

# **Multimeric Protein Structures of African Horsesickness Virus and their use as Antigen Delivery Systems**

**By**

**Francois Frederick Maree**

**A thesis submitted to the University of Pretoria in the Faculty of Biological and  
Agricultural Sciences (Department of Genetics) in fulfilment of the  
requirements for the degree of**

**PHILOSOPHY DOCTORALES**

**Pretoria**

**August 2000**

*Ek gee nuwe krag aan dié wat moeg is,  
Ek maak die moedlose weer vol moed.      Jer. 31:25*

*Hy gee die vermoeides krag,  
Hy versterk dié wat nie meer kan nie.  
Selfs jongmanne word moeg en raak afgemat,  
selfs manne in hulle fleur struikel en val,  
maar dié wat op die Here vertrou,  
kry nuwe krag.  
Hulle vlieg met arendsvlerke,  
hulle hardloop en word nie moeg nie,  
hulle loop en raak nie afgemat nie.      Jes. 40:29-31*

*Die Here my God gee vir my krag.  
Hy maak my voete soos dié van 'n ribbok  
op hoë plekke laat Hy my veilig loop.      Hab. 3:19*

## ACKNOWLEDGEMENTS

I wish to express my sincere appreciation to the following people:

Prof **H. Huismans** for his guidance, support and criticism throughout this study.

Dr **A.A. van Dijk** and Mrs **S. Maree** for their support, advice and assistance in the collaboration on the particle project.

Dr **Wade-Evans** for her idea on the use of VP7 crystals as peptide delivery systems.

The staff and students in the Department Genetics, especially Mrs **P. de Waal** and Mrs **M. van Niekerk**, for their useful discussions and encouragement.

Dr **J. Theron** and Dr **F. Joubert** for their interest and useful advice. Dr **F. Joubert** also assists with software regarding computer modelling.

Mr **A.N. Hall** and Mr **C. van der Merwe** for their assistance with electron microscopy.

The Foundation of Research and Development (**FRD**) for providing the necessary funding.

My wife, **Sonja Maree**, also a molecular biologist, for her valuable input in this study and continuing support and encouragement as well as proof reading of this document.

My family who supported me on so many levels throughout this study.

## CONTENTS

Acknowledgements	iii
Contents	iv
List of figures	xi
Summary	xvii
Abbreviations	xiii
<b>CHAPTER 1: LITERATURE OVERVIEW</b>	
1.1 General introduction	1
1.2 Classification of the genus <i>Orbivirus</i>	2
1.3 Epidemiology, transmission and pathogenesis of AHSV	5
1.4 Molecular biology and structure of orbiviruses	6
1.4.1 The virion	7
1.4.2 The viral genome	8
1.4.3 The viral proteins	11
1.4.3.1 The outer capsid polypeptides	11
1.4.3.2 The core polypeptides	12
1.4.3.3 The non-structural proteins	14
1.5 Orbivirus morphogenesis and viral replication	16
1.6 Orbivirus assembly	18
1.6.1 Three dimensional structure of orbivirus cores and core-like particles	18
1.6.2 Three dimensional atomic structure of core particles	21
1.6.3 X-ray crystallographic structure of VP7 trimers	23
1.6.4 Incorporation of the three minor proteins within CLPs	24
1.6.5 Three dimensional structure of virions and virus-like particles	25
1.7 Disease prevention and control: vaccination for protection against viral infection	26
1.7.1 Conventional live attenuated and inactivated virus vaccines	27
1.7.2 Recombinant subunit and peptide vaccines	28
1.7.2.1 AHSV antigenic outer capsid proteins and neutralisation	

	domains	29
1.7.2.2	Protection afforded by biosynthetic particulate structures	30
1.8	Expression systems for recombinant proteins	32
1.8.1	Baculovirus expression vector system	33
1.9	Summary and Aims	36

## CHAPTER 2

### CHARACTERISATION OF TUBULAR STRUCTURES COMPOSED OF NONSTRUCTURAL PROTEIN NS1 OF AHSV-6 EXPRESSED IN INSECT CELLS

2.1	Introduction	38
2.2	Materials and methods	40
2.2.1	Materials	40
2.2.2	Cells and viruses	40
2.2.3	Partial characterization of AHSV serotype 9 NS1 gene	40
2.2.4	Cloning of AHSV-6 segment 5 cDNA	41
	2.2.4.1 Preparation of <i>E. coli</i> competent cells	41
	2.2.4.2 Transformation of competent cells	41
2.2.5	Plasmid DNA extraction and purification	42
	2.2.5.1 Phenol-chloroform purification	42
	2.2.5.2 RNase-PEG precipitation	42
	2.2.5.3 CsCl density gradient centrifugation	43
2.2.6	Characterization of recombinant plasmids	43
	2.2.6.1 Preparation of radiolabelled dsDNA probes by nick translation	43
	2.2.6.2 Dot-blot hybridization for identification of recombinant clones	44
2.2.7	Restriction endonuclease mapping of AHSV-6 segment 5 cDNA	44
2.2.8	Subcloning of AHSV-6 NS1 gene	44
	2.2.8.1 Vector dephosphorylation	45
	2.2.8.2 Purification of restricted DNA fragments	45

