incubator for 1-2 h for cell absorption to occur. After 2 h the inoculum suspension was removed, and the cells were rinsed twice with calcium and magnesium free phosphate buffered saline (PBS-). Then 1 ml of culture medium was added, and the cultures were incubated at 37°C with 5% CO₂. After 24 h the media was changed by using a pipette to remove the media in the wells of the culture plate and added 1 ml of culture medium. Thereafter, media was changed once a week.

Briefly, the culture medium in the cell culture plate was discarded and the cells were washed twice with PBS- that is equal to half the volume of the growth medium. About 100 µl of trypsin was added to the cells and the plate was gently tilted to spread the trypsin over the entire surface of the cells. The cells detached and the cell layer separated after 5-10 minutes. The cells were incubated at 37°C for 1 minute to enhance the trypsinization process. Culture medium was added to the trypsin suspension to neutralize trypsin activity. The cell suspension was aspirated into a 2 ml sterile tube and centrifuged at 2000 x g for about 2 minutes. The supernatant was discarded carefully by a pipette making sure not to disturb the sedimented cells. The cells were gently dispersed with culture

medium using syringe with 18-gauge needle. The cells in suspension were transferred to a clean sterile 6-well cell culture plate containing culture medium and incubated at 37°C with 5% CO₂.

The cell cultures were examined using inverted microscope for cell growth and by visual inspection for any signs of microbial contamination (usually indicated by turbid media and dead/detached cells) daily. Also, using an inverted microscope the cells were examined for the cytopathic effect that demonstrate *E. ruminantium* in the endothelial cells. Small samples from the monolayer were removed by a sterile disposable cell scraper from which smears were made at days 7, 13, 19. The smears were air dried, methanol fixed and quick stained with Rapi-Diff II stain. Cell cultures which appeared to be infected with *E. ruminantium* colonies were tested for *E. ruminantium* by pCS20 qPCR.

3.4 Results

Ticks for salivary glands and gut extraction used as inoculum were *E. ruminantium* positive by the pCS20 Sol1 qPCR assay (Figure 3.1). Though the ticks were positive for *E. ruminantium*, the CT values of the positive ticks were above 31.

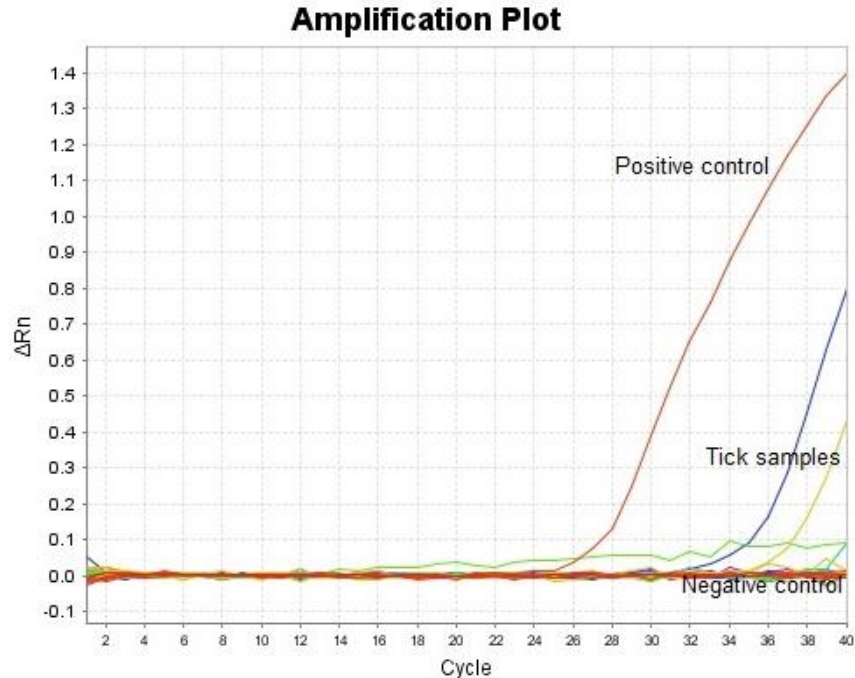


Figure 3.1: Representative amplification plot of *E. ruminantium* positive ticks used for extracting salivary glands and gut for *E. ruminantium in vitro* culture.

Throughout the 23 days, the cell cultures did not show any sign of infection, the medium was clear without any debris. Microscopic examination from the cell culture plate showed no cytopathic effect, cells looked normal and were multiplying. Dark purple colonies looking like *E. ruminantium* elementary bodies as shown in Figure 3.2 A and B were observed after staining with Rapi-Diff II stain 19 days post inoculation. However, the cell cultures were *E. ruminantium* negative by pCS20 Sol1 qPCR 19 days post inoculation. The cell cultures were negative even after 23 days post inoculation and the cell cultures showed signs of microbial contamination indicated by turbid media and detached cells. The contamination persisted and the cell cultures could not be salvaged. The contaminated cell cultures were discarded at day 25 post inoculation. The negative control cell culture remained negative throughout the 25 days.

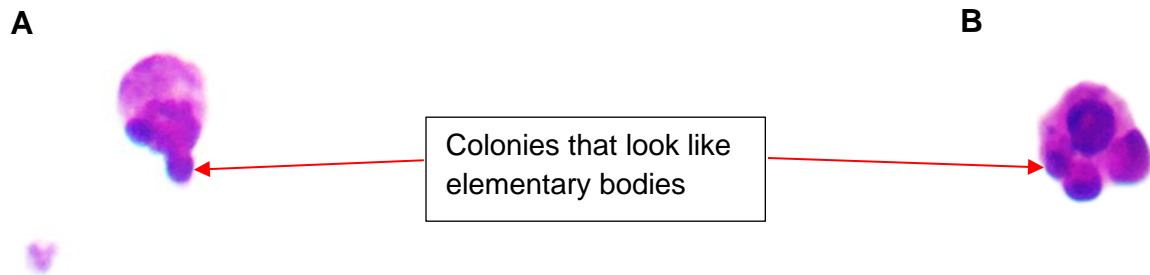
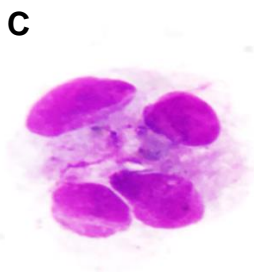


Figure 3.2 A & B: BPAAE cells 19 days post inoculation with tick gut and salivary glands (A and B). Dark purple colonies that resemble elementary bodies of *E. ruminantium* were observed. C is the negative control cell culture inoculated with culture medium 19 days after inoculation. The dark purple colonies that resemble elementary bodies of *E. ruminantium* were not present.



3.5 Discussion

Ehrlichia ruminantium is an intracellular rickettsial pathogen transmitted by *Amblyomma* ticks and causes heartwater, a major cause of livestock loss in sub-Saharan Africa. The pathogen is found in different anatomical sites within the mammalian host, including neutrophils and reticulo-endothelial cells (Du Plessis, 1975, Logan et al., 1987) and in tick midgut and salivary glands within the tick vector (Cowdry, 1925b). In 1926, Cowdry described the multiplication of *Rickettsia ruminantium* within the endothelial cells of an infected animal (Cowdry, 1926). It was not startling when Bezuidenhout et al. (1985) successfully propagated *E. ruminantium* in calf endothelial cells. *Ehrlichia ruminantium* was thought to be an obligate parasite of endothelial cells since it is often found *in vivo* in endothelial cells. However, the pathogen can be successfully propagated *in vitro* in non-endothelial cells: bovine foetal testis, cat ovary, donkey fibroblastoid, E₂, horse testis,

lamb foetal testis, mouse connective tissue and African Green monkey kidney (Zweygarth, 2003).

The use of mammalian host endothelial cells to propagate *E. ruminantium* from blood and cell culture has been extensively investigated (Byrom and Yunker, 1990, Byrom et al., 1991, Jongejan, 1991a, Martinez et al., 1993). Initiating *E. ruminantium in vitro* culture from blood requires infecting a healthy live animal with an *E. ruminantium* isolate. It is of paramount importance to optimize a cell culture system that will not be dependent on infecting an animal to get the infected blood to culture *E. ruminantium*.

The *in vitro* culture system has been applied in the modification of virulence of *E. ruminantium* isolate. Jongejan (1991a) observed the attenuation of *E. ruminantium* on serial passages without the loss of immunogenicity. Also, the culture system has been used in the development of inactivated vaccine. Although the cell culture system has potential for breakthrough in *E. ruminantium* research Yunker (1995) says, “workers in different laboratories, and even different workers in a single laboratory, commonly experience difficulties in consistently growing the heartwater organism.” Therefore, highlighting the need of the optimization of the culture system.

The current study used *E. ruminantium* positive tick gut and salivary glands to initiate *E. ruminantium in vitro*. The attempts were unsuccessful due to contamination and possibly low rickettsial load in the ticks. It is known that ticks are hosts to several pathogens with high natural bacterial load on the surface of ticks (Munderloh et al., 1994). Lesley Bell-Sakyi (personal communication) suggested that the ticks should be immersed in 0.1% benzalkonium chloride for 5 min, then in 70% ethanol and then rinsed with sterile water before the extraction of tick material to reduce the tick surface bacterial load. Furthermore, the culture medium used in the current study did not contain an antifungal agent which would have assisted in the control of unwanted fungal growth in cell culture (Perlman et

al., 1961). Additionally, in the current study, the culture medium was not further supplemented with 2 mM L-glutamine meaning the medium lacked enough nutrients required for the growth of *E. ruminantium in vitro* (Zweygarth et al., 2013, Palomar et al., 2019).

Also, low rickettsial load in the ticks could have negatively influenced the method as CT values of the *E. ruminantium* positive ticks were above 31. Therefore, it will be of benefit if the infectious material can be concentrated. A way to concentrate the infectious material is to dissect the salivary glands and midgut from several positive ticks collected from a single animal. Bezuidenhout et al. (1985) highlights that the source of the inoculum, choice of cell line and techniques of infection are important factors that contribute to a successful *E. ruminantium in vitro* culture.

A successful optimization of isolating *E. ruminantium* directly from ticks will pave a path for rapid isolation of field isolates and generation of genome sequences. Probably the question of what causes the lack of protection among the various *E. ruminantium* isolates may be answered once the whole genomes of these field isolates is known, leading to development of efficient vaccines.

3.6 Conclusion

The success of mammalian culture system for *in vitro* culture of *E. ruminantium* contributed to the understanding of the development of the organism in the ruminant host. While the use of tick cell cultures has piloted an increased knowledge and understanding of *E. ruminantium* development in the vector. It is without a doubt that there is a need for optimization of the *in vitro* culture system using tick material. The *in vitro* system will provide an easier way of isolating various *E. ruminantium* genotypes circulating in the field. Also, the system will eliminate the need of infecting a live animal with an *E. ruminantium* isolate to get the infected blood for the propagation of the *E. ruminantium*

isolate. Even though the current attempts of the culture system were without success, future attempts at initiating *E. ruminantium in vitro* culture will be done using tick gut and salivary glands stored at -80°C.

3.7 References

- ALLSOPP, B. A. 2010. Natural history of *Ehrlichia ruminantium*. *Veterinary Parasitology*, 167, 123-135.
- BEKKER, C. P., BELL-SAKYI, L., PAXTON, E. A., MARTINEZ, D., BENSALD, A. & JONGEJAN, F. 2002a. Transcriptional analysis of the major antigenic protein 1 multigene family of *Cowdria ruminantium*. *Gene*, 285, 193-201.
- BEKKER, C. P. J., POSTIGO, M., TAOUFIK, A., BELL-SAKYI, L., FERRAZ, C., MARTINEZ, D. & JONGEJAN, F. 2005. Transcription analysis of the major antigenic protein 1 multigene family of three *in vitro*-cultured *Ehrlichia ruminantium* isolates. *Journal of Bacteriology*, 187, 4782-4791.
- BELL-SAKYI, L. 2004. *Ehrlichia ruminantium* grows in cell lines from four ixodid tick genera. *Journal of Comparative Pathology*, 130, 285-93.
- BELL-SAKYI, L., DARBY, A., BAYLIS, M. & MAKEPEACE, B. L. 2018. The Tick Cell Biobank: A global resource for *in vitro* research on ticks, other arthropods and the pathogens they transmit. *Ticks and Tick-Borne Diseases*, 9, 1364-1371.
- BELL-SAKYI, L., PAXTON, E., WRIGHT, P. & SUMPTION, K. 2002. Immunogenicity of *Ehrlichia ruminantium* grown in tick cell lines. *Experimental and Applied Acarology*, 28, 177-85.
- BELL-SAKYI, L., PAXTON, E. A., MUNDERLOH, U. G. & SUMPTION, K. J. 2000. Growth of *Cowdria ruminantium*, the causative agent of heartwater, in a tick cell line. *Journal of Clinical Microbiology*, 38, 1238-40.
- BEZUIDENHOUT, J. D. 1987. The present state of *Cowdria ruminantium* cultivation in cell lines. *Onderstepoort Journal of Veterinary Research*, 54, 205-10.
- BEZUIDENHOUT, J. D. 2009. Heartwater: an abridged historical account. *Journal of the South African Veterinary Association*, 80, 208-9.
- BEZUIDENHOUT, J. D., PATERSON, C. L. & BARNARD, B. J. 1985. *In vitro* cultivation of *Cowdria ruminantium*. *Onderstepoort Journal of Veterinary Research*, 52, 113-20.

- BYROM, B. & YUNKER, C. E. 1990. Improved culture conditions for *Cowdria ruminantium* (Rickettsiales), the agent of heartwater disease of domestic ruminants. *Cytotechnology*, 4, 285-90.
- BYROM, B., YUNKER, C. E., DONOVAN, P. L. & SMITH, G. E. 1991. *In vitro* isolation of *Cowdria ruminantium* from plasma of infected ruminants. *Veterinary Microbiology*, 26, 263-8.
- CANGI, N., GORDON, J. L., BOURNEZ, L., PINARELLO, V., APRELON, R., HUBER, K., LEFRANÇOIS, T., NEVES, L., MEYER, D. F. & VACHIÉRY, N. 2016. Recombination Is a Major Driving Force of Genetic Diversity in the Anaplasmataceae *Ehrlichia ruminantium*. *Frontiers in Cellular and Infection Microbiology*, 6.
- COWDRY, E. V. 1925. Studies on the etiology of heartwater : I. Observation of a *Rickettsia*, *Rickettsia ruminantium* (N. SP.), in the tissues of infected animals. *Journal of Experimental Medicine*, 42, 231-52.
- COWDRY, E. V. 1925b. Studies on the etiology of heartwater: II. *Rickettsia ruminantium* (N.SP.) in the tissues of ticks transmitting the deases. . *Journal of Experimental Medicine*, 42, 253-274.
- COWDRY, E. V. 1926. Studies on the etiology of heartwater: III. The multiplication of *Rickettsia ruminantium* within the endothelial cells of infected animals and their discharge into circulation. *Journal of Experimental Medicine*, 44, 803-14.
- DU PLESSIS, J. L. 1975. Electron microscopy of *Cowdria ruminantium* infected reticulo-endothelial cells of the mammalian host. *Onderstepoort Journal of Veterinary Research*, 42, 1-13.
- JONGEJAN, F. 1991a. Protective immunity to heartwater (*Cowdria ruminantium* infection) is acquired after vaccination with *in vitro*-attenuated rickettsiae. *Infection and Immunity*, 59, 729-31.
- JONGEJAN, F., THIELEMANS, M. J. C., DE GROOT, M., VAN KOOTEN, P. J. S. & VAN DER ZEIJST, B. A. M. 1991b. Competitive enzyme-linked immunosorbent assay for heartwater using monoclonal antibodies to a *Cowdria ruminantium*-specific 32-kilodalton protein. *Veterinary Microbiology*, 28, 199-211.

- KOCAN, K. M. & BEZUIDENHOUT, J. D. 1987a. Morphology and development of *Cowdria ruminantium* in *Amblyomma* ticks. *Onderstepoort Journal of Veterinary Research*, 54, 177-82.
- LOGAN, L. L., WHYARD, T. C., QUINTERO, J. C. & MEBUS, C. A. 1987. The development of *Cowdria ruminantium* in neutrophils. *Onderstepoort Journal of Veterinary Research*, 54, 197-204.
- MARTINEZ, D., SHEIKBOUDOU, C., COURAUD, P. O. & BENSAID, A. 1993. *In vitro* infection of bovine brain endothelial cells by *Cowdria ruminantium*. *Research in Veterinary Science*, 55, 258-260.
- MUNDERLOH, U. G., JAURON, S. D., FINGERLE, V., LEITRITZ, L., HAYES, S. F., HAUTMAN, J. M., NELSON, C. M., HUBERTY, B. W., KURTTI, T. J., AHLSTRAND, G. G., GREIG, B., MELLENCAMP, M. A. & GOODMAN, J. L. 1999. Invasion and intracellular development of the human granulocytic ehrlichiosis agent in tick cell culture. *Journal of Clinical Microbiology*, 37, 2518-2524.
- MUNDERLOH, U. G., LIU, Y., WANG, M., CHEN, C. & KURTTI, T. J. 1994. Establishment, maintenance and description of cell lines from the tick *Ixodes scapularis*. *Journal of Parasitology*, 80, 533-43.
- OBBEREM, P. T. & BEZUIDENHOUT, J. D. 1987. The production of heartwater vaccine. *Onderstepoort Journal of Veterinary Research*, 54, 485-8.
- PALOMAR, A. M., PREMCHAND-BRANKER, S., ALBERDI, P., BELOVA, O. A., MONIUSZKO-MALINOWSKA, A., KAHL, O. & BELL-SAKYI, L. 2019. Isolation of known and potentially pathogenic tick-borne microorganisms from European ixodid ticks using tick cell lines. *Ticks Tick Borne Dis*, 10, 628-638.
- PERLMAN, D., GIUFFRE, N. A. & BRINDLE, S. A. 1961. Use of Fungizone® in Control of Fungi and Yeasts in Tissue Culture. *Proceedings of the Society for Experimental Biology and Medicine*, 106.
- POSTIGO, M., TAOUFIK, A., BELL-SAKYI, L., BEKKER, C. P. J., DE VRIES, E., MORRISON, W. I. & JONGEJAN, F. 2008. Host cell-specific protein expression *in vitro* in *Ehrlichia ruminantium*. *Veterinary Microbiology*, 128, 136-147.

