Studying the splicing of the wild type group II intron Sc. ai5g at non-physiological and near-physiological conditions

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The group II intron family represents a large class of non-coding RNA elements found in bacteria and lower eukaryotes. *In vitro,* group II introns are known to undergo Mg^{2+} dependent self-splicing during mRNA maturation. [1]. Under near physiological conditions the intron folding and splicing is assisted by a cofactor, namely the DEAD-box ATP dependent helicase Mss116 [2]. The aim of our research is to study these mechanisms in the wild type group II intron *Sc.* ai5γ from *Saccharomyces cerevisiae.* We are investigating the splicing during the mRNA maturation at non-physiological (high Mg^{2+}) or near-physiological (low Mg^{2+}) conditions and in the presence or the absence of the coenzyme Mss116. Intensive studies over the past decades have concentrated on an engendered intron model, whereas we are interested in the wild type molecule. *In vitro* splicing mechanism of the full-length intron will be followed by fluorescent native polyacrylamide gel electrophoresis (PAGE). We established a strategy for visualizing the splicing process by labelling the flanking exons with peptide nucleic acids (PNA) [3], both carrying fluorescence dyes. We are interested in the RNA splicing behavior at different salt concentration and in the presence of the cofactor. A comparison of the splicing between the wild type group II intron and the well-studied truncated model at non-physiological conditions will allow the investigation of two models at near natural or non-natural state and give insights of similarities and lead to a better understanding of the splicing processes

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