2.2.8.3	Ligation of DNA fragments and transformation	45
2.2.9	DNA sequencing of the cloned AHSV-6 NS1 gene	45
2.2.9.1	Denaturation of template DNA	46
2.2.9.2	The sequencing reactions	46
2.2.9.3	Polyacrylamide gel electrophoresis	46
2.2.10	Preparation of AHSV-6 NS1-encoding tailored cDNA by polymerase chain reaction	47
2.2.11	<i>In vitro</i> expression of the cloned NS1 gene	48
2.2.11.1	<i>In vitro</i> transcription	48
2.2.11.2	<i>In vitro</i> translation	48
2.2.11.3	SDS-polyacrylamide gel electrophoresis (PAGE)	48
2.2.11	Expression of NS1 in insect cells with the BAC-TO-BAC baculovirus expression system	49
2.2.12.1	Construction of a recombinant bacmid transfer vector	49
2.2.12.2	Transposition of recombinant bacmid DNA	49
2.2.12.3	Transfection of Sf9 cells with the recombinant baculovirus shuttle vector	50
2.2.12.4	Virus titration and plaque purification	50
2.2.13	Radiolabelling and SDS-PAGE analysis of recombinant viral proteins	50
2.2.14	Purification of NS1 tubules	51
2.2.15	Electron microscopy and biophysical analysis of tubule morphology	51
2.3	Results	52
2.3.1	Cloning and characterisation of AHSV-6 NS1 gene	53
2.3.2	Restriction enzyme mapping and subcloning of AHSV-6 NS1 gene	55
2.3.3	Characterisation of the AHSV-6 NS1 gene and deduced amino acid sequence	57
2.3.3.1	Nucleotide sequence of the AHSV-6 NS1 gene and comparison to cognate genes of other orbiviruses	57
2.3.3.2	Amino acid sequence of the AHSV-6 NS1 protein and comparison to the gene products of other orbiviruses	60
2.3.4	Modification and <i>in vitro</i> expression of the NS1 gene of AHSV-6	67

2.3.4.1	Modification of the NS1 gene for expression	67
2.3.4.2	<i>In vitro</i> expression of the NS1 gene	68
2.3.5	Expression of the NS1 gene of AHSV-6 in insect cells using a recombinant baculovirus	71
2.3.5.1	Construction of a recombinant baculovirus	71
2.3.5.2	Expression and purification of AHSV-6 NS1 protein	72
2.3.6	Electron microscopic analysis of the NS1 protein complex	75
2.3.7	Electron microscopy of thin sections of recombinant baculovirus-infected cells	77
2.3.8	The effect of biophysical conditions on the morphology of AHSV NS1 tubules	77
2.4	Discussion	80

### CHAPTER 3

#### ASSEMBLY OF EMPTY CORE-LIKE PARTICLES AND DOUBLE-SHELLED, VIRUS-LIKE PARTICLES OF AFRICAN HORSESICKNESS VIRUS BY CO-EXPRESSION OF FOUR MAJOR STRUCTURAL PROTEINS

3.1	Introduction	87
3.2	Materials and methods	89
3.2.1	Materials	89
3.2.2	DNA manipulations and construction of dual transfer vectors	89
3.2.2.1	Insertion of AHSV-9 VP3 and VP7 genes into pFBDual	89
3.2.2.2	Insertion of AHSV-9 or AHSV-3 VP2 genes with AHSV-9 VP3 into the dual transfer vector	90
3.2.2.3	Cloning of AHSV-9 VP5 and VP7 genes into the dual transfer vector	91
3.2.3	Generation and selection of recombinant baculoviruses	92
3.2.3.1	Construction of composite bacmid DNA by transposition	92
3.2.3.2	Isolation and selection of composite bacmid DNA	93
3.2.3.3	Transfection of Sf9 cells with bacmid DNA	93
3.2.3.4	<i>In vivo</i> mRNA hybridisation	94
3.2.4	Co-expression of AHSV capsid proteins in insect cells and	

