

P012 Dissecting the SUMOylation pathway in DT40

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One way in which cells regulate protein function is through post-translational modification with the Small Ubiquitin related modifier SUMO. Whilst yeast possesses a single SUMO protein, vertebrates have at least three SUMO paralogues, termed SUMO-1, SUMO-2 and SUMO-3. Based on their sequence these proteins fall into two distinct subclasses; SUMO-1 shares approximately 50% identity with SUMO-2 and SUMO-3, whereas the latter differ by only 3 amino acid residues. Whereas the majority of SUMO-1 is found conjugated to proteins, a large pool of SUMO2/3 remains free, becoming conjugated to its targets in response to cellular stress. However, very little is known about the functional differences between SUMO-1, SUMO-2 and SUMO-3.

To investigate the roles of these SUMO proteins in cells we have taken advantage of the genetically tractable vertebrate DT40 cell line. These cells, derived from avian B-cell lymphoma cells exhibit a high homologous targeting efficiency, enabling the generation of multiple gene disruptions in an isogenic background. Here we present our work analysing *sumo2*, *sumo3* and *sumo2sumo3* DT40 mutant cells, showing that SUMO-2 and SUMO-3 accumulate at the midbody during cell division suggesting a possible role in cytokinesis. We also examine the role of SUMO proteins in the cellular response to DNA damage.