"The *Trypanosoma brucei* DNA damage repairome"

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Trypanosoma brucei, is an extracellular parasite that has evolved to evade the host's immune system by antigenic variation, facilitated by an extensive variant surface glycoprotein (VSG) repertoire. Antigenic variation principally involves homologous recombination (HR), a complex process that requires both genetic factors and post-translational modifications (PTMs). Several reversible PTMs (phosphorylation, SUMOylation, ubiquitination, acetylation) are vital for the tight and accurate response to cellular damage but, until recently, only one DNA damage-associated phosphorylation site had been identified in *T. brucei*, that of γH2A. Using an unbiased single-locus biochemical screen, we characterised a double strand break (DSB) at a chromosomal internal region versus a bloodstream form expression site (BES). We detected 6500 phosphorylated sites, including a core set of 211 DSB-responsive phosphosites and found that dephosphorylation predominates at a BES, highlighting a key difference between breaks at these two genomic loci. We identified two additional DSB modifications on the H2A: S113 and S133, with only T131 and S133 being conserved amongst trypanosomatids, and a novel phosphorylation site at the C terminus of H2B (Tb927.10.10590), S39. Combined, these findings suggest that histone phosphorylation is important to the *T. brucei* DDR, possibly mediating access to associated chromatin. Additionally, we found two phosphosites on RPA1 (Replication Protein A1), S5 and S43, that play a role in efficient DNA repair. We aim to generate a map of repair interactions in trypanosomes and define the 'repairome', which has the potential to provide invaluable insights into the dynamics of VSG switching.