	purification of multimeric particles comprising different combinations of AHSV proteins	94
3.2.4.1	Analysis of polypeptides synthesised in infected insect cells	94
3.2.4.2	Co-expression of different combinations of AHSV capsid proteins in insect cells and purification of expressed multimeric particles	94
3.2.4.3	Stoichiometry of VP3 to VP7	95
3.2.5	Electron microscopy of purified particles	95
3.3	Results	96
3.3.1	Expression of the genes encoding the four major structural proteins of AHSV-9 or 3 in insect cells using dual recombinant baculovirus vectors	96
3.3.1.1	Construction of an AHSV-9 VP3 and VP7 dual-recombinant baculovirus transfer vector	97
3.3.1.2	Construction of a dual-recombinant baculovirus transfer vector containing either AHSV-3 or AHSV-9 segment 2 and AHSV-9 VP3	100
3.3.1.3	Construction of recombinant baculovirus transfer plasmids containing either AHSV-3 or AHSV-9 VP5 and AHSV-9 VP7 genes	104
3.3.1.4	Production of dual recombinant shuttle vectors (bacmids)	107
3.3.1.5	Construction of dual-recombinant baculoviruses	107
3.3.1.6	Detection of heterologous RNA synthesised in recombinant baculovirus infected cells	108
3.3.2	Investigation of heterologous gene expression in Sf9 cells	109
3.3.3	Co-expression, purification and electron microscopic evaluation of assembled particles	112
3.3.3.1	Particles formed by the assembly of VP3 and VP7 in insect cells	112
3.3.3.2	Assembly of VP2 or VP5 proteins onto CLPs	115
3.3.3.3	Co-expression of four major structural proteins of AHSV in insect cells	118
3.4	Discussion	119

## CHAPTER 4

### EFFECT OF SITE DIRECTED INSERTION MUTATION ON THE CRYSTAL FORMATION, SOLUBILITY AND CLP FORMATION OF AHSV-9 VP7

4.1	Introduction	124
4.2	Materials and methods	126
4.2.1	Materials	126
4.2.2	Site-directed insertion mutagenesis of VP7 and the construction of recombinant transfer vectors	126
4.2.3	Insertion of AHSV-9 VP2 epitopes into the VP7-encoding DNA and construction of recombinant baculovirus transfer vectors	128
4.2.4	Construction of recombinant pFastbacDual transfer vectors containing AHSV-9 VP3 and recombinant VP7 genes	129
4.2.5	Dye terminator cycle sequencing of the VP7 insertion mutants	129
4.2.5.1	Template purification and quantitation	130
4.2.5.2	Cycle sequencing reactions	130
4.2.5.3	ABI PRISM™ Sequencing	130
4.2.5.4	Structural modelling	131
4.2.6	Production of recombinant single and dual recombinant baculoviruses	131
4.2.7	Synthesis and purification of VP7 and recombinant protein complexes	131
4.2.8	Solubility assays and purification of recombinant VP7 proteins	132
4.2.9	Analysis by scanning electron microscopy	132
4.2.10	Purification and analysis of CLP formation	132
4.3	Results	133
4.3.1	Molecular structure modelling of the VP7 protein	133
4.3.2	Construction of recombinant baculovirus transfer vectors containing the mutagenised DNA copies of the VP7 gene	135
4.3.3	Sequence verification and molecular modelling of the recombinant VP7 proteins	140

4.3.4	The construction of dual recombinant baculovirus transfer vectors containing AHSV-9 VP3 in combination with VP7mt177, VP7mt200	145
4.3.5	Baculovirus expression of the VP7 insertion mutants	146
4.3.5.1	Construction and selection of recombinant baculoviruses	146
4.3.5.2	Expression of the modified VP7 proteins in Sf9 cells	146
4.3.6	Solubility and sedimentation analysis of the VP7 insertion mutants	146
4.3.7	Purification & electron microscopy analysis of modified VP7 complexes	151
4.3.8	CLP formation using VP7 insertion mutants	154
4.3.9	Construction of recombinant baculovirus transfer vectors containing VP7/TrVP2 chimeric genes	156
4.3.10	Expression of the two VP7/TrVP2 chimeric genes in insect cells	159
4.3.11	Sedimentation analysis and electron microscopy of the two VP7/TrVP2 chimeric proteins	161
4.4	Discussion	164
<b>CHAPTER 5: CONCLUDING REMARKS</b>		171
<b>PAPERS PUBLISHED AND CONGRESS CONTRIBUTIONS</b>		176
<b>REFERENCES</b>		178