- SMITH, G. E., ANDERSON, E. C., BURRIDGE, M. J., PETER, T. F. & MAHAN, S. M. 1998. Growth of *Cowdria ruminantium* in tissue culture endothelial cell lines from wild African mammals. *Journal of Wildlife Diseases*, 34, 297-304.
- SPICKLER, A. R. 2015. *Heartwater* [Online]. Available: <http://www.cfsph.iastate.edu/DiseaseInfo/factsheets.php> [Accessed 2022].
- TOTTÉ, P., BLANKAERT, D., ZILIMWABAGABO, P. & WÉRENNE, J. 1993. Inhibition of *Cowdria ruminantium* infectious yield by interferons alpha and gamma in endothelial cells. *Revue d'Elevage et de Médecine Vétérinaire des Pays Tropicaux*, 46, 189-194.
- VAN AMSTEL, S. R., & OBEREM, P. T. 1987. The treatment of heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 475-479.
- VAN DER MERWE, L. 1987. The infection and treatment method of vaccination against heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 489-91.
- YUNKER, C. E. 1995. Current status of *in vitro* cultivation of *Cowdria ruminantium*. *Veterinary Parasitology*, 57, 205-211.
- ZWEYGARTH, E. & JOSEMANS, A. I. 2003. *In vitro* infection by *Ehrlichia ruminantium* of baby hamster kidney (BHK), Chinese hamster ovary (CHO-K1) and Madin Darby bovine kidney (MDBK) cells. *Onderstepoort Journal of Veterinary Research*, 70, 165-8.
- ZWEYGARTH, E., JOSEMANS, A. I. & STEYN, H. C. 2008. *In vitro* isolation of *Ehrlichia ruminantium* from ovine blood into *Ixodes scapularis* (IDE8) cell cultures. *Onderstepoort Journal of Veterinary Research*, 75, 121-6.
- ZWEYGARTH, E., JOSEMANS, A. I. 2003. *In vitro* infection of non-endothelial cells by *Ehrlichia ruminantium*. *Annals of the New York Academy of Sciences*, 573-580.
- ZWEYGARTH, E., SCHÖL, H., LIS, K., CABEZAS CRUZ, A., THIEL, C., SILAGHI, C., RIBEIRO, M. F. & PASSOS, L. M. 2013. *In vitro* culture of a novel genotype of *Ehrlichia* sp. from Brazil. *Transboundary and Emerging Diseases*, 60 Suppl 2, 86-92.

Chapter 4

Development of a reverse transcription quantitative real-time PCR assay for the evaluation of a multivalent inactivated vaccine

4.1 Abstract

Heartwater is a tick-borne disease caused by *E. ruminantium* and occurs in sub-Saharan Africa region and Caribbean islands. The disease poses a threat to livestock farmers that want to introduce exotic high yielding breeds as mortality rate is up to 90% in susceptible animals. Heartwater is also a threat to livestock in areas where the disease does not occur yet the tick vector capable of transmitting the diseases is present. In southern Africa, the disease is controlled by regular use of acaricides especially in the warm rainy season where the tick vector is abundant. Another control strategy is immunization by live virulent blood vaccine and subsequent treatment with tetracyclines to prevent death. The nature of the vaccine requires cold chain storage and trained personnel to administer the vaccine. The major drawback of the vaccine is its limited cross protection against some virulent *E. ruminantium* isolates. Efficient alternative vaccines are a requirement in order to conquer the fight against heartwater. The developed vaccines must be tested for their ability to elicit protective immunity against heartwater. Hence, the aim of the study is to develop a reverse transcription quantitative real-time PCR (RT qPCR) assay for the evaluation of a multivalent inactivated vaccine. Sheep were vaccinated with an inactivated multivalent heartwater vaccine developed by Agricultural Research Council-Onderstepoort Veterinary Research (ARC-OVR) and blood was collected at different time points. Housekeeping genes were selected and validated for relative quantification of mRNA-levels of immune markers for protection. The selection and validation method were by statistical algorithm that include Ct mean, CV of RPKM values and CT values and the Δ Ct method and the genes were ranked using RefFinder. Immune markers for protection differentially expressed between surviving animals and treated animals were

identified using RNA-seq data from a previous study. Relative changes in gene expression of immune markers for protection were measured by RT qPCR. The best housekeeping genes were SDHA, RPL22, YWHAZ and GAPDH and the appropriate immune markers were CD41–ITGA2B, CD156A-ADAM8, CXCR5, CD8B, CD5, GZMB-LIKE, IFN- γ and TGFB1. The developed RT qPCR assay revealed that the immune markers for protection were differentially expressed at all time points. Although an increase in expression of the immune markers in all vaccinated animals at least one of the two time points post vaccination, it does not predict survival. Therefore, increase in expression of the immune markers post vaccination cannot be used to indicate protection.

Key words

RT qPCR, vaccine development, housekeeping genes, immune markers, inactivated vaccine

4.2 Introduction

Heartwater is a tick-transmissible infection caused by *E. ruminantium* and spread by *Amblyomma* genus ticks. Heartwater is a disease of goats, cattle and sheep and some wild ruminants in sub-Saharan Africa, Madagascar, Reunion, Mauritius, Zanzibar, the Comoros Islands, and Sao Tomé and three Caribbean islands: Guadeloupe, Marie-Galante, and Antigua (Spickler, 2015). The disease is indicated by fever, heavy breathing, loss of appetite, diarrhea, nervousness (inco-ordination and convulsion), lateral recumbency position with leg paddling and the buildup of liquid in the lungs, brain, thoracic cavity and pericardial sac (Bezuidenhout, 2009). Mortality of susceptible animals include: 6% in Persian or Afrikander sheep, 60% in cattle, 80% in Merino sheep and Angora goats (Mahan et al., 1992). Heartwater causes a notable decline in farmers productivity in areas where it is widespread and poses a significant threat in non-indigenous livestock that are moved into heartwater areas (Meltzer et al., 1996).

Heartwater is controlled by acaricides, antibiotic treatment of sick animals and vaccination of animals. Using a blood vaccine, vaccination employs the infection and treatment method. However, the infection and treatment vaccination method is laborious as mandatory daily monitoring of rectal temperature of the animal after vaccination is required, the necessary treatment of reacting animals with antibiotics, and the need for maintaining a cold chain for the distribution of the vaccine. Also, the vaccine isolate is live which present a risk of transmitting blood pathogens; and does not cross protect against all field isolates. The disadvantages of the infection and treatment vaccination method has led to investigations of developing more efficient vaccines.

The development of *in vitro* culture of *E. ruminantium* provided means of modifying the virulence of an isolate and supply antigens to be used for various vaccines (Jongejan, 1991a). Martinez et al. (1994) used cell culture derived inactivated elementary bodies mixed with Freund's adjuvant to immunize nine goats of which six survived the homologous challenge. Mahan et al. (1995b) reported similar results where 100% of

sheep immunized with inactivated elementary bodies mixed with Freund's adjuvant were protected and survived the challenge. The inactivated vaccine has been successfully used to immunize cattle and protected 100% of cattle against a homologous challenge (Totté et al., 1997). However, these promising results were regrettably not reproducible when tests were performed in a natural tick field situation, where varying genotypes with different immunogenicities are present.

It has been established that humoral immune response possibly contributes a minor role in the fight against *E. ruminantium* infection (Stewart, 1987). Protective immunity against heartwater is mediated by cellular immune responses (Du Plessis et al., 1991). Mwangi et al. (1998) reported that the cellular immune response to heartwater is characterized by the proliferation of CD4⁺, CD8⁺, $\gamma\delta$ T cells associated with T helper 1 (Th1) type. The T cells secrete high levels of IFN- γ , interleukin (IL)-2 receptor alpha and IL-6 (Byrom et al., 2000). Th1 cells are responsible for immunity mediated by cells, including delayed-type hypersensitivity reactions, recruitment and stimulation of inflammatory macrophages and leukocytes, cytolytic responses, leading to protection against intracellular pathogens (Esteves et al., 2004a).

It is important that a vaccine elicit a protective immune response. A protective immune response could be indicated by regulation of immune biomarkers of protection. Immune biomarkers are biological immune indicators that can be measured to determine responses to a therapeutic intervention (Libre and Duffy, 2018). The efficacy and effectiveness of a vaccine must be tested by challenging the animals with the disease-causing pathogen, further subjecting the animal to suffer from the symptoms of the disease. It is necessary to investigate and develop alternative methods to monitor immune responses induced in animals by determining the immune markers for protection and/or markers associated with a severe outcome. Therefore, the current study is aimed at developing an RT qPCR assay for the evaluation of a multivalent inactivated vaccine by monitoring the immune biomarkers for protection.

4.3 Materials and Methods

4.3.1 Selection of housekeeping genes as reference for a RT qPCR assay using RNA sequences obtained from sheep PBMC infected with *E. ruminantium*

Housekeeping genes were selected from literature as the most used for RT qPCR analyses. The RNA-seq analysis of these selected housekeeping genes were done using previous RNA-seq data sets prepared from peripheral blood mononuclear cells (PBMC) of animals infected and challenged with ticks infected experimentally with *E. ruminantium* Welgevonden using the methods by Nefefe et al. (2017). The data sets are considered confidential by the ARC and are not publicly available.

The RNA sequences were mapped to the sheep housekeeping homologues sequences selected from GenBank and are listed in table 4.1. The longest isoform (transcript variant X1, -X2, etc. indicated in the table), for a gene sequence was selected for RNA-seq mapping from GenBank, allowing complementarity to other transcripts of the same gene within the coding sequence.

Table 4.1: Summary of the candidate ovine housekeeping genes used in the RNA-seq analyses and evaluated in this study. The Gene symbol, Gene ID (the number allocated to the gene in the ovine genome sequence), Official name, Transcript variant (where applicable) and gene size are shown.

Gene symbol	Gene ID	Transcript variant	Protein name	Length (nt)
ACTB	443052	-	actin, beta	1839
ATP5F1B	101106318	-	ATP synthase, H + transporting, mitochondrial F0 complex, subunit B1	1775
B2M	443295	-	beta-2 microglobulin	385
CANX	101122273	-	calnexin	4047
EEF1A1	100101228	-	eukaryotic translation elongation factor 1 alpha 1	1744
GAPDH	443005	-	glyceraldehyde-3-phosphate dehydrogenase	1285
GUSB	101108802	-	glucuronidase, beta	4384
HPRT	100188975	-	hypoxanthine guanine phosphoribosyl transferase	1348
PGK1	100216440	-	phosphoglycerate kinase 1	1775
POLR2A	100144762	-	DNA-directed RNA polymerase II subunit RPB1	6736
PPIA	443258	X1	peptidyl-prolyl cis-trans isomerase A	815
PPIB	554319	-	peptidyl-prolyl cis-trans isomerase B	908
RPL13	443072	-	60S ribosomal protein L13	706
RPL22	101122293	-	60S ribosomal protein L22	463
RPL30	106990098	-	60S ribosomal protein L30	468
RPL31	101104219	-	60S ribosomal protein L31	438
RPL37	101103841	-	60S ribosomal protein L37	369
RPS18	100036761	X1	ribosomal protein S18	602
SDHA	100036762	-	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria	665
TBP	100144760	-	TATA box binding protein	1968
TFRC	100885768	X1	transferrin receptor	5882
YWHAZ	780452	X1	3 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	3429

From the animal trial described by Nefefe et al. (2017), four biological replicates taken as averages of three technical replicates, taken at eight time points from sheep PBMC isolated from heartwater infected animals were compared for this analysis. The RNA-seq data was analysed using the CLC Genomics Workbench 9.5. Data for each sample was imported and adapters and low-quality base reads were trimmed. To specifically focus on immune modulation by these cells, the reads were mapped, using the RNA-seq analysis tool, to the preselected ovine immune housekeeping reference gene sequences listed in table 4.2 obtained from NCBI (<https://www.ncbi.nlm.nih.gov>) using gene annotation and ID numbers updated on 16-August-2022. The RNA-seq mapping option settings were Mismatch cost (3); Insertion cost (3); Deletion cost (3); Length fraction (0.7) and Similarity fraction (0.8). The mapping data sets were further analysed using the transcriptomics analysis set up experiment tool of CLC. The RNA-seq data sets at each time point were collectively compared using the paired multi-comparison setting and normalised. Comparative transcriptomic experiments allowed for appropriate statistical analysis including Baggerley's test on proportions, T-test and the empirical analysis of digital gene editing (EDGE) tool.

Candidate housekeeping genes were selected by eliminating genes with a mean TPM of less than 100 and was filtered by determining the CV of TPM values for all data sets included in this analysis. The CV was calculated by dividing the standard deviation by the mean for each selected gene and the genes with the lowest CV values were selected as possible housekeeping genes. All qPCR primers were designed for selected genes using the latest sequence updates (August 2022) using the primer design software, OligoPerfect Primer Designer from ThermoFisher Scientific, (<https://apps.thermofisher.com/apps/oligoperfect>). Tm of these primers are all 60 °C and the length of PCR products vary from 96 bp to 150 bp. Some of the housekeeping genes are from Schulze et al. (2017) and were double checked using the latest sequence version if applicable. The primer sequences for amplification of the candidate housekeeping genes are listed in table 4.3 below (not highlighted).

4.3.2 Selection of immune markers using transcriptome sequence data

For the selection of immune markers, the same data sets as described by Nefefe et al. (2017) were used and the markers were selected by Dr Pretorius at the ARC-OVR (manuscript in preparation). Briefly, four sheep were vaccinated using a modified version of the infection and treatment method, where animals were infected with Welgevonden infected ticks and treated with tetracycline when a febrile reaction developed. These animals were challenged 30 days after they recovered from antibiotic treatment with experimentally infected ticks and all four survived the challenge without symptoms, while naïve animals (challenge controls) included in the study succumbed to heartwater.

The infection was monitored, and samples were collected at various time points after confirmed attachment of the male tick: (D1, D12 and D16 post infection [PI]) and (D1, D4 and D6 post challenge [PC]). These animals were challenged with experimentally infected ticks 30 days after they recovered from antibiotic treatment and all four survived the challenge without symptoms, while naïve animals (challenge controls) included in the study succumbed to heartwater. The ticks used to infect the sheep were tested with the pCS20 qPCR designed by Steyn et al. (2008) to determine infectivity, all ticks tested were infected with *E. ruminantium* Welgevonden. The presence of *E. ruminantium* in the blood of infected animals was also confirmed using the pCS20 qPCR where *E. ruminantium* DNA was detected on D12PI, and D16PI as well as in two animals on D1PC (Nefefe et al., 2017). Genes that were only upregulated post challenge and not during infection were identified and randomly selected for this assay. The selected markers are highlighted in table 4.2.

