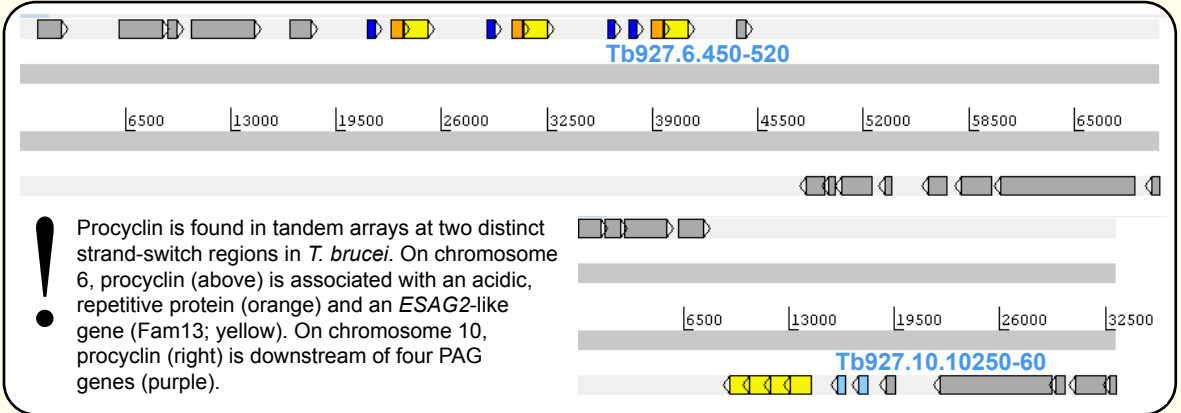


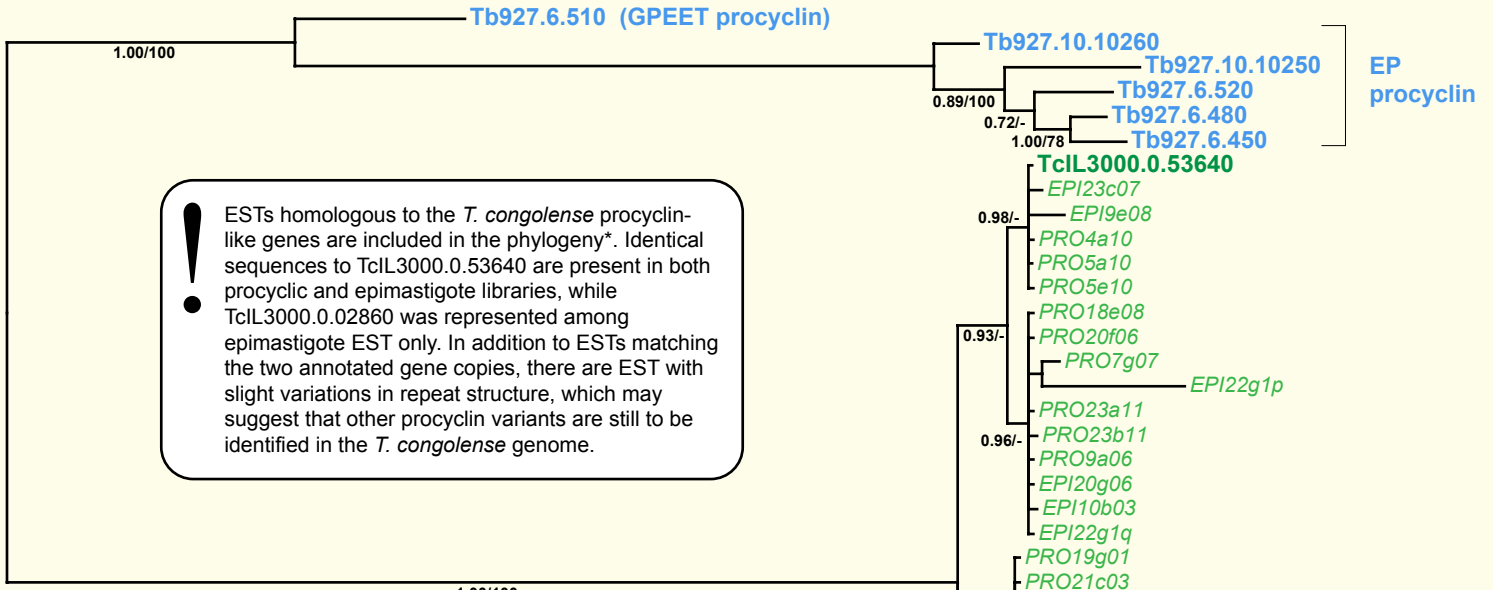
If you use these data, please cite:

Jackson, AP et al. 2012. A cell-surface phylome for African Trypanosomes. *manuscript submitted*.

# Fam12: Procyclin



0.5 rep/site



ESTs homologous to the *T. congolense* procyclin-like genes are included in the phylogeny\*. Identical sequences to TcIL3000.0.53640 are present in both procyclic and epimastigote libraries, while TcIL3000.0.02860 was represented among epimastigote EST only. In addition to ESTs matching the two annotated gene copies, there are EST with slight variations in repeat structure, which may suggest that other procyclin variants are still to be identified in the *T. congolense* genome.

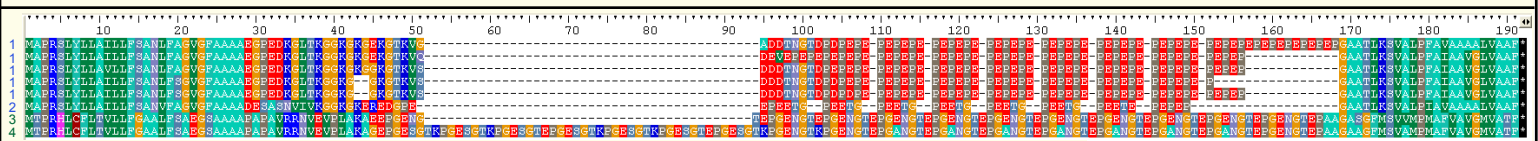
All procyclin genes in *T. brucei* encode proteins with predicted signal peptides and GPI anchors (below, a multiple alignment of procyclin amino acid sequences, dashes denote gaps). These two features are conserved in the *T. congolense* homologs. Between these features both species have amino acid repeat units. *T. brucei* has the 'EP' (1) and 'GPEET' (2) types, while *T. congolense* has 'EPGENG' (3; i.e. TcIL3000.0.53640) and 'EPGAN' (4; i.e. TcIL3000.0.02860).

Although *T. vivax* does not have a life stage within the insect midgut, there is sequence (TvY486\_0015640; 320aa) that is similar to procyclin in structure and length, and contains a 14-mer repeat 'GTEGDAEGVAEGGL' between predicted signal peptide and GPI anchors.

Key: **Tb927.**  
*T. brucei*

**TcIL3000.**  
*T. congolense*

**PRO23a11**  
*T. congolense*  
EST



**NOTES:** Fam12 consists of procyclin, the major surface glycoprotein of the procyclic (insect midgut) stage of *T. brucei*, in both EP and GPEET isoforms, and two *T. congolense* homologs. \* Helm et al. (2008) *Mol. Biochem. Parasitol.* **168**: 34–42.

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 597 characters, using MrBayes under default settings. The tree is mid-point rooted. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis under a GTR+Γ model.