## LIST OF FIGURES

<b>Figure 1.1:</b>	AHSV coding assignments.	9
<b>Figure 1.2:</b>	(A) A representation of the secondary structural elements of the BTV VP3(T2)B molecule. (B) The architecture of the VP3 layer of the BTV core particle. (C) A trimer and a monomer of orbivirus VP7 (T13). (D) The architecture of the VP7 (T13) layer of BTV.	20
<b>Figure 2.1:</b>	Autoradiograph of the 35S-methionine labelled in vitro translation product of AHSV-9 NS1 gene separated by SDS-PAGE.	52
<b>Figure 2.2:</b>	Cloning strategy for expression of NS1. A full-length cDNA copy of AHSV-6 NS1 gene was cloned by dG/dC-tailing into pBR322.	54
<b>Figure 2.3:</b>	(A) An autoradiograph representing dot blot hybridisation of a <sup>32</sup> P-labelled AHSV-9 segment 5-specific probe to the recombinant pBR322 plasmids to confirm the identity of the inserts. (B) Agarose gel electrophoretic analysis of recombinant plasmids, derived by cloning the cDNA copy of AHSV-6 segment 5 by means of dG/dC-tailing into the PstI site of pBR322.	55
<b>Figure 2.4:</b>	NS1 subclones prepared from NS1-specific cDNA clones p5.1 and p5.2 for sequencing, positioned relative to the full-length gene.	56
<b>Figure 2.5:</b>	The complete nucleotide sequence of the NS1-encoding segment 5 cDNA of AHSV-6.	58
<b>Figure 2.6:</b>	Alignment of the predicted amino acid sequences of the NS1 protein of AHSV serotypes 6, 4 and 9.	62
<b>Figure 2.7:</b>	Alignment of the predicted amino acid sequences of the NS1 protein of AHSV-6, -9, BTV-10, -13, -17 and EHDV-1 and -2.	63
<b>Figure 2.8:</b>	Percentage amino acid similarity in different NS1 proteins.	64
<b>Figure 2.9:</b>	Comparisons of the hydropathicity profiles (Kyte & Doolittle, 1982) of NS1 of AHSV-6 (A), BTV-10 (B) and EHDV-2 (C).	65
<b>Figure 2.10:</b>	(A) Comparisons of the location of hydrophobic regions of NS1 of AHSV-6 and BTV-10. (B) Schematic representation of the secondary structure prediction of the NS1 protein of the three orbiviruses (AHSV, BTV and EHDV).	66

- Figure 2.11:** Comparisons of the hydrophilicity profile (A) (Hopp & Woods, 1982) and antigenicity profile (B)(Welling et al., 1988) of AHSV-6 NS1. 66
- Figure 2.12:** (A) Agarose gel analysis of PCR amplified fragments of AHSV-6 NS1 specific cDNA. (B) Agarose gel analysis of the recombinant plasmid pBS-S5.2PCR, constructed by cloning the PCR-tailored NS1 gene into the Bam H1 site of pBS. 68
- Figure 2.13:** (A) An Agarose gel analysis of a partial Hind III digestion of the plasmid pBS-5.2PCR, through serial dilution. (B) Complete Hind III and Sty I digestions of pUC-5.2cDNA. (C) Agarose gel analysis of the recombinant plasmid pBS-S5.2Hybr. 69
- Figure 2.14:** Autoradiograph of the <sup>35</sup>S-methionine labelled in vitro translation products directed by mRNA synthesised from AHSV-6 NS1 chimeric gene. 70
- Figure 2.15:** Agarose gel electrophoretic analysis of the recombinant plasmid pFB-S5.2Hybr, constructed by cloning the PCR/cDNA chimeric NS1 gene into the Bam H1 site of pFastbacl. 71
- Figure 2.16:** (A) An autoradiograph representing dot-blot hybridisation of a <sup>32</sup>P-labelled NS1-specific probe (pBR-S5.2) to recombinant bacmid DNA. (B) Agarose gel analysis of PCR amplified fragments from composite bacmids. 72
- Figure 2.17:** SDS-PAGE analysis of the expression of the NS1 protein in insect cells infected with a recombinant baculovirus containing the NS1 gene. 73
- Figure 2.18:** Autoradiograph of SDS-PAGE separated cell lysates of insect cells infected with recombinant and wild-type baculoviruses. (B) Multimeric NS1 protein complexes were recovered by centrifugation through a 40% sucrose cushion. 74
- Figure 2.19:** Negative contrast electron micrographs. The recombinant baculovirus-expressed NS1 tubules were purified by sucrose gradient centrifugation and stained with 2% uranyl acetate. 76
- Figure 2.20:** Negative contrast electron micrographs of thin sections of insect cells infected with the recombinant baculovirus Bac-AH6NS1. 78
- Figure 2.21:** Electron micrographs of negatively stained tubules , treated with 1 M NaCl (A), buffer of pH > 8.0 (B) and buffer with pH 5.0 - 5.5 (C). 79

