



A novel transcription-based assay for identification of SUMO-modification in vivo and its application in proteomics.

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Background

Primary translation products are often modified by specific enzymatic reactions that catalyze a covalent addition of chemical/molecular groups to specific amino-acid residues. Ubiquitination, an extensively studied example of posttranslational modification, involves the transfer of a polypeptide called ubiquitin to lysine residue(s) of the target protein, which usually serves as a signal for degradation of the modified protein by the 26S proteasome.

Recently, a number of proteins have been discovered that share similarities to ubiquitin. A prominent example of these is "SUMO" ("small ubiquitin-like modifier"). In contrast to ubiquitination, SUMO-modification does not result in degradation of the target proteins but instead modulates protein function by enhancing protein stability, modulating specific protein-protein interactions and/or altering trafficking and localization of target proteins. There have been a number of SUMO-modification targets identified, including tumor suppressors p53 and PML, proto-oncogene MDM-2, nuclear-pore component RanGAP1 and others. Nevertheless, it is likely that many more SUMO-modified proteins which serve important functions under normal or abnormal cellular conditions remain to be discovered. Identification of new SUMO-modification targets is not only necessary to further understand the mechanisms and function of SUMO modifications, but also may provide novel targets for developing therapeutic drugs that regulate many important cellular processes.

Description of the Project

Dr. Samuels and his coworkers designed a novel transcription-based assay for SUMO-modification *in vivo*. This method has several advantages over other current methods of identification of SUMO-modification. Firstly, the assay is carried out in living cells and therefore utilizes the cellular enzymatic system for posttranslational modification. Secondly, this method is less time consuming and more sensitive than previously described assays. Finally, unlike other methods, Dr. Samuels's method eliminates the need for specific antibodies.

Applications

This novel transcription-based essay can be used to examine whether a protein is a potential target for SUMO-modification. It can also be used to identify new protein targets for this posttranslational modification. In addition, this method may be used to identify new components of the enzymatic machinery involved in SUMO-modification. For example, new candidate E3 ligases which can enhance SUMO-modification can be discovered. **Importantly**, this method can be scaled up to screen a large number of candidate proteins for SUMO-modification and thus may have useful implications in proteomics .

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