INTRODUCTION
Cattle theileriosis is a disease infamous for hampering the economic development of south, central and east African countries due to exorbitant numbers of cattle mortalities [1]. The disease is caused by Theileria parva, a tick-transmitted hemoprotozoan parasite that belongs to the phylum Apicomplexa [2]. Infection of cattle with cattle-derived T. parva isolates is responsible for East Coast fever while infections by buffalo-derived isolates results in Corridor disease. However, these causative agents bear similar morphological and serological characteristics and it is not clear why they cause different disease syndromes. Thus, a transcriptome study comparing the cattle-derived and buffalo-derived parasite isolates was performed to detect differentially expressed genes, using in silico methods. The aim of the study was to annotate functions of selected T. parva hypothetical proteins encoded by differentially expressed genes, using in silico approaches. The foundation of function annotation based on orthology is derived from the notion that proteins with similar sequences hint similar functions [5]. The SVSPs family is characterized by Nuclear Localization Signal (NLS) identified in 18 HPs, signal peptides detected in 17 HPs and FAINT domain found in 20 HPs. Proteins with NLSs are important as they are likely to contribute to the phenotypic changes of the host cell.

AIM
The aim of the study was to annotate functions of selected T. parva hypothetical proteins encoded by differentially expressed genes, using in silico methods.

METHOD/ APPROACH

RESULTS AND DISCUSSION
Classification of hypothetical proteins into functional families (Fig 2)

- Forty-three HPs were characterized into seven canonical protein families; most HPs are associated with binding proteins, catalytic activity and transcription factor activity.
- From binding proteins, four were shown to have a Zinc finger domain, and thus may be involved in regulation of apoptosis. Apoptosis contributes to the pathogenesis of a number of diseases [4].
- Five HPs were classified as enzymes. Enzymes facilitate the parasite’s survival within the host by carrying out several cellular processes making it viable for the course of infection within the host. Hypothetical proteins classified into functional families.

Homology/ Orthology

Fig 3. Schematic presentation of TP09_0882, a typical SVSP. This polypeptide of 607 amino acids has a signal peptide (SP; from residue 1-21) responsible for secretion, followed by two nuclear localization signals (NLS) for protein transportation to the nucleus and lastly two FAINT domains (from residue 146-343 and 520-577).

Homology analysis (Fig 4)

T. parva HPs had homologs, mostly in T. equi, H. sapiens and M. musculus. One homolog of interest was detected in N. caninum, belonging to the Acetyltransferase family protein (TP01_0669), known to be involved in virulence-associated functional roles such as invasion, colonization, evasion of host defence and immunomodulation [6,7].

Fig 4. Hypothetical proteins distribution in different related species. Subcellular localization predictions (Fig 5)

Information obtained from protein sub-cellular localization prediction can be used to infer protein functions and to find novel vaccine and/or drug targets [8]. Three HPs predicted to localize in the cytoplasm were identified as possible therapeutic targets.

CONCLUSION
Using in silico approaches, 266 of the 309 T. parva HPs investigated were successfully assigned probable functions. Secreton analysis revealed 57 HPs containing signal peptides, suggesting possible interactions with the host. Generally, the results of this study will facilitate a better understanding of the mechanism of pathogenesis of cattle theileriosis caused by T. parva and development of more effective disease control strategies.

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