Table 4.2: Selected housekeeping genes (not highlighted) and immune biomarkers (highlighted in blue)

Gene ID	Gene Symbol	Accession number	Primer sequences
		XM_042236905.1	F:5' AGGTGGAACGTGTGATCACC 3' R:5' GTTGTCTAGACCGTTGGCCA 3'
100036761	RPS18	XM_027975714.2	F:5' CTCTGGACTGTACCCACCCT 3' R:5' CGATTGTTACAACACCGCCA 3'
101122293	RPL22	XM_027972283.2	F:5' GCCATGGTTCAAGGGATGGA 3' R:5' CGCAAGGGTTTGTCAAGTTGG 3'
100101228	EEF1A1	XM_027980212.2	F:5' GAGTTCGTGCAGTTCCACCC 3' R:5' CTCTCACCTGGCTGTTGAT 3'
100036762	SDHA	NM_001190390.1	F:5' ACAGTCAAGGCAGAGAACGG 3' R:5' CCAGCATCACCCCACTTGAT 3'
443005	GAPDH	NM_001267887.1	F:5' GATGAAGCCATTGCTGAACTTGA 3' R:5' CAGCTTCGTCTCCTTGGGTA 3'
780452	YWHAZ	XM_015105023.3	F:5' TTCTTTGCCGACCTGTTGGA 3' R:5' TCACCTGTTGACTGGTCGTT 3'
100188975	HPRT1	NM_001009284.2	F:5' CTTGGTCCTTCTCGGGCTG 3' R:5' TCTGGCGGGTGTCTTGAGTAT 3'
443295	B2M	NM_001142516.1	F:5' CCTCTGGCATACTGTTGGC 3' R:5' CACCCACAGGTCCATTCCAC 3'
100216440	PGK1	XM_004003001.4	F:5' ACCTCAAATCAGCGCTGTCA 3' R:5' CAGCCTCACGTGGGACATAA 3'
100885768	TFRC	NM_001009784.3	F:5' GCAGATGTGGATCAGCAAGC 3' R:5' GGGTGTAAACGCAGCTAACAG 3'
443052	ACTB	XM_004018407.5	F:5' CACTGCCCCAGTCACATCAT 3' R:5' GGGCACTGTGGGGTAATTGA 3'
101112853	ALAS1	XM_004012836.4	F:5' AGCCTGTGACTGTCCATTCC 3' R:5' ACGTTACCTTCTCGGGCATT 3'
100270789	RPL19	XM_012178077.4	F:5' GTTGTGAAGGCCTACCTCCC 3' R:5' GCCAGTGGTCAAACACACAC 3'
101115719	CD41	XM_004012986.5	F:5' CGAGATGAGACCGACTTCCG 3' R:5' ATGTGGGTGTCTCCATGCAG 3'
105605819	ITGA2B	XM_042238593.1	F:5' AAAGCAGGTCATCAAGCCGA 3' R:5' CTTCTGGGTCAACAGCTTCCT 3'
101104174	CD156A-ADAM8	XM_042232717.1	F:5' GACAGCTATCTCTCCGTGGC 3' R:5' CTGGGGAAGAAGTGGCAGAG 3'
101103712	CXCR5	XM_004007264.5	T F:5' TGGGCTGGGAACTTTGTGT 3' R:5' CCAAGGGGACGCATCCTATC 3'
443328	CD8B	XM_012101941.4	F:5' AACTCATCTGTGCAGCCCTC 3' R:5' GCTCCAGGGAGTTGCATCTT 3'
101108034	CD5	XM_027957506.2	F:5' AGACATCAGCTGTGAAGCCC 3' R:5' CTCCTGCACGGTCAGCTTTA 3'
443396	GZMB-LIKE	NM_001009803.1	F:5' CTCCGGCCTAACTCTCTCCT 3' R:5' AAGAGGCCACCCCTTAGCTA 3'
443417	IFNG	NM_001009400.2	F:5' GAGCCCTGGACACCAACTAC 3' R:5' GTAGCCCTTGGGTTCTGTGAA 3'
	TGFB1		

4.3.3 Validation of the housekeeping genes and immune markers selected for the RT-qPCR using RNA isolated from a current inactivated vaccine trial

4.3.3.1 Propagation of *E. ruminantium*

The infection of Bovine Aorta endothelial cells (BA886) with the *E. ruminantium* Welgevonden isolate was done according to Zweygarth et al. (1997) and Tjale et al. (2018). The *E. ruminantium* Welgevonden isolate was originally collected on the Welgevonden farm in the Northern Transvaal (Limpopo province) in South Africa from an *A. hebraeum* male tick (Du Plessis, 1985). For the current study the *E. ruminantium* Welgevonden isolate used was kept in liquid nitrogen and stored in 500 µl sucrose-potassium phosphate glutamate medium (SPG) composed of 0.218 M sucrose, 3.8 mM KH₂PO₄, 7.1 mM K₂HPO₄, 4.9 mM C₅H₈NO₄K. The cells were grown in Dulbecco's modified eagle's medium/Ham's nutrient mixture: F12 containing L-glutamine, 15 mM HEPES and sodium bicarbonate (DME/F-12). The medium was further supplemented with 10% heat inactivated fetal bovine serum, 1.2 g/L sodium bicarbonate and 100 IU penicillin and 100 µg/ml streptomycin. The monolayer of the BA886 cells in 25 cm² or 75 cm² flasks were incubated at 37 °C with CO₂. The infective material used to inoculate the BA886 cells in the current study was *E. ruminantium* Welgevonden elementary bodies at passage 179. Cytopathic effect was observed after 6 days, and the elementary bodies were harvested from cells that were 90% infected and could be visualized with Rapi-Diff II stain. The elementary bodies were purified according to the method provided by CIRAD. Briefly, the cells were gently scraped, and the lysate transferred into a 50 ml Falcon tube and lysed by aspiration with a 25 G needle. The lysate is then centrifuge for 15 minutes at 1800 x g at 4°C. The supernatant was transferred to a PPCO Nalgene tube and centrifuge for 30 minutes at 20 000 x g at 4°C. The supernatant was discarded, and pellet (EB) resuspended with approximately 1 ml of physiological saline.

4.3.3.2 Preparation of the inactivated vaccine

Elementary bodies were inactivated for 24 hours at 4 °C with 0.1% sodium azide, and a 10 µl aliquot was collected before and after inactivation to test efficiency using the Live/Dead bacterial kit from Invitrogen. The Live/Dead bacterial kit from Invitrogen makes use of a combination of two nucleic acid stains, green fluorescent SYTO® 9 dye and red-fluorescent propidium iodide for viability determinations, and a calibrated suspension of microspheres for precise sample volume measurements. The samples were diluted 1:100 to 1:1000 in saline and 1 µl of each dye was added. The elementary body viability was assessed, and concentration determined after an incubation time of 15 minutes at 37 °C. Protein concentration was assessed using the BSA method using the Pierce™ BCA Protein Assay Kit according to the manufacturer's instruction. The protein was mixed 40:60 with the Montanide ISA 61VG (Seppic) adjuvant using an ULTRA-TURRAX® Tube Drive mixer.

4.3.3.3 Infection of ticks with *E. ruminantium* Welgevonden

Uninfected *A. hebraeum* nymphs from the naïve tick colony at the ARC-OVR, were infected by feeding uninfected *A. hebraeum* nymphs on sheep infected intravenously with *E. ruminantium* Welgevonden (Tjale et al., 2018). The nymphs were placed into an acaridarium where they moulted into adults. A portion of adult ticks were tested for the presence of *E. ruminantium* by pCS20 qPCR to approximate the infectivity of the ticks. Screening for *E. ruminantium* infection was performed on individual tick.

4.3.3.4 Animal trial and collection of samples

An animal trial was done at ARC-OVR, the trial consisted of four groups of 7 animals as outlined in table 4.3, Group 1 (G1), G2 and two control groups (G3 and G4). Group 1 and G2 were vaccinated subcutaneously with inactivated *E. ruminantium* Welgevonden vaccine. The animals were challenged 2 months after the second boost (G1) with 10 ticks experimentally infected with the *E. ruminantium* Welgevonden strain and were monitored

for onset of disease by measuring their temperatures daily and monitoring for typical heartwater symptoms. Once an animal has an increased temperature of 41.5 °C for about 2 days, it was treated with 100 (1 ml/10 kg) Terramycin® and considered dead.

Table 4.3: Animal groups for animal trial

Group number	Immunized with	No of animals	Challenged with
Group 1 (trial group)	2x with 100 µg inactivated <i>E. ruminantium</i> Welgevonden in adjuvant	7	Welgevonden infected ticks
Group 2 (trial group)	1x with 200 µg inactivated <i>E. ruminantium</i> Welgevonden in adjuvant	7	Welgevonden infected ticks
Group 3 (control group)	1x Adjuvant	7	Welgevonden infected ticks
Group 4 (control group)	None, Naive	7	Welgevonden infected ticks

4.3.3.5 Blood collection, RNA extraction

Whole blood samples for RT qPCR were collected from the animal trial on D0 (before vaccination); D1; D4 and D7 post vaccination (PV) and D10 post challenge (PC). Blood (10 ml) was collected in BD Vacutainer® EDTA tubes (Becton, Dickinson). A total of 1 mL blood was centrifuged at 1500 x g for 5 min and the plasma was removed. To reduce the volume of the cell pellet that should not exceed 25% of the total volume of Trizol added (i.e 250 µl if 1 ml Trizol is added), most of the remaining red blood cells were lysed by adding 1 ml 1x BD lyse buffer and incubated for 10 minutes at room temperature. The cells were pelleted at 1500 x g for 5 min. The supernatant was removed, and the remaining pellet were mixed with 750 µL Trizol and stored at -20 °C until processed according to the instructions of the manufacturer. After total RNA isolation, the genomic DNA was removed using a DNA-free kit (Ambion, Invitrogen) according to the instructions of the manufacturer and stored in 75% Ethanol at -20 °C or in Diethyl pyrocarbonate (DEPC) treated water at -70 °C until used for RT qPCR.

4.3.3.6 Validation of housekeeping genes

Three different statistical algorithms (Ct mean, CV of RPKM values and CT values and the Δ Ct method) were applied to estimate the expression stability of each housekeeping gene from the isolated RNA and an online tool, RefFinder was used to rank the identified housekeeping genes for RT qPCR data normalization (Schulze et al., 2017).

4.3.3.7 Reverse transcription quantitative real-time qPCR

Relative changes in gene expression of immune markers were measured by RT qPCR according to Livak and Schmittgen (2001). Each reaction was performed in a final volume of 20 μ l containing 1X QuantiTect SYBR Green RT PCR Mix, a final concentration 0.5 μ M of each primer (primers highlighted in table 4.3), 0.25 μ l QuantiTect RT mix, 1 μ l template RNA (pools) (see supplementary table 4.3 and 4.4 for how the pools for template RNA were achieved). The fold change at which it is considered that a gene is upregulated or downregulated is at least >1.5 and significant with the T-test.

4.4 Results

4.4.1 Identification of candidate housekeeping genes using transcriptome data

Based on Nefefe et al. (2017), the analysis of RPKM values revealed that there are a number of genes that are expressed at different expression levels with CANX and POLR2A having the highest levels of variation between the 24 data sets analysed as shown in the box-and-whisker plots indicating the range of normalized RPKM values calculated in CLC of the selected candidate reference genes (Figure 4.1). Fourteen housekeeping genes that had stable expression were determined using the CV method calculated by dividing the TPM average for each gene, by the standard deviation between all 24 data sets (table 4.5) were used for validation using the RNA extracted from samples obtained from the inactivated vaccine animal trial.

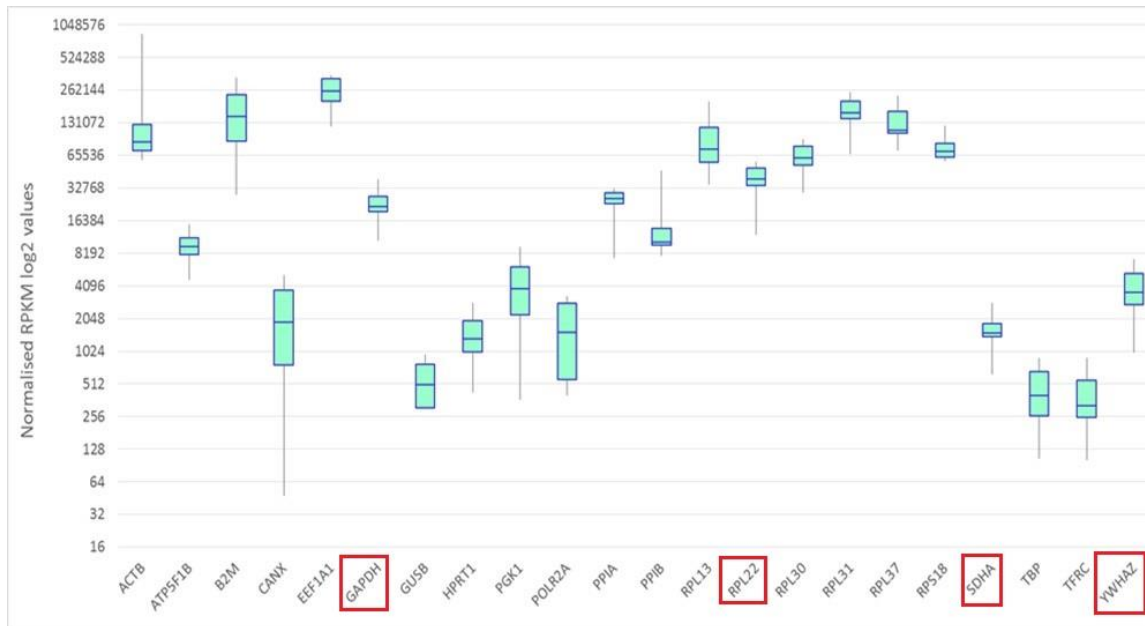


Figure 4.1. Box-and-whisker plots indicating the range of normalised RPKM values calculated in CLC of the selected candidate reference genes throughout *E. ruminantium* infection. The whiskers represent standard deviation of n samples (n = 24).

4.4.2 Selection of immune markers for protection

Using RNA-seq data from a previous study (Nefefe et al., 2017), potential genes differentially expressed were identified (Figure 4.2). For the RT qPCR, functional markers expressed on the surface of cells or cytokines produced by the cells were selected and the intracellular markers of transcription were excluded. The intracellular transcription factor regulation markers can be expressed by non-immune cells as well.

CD8B, CD5 and CXCR5 were also downregulated at D1PC in positive control animals. One of the reasons for this is that the cells are homing to the site of infection, although further analysis must be done at the infection sites to confirm this in future. CD8B and Granzyme B (GZMB) are markers specific to CD8⁺ T cells (cytotoxic T cells) while CD5 is expressed by most T cells and a subset of B cells. A subset of CD4⁺ T cells expressing CXCR5 is similar to Thf cells and exist in blood. Thf cells expressing the CXCR5 receptor

could activate B cells to produce antibodies. CD41 is expressed on blood platelets and the immune response induced by these cells in response to heartwater infection has not been investigated since most assays used purified PBMCs and not whole blood. CD156A is expressed on antigen presenting cells and could suggest that the *E. ruminantium* is processed and assimilated. IFN- γ was included even though it was expressed at all time points since it has long been considered a biomarker for protection.

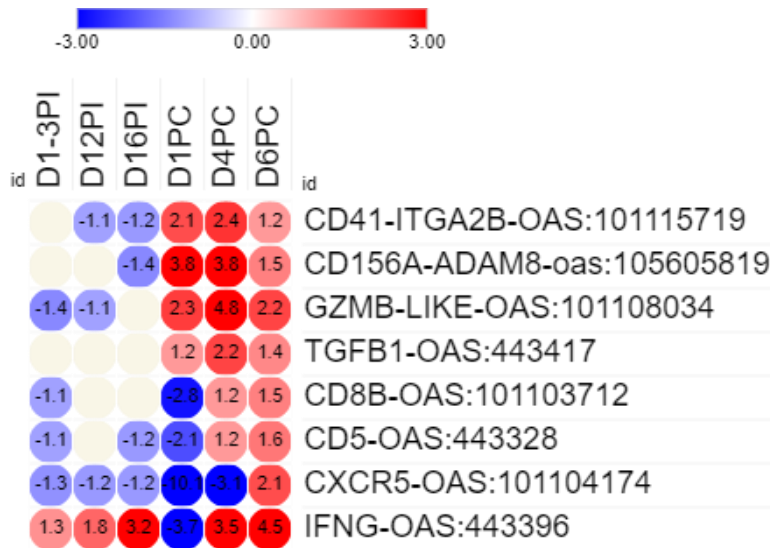


Figure 4.2: Markers selected that were upregulated in animals that survived heartwater challenge. This shows the heat map of markers that were upregulated at the post challenge time points (PC) but not during infection.

4.4.3 Animal trial

All the animals were treated except one sheep (nr 15), in group 2. It was observed that some of the animals in G1 (sheep 5, 9 and 10) and sheep 18 in G2 had less severe symptoms and survived on average longer than the rest of the animals (29-35 days) while the controls were treated within 26 days. These animals also recovered faster than the control group animals after antibiotic treatment. Similar results were obtained between the group of animals that were boosted and the group receiving a single shot.



Figure 4.3: Survival plot of animals in group 1, 2, 3, and 4

4.4.4 qPCR validation of housekeeping genes to use using total RNA samples collected during animal trial

Total RNA was isolated from whole blood collected D0; D1; D4 and D7PV and D10PC as described above (animal trial), and using the survival outcome results from the trial, the RNA samples were pooled as described in table 4.4 to determine the best housekeeping genes to include in the final assay using Ct, STDEV, CV and the delta Ct methods to rank the housekeeping genes in a pairwise comparison.

Table 4.4 Animal groups for the animal trial pooled for qPCR screening.

Group number	Immunized with		Time points and pools			
			D0	D1PV	D7PV	D10PC
Group 1	2x with 100 µg Welgevonden, adjuvant	Lived longer [Sheep 4, 5, 9 and 10]	Pool 1	Pool 2	Pool 3	Pool 4
		Treated [Sheep 6, 7, 11]	Pool 5	Pool 6	Pool 7	Pool 8
Group 2	1x with 200 µg Welgevonden, adjuvant	Lived longer [Sheep 15 and 18]	Pool 9	Pool 10	Pool 11	Pool 12
		Treated [12, 13, 14, 16 and 17]	Pool 13	Pool 14	Pool 15	Pool 16
Group 3	1x Adjuvant	Treated [19, 20, 21, 22, 23, 25 and 26]	Pool 17	Pool 18	Pool 19	Pool 20

To test the expression stability of the 14 selected housekeeping genes, five pools were randomly selected for the qPCR and the methods above were done to determine the top 4 genes to be included in the final RT qPCR assay. After total RNA extraction was completed, the samples were suspended in 50 µl DEPC treated water and concentration determined using the Nano drop. For each group listed in table 4.2, 1 µg total RNA of each animal/group was pooled prior to the first qPCR screening. Only those that had a positive fold change in the group were further tested to determine if each individual animal reacted similarly. SDHA, RPL22, YWHAZ and GAPDH was detected at similar Ct points, had the most stable expression between samples (STDEV and CV methods) and the least variation with the Delta Ct method. The qPCR results thus also correlated with the transcriptome data sets where the CV were calculated based on the TPM values generated in CLC (Table 4.3).

