

P046 Modelling human meiotic recombination
in *Saccharomyces cerevisiae*

**Patricia M R Aldred¹, Eva R Hoffmann²,
Maria Almedia³ and Rhona H Borts¹**

¹Department of Genetics, University of Leicester, University
Road, Leicester, LE1 7RH, UK, ²MRC Genome Damage
and Stability Centre, University of Sussex, Falmer, BN1
9RQ, UK, ³Institute of Molecular Medicine, GenoMed,
Av Professor Egas Moniz, 1649-028 Lisbon, Portugal

Errors during meiosis can cause problems with infertility and aneuploidy. We aim to use *Saccharomyces cerevisiae* as a model system through which to study the functional effects of polymorphisms in human meiotic recombination genes.

Our project involves deleting *S. cerevisiae* genes and expressing the human orthologue in the deletion strain with the aim of complementing the function of the yeast gene. Complementation is assessed by study of meiotic recombination rate. Ultimately, known polymorphisms will be introduced into the human gene sequences and their functionality and affect on recombination assessed.

Preliminary results suggest that hMSH2 and hMSH6 expressed together from plasmids can complement the mismatch repair function of yeast Msh2p and Msh6p. Eventually all of the human genes studied will be inserted as single copies to present expression levels similar to the native yeast protein. Once a human gene sequence is inserted into the yeast genome, simple transformation and homologous recombination will allow site-specific mutagenesis to introduce point mutations.

This project emphasises the powerful diagnostic potential of using yeast to model human genes and potentially functional DNA changes.