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Nuclear Chromatin Interactions Underlie Epigenetic Regulation of Antigenic Variation

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In the mammalian host, bloodstream trypanosomes elude the immune response by periodically changing their main surface antigen, the Variant Surface Glycoprotein (VSG). To achieve the expression of a single type of VSG on the surface, only one out of ~15 possible subtelomeric VSG expression sites (ESs) is transcribed at a given time. Unusually, the active VSG-ES is transcribed by RNA polymerase I and is located in an extra-nucleolar nuclear body named the expression site body (ESB)¹. It has been suggested that maintenance of the epigenetic state of monoallelic expression of the active VSG-ES locus could be mediated by exclusive association to the nuclear ESB^{1,2,3}.

Using GFP tagging of chromosomes in trypanosomes⁴, we have recently shown that during the cell cycle sister chromatids of the active VSG-ES remain held together longer than other loci. Interestingly, sister chromatids remain associated to the unique ESB present in the nucleus until chromosome segregation. The cohesin complex is important in preserving VSG-ES activity, as the knockdown of cohesin subunits lead to premature separation of sister chromatids of the active VSG-ES and promotes a transcriptional switch from the active VSG-ES to a previously inactive one. These results suggest that cohesins play a crucial role in ensuring proper epigenetic inheritance of the VSG transcriptional state⁵.

The DNA-binding protein CTCF operates as a transcriptional insulator and functionally associates with cohesins^{6,7}. Removal of cohesins could then hamper the proper insulation of the active VSG-ES. A trypanosome CTCF functional orthologue was identified together with its binding sequences, which loop upstream of the VSG-ES promoter, as suggest by EMSA and 3C experiments. Knockdown of TbCTCF results in 15 fold down-regulation of active 221 VSG-ES transcription. In sum, we have identified a transcriptional insulator in *T. brucei* and described a functional association between cohesins and TbCTCF in the regulation of VSG monoallelic expression.

Bibliography

- 1 Navarro, M. & Gull, K. A pol I transcriptional body associated with VSG mono-allelic expression in *Trypanosoma brucei*. *Nature* **414**, 759-763 (2001).
- 2 Borst, P. Antigenic variation and allelic exclusion. *Cell* **109**, 5-8 (2002).
- 3 Navarro, M., Penate, X. & Landeira, D. Nuclear architecture underlying gene expression in *Trypanosoma brucei*. *Trends Microbiol* **15**, 263-270 (2007).
- 4 Landeira, D. & Navarro, M. Nuclear repositioning of the VSG promoter during developmental silencing in *Trypanosoma brucei*. *J Cell Biol* **176**, 133-139 (2007).
- 5 Landeira, D., Bart, J. M., Van Tyne, D. & Navarro, M. Cohesin regulates VSG monoallelic expression in trypanosomes. *J Cell Biol* **186**, 243-254, (2009).
- 6 Parelho, V. *et al.* Cohesins functionally associate with CTCF on mammalian chromosome arms. *Cell* **132**, 422-433 (2008).
- 7 Wendt, K. S. *et al.* Cohesin mediates transcriptional insulation by CCCTC-binding factor. *Nature* **451**, 796-801 (2008).

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