

**The organisation of congopain-family genes of *Trypanosoma congolense*.  
Insight into genetic diversity of trypanosomes cysteine proteinase  
genes .**

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Congopain is a major cysteine proteinase of *T. congolense* and is thought to contribute to pathogenesis in cattle<sup>1</sup>. The ultimate goal being to generate an immunogen for an anti-disease vaccine strategy, it was important to investigate the variability of genes encoding congopain and related enzymes. Genomic organisation was studied by Southern blot. The pattern was characteristic of genes located in a single locus and organised in tandem repeats of 12-14 copies. To gain insight into the variability of these genes, we cloned the locus through construction and screening of a cosmid library. As homogeneity of the gene units hampered conventional sequencing strategies, a library of gene units was constructed and 50 random clones sequenced. They appeared highly homogenous, both in coding and untranslated region, clustering in three families differently represented. Interestingly, one cluster of genes (7/50) shows a crucial substitution of the active site cysteine by a serine. It was established by reverse transcription that the gene(s) is indeed translated. Through expression in *Pichia pastoris*, indirect evidences suggest that the enzyme is active. Possible implications of this enzyme in host-parasite relationships remain to be investigated. A PCR approach using a few sets of degenerated primers was used to explore variability across *T. congolense* strains and across trypanosome species. Despite the limited number of trypanosome clones tested, this study showed remarkable CP sequence conservation in a given species. Once again, genes showing a cys/ser substitution appear common in all African trypanosome species tested.

1. Authié E. 1994. Parasitol. Today 10, 360-364.