- Figure 3.1:** (A) A schematic diagram showing the strategy for cloning both AHSV-9 VP3 and VP7 genes into the dual expression transfer vector, pFastbac-Dual. (B) A schematic representation of a partial restriction map of the dual recombinant plasmid, pFBd-S3.9-S7.9. (C) Agarose gel electrophoretic analysis of pFBd-S3.9-S7.9. 98
- Figure 3.2:** A schematic diagram of the strategy employed for the respective cloning of AHSV-3 and AHSV-9 VP2 genes in combination with AHSV-9 VP3 into the transfer vector pFastbac-Dual. 101
- Figure 3.3:** (A) A schematic representation of a partial restriction map of the plasmid pFBd-S2.9-S3.9, containing AHSV-9 VP2 and VP3 genes in the correct transcriptional orientation for expression by the polyhedrin and p10 promoters, respectively. (B) A restriction analysis of pFBd-S2.9-S3.9. 102
- Figure 3.4:** (A) A schematic representation of a partial restriction map of the plasmid pFBd-S2.3-S3.9, containing AHSV-3 VP2 and AHSV-9 VP3 genes in the correct transcriptional orientation for expression by the polyhedrin and p10 promoters, respectively. (B) A restriction analysis of pFBd-S2.3-S3.9. 103
- Figure 3.5:** (A) A schematic diagram showing the cloning strategy for inserting both AHSV-9 VP5 and VP7 into the dual expression transfer vector, pFastbac-Dual. (B) A schematic representation of a partial restriction map of the recombinant dual transfer vector, pFBd-S6.9-S7.9. (C) An agarose gel electrophoretic analysis of the dual recombinant plasmid, pFBd-S6.9-S7.9. 105
- Figure 3.6:** In situ Northern blot analysis of Sf 9 cells infected with dual recombinant baculoviruses. 108
- Figure 3.7:** (A) SDS-PAGE analysis of cell lysates of insect cells infected with recombinant and wild-type baculoviruses. (B) Autoradiograph of <sup>35</sup>S-methionine labelled proteins separated by SDS-PAGE. 110
- Figure 3.8:** Autoradiograph of SDS-PAGE analysis of <sup>35</sup>S-methionine labelled proteins from cell lysates of insect cells infected with VP3/VP2 dual recombinant and wild-type baculoviruses. 110
- Figure 3.9:** Autoradiograph of SDS-PAGE analysis of <sup>35</sup>S-methionine labelled proteins from cell lysates of insect cells infected with VP5/VP7 dual recombinant and wild-type baculoviruses. 111

- Figure 3.10:** (A) Electron micrographs of empty AHSV CLPs synthesised in insect cells by a recombinant baculovirus expressing the two major AHSV core proteins VP3 and VP7. (B) Negative contrast electron micrographs of the purified CLPs bound to VP7 monoclonal antibodies. 114
- Figure 3.11:** (A) Electron micrograph of partial VLPs synthesised in insect cells by co-infection of a dual VP3/VP7 recombinant baculovirus and a VP5 single recombinant baculovirus. (B) Negative contrast electron micrographs of the purified partial VLPs (CLPs & VP5) decorated with VP5 monospecific antisera and stained with uranyl acetate. 116
- Figure 3.12:** Electron micrograph of partial VLPs synthesised in insect cells by co-infection of a dual VP3/VP7 recombinant baculovirus and a VP2 single recombinant baculovirus. 117
- Figure 3.13:** Electron micrograph of VLPs synthesised in insect cells. In (A) the particles were synthesised by co-infection of a VP2/VP3 and a VP5/VP7 dual recombinant baculoviruses. In (B) the empty AHSV double-shelled VLPs were synthesised by the co-infection of a VP2/VP5 and a VP3/VP7 dual recombinant baculoviruses. 118
- Figure 4.1:** Hydrophilicity (a) and antigenicity profiles (b) of AHSV-9 VP7 in comparison with the predicted solvent-accessibility (c). 134
- Figure 4.2:** A schematic representation of the three-dimensional structure of AHSV VP7 trimer, looking vertically into the top of the trimer. 135
- Figure 4.3:** Schematic representation of the first PCR method used to construct the recombinant transfer vectors containing the mutagenised DNA copies of the VP7 gene. 137
- Figure 4.4:** Agarose gel electrophoretic analysis of the DNA products obtained by PCR amplification of the AHSV-9 VP7 gene (pBR-S7cDNA), using two inverted tail-to-tail mutagenic primers in combination with VP7 5' and 3' end specific primers. 138
- Figure 4.5:** In the second method used for insertion mutagenesis the insertion was performed in a one step PCR process. 139
- Figure 4.6:** (Previous page) Alignment of the nucleotide sequences of the two insertion mutants mt177 and mt200 with the VP7 gene. 141
- Figure 4.7:** Comparison of the deduced amino acid sequences of VP7 and insertion mutants 177 and 200. 142

