Title:	Investigations on the intersection between folate & methionine pathways in Saccharomyces cerevisiae
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Abstract:	The folate and methionine cycles are part of a fundamental metabolic pathway, one-carbon metabolism, in all living cells. The folate cycle serves to produce activated one-carbon units and transfers them to the methionine cycle for the production of methionine. Unlike animals, yeasts can synthesize folates de novo using their folate biosynthetic pathway, which converts GTP into THF and THF enters the folate cycle. The conversion is catalyzed by enzymes encoded by three FOL genes, FOL1, FOL2 & FOL3. The FOL3 gene has a paralog, RMA1, whose gene product shares similarity with that of FOL3. One of the objectives of the study is to examine if RMA1 is a functional homolog of FOL3. The SAM is synthesized from methionine in the methionine cycle and is a major methyl donor for various cellular metabolism reactions, being the second-only entity after ATP. The SAM4 gene was identified to code for SAM-homocysteine methyl transferase enzyme catalyzing the reaction that majorly recycles the SAM in cells apart from the two already known pathways: methionine cycle and MTA salvage pathway. It was observed that SAM4 gets upregulated in a methionine-supplemented environment, unlike any other classical MET genes of the methionine pathway. However, it gets downregulated when the cells are starved for folate despite the presence of methionine. The study aims to investigate this unique behaviour of SAM4 by identifying the regulatory regions in the promoter region. In vivo homology-based cloning using yeast was implemented to investigate the two genes, which is a simple and robust alternative to conventional cloning. The present study adds on the split-vector strategy, which has been previously used for genome assembly (Kuipers et al., 2013) to clone the gene/ promoters of interest, expanding its applications.
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