According to the ranking of the selected housekeeping genes (table 4.5), it was identified that SDHA, RPL22, YWHAZ and GAPDH are the most suitable choice combination of housekeeping genes for normalization of RT qPCR results for mRNA-levels of target

markers. These four housekeeping genes showed the least expression variation throughout the experimental conditions at any given time point.

Table: 4.5: The ranking of the selected housekeeping genes

	Ct mean values	STDEV	Rank	CV Ct (stdev/av)	Rank	TPM CV	Rank	Delta CT mean SD	Rank	Overall	Rank
				(Determined the CV from the mean Ct and STEV in column one and two)		(Determined the CV from the mean TPM and STEV From original sequencing data)		Mean STDEV as determined by the Delta Ct method (next sheet) in a pairwise comparisson)		Combination of the four methods used to determine final ranking	
SDHA	13,836	0,13	1	0,10	1	0,31	4	1,6	3	2,3	1
RPL22	13,051	1,73	3	0,13	3	0,28	2	2,5	12	5,0	2
RPS18	14,635	2,31	8	0,22	8	0,17	1	1,3	1	4,5	3
YWHAZ	13,567	2,45	5	0,18	5	0,43	6	2,3	9	6,3	4
GAPDH	13,064	2,60	7	0,20	7	0,37	5	2,3	8	6,8	5
EEF1A1	14,987	6,39	12	0,43	12	0,31	3	1,5	2	7,3	6
ALAS1	15,246	1,83	2	0,12	2		12	2,6	13	7,3	7
B2M	23,567	3,93	4	0,17	4	0,53	8	2,6	14	7,5	8
TFRC	15,396	2,96	6	0,19	6	0,69	10	2,3	10	8,0	9
PGK1	14,845	3,43	9	0,23	9	0,56	9	2,1	7	8,5	10
ACTB	12,403	6,17	13	0,50	13	1,30	11	1,6	4	10,3	11
RPL19	13,613	4,03	11	0,30	11		14	1,9	5	10,3	12
HPRT1	18,026	10,67	14	0,59	14	0,52	7	2,1	6	10,3	13
EEF2	14,741	3,80	10	0,26	10		13	2,4	11	11,0	14

4.4.5 Expression levels of the selected markers for protection using RT-qPCR with the validated housekeeping genes using RNA from the animal trial

All the markers were upregulated at D1PV for all the pools except for animals that died in group G1 (pool [P] 6) and in group G3 (P18) where the animals were immunized with the adjuvant. However, at D7PV transcripts in P11 and P15 from animals in G2 that received one dose of vaccine were detected (table 4.6). CD41, Granzyme and IFN- γ were upregulated in the adjuvant only group at D7PV. At D10PC, upregulated transcripts for all genes were detected in P12 except CD5 and TGFB1, the animals that lived longer during the experimental tick challenge. Overall, significant differences in the expression of markers in vaccinated animals in comparison with the adjuvant only group were detected. The detection of these transcripts can be considered as indicative of immunological memory that was activated after vaccination and the expression patterns depended on the treatment that the animals received.

However, these selected markers were detected in both animals that survived and those that succumbed to infection. For instance, the expression of the CD156A marker was detected in 4 of the 6 pools that represents G2 and was upregulated in both animals that survived and those that died. Similarly, IFN- γ and GZMB at D7PV were upregulated for G2 animals that survived longer (pool 10) and that died (pool 15). Both markers were also upregulated at D7PV in the adjuvant only animal group that were severely infected and required treatment.

Marker TGFB1 was downregulated at all time points in G3 (adjuvant only) and upregulated in vaccinated animals in pools 2, 8, 10 14 and 15.

IFN- γ was upregulated at D1PV or D7PV for all animal groups including the control animal group (adjuvant only). The expression of IFN- γ decreased at D7PV for animal G1 but were increased in pool 15 and the control animal group (P19). However, at D10PC, IFN- γ was downregulated in animal G1, but upregulated in both animals that survived and those that died in G2.

Table 4.6: $2^{-\Delta\Delta CT}$ to analyze the significant relative fold changes in gene expression of the immune markers.

Fold change (the shading indicate upregulation that is statistically significant)

Gene (transcript)	G1: 2x 100 µg Inactivated Welgevonden vaccine						G2: 1x 200 µg Inactivated Welgevonden vaccine						G3: 1x Adjuvant		
	Lived longer			Died			Lived longer			Died			Died		
	D1PV	D7PV	D10PC	D1PV	D7PV	D10PC	D1PV	D7PV	D10PC	D1PV	D7PV	D10PC	D1PV	D7PV	D10PC
	P2	P3	P4	P6	P7	P8	P10	P11	P12	P14	P15	P16	P18	P19	P20
CD41	10.6	0.6	0.4	0.0	0.0	0.0	1.4	0.5	94.0	1.3	14.9	0.3	0.0	3.2	3.0
CD156A	5.7	0.8	0.2	0.2	0.0	0.1	2.6	1.0	3.7	9.2	26.0	0.6	0.0	0.3	1.2
CXCR5	5.2	0.5	0.1	0.2	0.1	0.1	2.5	0.9	33.4	6.7	14.7	6.4	0.1	0.8	0.0
CD8B	3.0	0.8	0.2	0.1	0.0	0.1	2.7	1.0	7.3	5.8	15.5	1.5	0.0	0.0	0.0
CD5	1.7	0.3	0.2	0.7	0.4	0.7	2.5	0.9	0.2	2.2	4.1	1.7	0.1	0.6	0.0
GZMB	7.0	0.6	0.5	0.0	0.0	0.1	10.4	3.9	171.8	0.8	21.6	3.2	0.1	1.6	0.0
IFNG	14.0	0.5	0.3	0.0	0.0	0.0	4.7	10.0	108.0	0.0	18.2	0.0	0.1	8.2	0.0
TGFB1	2.9	1.2	1.2	0.0	0.0	107.3	1.9	0.7	0.0	15.7	3.0	1.8	0.0	0.0	0.0

4.5 Discussion

When investigating a specific experimental model, it is important to validate the expression of housekeeping genes to obtain reproducible and reliable results for relative quantification of mRNA-levels in target genes of interest (Kozera and Rapacz, 2013). A housekeeping gene should have a similar expression in all tissues and experimental conditions (Garrido et al., 2020). Prediction using RPKM values correlated with the stability detected using the delta CT method after RT-qPCR for the markers selected for use in the RT qPCR assay. Therefore, RNA-seq can be used to select housekeeping genes.

The markers selected for use in the RT qPCR assay were based on data from animals that were immunized by infection and treatment; the markers were only detected after a subsequent challenge and not during the initial infection (Nefefe et al., 2017). However, these were regarded as markers for protection of sheep with immunity acquired after natural *E. ruminantium* infection transmitted by ticks after treatment. In the present inactivated heartwater vaccine trial, these markers were also upregulated in at least one of the two time-points after vaccination of sheep and these were downregulated at the same time points in the adjuvant only group except for CD41, IFN- γ and GZMB at D7PV. In the present inactivated vaccine trial, these markers were also up regulated after vaccination of sheep. In contrast, these markers were down regulated both post vaccination and post challenge in the adjuvant only negative control group (except for CD41, IFN- γ and GZMB at D7PV and CD41 at D10PC), thus confirming that these markers are not detected during primary infection of heartwater in naïve animals.

However, if these markers were to be used to predict if animals will be protected from heartwater after vaccination, the prediction will be dependent on the time point of sample collection. In G1 animals, a difference in expression could only be seen at D1PV where upregulated genes were detected in animals that lived longer but not in animals that died.

The fact that these genes were not upregulated after challenge may indicate that despite living longer, sufficient memory and adaptive immune responses were not activated. PC and these animals would not survive. In G2, all animals reacted at some point PV, but only the animals that survived/lived longer had a high response at D10PC (P12) as well, and perhaps the detection of these transcripts (except CD5 and TGFB1) after challenge can be used to predict if an animal will survive the challenge or not. None of the selected markers could predict protection after vaccination and new or additional markers that will be an early indication of protection PV will have to be selected in future using transcriptome studies.

In addition to the primary role as regulators of haemostasis and thrombosis, platelets have been found to play an important role in both innate and adaptive immune responses (Ali et al., 2015). Among other cells, platelets are the first cells to detect endothelial injury and invasion of pathogens to the bloodstream or tissue through their receptors resulting in platelet activation. Once a pathogen successfully invades the host, chemokines and cytokines are secreted by activated platelets and direct lymphocytes, neutrophils and monocytes to site of inflammation (Portier and Campbell, 2021). The chemokines and cytokines target the pathogen, preventing the infection from spreading. Expression of platelets due to heartwater infection has not been previously reported and in the current study, CD41 was upregulated D1PV. However, its expression decreased on D7PV and D10PC in G1 animals. The first exposure to antigen could elicit a radical immune response hence the high expression of the markers at D1PV in G1 animals after the second boost.

A fluctuation in the expression of CD156A between D7PV and D10PC was observed between immunized animal group 1 and 2. CD156A is expressed on antigen presenting cells and may be indicative of *E. ruminantium* antigen uptake. Also, the marker is expressed in neutrophils which are first responders to invaders and produce antimicrobial enzymes that attack the pathogen. When the antigen is introduced for the first time to the

host, the attack on the antigen is expected to be high hence the high level of expression of the marker at D1PV in G1. However, at D10PC the expression of the marker decreased.

CXCR5 is a receptor for the chemokine CXCL13 that is expressed in lymphatic tissues, such as follicles in lymph nodes as well as in spleen. The CXCR5 is expressed in mature B lymphocytes and by a CD4 T helper cell subset, T follicular B helper T cells (T_{FH}) (Chevalier et al., 2011). CXCR5 is essential for directing B cells to lymphoid tissues and in humoral response (Han, 2014). *Ehrlichia ruminantium* in mammalian host replicate first within the regional lymph nodes and is found in spleen of infected animals. The upregulation of CXCR5 in P2, P10 and P12-15 in the animal experiment could be the result of activation of immune cells in the lymph nodes and spleen to fight the infection.

CD8B and Granzyme B (GZMB) are markers specific to CD8⁺ T cells (cytotoxic T cells) that induce lysis of their target. The current study observed that both markers are expressed in both severely infected and protected animals. However, for the negative control group the markers were hardly expressed. IFN- γ been regarded as an immune marker for protection. The current study shows that it is expressed in both severely infected and treated animals. More data is needed to certify IFN- γ as a biomarker for protection in heartwater infection. Though some animals lived longer than other animals, post tick challenge all animals showed heartwater symptoms and were treated except for S15.

4.6 Conclusion

The housekeeping genes were selected and validated for the purpose of developing a RT qPCR to relatively quantify changes in gene expression of immune markers for protection. The RT qPCR assay was developed to evaluate a multivalent inactivated vaccine against heartwater. The assay was successfully developed and can be validated.

Using a total dosage of 200 μg antigen, the vaccine did not protect the animals against heartwater. The expression levels of the immune markers for protection did not indicate the protective immunity against the disease post vaccination. More research on optimizing antigen dosage is required to comprehend the protective immunity against heartwater. Additional markers that indicate protection post-immunization must be identified and a larger pool of animals that survived challenge need to be included in the analysis.

4.7 References

- ALI, R. A., WUESCHER, L. M. & WORTH, R. G. 2015. Platelets: essential components of the immune system. *Current Trends in Immunology*, 16, 65-78.
- BEZUIDENHOUT, J. D. 2009. Heartwater: an abridged historical account. *Journal of the South African Veterinary Association*, 80, 208-9.
- BYROM, B., OBWOLO, M., BARBET, A. F. & MAHAN, S. M. 2000. A polarized Th1 type immune response to *Cowdria ruminantium* infection is detected in immune DBA/2 mice *The Journal of Parasitology*, 86, 983-992.
- CHEVALIER, N., JARROSSAY, D., HO, E., AVERY, D. T., MA, C. S., YU, D., SALLUSTO, F., TANGYE, S. G. & MACKAY, C. R. 2011. CXCR5 expressing human central memory CD4 T cells and their relevance for humoral immune responses. *Journal of Immunology*, 186, 5556–5568.
- DU PLESSIS, J. L. 1985. A method for determining the *Cowdria ruminantium* infection rate of *Amblyomma hebraeum*: effects in mice injected with tick homogenates. *Onderstepoort Journal of Veterinary Research*, 52, 55-61.
- DU PLESSIS, J. L., BERCHE, P. & VAN GAS, L. 1991. T cell-mediated immunity to *Cowdria ruminantium* in mice: the protective role of Lyt-2+ T cells. *Onderstepoort Journal of Veterinary Research*, 58, 171-9.
- ESTEVEZ, I., VACHIÉRY, N., MARTINEZ, D. & TOTTE, P. 2004a. Analysis of *Ehrlichia ruminantium*-specific T1/T2 responses during vaccination with a protective killed vaccine and challenge of goats. *Parasite Immunology*, 26, 95-103.
- GARRIDO, J., AGUILAR, M. & PRIETO, P. 2020. Identification and validation of reference genes for RT-qPCR normalization in wheat meiosis. *Scientific Reports*, 10.
- HAN, X. 2014. Constitutively Active Chemokine CXC Receptors. In: TAO, Y. (ed.) *Pharmacology and Therapeutics of Constitutively Active Receptors*. United States of America: © Academic Press 2014.
- JONGEJAN, F. 1991a. Protective immunity to heartwater (*Cowdria ruminantium* infection) is acquired after vaccination with *in vitro*-attenuated rickettsiae. *Infection and Immunity*, 59, 729-31.

- KOZERA, B. & AND RAPACZ, M. 2013. Reference genes in real-time PCR. *Journal of Applied Genetics*, 54, 391-406.
- LIVAK, K. J. & SCHMITTGEN, T. D. 2001. Analysis of Relative Gene Expression Data Using RealTime Quantitative PCR and the 22DDCT Method. *Methods*, 25, 402-408.
- LLIBRE, A. & DUFFY, D. 2018. Immune response biomarkers in human and veterinary research. *Comparative Immunology, Microbiology and Infectious Diseases*, 59, 57-62.
- MAHAN, S. M., ANDREW, H. R., TEBELE, N., BURRIDGE, M. J. & BARBET, A. F. 1995b. Immunisation of sheep against heartwater with inactivated *Cowdria ruminantium*. *Research in Veterinary Science*, 58, 46-9.
- MAHAN, S. M., WAGHELA, S. D., MCGUIRE, T. C., RURANGIRWA, F. R., WASSINK, L. A. & BARBET, A. F. 1992. A cloned DNA probe for *Cowdria ruminantium* hybridizes with eight heartwater strains and detects infected sheep. *Journal of Clinical Microbiology*, 30, 981-6.
- MARTINEZ, D., MAILLARD, J. C., COISNE, S., SHEIKBOUDOU, C. & BENSALD, A. 1994. Protection of goats against heartwater acquired by immunisation with inactivated elementary bodies of *Cowdria ruminantium*. *Veterinary Immunology and Immunopathology*, 41, 153-163.
- MELTZER, M. I., PERRY, B. D. & DONACHIE, P. L. 1996. Mortality percentages related to heartwater and the economic impact of heartwater disease on large-scale commercial farms in Zimbabwe. *Preventive Veterinary Medicine*, 26, 187-199.
- MWANGI, D. M., MAHAN, S. M., NYANJUI, J. K., TARACHA, E. L. & MCKEEVER, D. J. 1998. Immunization of cattle by infection with *Cowdria ruminantium* elicits T lymphocytes that recognize autologous, infected endothelial cells and monocytes. *Infection and immunity*, 66, 1855-1860.
- NEFEFE, T., LIEBENBERG, J., VAN KLEEF, M., STEYN, H. C. & PRETORIUS, A. 2017. Innate immune transcriptomic evaluation of PBMC isolated from sheep after infection with *Eruminantium. ruminantium* Welgevonden strain. *Molecular Immunology*, 91, 238-248.

- PORTIER, I. & CAMPBELL, R. A. 2021. Role of Platelets in Detection and Regulation of Infection. *Arteriosclerosis, Thrombosis, and Vascular Biology*, 41, 70-78
- SCHULZE, F., MALHAN, D., KHASSAWNA, T. E. I., HEISS, C., SECKINGER, A., HOSE, D. & RÖSEN-WOLFF, A. 2017. A tissue-based approach to selection of reference genes for quantitative real-time PCR in a sheep osteoporosis model. *BioMed Central Genomics*, 18.
- SPICKLER, A. R. 2015. *Heartwater* [Online]. Available: <http://www.cfsph.iastate.edu/DiseaseInfo/factsheets.php> [Accessed 2022].
- STEWART, C. G. 1987. Specific immunity in farm animals to heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 341-2.
- STEYN, H. C., PRETORIUS, A., MCCRINDLE, C. M. E., STEINMANN, C. M. L. & VAN KLEEF, M. 2008. A quantitative real-time PCR assay for *Ehrlichia ruminantium* using pCS20. *Veterinary Microbiology*, 131, 258-265.
- TJALE, M. A., PRETORIUS, A., JOSEMANS, A., VAN KLEEF, M. & LIEBENBERG, J. 2018. Transcriptomic analysis of *Ehrlichia ruminantium* during the developmental stages in bovine and tick cell culture. *Ticks and Tick-Borne Diseases*, 9, 126-134.
- TOTTÉ, P., MCKEEVER, D., MARTINEZ, D. & BENSALD, A. 1997. Analysis of T-cell responses in cattle immunized against heartwater by vaccination with killed elementary bodies of *Cowdria ruminantium*. *Infection and Immunity*, 65, 236-41.
- ZWEYGARTH, E., VOGEL, S. W., JOSEMANS, A. I. & HORN, E. 1997. In vitro isolation and cultivation of *Cowdria ruminantium* under serum-free culture conditions. *Research in Veterinary Science*, 63, 161-4.