<b>Figure 4.8:</b> Comparison of the hydrophilicity profiles of AHSV-9 VP7 with that of the two insertion mutants mt177 and mt200.	143
<b>Figure 4.9:</b> A schematic representation of the structure of the insertion mutants mt177 and mt200 monomers as predicted by the MODELLER package.	144
<b>Figure 4.10:</b> Agarose electrophoretic analysis of pFBd-S3.9-mt177 and pFBd-S3.9-mt200.	145
<b>Figure 4.11:</b> SDS-PAGE analysis of the recombinant VP7 protein expression in insect cells.	148
<b>Figure 4.12:</b> Differential centrifugation of the cytoplasmic extracts from Bac-AH9VP7, Bac-mt200 and Bac-mt177 infected cells.	148
<b>Figure 4.13:</b> Sedimentation analysis of the cytoplasmic extracts from Bac-AH9VP7 (A) and Bac-mt177 (B) infected cells by sucrose density centrifugation.	149
<b>Figure 4.14:</b> Sedimentation analysis of the cytoplasmic extracts from Bac-AH9VP7 and Bac-mt177 infected cells by sucrose density centrifugation.	150
<b>Figure 4.15:</b> Scanning electron micrographs of sucrose gradient purified VP7 (A) and mt200 (B1-3) crystals.	152
<b>Figure 4.16:</b> Scanning electron micrographs of purified VP7 crystals (A) and mt177 ball-like structures (B1-3).	153
<b>Figure 4.17:</b> Autoradiograph of <sup>35</sup> S-methionine labelled proteins resolved by SDS-PAGE to evaluate co-expression of AHSV-9 VP3 and the VP7 insertion mutants in insect cells by dual recombinant baculoviruses.	154
<b>Figure 4.18:</b> Electron microscopy of purified CLPs obtained from the co-expression of the two VP7 insertion mutants mt200 (A) and mt177 (B) with AHSV-9 VP3 in insect cells.	156
<b>Figure 4.19:</b> (A) A schematic diagram of the cloning strategy for the construction of two VP7/TrVP2 chimeric genes for expression in the Bac-to-Bac baculovirus system. (B) Agarose gel electrophoretic analysis of the two recombinant chimeric VP7 gene cloned into pFastbac transfer vector.	157
<b>Figure 4.20:</b> Comparison of the hydrophilicity profiles of the two chimeric proteins mt177/TrVP2 and mt200/TrVP2. Hydrophilicity was predicted according to	

Hopp & Woods (1981) utilising the ATHEPROT computer program. 160

**Figure 4.21:** SDS-PAGE analysis of the recombinant VP7 protein expression. Lane 1 contains rainbow molecular weight marker. 161

**Figure 4.22:** A graph representing the sedimentation analysis of the cytoplasmic extracts from Bac-177/TrVP2 infected cells by sucrose density centrifugation. 162

**Figure 4.23:** Scanning electron micrographs of purified chimeric VP7/TrVP2 ball-like structures. (A) Represent structures from 177/TrVP2 and (B) 200/TrVP2. 163

## SUMMARY

*African horsesickness virus* (AHSV), a member of the genus *Orbivirus* in the family *Reoviridae*, is the aetiological agent of African horsesickness, a highly infectious non-contagious disease of equines. The AHSV virion is composed of seven structural proteins organised into a double layered capsid, which encloses ten double-stranded RNA segments. The double stranded (ds) RNA genome of AHSV encodes, in addition to the seven structural proteins, at least three non-structural proteins (NS1 to NS3). The assembly of viral proteins in AHSV-infected cells results in at least three characteristic particulate structures. The first of these structures are the complete virions and viral cores. Empty virions or particles that simulate the virion surface can be produced synthetically by the co-expression of various combinations of AHSV structural genes in insect cells. Apart from the core particles and complete virions, there are two additional structures observed in AHSV-infected cells. Unique virus-specified tubular structures, composed of NS1, are observed in the cytoplasm of all orbivirus-infected cells. The second structure, distinctive hexagonal crystals, is unique to AHSV and is composed entirely of VP7, the major core protein. The assembly of all these particles can be produced synthetically when expressed individually in an insect cell expression system. The aim of this investigation was first of all to investigate the structure and assembly of these structures and secondly to evaluate their use as vehicles for foreign immunogens.

