wellcome trust
Sanger institute

Gene DB

Fam1: **Proline-rich VSG-like protein**

T. brucei 927

T. b. gambiense 972

Tb927.6.1310

Tb927.6.1370
Tb927.6.1390

1.00/100

1.00/100

Tb927.6.1350

Tb927.6.1330

0.1 sub/site
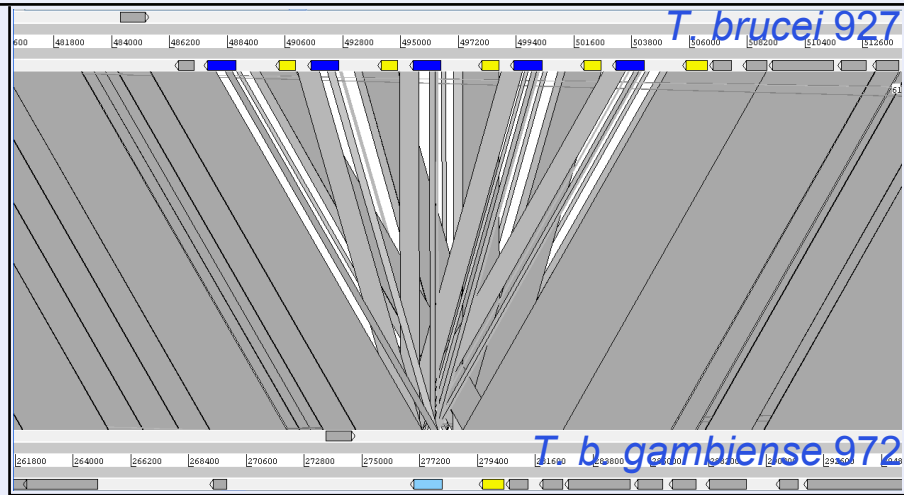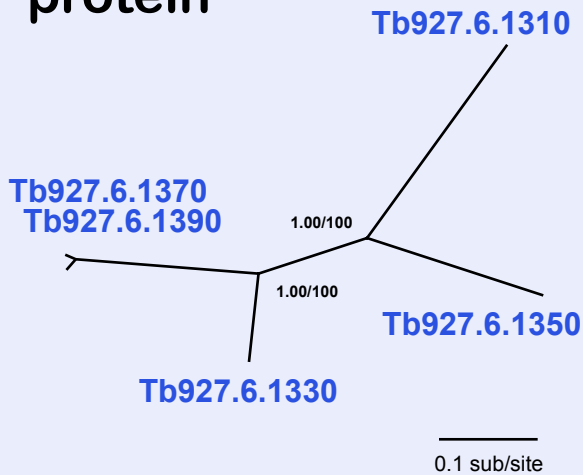
! Fam1 occurs at a single strand-switch region in *T. brucei*, and its copy number may differ between strains (*inset, ACT comparison of* T. brucei *and* T. b. gambiense; *genes are shaded blue (Fam1) or yellow (putative cyclophilin-type peptidyl-prolyl cis-trans isomerase)*). The gene encodes a 347aa protein with a b-VSG-like core, terminating in a proline string and a unique C-terminal domain. Each protein has a predicted signal peptide and GPI-anchor. Fam1 proteins are localized in *T. brucei* to the flagellar pocket and endosomes (*below*), and may be preferentially expressed in metacyclic cells within the insect salivary gland*.

	HA::Tb927.6.1310	ConA	Merge	Merge + phase
4°C no detergent				
12°C + detergent				

2μm
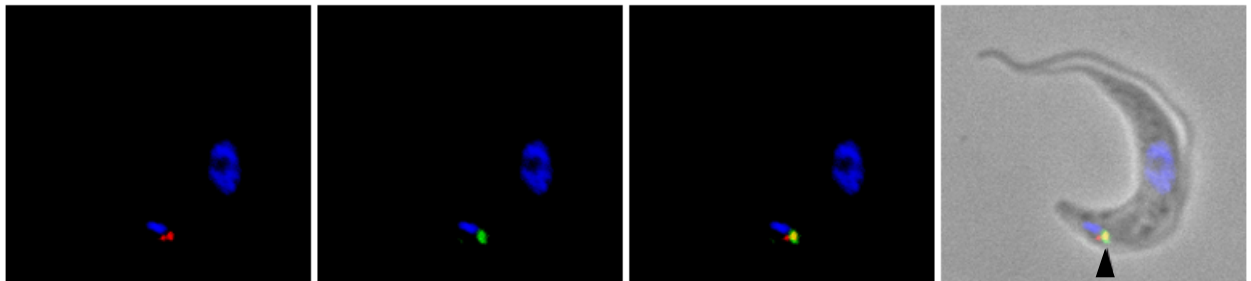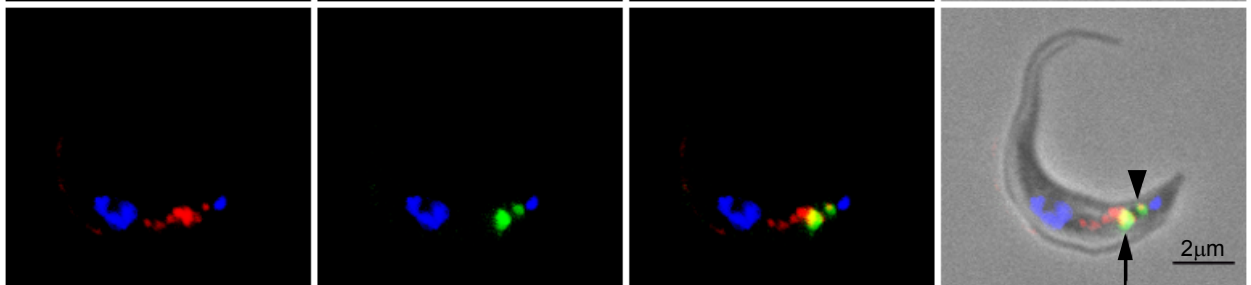
NOTES: **Fam1** consists of five, non-identical tandem gene copies at a strand-switch region on chromosome 5, which is unique to *T. brucei*.

Immunofluorescence analysis (Harriet Allinson & Mark Field, University of Cambridge): Tb927.6.1310 was N-terminally HA epitope-tagged and expressed in bloodstream-form cells. Cells expressing HA::Tb927.6.1310 were loaded with FITC-concanavalin-A in serum-free media and incubated at either 4oC (upper panel) or 12oC (lower panel). ConA is restricted to the flagellar pocket at the lower temperature, whereas it is transported to, and trapped within, Rab5A positive early endosomes at 12oC. Columns in each panel (from left to right); fluorescent stain of HA epitope tag (red); FITC-ConA fluorescence (green); merged images for fluorescence; merged images from phase and fluorescence. DAPI-stain of the nucleus and kinetoplast is shown in blue. HA::Tb927.6.1310 colocalises with ConA at the flagellar pocket (indicated with arrow head) and early endosomes (indicated with a whole arrow). * Savage *et al*. 2012. PLoS Negl Trop Dis 6(6): e1708.

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 1068 characters, using MrBayes under default settings. The tree is midpoint-rooted. Nodes are supported by posterior probability values and non-parametric bootstraps generated from a maximum likelihood analysis using an GTR+Γ model.