4.8 Supplementary data

Supplementary Table 4.1: Animal groups and individual animals combined to make RNA pools at different time points to be tested for immune markers

Group number	Immunized with		Time points and pools			
			D0	D1PV	D7PV	D10PC
Group 1A	2X 100 µg inactivated <i>E. ruminantium</i> Welgevonden in adjuvant	Lived longer [sheep 4, 5, 9 and 10]	Pool 1	Pool 2	Pool 3	Pool 4
Group 1B		Treated [sheep 6, 7, 11]	Pool 5	Pool 6	Pool 7	Pool 8
Group 2A	1X 200 µg inactivated <i>E. ruminantium</i> Welgevonden in adjuvant	Lived longer [15 and 18]	Pool 9	Pool 10	Pool 11	Pool 12
Group 2B		Treated [12, 13, 14, 16 and 17]	Pool 13	Pool 14	Pool 15	Pool 16
Group 3	1X Adjuvant	Treated [19, 20, 21, 22, 23, 25 and 26]	Pool 17	Pool 18	Pool 19	Pool 20

Supplementary Table 4.2: Sheep numbers with their RNA concentrations

Sheep no	D0 ng/µl	D1PI ng/µl	D7PI ng/µl	D10PC ng/µl
4	315.2	441.6	324.2	154.8
5	471.2	372.7	229.5	200.5
9	679.8	627.8	184.5	170.9
10	843.8	310.9	358.5	238.6
6	138.6	177.4	103.3	137.4
7	374.5	250.0	100.2	249.3
11	306.5	153.6	196.6	390.5
15	337.8	1043.8	500.3	504.8
18	284.9	225.6	866.0	279.1
12	174.0	NA	613.5	427.2
13	132.7	378.6	373.6	420.3
14	437.6	468.1	814.6	832.7
16	154.5	438.8	464.4	128.8
17	490.1	536.1	464.1	546.4
19	364.9	938.2	203.1	596.6
20	266.9	405.5	428.3	256.1
21	431.0	42.2	89.7	585.3
22	532.9	91.7	92.9	220.2
23	1414.2	54.0	107.6	183.2
25	608.6	89.4	302.6	455.4
26	610.0	49.0	388.0	426.1

NA: not available

Supplementary Table 4.3: Volume of RNA for each sheep needed to make the pools.

Sheep no	D0 μ l	D1PI μ l	D7PI μ l	D10PC μ l
4	3.17	2.26	3.08	6.45
5	2.12	2.68	4.35	4.98
9	1.47	1.59	5.42	5.85
10	1.18	3.21	2.78	4.19
6	7.21	5.63	9.68	7.27
7	2.67	4.00	9.98	4.01
11	3.26	6.51	5.08	2.56
15	2.96	0.95	1.99	1.98
18	3.51	4.43	1.15	3.58
12	5.74	NA	1.62	2.34
13	7.53	2.64	2.67	2.37
14	2.28	2.13	1.22	1.20
16	6.47	2.27	2.15	7.76
17	2.04	1.86	2.15	1.83
19	2.74	1.06	4.92	1.67
20	3.74	2.46	2.33	3.90
21	2.30	23.69	11.14	1.70
22	1.87	10.90	10.76	4.54
23	0.70	18.51	9.29	5.45
25	1.64	11.18	3.30	2.19
26	1.63	20.40	2.57	2.34

NA: not available

Total concentration must be 1000 ng in each pool

Example: Sheep 4 D0 RNA concentration is 315 ng/ μ l

315 ng in 1 μ l

1000 ng in X μ l

[315 ng] [X] = [1000 ng] [1 μ l]

X = [1000 ng] [1 μ l] / [315 ng]

X = 3.17 μ l

Supplementary Table 4.4: Volume of RNA, buffer and H₂O needed for making each pool

Sheep	D0	D1PI	D7PI	D10PC
4	Pool 1	Pool 2	Pool 3	Pool 4
5	7.94 µl RNA	9.74 µl RNA	15.63 µl RNA	21.47 µl RNA
9	5 µl buffer	5 µl buffer	5 µl buffer	5 µl buffer
10	37.06 µl H ₂ O	35.26 µl H ₂ O	29.37 µl H ₂ O	23.53 µl H ₂ O
6	Pool 5	Pool 6	Pool 7	Pool 8
7	13.14 µl RNA	16.14 µl	24.74 µl RNA	13.84 µl RNA
11	5 µl buffer	5 µl buffer	5 µl buffer	5 µl buffer
	31.86 µl H ₂ O	28.86 µl H ₂ O	20.26 µl H ₂ O	31.16 µl H ₂ O
15	Pool 9	Pool 10	Pool 11	Pool 12
18	6.47 µl RNA	5.38 µl RNA	3.14 µl RNA	5.56 µl RNA
	5 µl buffer	5 µl buffer	5 µl buffer	5 µl buffer
	38.53 µl H ₂ O	39.61 µl H ₂ O	41.86 µl H ₂ O	39.44 µl H ₂ O
12	Pool 13	Pool 14	Pool 15	Pool 16
13	24.06 µl RNA	8.9 µl RNA	9.81 µl RNA	15.5 µl RNA
14	5 µl buffer	5 µl buffer	5 µl buffer	5 µl buffer
16	20.94 µl H ₂ O	36.1 µl H ₂ O	35.19 µl H ₂ O	29.5 µl H ₂ O
17				
19	Pool 17	Pool 18	Pool 19	Pool 20
20	14.62 µl RNA	88.2/2 =44,1 µl	44.31 µl RNA	27.31 µl RNA
21	5 µl buffer	RNA (pool split)	5 µl buffer	5 µl buffer
22	30.38 µl H ₂ O	5 µl buffer	0.7 µl H ₂ O	17.69 µl H ₂ O
23		0.9 µl H ₂ O		
25				
26				

Chapter 5

General Discussion, Recommendations and Conclusion

Heartwater, a disease caused by *E. ruminantium* in some wild and domestic ruminants still poses a threat to farmers even many centuries after its discovery. The heartwater causing agent, *E. ruminantium* has diverse immunogenicity and evidence of the occurrence of recombination between strains resulting in new strains has been reported (Allsopp and Allsopp, 2007, Cangi et al., 2016). The only vaccine currently in use is made up of a live Ball3 strain in sheep blood and employs the infection and treatment method (Van der Merwe, 1987). This vaccination method is laborious and limiting to some rural small holder farmers as the vaccine requires cold chain storage. Also, the vaccine lacks cross protection against some virulent and field isolates (Allsopp, 2010). An inactivated vaccine with broad protective ability is of importance. Some requirements for developing an effective vaccine are to isolate field strains in *in vitro* culture to provide the antigen required for the vaccine, and to genetically characterize the isolates to determine the possibility of their use in an inactivated cocktail vaccine. Then, the vaccine can be developed and tested.

MLST is a useful tool to use for genotypic characterization of *E. ruminantium* as it reveals genetic diversity among tested field isolates (Adakal et al., 2009). The MLST method has been extensively explored using different structural genes (Adakal et al., 2010, Nakao et al., 2011). The success of the method is not limited to the genotypic characterization of *E. ruminantium* but other pathogens such as *Neisseria meningitidis* and “*Candidatus Neoehrlichia mikurensis*”, a tickborne agent of neoehrlichiosis (Jolley et al., 2000, Grankvist et al., 2015).

In the current study, the isolates were successfully genetically characterized by MLST. Genetic diversity in the sequenced regions was informed by SNPs observed. The same observations were reported by Allsopp et al. (2003) and Adakal et al. (2009). An obvious observation is distinction of West African isolates from other geographic isolates (Cangi et al., 2016). Based on the regularly observed distinction of West African isolates, it is pivotal to genotype circulating field isolates in West Africa using different genes to determine if the distinction remains. Additionally, researchers must investigate the phenotypic features of the West Africa isolates for the purpose of cross protection against the diverse southern Africa isolates.

MLST is based on structural genes and does not inform virulence or immunogenicity of isolates. A gene that could be used to extrapolate phenotypic features of isolates and was used as a DNA vaccine that elicited protective immunity in mice is *map1* (Nyika et al., 2002). The use of the gene to genetically characterize diversity of *E. ruminantium* isolates has been reported (Ralinaiaina et al., 2010). However, *map1* gene is highly polymorphic which presents a challenge for designing primers that can detect all genotypes (Allsopp et al., 2001). The polymorphic nature of *map1* gene disqualifies it as a candidate for genotypic characterization. It is evident that there is a need for extensive research to ascertain characterization genes that can reveal phenotypic features of *E. ruminantium* isolates, such as immunogenicity and virulence. That will alleviate the persistent challenges of determining best vaccine isolates and establish improved treatment protocols.

If a genotypic characterization method that inform virulence and immunogenicity of isolates could be developed, it would be beneficial if these *E. ruminantium* isolates could be propagated *in vitro* using salivary glands and gut from ticks directly from the field. The conventional method of isolating *E. ruminantium* involves the use of blood stabilate and other infected cell lines as inoculum (Bell-Sakyi et al., 2000, Logan et al., 1987). Isolating

E. ruminantium from tick material compared to using blood would be cost effective, less time consuming since there is no need for infecting live animals and waiting for incubation period of the disease and considers the welfare of animals as it eliminates the use of blood donor animals. Although *in vitro* isolation of *E. ruminantium* from tick material has potential for successful application, the culture system needs to be optimized. The system is not feasible when large sample size is required. DNA from tick is attained by cutting two tick legs close to the body of tick to get the hemolymph and that requires precision, ticks must be kept alive while testing for *E. ruminantium* positivity.

It is recommended that a smaller sample size be used, and both antifungal and antibiotics are included in the culture medium. Also, observing the cultures for more than 30 days without any contamination can be considered to conclusively decide a negative result as ticks could have low copy number of *E. ruminantium*. Furthermore, it could be of interest to test the contamination in the cultures so that when cell culture is repeated an antimicrobial drug effective against that specific contaminating agent is included in the culture medium.

For subsequent propagation of vaccine isolates and development of vaccine, methods to determine success of the vaccine must be considered. In this study, an animal trial was conducted to test the effectiveness of the developed inactivated vaccine using a total of 200 µg of antigen to immunize sheep. Moreover, a RT qPCR to relatively quantify changes in gene expression of immune markers for protection was developed. The results showed conclusively that immunization with the antigen at the dose of 200 µg did not protect sheep against a homologous tick challenge as all sheep except one sheep were treated with antibiotic post challenge. The immune markers for protection were differentially expressed throughout the experiment and upregulation of the markers did not correlate to protection as both experimental and control group animals died.

It is recommended that more research to determine optimum dosage of the vaccine be conducted before concluding that the vaccine does not offer protective immunity. Also, additional immune markers should be included and tested for any developed heartwater vaccine. The above-mentioned recommendations could be a breakthrough to understanding specific protective immunity against heartwater.

In conclusion, the study showed genetic diversity among *E. ruminantium* field isolates from ticks collected from cattle in three provinces of South Africa. The RT qPCR assay developed to evaluate a multivalent inactivated vaccine against heartwater can be validated and applied in further studies. Also, there is a need for alternate genotypic genes that reveal immunogenicity of isolates and optimization of *E. ruminantium in vitro* culture systems, using tick salivary gland and gut as inoculum is of paramount importance to be able to establish a pan-African biobank of *E. ruminantium* isolates.

5.1 References

- ADAKAL, H., GAVOTTE, L., STACHURSKI, F., KONKOBO, M., HENRI, H., ZOUNGRANA, S., HUBER, K., VACHIERY, N., MARTINEZ, D., MORAND, S. & FRUTOS, R. 2010. Clonal origin of emerging populations of *Ehrlichia ruminantium* in Burkina Faso. *Infection, Genetics and Evolution*, 10, 903-912.
- ADAKAL, H., MEYER, D. F., CARASCO-LACOMBE, C., PINARELLO, V., ALLÈGRE, F., HUBER, K., STACHURSKI, F., MORAND, S., MARTINEZ, D., LEFRANÇOIS, T., VACHIERY, N. & FRUTOS, R. 2009. MLST scheme of *Ehrlichia ruminantium*: Genomic stasis and recombination in strains from Burkina-Faso. *Infection, Genetics and Evolution*, 9, 1320-1328.
- ALLSOPP, B. A. 2010. Natural history of *Ehrlichia ruminantium*. *Veterinary Parasitology*, 167, 123-135.
- ALLSOPP, M. T. E. P. & ALLSOPP, B. A. 2007. Extensive genetic recombination occurs in the field between different genotypes of *Ehrlichia ruminantium*. *Veterinary Microbiology*, 124, 58-65.
- ALLSOPP, M. T. E. P., DORFLING, C. M., MAILLARD, J. C., BENSALD, A., HAYDON, D. T., VAN HEERDEN, H. & ALLSOPP, B. A. 2001. *Ehrlichia ruminantium* Major Antigenic Protein Gene (*map1*) Variants Are Not Geographically Constrained and Show No Evidence of Having Evolved under Positive Selection Pressure. *Journal of Clinical Microbiology*, 39, 4200-4203.
- ALLSOPP, M. T. E. P., VAN HEERDEN, H., STEYN, H. C. & ALLSOPP, B. A. 2003. Phylogenetic Relationships among *Ehrlichia ruminantium* Isolates. *Annals of the New York Academy of Sciences*, 990, 685-691.
- BELL-SAKYI, L., PAXTON, E. A., MUNDERLOH, U. G. & SUMPTION, K. J. 2000. Growth of *Cowdria ruminantium*, the causative agent of heartwater, in a tick cell line. *Journal of Clinical Microbiology*, 38, 1238-40.
- CANGI, N., GORDON, J. L., BOURNEZ, L., PINARELLO, V., APRELON, R., HUBER, K., LEFRANÇOIS, T., NEVES, L., MEYER, D. F. & VACHIÉRY, N. 2016. Recombination Is a Major Driving Force of Genetic Diversity in the

- Anaplasmataceae *Ehrlichia ruminantium*. *Frontiers in Cellular and Infection Microbiology*, 6.
- GRANKVIST, A., MOORE, E. R. B., SVENSSON STADLER, L., PEKOVA, S., BOGDAN, C., GEIßDÖRFER, W., GRIP-LINDÉN, J., BRANDSTRÖM, K., MARSAL, J., ANDRÉASSON, K., LEWERIN, C., WELINDER-OLSSON, C. & WENNERÅS, C. 2015. Multilocus sequence analysis of clinical “Candidatus Neoehrlichia mikurensis” strains from Europe. *Journal of Clinical Microbiology*, 53, 3126-3132.
- JOLLEY, K. A., KALMUSOVA, J., FEIL, E. J., GUPTA, S., MUSILEK, M., KRIZ, P. & MAIDEN, M. C. J. 2000. Carried Meningococci in the Czech Republic: a Diverse Recombining Population. *Journal of Clinical Microbiology*, 38, 4492-4498.
- LOGAN, L. L., WHYARD, T. C., QUINTERO, J. C. & MEBUS, C. A. 1987. The development of *Cowdria ruminantium* in neutrophils. *Onderstepoort Journal of Veterinary Research*, 54, 197-204.
- NAKAO, R., MAGONA, J. W., ZHOU, L., JONGEJAN, F. & SUGIMOTO, C. 2011. Multi-locus sequence typing of *Ehrlichia ruminantium* strains from geographically diverse origins and collected in *Amblyomma variegatum* from Uganda. *Parasites & Vectors*, 4, 137.
- NYIKA, A., BARBET, A. F., BURRIDGE, M. J. & MAHAN, S. M. 2002. DNA vaccination with map1 gene followed by protein boost augments protection against challenge with *Cowdria ruminantium*, the agent of heartwater. *Vaccine*, 20, 1215-1225.
- RALINIAINA, M., MEYER, D. F., PINARELLO, V., SHEIKBOUDOU, C., EMBOULÉ, L., KANDASSAMY, Y., ADAKAL, H., STACHURSKI, F., MARTINEZ, D., LEFRANÇOIS, T. & VACHIÉRY, N. 2010. Mining the genetic diversity of *Ehrlichia ruminantium* using map genes family. *Veterinary Parasitology*, 167, 187-195.
- VAN DER MERWE, L. 1987. The infection and treatment method of vaccination against heartwater. *Onderstepoort Journal of Veterinary Research*, 54, 489-91.

Appendices

Appendix 1

CLUSTAL multiple sequence alignment of concatenated nucleotide sequences of housekeeping genes (*sodB*, *secY*, *lipB*, and *lipA*) partial sequences. The asterisk at the end of the alignment represent a conserved region.

```

E67      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W47      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
U66      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W36      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Welg     TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Ball3    TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Blaauw   TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Kwany    TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Nonile   TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
SBF4     TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
SBF7     TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
UmBanein TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Mara     TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Gardel   TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTAGAGG-GTATTGCTAATAAG
Senegal  TACCTTATGATAAAGCTATGTGTTTTATGCAACAGAGGGTAGAGG-GTATTGCTAATAAG
Sankat   TACCTTATGATAAAGCTATGTGTTTTATGCAACAGAGGGTAGAGG-GTATTGCTAATAAG
L52      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
U11      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
U89      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W25      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W102     TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W26      TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W54      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
L60      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
L53      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
W91      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
Kumm2    TACCTTATGAGCAGGCTGTAAGTTTGATGCAACAAAGAGTAGAGG-GTATAGCTAGTAAG
River    TACCTTATGAGCAGGCTGTAAGTTTGATGCAACAAAGAGTAGAGG-GTATAGCTAGTAAG
Omatjenne TACCTTATGAGCAGGCTGTAAGTTTGATGCAACAAAGAGTAGAGG-GTATAGCTAGTAAG
C25      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C38      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C49      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C52      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C69      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C87      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C97      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C98      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I34      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I55      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I56      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I70      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I77      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I81      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
M3       TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
M11      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
M19      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
M22      TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
  
```

M56 TACCTTATGATAAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C14 TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
C57 TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
I72 TACCTTATGATGAAGCTATGTGTTTTATGCAACAAAGGGTCGAGG-GTATTGCTAATAAG
***** * ** * ***** ** * ** * ** * ** * ** *

E67 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W47 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
U66 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W36 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Welg ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Ball3 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Blaauw ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Kwany ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Nonile ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
SBF4 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
SBF7 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
UmBanein ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Mara ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Gardel ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Senegal ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCATTATATACAGCTGGTACTAGT
Sankat ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCATTATATACAGCTGGTACTAGT
L52 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
U11 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
U89 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W25 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W102 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W26 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W54 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCATTATATACAGCTGGTACTAGT
L60 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
L53 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
W91 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
Kumm2 TTGCAGGATGAGCTAGTGTGGTTGCTTGAACATTTTCCATTGTATACAGCTGGTACTAGT
River TTGCAGGATGAGCTAGTGTGGTTGCTTGAACATTTTCCATTGTATACAGCTGGTACTAGT
Omatjenne TTGCAGGATGAGCTAGTGTGGTTGCTTGAACATTTTCCATTGTATACAGCTGGTACTAGT
C25 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C38 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C49 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C52 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C69 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C87 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C97 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C98 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I34 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I55 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I56 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I70 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I77 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I81 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
M3 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
M11 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
M19 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
M22 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
M56 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C14 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
C57 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
I72 ACACAAGATGAACTAGTATGGTTACTTGAACATTTTCCGTTATATACGGCTGGTACTAGT
** ***** ***** ***** ***** ***** ***** ***** *****

E67 GCAAGGAGTGAGGAATTACTAACCGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
W47 GCAAGGAGTGAGGAATTACTAACCGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
U66 GCAAGGAGTGAGGAATTACTAACCGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
W36 GCAAGGAGTGAGGAATTACTAACCGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT

Welg	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
Ball3	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
Blaauw	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
Kwany	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
Nonile	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
SBF4	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
SBF7	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
UmBanein	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
Mara	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
Gardel	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
Senegal	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTATATATTCTACAGGTAGAGGT
Sankat	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTATATATTCTACAGGTAGAGGT
L52	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
U11	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
U89	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
W25	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
W102	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
W26	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
W54	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
L60	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
L53	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
W91	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
Kumm2	GCAAAAAGGTGAAGAGTTATTAAGTATAGTTTATTTCCCTGTATATACTACAGGTAGGGGT
River	GCAAAAAGGTGAAGAGTTATTAAGTATAGTTTATTTCCCTGTATATACTACAGGTAGGGGT
Omatjenne	GCAAAAAGGTGAAGAGTTATTAAGTATAGTTTATTTCCCTGTATATACTACAGGTAGGGGT
C25	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
C38	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C49	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C52	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C69	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C87	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C97	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
C98	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I34	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I55	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I56	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I70	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I77	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I81	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
M3	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
M11	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
M19	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
M22	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
M56	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTATTTCCCTGTATATTCTACAGGTAGAGGT
C14	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
C57	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
I72	GCAAGGAGTGAGGAATTACTAACCAGATAGTTTGTTCCTGTGTATTCTACAGGTAGAGGT
	***** ** ** ** * ** ** * ** ** * ** ** * ** ** *
E67	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
W47	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
U66	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
W36	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Welg	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Ball3	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Blaauw	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Kwany	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Nonile	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
SBF4	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
SBF7	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
UmBanein	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Mara	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA
Gardel	GGTAAATACACTTATCATGGTCCTGGTCAAAGAATTGCTTATGTGATGATGGATTTAAAA

L53 GCAAGAGATAAATGTAATGTTAGGTTGTATATTGAAACTTTGGGTGAGTGGATTGTTAAA
W91 GCAAGAGATAAATGTAATGTTAGGTTGTATATTGAAACTTTGGGTGAGTGGATTGTTAAA
Kumm2 GTAAGAAATATATGTAATGTTAAATTATATATTGAGAGTTTGGGGAAATGGATTGTTGAA
River GTAAGAAATATATGTAATGTTAAATTATATATTGAGAGTTTGGGGAAATGGATTGTTGAA
Omatjenne GTAAGAAATATATGTAATGTTAAATTATATATTGAGAGTTTGGGGAAATGGATTGTTGAA
C25 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C38 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C49 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C52 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C69 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C87 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C97 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C98 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I34 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I55 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I56 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I70 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I77 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I81 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
M3 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
M11 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
M19 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
M22 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
M56 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C14 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
C57 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
I72 GCAAGAGATAAATGTAATGTTAGGTTGTATGTTGAAACTTTGGGTGAGTGGATTGTTAAA
* **** * * ***** ** * * * * * * * * * * * * * * * * *

E67 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W47 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
U66 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W36 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Welg ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Ball3 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Blaauw ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Kwany ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Nonile ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
SBF4 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
SBF7 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
UmBanein ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Mara ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Gardel ACTTTAAACATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Senegal ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Sankat ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
L52 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
U11 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
U89 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W25 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W102 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W26 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W54 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
L60 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
L53 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
W91 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
Kumm2 ACATTGAAGCATTTTTCAATACAATCATATTTTAATCC-TAACTTAATAGGGG--TGTGG
River ACATTGAAGCATTTTTCAATACAATCATATTTTAATCC-TAACTTAATAGGGG--TGTGG
Omatjenne ACATTGAAGCATTTTTCAATACAATCATATTTTAATCC-TAACTTAATAGGGG--TGTGG
C25 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C38 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C49 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C52 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C69 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG

C87 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C97 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C98 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I34 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I55 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I56 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I70 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I77 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I81 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
M3 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
M11 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
M19 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
M22 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
M56 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C14 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
C57 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
I72 ACTTTAAAGCATTTTTCAATACGATCATATTTTAATCC-TAATTTAATAGGGG--TATGG
** ** * * * **

E67 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W47 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
U66 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W36 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Welg GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Ball3 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Blaauw GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Kwany GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Nonile GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
SBF4 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
SBF7 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
UmBanein GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Mara GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Gardel GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Senegal GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Sankat GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
L52 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
U11 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
U89 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W25 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W102 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W26 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W54 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
L60 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
L53 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
W91 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
Kumm2 ATAGACC-ATAATGGAGTTAAAGAAAAAAAAATTGCTGCATTGGTATTAGAATAAAAAAGAT
River ATAGACC-ATAATGGAGTTAAAGAAAAAAAAATTGCTGCATTGGTATTAGAATAAAAAAGAT
Omatjenne ATAGACC-ATAATGGAGTTAAAGAAAAAAAAATTGCTGCATTGGTATTAGAATAAAAAAGAT
C25 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C38 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C49 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C52 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C69 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C87 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C97 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
C98 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I34 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I55 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I56 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I70 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I77 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
I81 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT
M3 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTGGCATTAGAATAAAAAAGAT

M11 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
M19 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
M22 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
M56 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
C14 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
C57 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
I72 GTTAACC-ATAATGGTAGTGAAAAAAAAAATTGCTGCATTTGGCATTAGAATAAAAAAGAT
* ** * **** * ** * **** * **** * **** *

E67 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W47 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
U66 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W36 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Welg GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Ball3 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Blaauw GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Kwany GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Nonile GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
SBF4 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
SBF7 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
UmBanein GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Mara GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Gardel GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Senegal GATTTAGCCCCATATTTGAGTGCTAATGTGTTAAATTATCACTA-TGGAAAGCATCATCA
Sankat GATTTAGCCCCATATTTGAGTGCTAATGTGTTAAATTATCACTA-TGGAAAGCATCATCA
L52 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
U11 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
U89 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W25 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W102 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W26 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W54 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
L60 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
L53 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
W91 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
Kumm2 GATTTAGTACCATATTTAAGTGCTAGTGTGTTAGACTATCATTAT-TGGTAAACATCATCA
River GATTTAGTACCATATTTAAGTGCTAGTGTGTTAGACTATCATTAT-TGGTAAACATCATCA
Omatjenne GATTTAGTACCATATTTAAGTGCTAGTGTGTTAGACTATCATTAT-TGGTAAACATCATCA
C25 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C38 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C49 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C52 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C69 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C87 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C97 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C98 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I34 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I55 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I56 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I70 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I77 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I81 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
M3 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
M11 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
M19 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
M22 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
M56 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C14 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
C57 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
I72 GATTTAGCCCCATATTTGAGTGCTAATGTGTTGAATTATCACTA-TGGAAAGCATCATCA
***** ***** ***** ***** * ***** ** * ** *****

E67 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTCAGGGACTGATTTCTGTACATGTACGA

W47 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 U66 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 W36 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Welg AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Ball3 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Blaauw AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Kwany AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Nonile AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 SBF4 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 SBF7 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 UmBanein AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Mara AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 Gardel AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Senegal AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Sankat AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 L52 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 U11 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 U89 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 W25 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 W102 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 W26 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 W54 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 L60 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 L53 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 W91 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 Kumm2 AGGTTATGTAAATGCTTTAAA-CAATCTTGTTGCAGGGACTGATTTTGTACTTATACAA
 River AGGTTATGTAAATGCTTTAAA-CAATCTTGTTGCAGGGACTGATTTTGTACTTATACAA
 Omatjenne AGGTTATGTAAATGCTTTAAA-CAATCTTGTTGCAGGGACTGATTTTGTACTTATACAA
 C25 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 C38 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 C49 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 C52 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 C69 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 C87 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 C97 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 C98 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I34 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 I55 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I56 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I70 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I77 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I81 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 M3 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 M11 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 M19 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 M22 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 M56 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 C14 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACATGTACGA
 C57 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 I72 AGGTTATGTAAATGCTTTAAA-TAATCTTGTTGCAGGGACTGATTTCTGTACCTGTACGA
 ***** * * * * *

E67 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 W47 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 U66 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 W36 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 Welg ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 Ball3 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 Blaauw ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 Kwany ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 Nonile ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 SBF4 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
 SBF7 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT

UmBanein ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
Mara ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
Gardel ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
Senegal ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
Sankat ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
L52 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
U11 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
U89 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
W25 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
W102 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
W26 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
W54 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
L60 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
L53 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
W91 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
Kumm2 ATGAAGATTTACCTACAGTTATTAAGGCTACGCATGGTAATTTAGCAACCAGATCAATAT
River ATGAAGATTTACCTACAGTTATTAAGGCTACGCATGGTAATTTAGCAACCAGATCAATAT
Omatjenne ATGAAGATTTACCTACAGTTATTAAGGCTACGCATGGTAATTTAGCAACCAGATCAATAT
C25 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C38 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C49 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C52 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C69 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C87 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAAATCAATAT
C97 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C98 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I34 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I55 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I56 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I70 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAAATCAATAT
I77 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I81 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
M3 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
M11 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
M19 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
M22 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
M56 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C14 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
C57 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
I72 ATGAAGATTTACCTGCGGTTATTAAGCTACACATAGTGATTTAGCAACTAGATCAATAT
***** * ***** ***** ** * ***** * *****

E67 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
U47 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
U66 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
W36 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Welg TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Ball3 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Blaauw TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
Kwany TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
Nonile TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
SBF4 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
SBF7 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
UmBanein TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Mara TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Gardel TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Senegal TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
Sankat TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
L52 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
U11 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
U89 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
W25 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
W102 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG

W26 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
W54 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
L60 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
L53 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
W91 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
Kumm2 TTAATAATGCTGGTCAAGTATGGAATCATAACTTTTTATTGGCAGTCTATCAAAAAGAATG
River TTAATAATGCTGGTCAAGTATGGAATCATAACTTTTTATTGGCAGTCTATCAAAAAGAATG
Omatjenne TTAATAATGCTGGTCAAGTATGGAATCATAACTTTTTATTGGCAGTCTATCAAAAAGAATG
C25 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C38 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C49 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C52 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C69 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C87 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C97 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C98 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I34 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I55 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I56 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I70 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I77 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I81 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
M3 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
M11 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAGTCTATAACAAAGAATG
M19 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
M22 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
M56 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C14 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
C57 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
I72 TTAATAATGCTGGTCAAGTATGGAATCATAATTTTTATTGGCAATCTATAACAAAGAATG
***** * *****

E67 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W47 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
U66 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W36 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Welg GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Ball3 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Blaauw GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Kwany GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Nonile GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
SBF4 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
SBF7 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
UmBanein GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Mara GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Gardel GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Senegal GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTATTG
Sankat GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTATTG
L52 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
U11 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
U89 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W25 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W102 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W26 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W54 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
L60 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
L53 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
W91 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
Kumm2 GAGGTATAGCTCCTACAGGAGAATTACTCAATAGAATTAATAAAGATTTTGAAAGTATTG
River GAGGTATAGCTCCTACAGGAGAATTACTCAATAGAATTAATAAAGATTTTGAAAGTATTG
Omatjenne GAGGTATAGCTCCTACAGGAGAATTACTCAATAGAATTAATAAAGATTTTGAAAGTATTG
C25 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG
C38 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTTG

C49 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C52 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C69 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C87 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C97 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C98 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I34 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I55 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I56 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I70 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I77 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I81 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 M3 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 M11 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 M19 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 M22 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 M56 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C14 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 C57 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 I72 GTGTTGTTACGCCTAAAGGAGAGTTATTAGATAGAATAAAATAAAGATTTTGAAAGTGTG
 *

E67 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W47 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 U66 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W36 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Welg AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Ball3 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Blaauw AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Kwany AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Nonile AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 SBF4 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 SBF7 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 UmBanein AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Mara AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Gardel AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Senegal AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Sankat AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 L52 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 U11 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 U89 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W25 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W102 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W26 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W54 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 L60 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 L53 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 W91 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 Kumm2 ACAAGTTTAATCATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGTTGGATAT
 River ACAAGTTTAATCATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGTTGGATAT
 Omatjenne ACAAGTTTAATCATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGTTGGATAT
 C25 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C38 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C49 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C52 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C69 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C87 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C97 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 C98 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 I34 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 I55 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 I56 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
 I70 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT

I77 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
I81 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
M3 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
M11 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
M19 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
M22 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
M56 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
C14 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
C57 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
I72 AAAAGTTTAATAATGCTTTTACTGAAGCTGGAAAAGGTCATTTTGGTAGTGGATGGGTAT
* * * * *
E67 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W47 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
U66 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W36 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Welg GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Ball3 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Blaauw GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Kwany GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Nonile GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
SBF4 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
SBF7 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
UmBanein GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Mara GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Gardel GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Senegal GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Sankat GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
L52 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
U11 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
U89 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W25 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W102 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W26 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W54 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
L60 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
L53 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
W91 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
Kumm2 GGTTAGTTTTTGATATTACAGAACAACAAAACCTAAGATTCTTTGTACAGC-TAATGGTGAT
River GGTTAGTTTTTGATATTACAGAACAACAAAACCTAAGATTCTTTGTACAGC-TAATGGTGAT
Omatjenne GGTTAGTTTTTGATATTACAGAACAACAAAACCTAAGATTCTTTGTACAGC-TAATGGTGAT
C25 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C38 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C49 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C52 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C69 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C87 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C97 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C98 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I34 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I55 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I56 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I70 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I77 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I81 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
M3 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
M11 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
M19 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
M22 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
M56 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C14 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
C57 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT
I72 GGTTGGTTTTTGATACTGTAGAGCAAAAACCTAAAATTTTGTGTACAGC-TAATGGTGAT

***** * * * * *

E67 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W47 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
U66 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W36 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Welg ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Ball3 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Blaauw ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Kwany ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Nonile ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
SBF4 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
SBF7 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
UmBanein ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Mara ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Gardel ACTCCTATTACT-CAATATCCTGATACATATCCATTACTGACTATGGATGTAGTTTGGCT
Senegal ACTCCTATTACT-CAATATCCTGATACATATCCATTACTGACTATGGATGTAGTTTGGCT
Sankat ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
L52 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
U11 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
U89 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W25 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W102 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W26 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W54 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
L60 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
L53 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
W91 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
Kumm2 ACTCCTATTACT-CAGTATCCTGATACATATCCATTATTGACTATGGATGTAGCCTAGCT
River ACTCCTATTACT-CAGTATCCTGATACATATCCATTATTGACTATGGATGTAGCCTAGCT
Omatjenne ACTCCTATTACT-CAGTATCCTGATACATATCCATTATTGACTATGGATGTAGCCTAGCT
C25 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C38 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C49 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C52 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C69 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C87 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C97 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C98 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I34 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I55 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I56 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I70 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I77 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I81 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
M3 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
M11 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
M19 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
M22 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
M56 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C14 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
C57 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
I72 ACTCCTATTACT-CAATATCCTGATACATACCCATTACTGACTATGGATGTAGTTTGGCT
***** * * * * *