The NS1 gene of AHSV-6 was cloned as a complete and full-length cDNA fragment from purified dsRNA genome segment 5 and the complete nucleotide sequence determined. The gene was found to be 1749 bp in length with one major open reading frame (ORF) of 1645 bp, encoding a protein comprising 548 amino acids. The 5' and 3' termini of the gene were found to contain the conserved terminal hexanucleotide sequences of AHSV RNA fragments, followed by inverted heptanucleotide repeats. The deduced amino acid sequence was analysed and found to define a hydrophobic protein of 63 kDa. Antigenic profile analysis indicated a hydrophilic domain with relative high antigenicity in the C-terminus of the protein. This represents a possible insertion site for immunogenic epitopes. The cloned NS1 gene of AHSV-6 was modified at the 5' and 3' terminal ends to facilitate expression of the gene. *In vitro* expression yielded a protein corresponding to the predicted size of NS1. The gene was also expressed in insect cells, using a recombinant baculovirus and yields of approximately 1.0mg NS1 protein/10<sup>6</sup> cells were obtained. Expression of NS1 in insect cells resulted in the intracellular formation of tubular structures with diameters of 23 ±2 nm. Biophysical analysis of the AHSV tubules suggests that they are more fragile and unstable than BTV NS1 tubules.

To gain more insight into the structure, assembly and the biochemical characteristics of AHSV cores and virions, a number of baculovirus multigene expression vectors have been developed and utilised to co-express various combinations of AHSV genes. Cells infected with a dual-recombinant baculovirus, expressing AHSV-9 VP3 and VP7 genes, contained high levels of VP7 and low levels of VP3. The simultaneous expression of the two proteins resulted in the spontaneous intracellular assembly of empty multimeric core-like particles (CLPs) with a diameter of approximately 72 nm. These particles structurally resembled authentic AHSV cores in size and appearance. The yield of CLP production was low as a result of the insolubility of VP7, which aggregates preferably into large hexagonal crystal as well as the low yield of VP3. The interaction of CLPs with either VP2 or VP5 was investigated by co-infection of the VP3 and

VP7 dual recombinant baculovirus with a VP2 or VP5 single recombinant baculovirus. Each of the outer capsid proteins interacted separately with CLPs. Co-expression of all four major structural proteins of AHSV, using two dual recombinant baculoviruses one expressing VP2 and VP3, the other VP5 and VP7, resulted in the spontaneous assembly of empty virus-like particles with a diameter of 82 nm. Although co-expression of the different combinations of AHSV proteins was obtained, the levels of expression were low. This low levels of the AHSV capsid proteins and the aggregation of VP7 downregulated the assembly process.

In order to investigate the possibility of the use of CLPs and VP7 crystals as particulate delivery systems, insertion analysis of VP7 was used to identify certain sequences in the VP7 protein that are not essential for the assembly of CLPs or trimer-trimer interactions in the crystals. Two insertion mutants of VP7 (mt177 and mt200) were constructed. In each case three unique restriction enzyme sites were introduced that coded for six amino acids. In mt177 these amino acids were added to the hydrophilic RGD loop at position 177 - 178 and for mt200 to amino acid 200 - 201. Both regions were located in the top domain of VP7. Insertion mt177 increased the solubility of VP7, but did not abrogate trimerisation and CLP formation with VP3. The yield of mutant CLPs was significantly higher than the normal CLPs, possibly due to the increased solubility and availability of VP7 trimers. Evidence about the size of an insert that can be accommodated by VP7 was provided by the insertion of a 101 amino acid region of VP2, containing a previously identified immunodominant region of VP2. The two chimeric VP7/TrVP2 proteins were investigated for their ability to form crystal structures and CLPs. The chimeric proteins did not produce the typical hexagonal crystal structure, but rather small ball-like structures.

This investigation yielded valuable information regarding the structure and assembly of AHSV tubules, CLPs and VLPs. These findings also have practical value, since the multimeric structures can be utilised as delivery systems for immunogens, like the AHSV VP2 immunodominant epitopes.

