

## **Xth EUROPEAN MULTICOLLOQUIUM OF PARASITOLOGY – from satellites to microsattellites, Paris, August 24-29, 2008.**

### **Molecular characterisation of total and differentially expressed secretome of *Trypanosoma congolense*: identification of novel virulence and/or pathogenic factors.**

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Animal trypanosomosis is one of the most severe constraints to agricultural development in Sub-Saharan Africa and is also an important disease of livestock in Latin America and Asia. The causative agents are various species of protozoan parasites belonging to the genus *Trypanosoma*, among which *T. congolense* and *T. evansi* are the major pathogenic species. The extracellular position of the trypanosomes implies to consider both the parasite and its excreted-secreted factors in the course of both parasite multiplication in the host and the physiopathological processes. The postgenomic era stimulated the development of new techniques (e.g. 2-DE and MS) and bioinformatics tools to identify the locations, functions and interactions of the gene products in tissues and/or cells of living organisms. Both 2-D Electrophoresis and Mass Spectrometry have been very successfully employed to identify in particular proteins involved in host-pathogen interactions. These advances in proteomics led us to propose both a global and a comparative approach of the secretome (*i.e.* naturally excreted-secreted molecules) of *T. congolense* and *T. evansi*. *T. congolense* clones of differing virulence and pathogenicity were used as a model to improve the proteomic approach to highlight novel A molecules related to virulence and pathogenicity. The molecular identification of differentially expressed trypanosomes molecules correlated with either the virulence process or exhibiting potential properties to induce pathogenic dysregulation are promising to define new potential molecular targets for improved field diagnosis and new strategies of interference with the infectious process of animal trypanosomosis.