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 Jackson, AP et al. 2011. Divergent evolution
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Fam0a: a-type VSG



! Telomeric VSG from bloodstream expression sites are shown here in yellow boxes. These are largely taken from *T. brucei* 427, and the expression site number is given*. Three VSG from *T. brucei* 927 expression sites are also included (marked with a hash #). Telomeric VSG from metacyclic expression sites are shown in orange and labelled with their database accession number.

It is clear from their distribution that telomeric VSG are not a distinct subset of all VSG, but are instead a random sample of total diversity.

Similarly, two VSG taken from a published mini-chromosome sequence in *T. brucei* 927**, and highlighted in pink, cluster among subtelomeric VSG, and so do not appear to be structurally distinct.

NOTES:

Fam0a includes the a-type variant surface glycoprotein genes from *T. brucei*. All full-length genes and pseudogenes (n=427) were selected from vsgDB (www.vsgdb.net).

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 2035 characters, using MrBayes with a GTR+ Γ model and default settings. This included the C-terminal domain. The tree is rooted using transferrin-receptor-like sequences from *T. brucei* and *T. congolense*. Selected nodes are supported by posterior probability values.

* Hertz-Fowler et al. (2008). *PLoS One*, 3(10): e3527. ** Alford et al. (2001). *Mol. Biochem. Parasitol.* 113(1):79-88.

Outgroup:
 Transferrin-
 receptor
 genes