## LIST OF ABBREVIATIONS

AcNPV	-	<i>Autographa californica</i> nuclear polyhedrosis virus
AHS	-	African horsesickness
AHSV	-	African horsesickness virus
AHSV-9	-	African horsesickness virus serotype 9
ATP	-	adenosine-5'-triphosphate
amp	-	ampicillin
BHK	-	Baby hamster kidney cells
bp	-	base pairs
BRDV	-	Broadhaven virus
BSA	-	bovine serum albumin
BT	-	bluetongue
BTV	-	bluetongue virus
°C	-	degrees Celcius
ca.	-	approximately
cDNA	-	complementary DNA
ccc	-	covalently closed circular
CF	-	complement fixation
Ci	-	Curie
CIP	-	calf intestinal alkaline phosphatase
CLP	-	core-like particle
cm <sup>2</sup>	-	square centimetre
cpm	-	counts per minute
CsCl	-	cesium chloride
Da	-	dalton
ddH <sub>2</sub> O	-	deionized distilled water
DEPC	-	deithylpyrocarbonate
dATP	-	2'-deoxyadenosine-5'-triphosphate
dCTP	-	2'-deoxycytidine-5'-triphosphate
dGTP	-	2'-deoxyguanosine-5'-triphosphate
dTTP	-	2'-deoxythymidine-5'-triphosphate
dNTP	-	deoxyribonucleoside-triphosphate
ddATP	-	2',3'-dideoxyadenosine-5'-triphosphate
ddCTP	-	2',3'-dideoxycytidine-5'-triphosphate
ddGTP	-	2',3'-dideoxyguanosine-5'-triphosphate
ddTTP	-	2',3'-dideoxythymidine-5'-triphosphate
DNA	-	deoxyribonucleic acid
DNAse	-	Deoxyribonuclease
ds	-	double stranded
DTT	-	1,4-dithiothreitol
EDTA	-	ethylenediaminetetra-acetic acid
EEV	-	Equine encephalosis virus
e.g.	-	<i>exempli gratia</i> (for example)

EHDV	-	epizootic haemorrhagic disease virus
<i>et al.</i>	-	<i>et alia</i> (and others)
etc.	-	<i>et cetera</i> (and so forth)
EtBr	-	ethidium bromide
FCS	-	fetal calf serum
FESEM	-	Field emission scanning electron microscopy
Fig.	-	figure
g	-	gram / gravitational acceleration
GTP	-	guanosine-5'-triphosphate
GST	-	glutathione S-transferase
h	-	hour
HPRI	-	human placental RNase inhibitor
IgA	-	immunoglobulin class A
IgG	-	immunoglobulin class G
IPTG	-	isopropyl- $\beta$ -D-thiogalactopyranoside
kb	-	kilobase pairs
kDa/kd	-	kilodalton
l	-	litre
LB	-	Luria-Bertani
log	-	logarithmic
M	-	Molar
mA	-	milliampere
MAb	-	monoclonal antibody
MCS	-	multiple cloning site
mg	-	milligram
min	-	minute
ml	-	millilitre
mM	-	millimolar
mmol	-	millimole
MMOH	-	methylmercuric hydroxide
MOI	-	multiplicity of infection
$M_r$	-	molecular weight
mRNA	-	messenger ribonucleic acid
m/v	-	mass per volume
N	-	normal
NaAc	-	sodium acetate
nm	-	nanometre
NS	-	non-structural
OD <sub>550</sub>	-	optical density at 550 nm
OD <sub>260</sub>	-	optical density at 260 nm
ORF	-	open reading frame
OVI	-	Onderstepoort Veterinary Institute

PAGE	-	polyacrylamide gel electrophoresis
PCR	-	polymerase chain reaction
p.f.u.	-	plaque forming units
p.i.	-	post infection
pmol	-	picomole
PSB	-	protein solvent buffer
PSV	-	perdesiekte virus
RE	-	restriction endonuclease
RNA	-	ribonucleic acid
RNAse	-	ribonuclease
rpm	-	revolutions per minute
RT	-	room temperature
RT-PCR	-	reverse transcriptase PCR
s	-	second
S	-	Svedberg unit
S 1-10	-	segment 1-10
SDS	-	sodium dodecyl sulphate
SEM	-	Scanning electron microscopy
Sf9	-	<i>Spodoptera frugiperda</i>
ss	-	single stranded
T <sub>An</sub>	-	annealing temperatures
TC	-	transcriptase complex
TdT	-	terminal deoxynucleotidyl transferase
TEM	-	Transmission electron microscopy
TEMED	-	N,N,N',N'-tetramethylethylenediamine
tet	-	tetracycline hydrochloride
TFB	-	Transformation buffer
Tris	-	Tris(hydroxymethyl)-aminomethane
TSB	-	Transformation suspension buffer
TSBG	-	Transformation suspension buffer with glucose
TX-100	-	Triton X-100
U	-	units
μCi	-	microcurie
μg	-	microgram
μl	-	microlitre
UV	-	ultraviolet
V	-	volts
v	-	volume
VIB	-	viral inclusion body
VLP	-	virus-like particle
VP	-	viral protein
VT	-	viral tubules

- v/v - volume per volume
- W - watt
- X-gal - 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside