*Poster*

# Identification and characterization of a mutant that shows genomic instability.


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## ABSTRACT

**Motivation:** The fission yeast, Schizosaccharomyces pombe, is an important model organism for the study of eukariotic molecular and celular biology, including processes like cell cycle control that attracts an especial interest due to their relation with cancer and tumorigenesis [1]. Previous work of our group showed that RNA metabolism is the primary target of formamide in vivo, probably by weakening RNA secondary structure and its interaction with other proteins. In this study 35 Formamide Sensitive Mutant strains (fsm) have been isolated [2]. In the present work, we aim to identify and characterize one of these mutants (fsm43), which presents an interesting phenotype since it shows defects in chromosome segregation and aberrant cell division. These phenotypes are usually involved in tumoral processes so its study and characterization may identify new oncogenic mutations and reveal new treatment targets.

**Methods:** Provided that this mutation has been proved very difficult to complement by genomic libraries, As a first step in this project, a genetic mapping of the formamide sensitive mutation in fsm43 will be carried out to determine its position in the genome. The methodology to follow is described in Anders et al.[3] and it is based on the amplification of linkage distance using two gene deletions, rec12 and swi5. Together, the two methods allow an approximate determination of map position in only a small number of crosses. First we used rec12 deletion that produce a recombition-deficient that allow choose an individual chromosome, and then swi5 mutants that have a reduced frequency of both intragenic and intergenic recombination. Then we use a classical method of linkage proving different genes that are in the region that we determinate previously. In parallel we have initiated cellular characterization of the mutant phenotype under permisive and restrictive conditions.

**Results:** So far, by long range analysis we have been able to map the mutation on chromosome III. Swi5 deletion background show that the gene is on the right arm of the chromosome between markers tea1 and ima1. Current analysis by classical linkcage on the region, will determine the precise location of fms43 mutation.

**Conclusions:** Fsm43 is a recessive mutation that leads to severe genomic instability. This mutant can not be complemented by genomic libraries but is amenable for linkage analysis. The mutation lies on right chromosme III arm within tea1 and ima1 markers (45 Kb).

## REFERENCES

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