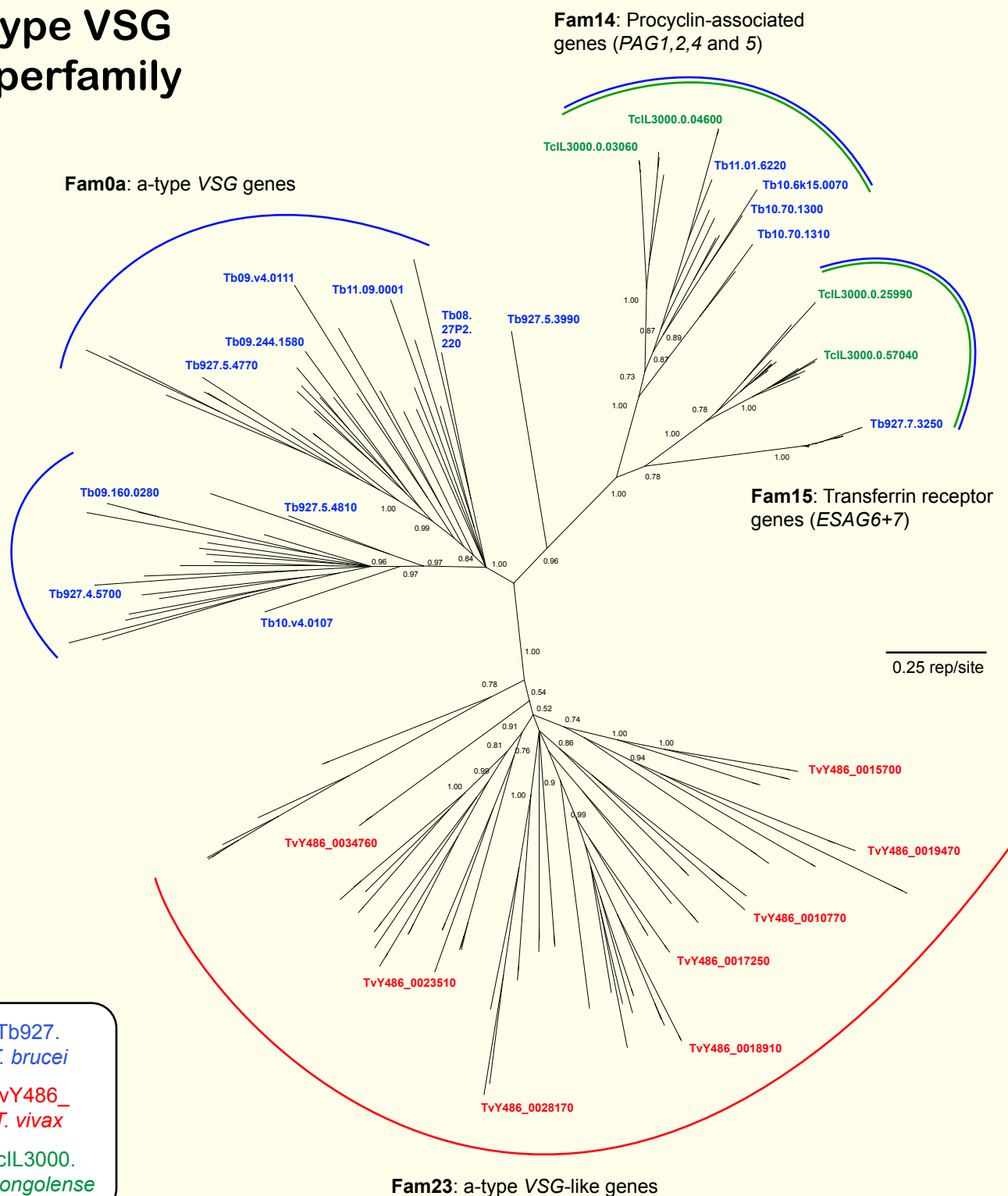


If you use these data, please cite:

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

a-type VSG superfamily



NOTES: The Bayesian consensus phylogram was estimated from a multiple protein sequence alignment of 421 characters, using MrBayes with a WAG model and corrections for rate heterogeneity. Four MCMC chains were run for 5000000 generations to encourage maximal convergence of model parameters. The tree is unrooted. Selected nodes are supported by posterior probability values and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity, executed using RAXML.

a-VSG from *T. brucei*, Fam23 from *T. vivax* and transferrin receptor-like genes from both *T. brucei* and *T. congolense* form three robust clades. Example gene names are given for each clade. Fam0a splits into two distinct clades, which correspond to sequences with (upper) and without (lower) the 'GRIDE' motif generally characteristic of a-type VSG families (see Fam0a and Fam23 pages for more information).