E67 AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W47 AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
U66 AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W36 AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Welg AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Ball3 AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Blaauw AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Kwany AAAGCTGTTAGTTCGTTGAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC

Nonile AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
SBF4 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
SBF7 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
UmBanein AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Mara AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Gardel AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Senegal AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Sankat AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
L52 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
U11 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
U89 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W25 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W102 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W26 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W54 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
L60 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
L53 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
W91 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
Kumm2 AAGGCTGTAAGTTTACTAAAAGTTACAGCATGTTGTTATCACATCTGTAGATAGGGATGAT
River AAGGCTGTAAGTTTACTAAAAGTTACAGCATGTTGTTATCACATCTGTAGATAGGGATGAT
Omatjenne AAGGCTGTAAGTTTACTAAAAGTTACAGCATGTTGTTATCACATCTGTAGATAGGGATGAT
C25 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C38 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C49 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C52 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C69 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C87 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C97 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C98 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I34 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I55 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I56 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I70 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I77 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I81 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
M3 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
M11 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
M19 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
M22 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
M56 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C14 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
C57 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
I72 AAAGCTGTTAGTTCGTTGAAAGTTACAGCATGTTGTAATTACATCTGTGGATCGAGATGAC
** ** * * * * *

E67 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
W47 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
U66 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
W36 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Welg TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Ball3 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Blaauw TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Kwany TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Nonile TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
SBF4 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
SBF7 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
UmBanein TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Mara TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Gardel TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
Senegal TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAGATACGCAAAGAGAT
Sankat TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAGATACGCAAAGAGAT
L52 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGCAAAGGGAT
U11 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACGTAAGGGAT

U89 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
W25 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
W102 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
W26 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
W54 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
L60 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
L53 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
W91 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
Kumm2 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
River TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
Omatjenne TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
C25 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
C38 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C49 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C52 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C69 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C87 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C97 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
C98 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I34 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I55 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I56 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I70 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I77 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I81 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
M3 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
M11 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
M19 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
M22 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
M56 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG TAAAAGGGAT
C14 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
C57 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
I72 TTAGAAGATGGTGGTGC TGGGCATTTTGTAGAATGTATAGAAGAAATACG CAAAAGGGAT
***** ** ** ** **

E67 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W47 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
U66 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W36 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Welg AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Ball3 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Blaauw AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Kwany AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Nonile AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
SBF4 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
SBF7 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
UmBanein AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Mara AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Gardel AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Senegal AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Sankat AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
L52 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
U11 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
U89 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W25 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W102 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W26 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W54 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
L60 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
L53 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
W91 AGTAATGTCACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
Kumm2 AACAAATGTTACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT
River AACAAATGTTACTATTGAAATATTAAC TCCAGATTTTTTAAATAAACATGATGCAATTGAT

I55 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 I56 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 I70 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 I77 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 I81 AAAATTGCTAAAGCATTTCCTGATGTGTATAACCATAATGTAGAAACAGTACCAAGGCTA
 M3 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 M11 AAAATTGCTAAAGCATTTCCTGATGTGTATAACCATAATGTAGAAACAGTACCAAGGCTA
 M19 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 M22 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 M56 AAAATTGCTAAAGCATTTCCTGATGTGTATAACCATAATGTAGAAACAGTACCAAGGCTA
 C14 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 C57 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG
 I72 AAAATTGCTAAAGCATTTCCTGATGTGTATAATCATAATGTAGAAACAGTACCAAGGCTG

E67 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W47 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 U66 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W36 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Welg TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Ball3 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Blaauw TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Kwany TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Nonile TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 SBF4 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 SBF7 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 UmBanein TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Mara TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Gardel TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Senegal TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Sankat TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 L52 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 U11 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 U89 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W25 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W102 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W26 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W54 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 L60 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 L53 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 W91 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 Kumm2 TATGCCAAAATTAGACCAAGGGCACGATATTTTCATTCTTTATATTTGCTTAAAACGATC
 River TATGCCAAAATTAGACCAAGGGCACGATATTTTCATTCTTTATATTTGCTTAAAACGATC
 Omatjenne TATGCCAAAATTAGACCAAGGGCACGATATTTTCATTCTTTATATTTGCTTAAAACGATC
 C25 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C38 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C49 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C52 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C69 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C87 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C97 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 C98 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I34 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I55 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I56 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I70 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I77 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 I81 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 M3 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 M11 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 M19 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 M22 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
 M56 TATGCTAAGATTAGACCAAAAAGCACGTTATTTTCATTCTTTATATTTGCTAAAAACAATA

C14 TATGCTAAGATTAGACCAAAGCAGGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
C57 TATGCTAAGATTAGACCAAAGCAGGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
I72 TATGCTAAGATTAGACCAAAGCAGGTTATTTTCATTCTTTATATTTGCTAAAAACAATA
***** ** *****

E67 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W47 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
U66 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W36 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Welg AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Ball3 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Blaauw AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Kwany AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Nonile AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
SBF4 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
SBF7 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
UmBanein AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Mara AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Gardel AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Senegal AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Sankat AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
L52 AAGCAGAAAAACCTAGGATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
U11 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
U89 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W25 AAGCAGAAAAACCTAGGATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W102 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W26 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W54 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
L60 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
L53 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
W91 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
Kumm2 AAACAAAAAATCCTCAAATATTTACTAAATCTGGAATAATGTTGGGCTTAGGGGAAATG
River AAACAAAAAATCCTCAAATATTTACTAAATCTGGAATAATGTTGGGCTTAGGGGAAATG
Omatjenne AAACAAAAAATCCTCAAATATTTACTAAATCTGGAATAATGTTGGGCTTAGGGGAAATG
C25 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C38 AAGCAGAAAAACCTAGGATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C49 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C52 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C69 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C87 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C97 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C98 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I34 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I55 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I56 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I70 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I77 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I81 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
M3 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
M11 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
M19 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
M22 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
M56 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C14 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
C57 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
I72 AAGCAGAAAAACCTAGAAATATTTACTAAGTCAGGTATAATGGTAGGATTGGGAGAACTA
** ** ***** ** ***** ** ** ***** * ** ** * ** * ** *

E67 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTCAGTGGGTGTTTTAGG
W47 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTCAGTGGGTGTTTTAGG
U66 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTCAGTGGGTGTTTTAGG
W36 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTCAGTGGGTGTTTTAGG
Welg AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTCAGTGGGTGTTTTAGG

Ball3 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 Blaauw AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Kwany AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Nonile AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 SBF4 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 SBF7 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 UmBanein AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Mara AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Gardel AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Senegal AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Sankat AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 L52 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 U11 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 U89 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 W25 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 W102 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 W26 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 W54 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 L60 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 L53 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 W91 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 Kumm2 AAAGAGGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTATTTTTAGG
 River AAAGAGGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTATTTTTAGG
 Omatjenne AAAGAGGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTATTTTTAGG
 C25 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C38 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C49 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 C52 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C69 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C87 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C97 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C98 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 I34 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 I55 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 I56 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 I70 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 I77 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 I81 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 M3 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 M11 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 M19 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 M22 AAAGAAGAGATATACCAAGATAGATGCAGTTATATCAAAACATTTCAGTGGGTGTTTTAGG
 M56 AAAGAAGAGATATATCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C14 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 C57 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG
 I72 AAAGAAGAGATATACCAAGATAGATGCAGTTATCTCAAAACATTTCAGTGGGTGTTTTAGG

E67 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 W47 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 U66 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 W36 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Welg TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Ball3 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Blaauw TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Kwany TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Nonile TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 SBF4 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 SBF7 TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 UmBanein TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Mara TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Gardel TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
 Senegal TATTTTTAATGTATTTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT

Sankat TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCTCTTAATGT
L52 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
U11 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
U89 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
W25 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
W102 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
W26 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
W54 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
L60 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
L53 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
W91 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
Kumm2 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGGAGAATGACAATTTTTGCTCTAAATGT
River TATTTTTAATGTATTTCTGGTGGTGCCTTAGGGAGAATGACAATTTTTGCTCTAAATGT
Omatjenne TATTTTTAATGTATTTCTGGTGGTGCCTTAGGGAGAATGACAATTTTTGCTCTAAATGT
C25 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C38 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C49 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C52 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C69 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C87 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C97 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C98 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I34 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I55 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I56 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I70 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I77 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I81 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
M3 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
M11 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
M19 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
M22 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
M56 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C14 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
C57 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
I72 TATTTTTAATGTATTTCTGGTGGTGCCTTAGGTAGAATGACAATTTTTGCCCTTAATGT
***** ** *****

E67 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W47 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
U66 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W36 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Welg TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Ball3 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Blaauw TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Kwany TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Nonile TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
SBF4 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
SBF7 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
UmBanein TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Mara TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Gardel TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Senegal TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
Sankat TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
L52 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
U11 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
U89 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W25 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W102 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W26 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
W54 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
L60 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
L53 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT

W91 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 Kumm2 TATGCCATATATAGTATCTTCTATAAATTATGCAGTTGTTATCAGTGACAATTCAAAAT
 River TATGCCATATATAGTATCTTCTATAAATTATGCAGTTGTTATCAGTGACAATTCAAAAT
 Omatjenne TATGCCATATATAGTATCTTCTATAAATTATGCAGTTGTTATCAGTGACAATTCAAAAT
 C25 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C38 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C49 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C52 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C69 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C87 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C97 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C98 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I34 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I55 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I56 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I70 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I77 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I81 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 M3 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 M11 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 M19 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 M22 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 M56 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C14 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 C57 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 I72 TATGCCATATATAGTTTCTTCTATAAATTATGCAGTTACTTTCAGTTACAATTCCAAGATT
 ***** * ***** ** ***** **

E67 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W47 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 U66 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 W36 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 Welg GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 Ball3 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 Blaauw AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Kwany AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Nonile GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 SBF4 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 SBF7 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 UmBanein GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Mara AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Gardel GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Senegal AAATGAGATGAGGCAAAGTGGTGAATTAGGTAGGTAAGATTAATACTTATGTACGATA
 Sankat AAATGAGATGAGGCAAAGTGGTGAATTAGGTAGGTAAGATTAATACTTATGTACGATA
 L52 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 U11 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 U89 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W25 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W102 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W26 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W54 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 L60 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 L53 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 W91 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 Kumm2 GAATGAAATGAGGCAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGGTA
 River GAATGAAATGAGGCAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGGTA
 Omatjenne GAATGAAATGAGGCAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGGTA
 C25 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C38 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C49 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 C52 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C69 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C87 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA

C97 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C98 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 I34 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 I55 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 I56 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 I70 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 I77 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 I81 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 M3 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 M11 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 M19 AAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 M22 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTAAAGATA
 M56 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C14 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 C57 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA
 I72 GAATGAGATGAGACAAAGTGGTGAATTAGGTAGGGTAAAGATTAATACTTATGTACGATA

E67 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W47 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 U66 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W36 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Welg TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Ball3 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Blaauw TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Kwany TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Nonile TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 SBF4 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 SBF7 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 UmBanein TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Mara TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Gardel TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Senegal TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Sankat TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 L52 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 U11 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 U89 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W25 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W102 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W26 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W54 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 L60 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 L53 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 W91 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 Kumm2 TATAACTATTCTGTTTTGTTAATTCAAGGTTCTATTATCTTACTTGGATTAGAAAAAAT
 River TATAACTATTCTGTTTTGTTAATTCAAGGTTCTATTATCTTACTTGGATTAGAAAAAAT
 Omatjenne TATAACTATTCTGTTTTGTTAATTCAAGGTTCTATTATCTTACTTGGATTAGAAAAAAT
 C25 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C38 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C49 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C52 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C69 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C87 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C97 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 C98 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I34 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I55 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I56 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I70 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I77 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 I81 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 M3 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
 M11 TATAACTATTGTTTTCTGTTAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT

M19 TATAACTATTGGTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
M22 TATAACTATTGTTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
M56 TATAACTATTGTTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
C14 TATAACTATTGTTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
C57 TATAACTATTGTTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
I72 TATAACTATTGTTTTCTGTTTAAATTCAAGGTTCTATTATCTTGCTTGGGTTAGAAAAAAT
***** ** *****

E67 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W47 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
U66 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W36 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Welg GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Ball3 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Blaauw GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Kwany GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Nonile GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
SBF4 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
SBF7 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
UmBanein GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Mara GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Gardel GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Senegal GAATACACAGACTAGTATTGTAGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Sankat GAATACACAGACTAGTATTGTAGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
L52 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
U11 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
U89 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W25 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W102 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W26 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W54 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
L60 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
L53 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
W91 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
Kumm2 GAATACAGAAGCTAGTATTGTAGTGATTGATCCTGGTTTATTATTTAGAGTAGTAGGTAT
River GAATACAGAAGCTAGTATTGTAGTGATTGATCCTGGTTTATTATTTAGAGTAGTAGGTAT
Omatjenne GAATACAGAAGCTAGTATTGTAGTGATTGATCCTGGTTTATTATTTAGAGTAGTAGGTAT
C25 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C38 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C49 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C52 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C69 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C87 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C97 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C98 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I34 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I55 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I56 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I70 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I77 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I81 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
M3 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
M11 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
M19 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
M22 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
M56 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C14 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
C57 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
I72 GAATACACAGACTAGTATTGTGGTAATTGATCCTGGTTTGTATTTAGGGTAGTAGGTAT
***** * ***** ** *****

E67 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAG
W47 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAG

U66 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
W36 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Welg TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Ball3 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Blaauw TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Kwany TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Nonile TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
SBF4 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
SBF7 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
UmBanein TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
Mara TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Gardel TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Senegal TAGTAGCTTGTAGGCGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Sankat TAGTAGCTTGTAGGCGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
L52 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
U11 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
U89 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
W25 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
W102 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
W26 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
W54 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
L60 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
L53 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
W91 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
Kumm2 TAGTAGCTTACTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
River TAGTAGCTTACTAGGTGGGACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
Omatjenne TAGTAGCTTACTAGGTGGGACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
C25 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
C38 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
C49 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
C52 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
C69 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
C87 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
C97 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
C98 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
I34 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
I55 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
I56 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
I70 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
I77 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
I81 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
M3 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
M11 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
M19 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
M22 TAGTAGCTTGTAGGTGGTACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
M56 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTCTGGTTAGGTGATAGTATAAATAAAAG
C14 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
C57 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
I72 TAGTAGCTTGTAGGTGGCACAATGTTTCTACTTTGGTTAGGTGATAGTATAAATAAAAG
***** **

E67 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
W47 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
U66 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
W36 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
Welg GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
Ball3 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
Blaauw GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
Kwany GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
Nonile GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
SBF4 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
SBF7 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
UmBanein GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG

Mara GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAATCGCAGAGTTACCAGG
 Gardel GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 Senegal GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAATTACCAGG
 Sankat GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 L52 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 U11 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 U89 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 W25 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 W102 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 W26 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 W54 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 L60 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 L53 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 W91 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 Kumm2 GGGGATTGGTAATGGAGTCTCCATGATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 River GGGGATTGGTAATGGAGTCTCCATGATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 Omatjenne GGGGATTGGTAATGGAGTCTCCATGATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C25 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C38 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C49 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C52 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C69 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C87 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C97 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C98 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I34 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I55 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I56 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I70 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I77 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I81 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 M3 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 M11 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 M19 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 M22 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 M56 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C14 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 C57 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 I72 GGGTATTGGTAATGGGATTTCTCTAATTATATTTACAGGAATAAATGCGAGAGTTACCAGG
 *** ***** * ** * ***** ***** *****

E67 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 W47 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 U66 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 W36 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Welg TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Ball3 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Blaauw TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Kwany TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Nonile TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 SBF4 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 SBF7 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 UmBanein TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Mara TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Gardel TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Senegal TTCTTTTTCTGCCATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 Sankat TTCTTTTTCTGCCATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 L52 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 U11 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 U89 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 W25 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 W102 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT
 W26 TTCTTTTTCTGCTATGTTTTTATTAGGTAAAAATGGCAATGTGCCAATATTTGTGATTTT

W54 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
L60 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
L53 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
W91 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
Kumm2 TTCTTTCTCTCTATGTTTTTATTAGGTA AAAATGGTAATGTACCAATCTTTGTTATCTT
River TTCTTTCTCTCTATGTTTTTATTAGGTA AAAATGGTAATGTACCAATCTTTGTTATCTT
Omatjenne TTCTTTCTCTCTATGTTTTTATTAGGTA AAAATGGTAATGTACCAATCTTTGTTATCTT
C25 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C38 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C49 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C52 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C69 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C87 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C97 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C98 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I34 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I55 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I56 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I70 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I77 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I81 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
M3 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
M11 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
M19 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
M22 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
M56 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C14 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
C57 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
I72 TTCTTTTTCTGCTATGTTTTTATTAGGTA AAAATGGCAATGTGCCAATATTTGTGATTTT
***** ** * *****

E67 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W47 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
U66 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W36 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Welg ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Ball3 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Blaauw ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Kwany ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Nonile ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
SBF4 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
SBF7 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
UmBanein ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Mara ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Gardel ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Senegal ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Sankat ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
L52 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
U11 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
U89 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W25 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W102 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W26 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W54 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
L60 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
L53 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
W91 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Kumm2 ATTAATGATATTGGTATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
River ATTAATGATATTGGTATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
Omatjenne ATTAATGATATTGGTATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
C25 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
C38 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA
C49 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTCGTTGAAAAATCTTA

