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Title:	Molecular evolution of Sde2
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Abstract:	Ubiquitination is one of the most common post-translational modification in eukaryotes. Ubiquitin usually regulates protein function by serving as a tag for degradation. A special group of enzymes called deubiquitinating enzymes (DUBs) perform the task of removing ubiquitin moieties from proteins. Recently, DUBs have also been reported to cleave the ubiquitin fold (Sde2-UBL) from the splicing regulator Sde2 in Schizosaccharomyces pombe (fission yeast). Such a resemblance in the structural architecture and processing machinery of ubiquitin and Sde2-UBL tempted us to trace the evolutionary origins of the two. Our study suggests the likely possibility that Sde2-UBL might have evolved from ubiquitin by diverging from it as a consequence of minimal selection pressure. In the latter parts of our study, we also attempted to analyse our results in the context of the factors that would determine the specificity of the DUBs towards Sde2-UBL. We infer that the ubiquitin fold of Sde2-UBL itself may not play an important role in determining the specificity of the DUBs, but a meagre 8 amino acid sequence at the C-terminus of Sde2-UBL might be the key player in dictating specificity to the DUBs.
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