C52 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C69 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C87 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C97 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C98 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I34 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I55 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I56 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I70 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I77 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I81 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 M3 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 M11 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 M19 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 M22 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 M56 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C14 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 C57 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 I72 ATTAATGATATTAATATTTTTTGCATTACTATTGTTAATCATTTTTCGTTGAAAAATCTTA
 ***** ** * ** *****

E67 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W47 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 U66 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W36 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Welg TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Ball3 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Blaauw TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Kwany TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Nonile TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 SBF4 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 SBF7 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 UmBanein TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Mara TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Gardel TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Senegal TCGAAAAATTTTGGTACAATATCCAAAAAGGCAGGTTAAAAATAAGTTATATAAT
 Sankat TCGAAAAATTTTGGTACAATATCCAAAAAGGCAGGTTAAAAATAAGTTATATAAT
 L52 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 U11 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 U89 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W25 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W102 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W26 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W54 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 L60 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 L53 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 W91 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Kumm2 TCGTAAGATTTTAGTACAGTACCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 River TCGTAAGATTTTAGTACAGTACCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 Omatjenne TCGTAAGATTTTAGTACAGTACCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C25 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C38 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C49 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C52 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C69 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C87 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C97 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 C98 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 I34 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 I55 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 I56 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 I70 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
 I77 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT

```
I81 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
M3 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
M11 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
M19 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
M22 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
M56 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
C14 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
C57 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
I72 TAGAAAAATTTTAGTACAATATCCAAAAAGGCAGGTTAAAAATAAATTATATAAT
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

Appendix 2

Approval Documents



Faculty of Veterinary Science

Research Ethics Committee

Project Title	Assessment of an inactivated multivalent heartwater vaccine under field conditions
Project Number	REC205-19
Researcher / Principal Investigator	Ms Z Lukanji

Dissertation / Thesis submitted for	Doctoral
-------------------------------------	-----------------

Supervisor	Prof LCBGD Neves
------------	-------------------------

Conditions	<p>Please address the following: An informed consent document should be uploaded for the sampling of animals and collection of ticks. DAFF section 20 approval is required prior to tick sampling - uploaded approval only corresponds to the collection of blood from HW affected animals.</p> <p>The DAFF section 20 requires that only FMD PCR negative samples may be moved from HH to DVTD. This portion / testing should be inserted into the M&M section of the application.</p>
------------	---

CONDITIONALLY APPROVED	Date: 2019-11-08
CHAIRMAN: UP Research Ethics Committee	Signature: 



**Faculty of Veterinary Science
Animal Ethics Committee**

5 December 2019

**Approval Certificate with Conditions
New Application**

AEC Reference No.: REC205-19
Title: Assessment of an inactivated multivalent heartwater vaccine under field conditions
Researcher: Ms Z Lukanji
Student's Supervisor: Prof LCBGD Neves
Dear Ms Z Lukanji,

The **New Application** as supported by documents received between 2019-09-10 and 2019-11-25 for your research, was approved by the Animal Ethics Committee on its quorate meeting of 2019-11-25.

Please note the following about your ethics approval:

1. The use of species is approved:

Species	Number
Cattle (for tick collection only)	144 max
Goats (blood collection only)	54 max
Sheep (blood collection only)	54 max
Samples	
Blood collection (sheep, goats)	54 per species (Total 108 samples max)
Ticks (<i>A. hebraeum</i>)	432 max (total to be collected from Cattle)

2. Ethics Approval is valid for 1 year and needs to be renewed annually by 2020-12-05.
3. Please remember to use your protocol number (REC205-19) on any documents or correspondence with the AEC regarding your research.
4. Please note that the AEC may ask further questions, seek additional information, require further modification, monitor the conduct of your research, or suspend or withdraw ethics approval.
5. **Condition of approval: CAN NOT collect samples above what is approved by AEC.**

Ethics approval is subject to the following:

- The ethics approval is conditional on the research being conducted as stipulated by the details of all documents submitted to the Committee. In the event that a further need arises to change who the investigators are, the methods or any other aspect, such changes must be submitted as an Amendment for approval by the Committee.

We wish you the best with your research.
Yours sincerely

Prof V Naidoo
CHAIRMAN: UP-Animal Ethics Committee

Room 6-13, Arnold Theiler Building, Onderstepoort
Private Bag X04, Onderstepoort 0110, South Africa
Tel +27 12 529 8483
Fax +27 12 529 8321
Email aec@up.ac.za
www.up.ac.za

Fakulteit Veeartsenykunde
Lefapha la Diseanse tsa Bongakadiriwa



Faculty of Veterinary Science
Animal Ethics Committee

12 October 2021

**Approval Certificate
Annual Renewal
(EXT2)**

AEC Reference No.: REC205-19
Title: Assessment of an inactivated multivalent heartwater vaccine under field conditions
Researcher: Ms Z Lukanji
Student's Supervisor: Dr D Morar-Leather

Dear Ms Z Lukanji,

The **Annual Renewal** as supported by documents received between 2021-08-16 and 2021-10-01 for your research, was approved by the Animal Ethics Committee on its quorate meeting of 2021-10-01.

Please note the following about your ethics approval:

1. The use of species is approved:

Species	Number Available
Cattle (blood collection only)	144 max
Goats (blood collection only)	54 max
Sheep (blood collection only)	54 max
Samples	
Blood collection (sheep, goats)	54 per species (Total 108 samples max)
Ticks (<i>A. hebraeum</i>)	432 max (total to be collected from Cattle)

- Ethics Approval is valid for 1 year and needs to be renewed annually by 2022-10-12.
- Please remember to use your protocol number (REC205-19) on any documents or correspondence with the AEC regarding your research.
- Please note that the AEC may ask further questions, seek additional information, require further modification, monitor the conduct of your research, or suspend or withdraw ethics approval.
- All incidents** must be reported by the PI by email to Ms Marleze Rheeder (AEC Coordinator) within 3 days, and must be subsequently submitted electronically on the application system within 14 days.
- The committee also requests that you record major procedures undertaken during your study for own-archiving, using any available digital recording system that captures in adequate quality, as it may be required if the committee needs to evaluate a complaint. However, if the committee has monitored the procedure previously or if it is generally can be considered routine, such recording will not be required.

Ethics approval is subject to the following:

- The ethics approval is conditional on the research being conducted as stipulated by the details of all documents submitted to the Committee. In the event that a further need arises to change who the investigators are, the methods or any other aspect, such changes must be submitted as an Amendment for approval by the Committee.

Room 6-13, Arnold Theiler Building, Onderstepoort
Private Bag X04, Onderstepoort 0110, South Africa
Tel +27 12 529 8434
Fax +27 12 529 8324
Email: marleze.rheeder@up.ac.za

Fakulteit Veeartsenykunde
Lefapha la Diseense tša Bongakadiruiwa

We wish you the best with your research.

Yours sincerely


Prof V Naidoo
CHAIRMAN: UP-Animal Ethics Committee



**Faculty of Veterinary Science
Animal Ethics Committee**

29 May 2023

**Approval Certificate
Amendment 1**

AEC Reference No.: REC205-19 Line 4
Title: Molecular characterization of South African Ehrlichia ruminantium field isolates and development of a qPCR assay for the evaluation of a multivalent inactivated vaccine
Researcher: Ms Z Lukanji
Student's Supervisor: Prof LCBGD Neves

Dear Ms Z Lukanji,

The **Amendment** as supported by documents received between 2023-03-28 and 2023-05-29 for your research, was approved by the Animal Ethics Committee on its quorate meeting of 2023-05-29.

Please note the following about your ethics approval:

1. The change in the Title is approved: (new title) **Molecular characterization of South African Ehrlichia ruminantium field isolates and development of a qPCR assay for the evaluation of a multivalent inactivated vaccine**
2. The change in species/animals/ samples is approved

Species	No Approved	Additional Required	Total Approved
Cattle - N/A	144	108	252
Samples	No Approved	Additional Required	Total Approved
A. hebraeum - Tick DNA - Bushbuckri - Stored	427	0	427
A. hebraeum - Ticks - South Afri - Live	292	1152	1444
Blood - Bushbuckri - Live	0	0	0

3. Please note that the approved date(s) from the original application certificate / annual renewal certificate will be applicable to this amendment.
4. Please remember to use your protocol number (REC205-19) on any documents or correspondence with the AEC regarding your research.
5. Please note that the AEC may ask further questions, seek additional information, require further modification, monitor the conduct of your research, or suspend or withdraw ethics approval.
6. **All incidents** must be reported by the PI by email to Ms Marleze Rheeder (AEC Coordinator) within 3 days, and must be subsequently submitted electronically on the application system within 14 days.
7. The committee also requests that you record major procedures undertaken during your study for own-archiving, using any available digital recording system that captures in adequate quality, as it may be required if the committee needs to evaluate a complaint. However, if the committee has monitored the procedure previously or if it is generally can be considered routine, such recording will not be required.

Ethics approval is subject to the following:

- The ethics approval is conditional on the research being conducted as stipulated by the details of all documents submitted to the Committee. In the event that a further need arises to change who the investigators are, the methods or any other aspect, such changes must be submitted as an Amendment for approval by the Committee.

We wish you the best with your research.

Yours sincerely


Prof. V. Naidoo

CHAIRMAN: UP-Animal Ethics Committee

investigators are, the methods or any other aspect, such changes must be submitted as an Amendment for approval by the Committee.

We wish you the best with your research.

Yours sincerely

Prof V Naidoo
CHAIRMAN: UP-Animal Ethics Committee



agriculture, forestry & fisheries

Department:
Agriculture, Forestry and Fisheries
REPUBLIC OF SOUTH AFRICA

Directorate Animal Health, Department of Agriculture, Forestry and Fisheries
Private Bag X138, Pretoria 0001

Enquiries: Mr Herry Gololo • Tel: +27 12 319 7532 • Fax: +27 12 319 7470 • E-mail: HerryG@daff.gov.za
Reference: 12/11/1/6 (1210)

Ms Zinathi Lukanji
University of Pretoria
Tel: 012 529 8268
E-mail: zinathi.lukanji@up.ac.za

Dear Ms Lukanji

RE: PERMISSION TO DO RESEARCH IN TERMS OF SECTION 20 OF THE ANIMAL DISEASES ACT, 1984 (ACT NO 35 OF 1984)

Your application dated 27 June 2019 requesting permission under Section 20 of the Animal Disease Act, 1984 (Act No. 35 of 1984) to perform a research project or study, refers. I am pleased to inform you that permission is hereby granted to perform the following study, with the following conditions:

Conditions:

1. This permission does not relieve the researcher of any responsibility which may be placed on him by any other act of the Republic of South Africa;
2. This permit is valid only for the collection and analysis of blood collected from cases of Heartwater in animals, the collection and analysis of ticks and the culturing of *E. ruminantium*. A separate Section 20 permit must be obtained prior to the manufacturing or testing of any Heartwater vaccine. Please apply in writing to HerryG@daff.gov.za;
3. Written permission from the Director: Animal Health must be obtained prior to any deviation from the conditions approved for this research project under this Section 20 permit. Please apply in writing to HerryG@daff.gov.za;

4. If required, an application for an extension must be made by the responsible researcher at least one month prior to the expiry of this Section 20 permit. Please apply in writing to HerryG@daff.gov.za;
5. No part of this research project may begin until the valid ethical approval has been obtained in writing from the relevant South African authority;
6. The following samples may be collected:
 - 6.1. Blood may be collected from ruminants showing clinical signs of Heartwater at the Hluvukani Animal Health Centre;
 - 6.2. Ticks may be collected from the following areas in the Foot and mouth disease (FMD) free zone: Ekuphindisweni, Ocilwane and Mvutshini diptanks in Kwa Zulu Natal Province, Makhuduthamaga Municipality in Limpopo Province;
 - 6.3. Ticks may be collected from the following areas in the FMD controlled area: Utah, Welverdiend, Hluvukani and Hlavekisa in Bushbuckridge, Mpumalanga Province;
7. It is the responsibility of the researcher to consult with the relevant state veterinarian to ensure no restrictions have been placed on the above mentioned areas prior to collection and to facilitate the issuing of movement permits as may be required;
8. All ticks and blood samples collected from the FMD controlled area must be transported to the Hans Hoheisen Wildlife Research Station (HHWRS) BSL 2+ facility;
9. With regard to the removal of samples from the HHWRS:
 - 9.1. Extracted DNA may be moved from HHWRS to the Department of Veterinary Tropical Diseases (DVTD). Please contact the Skukuza state veterinary office to arrange for the necessary veterinary movement permits;
 - 9.2. Only cultures of *E. ruminantium* that test negative on PCR for FMD virus at the DAFF approved Transboundary Animal Diseases Programme (TAD-P) facility, may be moved to the DVTD. Please contact the Skukuza state veterinary office to arrange for the necessary veterinary movement permits;
10. Ticks collected in the FMD free zone may be moved directly to DVDT;
11. Any incidence or suspected incidence of a controlled or notifiable disease in terms of the Animal Diseases Act 1984 (Act no 35 of 84), must be reported immediately to the state veterinarian of the area;
12. All ticks and samples must be packaged and transported in accordance with International Air Transport Association (IATA) requirements and the National Road

- Traffic Act, 1996 (Act No. 93 of 1996). Live ticks must be packaged in such a manner as to prevent escape during transport;
13. All potentially infectious material utilised or generated during or by the research project is to be destroyed at completion of the research project. Only a registered waste disposal company may be used for the removal of all potentially infectious waste from the research project;
 14. Records must be kept for five years for auditing purposes;
 15. A dispensation on point 13 above is attached;

Title of research/study: Assessment of an inactivated multivalent heartwater vaccine in South Africa

Researcher: Ms Zinathi Lukanji

Institution: BSL 2+ Laboratory, Hans Hoheisen Wildlife Research Station; Research and Training Laboratories, Department of Veterinary Tropical Diseases, Onderstepoort Faculty of Veterinary Science; Hluvukani Animal Health Centre, Bushbuckridge, Mpumalanga Province; Transboundary Animal Diseases Programme, Onderstepoort.

Permit Expiry date: 31 July 2020

Our ref Number: 12/11/1/1/6 (1210)

Your ref: None Provided.

Kind regards,



DR. MPHOMAJA
DIRECTOR OF ANIMAL HEALTH

Date: 2019 -07- 3 0



agriculture, forestry & fisheries

Department:
Agriculture, Forestry and Fisheries
REPUBLIC OF SOUTH AFRICA

Directorate Animal Health, Department of Agriculture, Forestry and Fisheries
Private Bag X138, Pretoria 0001

Enquiries: Mr Herry Gololo • Tel: +27 12 319 7532 • Fax: +27 12 319 7470 • E-mail: HerryG@dalrrd.gov.za
Reference: 12/11/11/6A (1210) (JD)

Responsible person: Ms Zinathi Lukanji

Institution: Department of Veterinary Tropical Diseases, Faculty of Veterinary Science,
University of Pretoria

Email: zinathi.lukanji@up.ac.za

Dear Ms Lukanji

**RE: AMENDMENT OF SECTION 20 APPROVAL IN TERMS OF THE ANIMAL DISEASES
ACT, 1984 (ACT NO 35 OF 1984) – EXTENSION OF THE EXPIRY DATE**

**Title of research project / study: “Assessment of an inactivated multivalent heartwater
vaccine in South Africa”**

An amendment is hereby granted on the attached Section 20 approval that was issued for
the above mentioned study on 2019-07-30.

- i) As requested, the validity of the section 20 approval is extended to 31 December 2021;
- ii) All other conditions as specified in the Section 20 approval of 2019-07-30 remain in full effect. This includes the validity of laboratory approvals in terms of SANAS and DALRRD.

Kind regards,

Dr Mpho Maja
DIRECTOR: ANIMAL HEALTH

Date: 2020 -10- 13



agriculture, forestry & fisheries

Department:
Agriculture, Forestry and Fisheries
REPUBLIC OF SOUTH AFRICA

Directorate Animal Health, Department of Agriculture, Forestry and Fisheries
Private Bag X138, Pretoria 0001

Enquiries: Ms Marna Laing • Tel: +27 12 319 7442 • Fax: +27 12 319 7470 • E-mail: MarnaL@dalrrd.gov.za
Reference: 12/11/1/1/6A (1210) (JD)

Responsible person: Ms Zinathi Lukanji
Institution: Department of Veterinary Tropical Diseases, Faculty of Veterinary Science,
University of Pretoria
Email: zinathi.lukanji@up.ac.za

Dear Ms Lukanji,

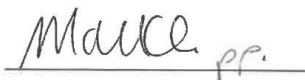
**RE: AMENDMENT OF SECTION 20 APPROVAL IN TERMS OF THE ANIMAL DISEASES
ACT, 1984 (ACT NO 35 OF 1984) – EXTENSION OF THE EXPIRY DATE**

**Title of research project / study: “Assessment of an inactivated multivalent heartwater
vaccine in South Africa”**

An amendment is hereby granted on the Section 20 approval that was issued for the above
mentioned study on 2019-07-30.

- i) As requested, the validity of the section 20 approval is extended to 31 December 2022;
- ii) All other conditions as specified in the Section 20 approval of 2019-07-30 remain in full effect. This includes the validity of laboratory approvals in terms of SANAS and DALRRD.

Kind regards,



Dr Mpho Maja
DIRECTOR: ANIMAL HEALTH

Date: 2021-10-12