Meiotic Recombination in Barley

Approaches to analyze barley desynaptic mutants

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Introduction

During meiosis, homologous chromosomes recognize each other, align and pair via chiasmata, ensuring correct segregation at metaphase and thus avoiding aberrant chromosome numbers within gametes. This process also ensures the fundamental process of recombination between parental alleles within progeny that underpins much of genetics and breeding programmes. In crops such as wheat or barley, the distribution of chiasmata is markedly skewed towards the telomere, meaning that a considerable proportion of the genome rarely recombines. An ability to modify the pattern of recombination in these species could therefore have profound impact on the breeding of the crops. As part of the EU FP7 project 'MeioSys', information and data derived from the model plant Arabidopsis *thaliana* is providing a basis for the development of reverse genetics strategies to understand and thus modify recombination in barley. In addition, a collection of barley desynaptic mutants provides a complementary forward genetics strategy for understanding the control of meiosis in cereals. These lines are being assessed both cytologically and genetically to assess the impact of the mutations on recombination.

The barley desynaptic mutant *des7*

Mapping

Des7 is part of a collection of 14 non-allelic *des* mutants that have been backcrossed into a common Bowman background (J.D. Francowiak). The position of the introgression and thus the putative map position of the mutation for des7 has been delineated to a small interval on 2H through SNP genotyping (A. Druka). A segregating population derived from a backcross line is currently being used for fine mapping.

Phenotype

Des7 shows varying degrees of semi-sterility (fig1) from having a few seeds missing to a completly sterile spike when compared to the wild type.

Fig1: *Des7* Fertility

Cytology

In barley, metaphase exhibits seven ring bivalents (Fig2a), resulting in equal reduction of the homologues at Anaphase I (Fig2d). *Des7* has abnormal metaphases, exhibiting mainly Rod-bivalents and univalents (Fig2b,c) resulting in abberant segregation and chromosome loss (Fig2d). It sometimes shows chromosome bridges at anaphase (Fig2f, white arrow).

The protein ASY1 loads on the chromosome at G2/leptotene to fully coat the chromatin at zygotene (Fig2g). Immunolocalization of ASY1 in *des7* shows a normal loading (Fig2h) although we can notice some very condensed foci in the nucleus (Fig2j).

Mid-zygotene, the protein Zyp1 starts loading on the chromosomes to bring the homologues together to be fully synapsed at pachytene (Fig2k). Confocal images of pachytene nuclei from *des7* show colocalization of ASY1 (Fig2l) and ZYP1 like in the wild type. 3D-SIM images of des7 clearly show the 2 homologues labelled with ASY1 (Fig2m) linked together via ZYP1 (Fig2n,o).

Des7 initially called "desynaptic" as regard for its abnormal metaphase shows a normal synapsis suggesting that the mutation does not affect the mechanism involving the proteins ASY1 and ZYP1. Further analysis with meiotic protein and time course analysis (BrdU) will be done to understand what could be the cause of the semi -sterility phenotype.

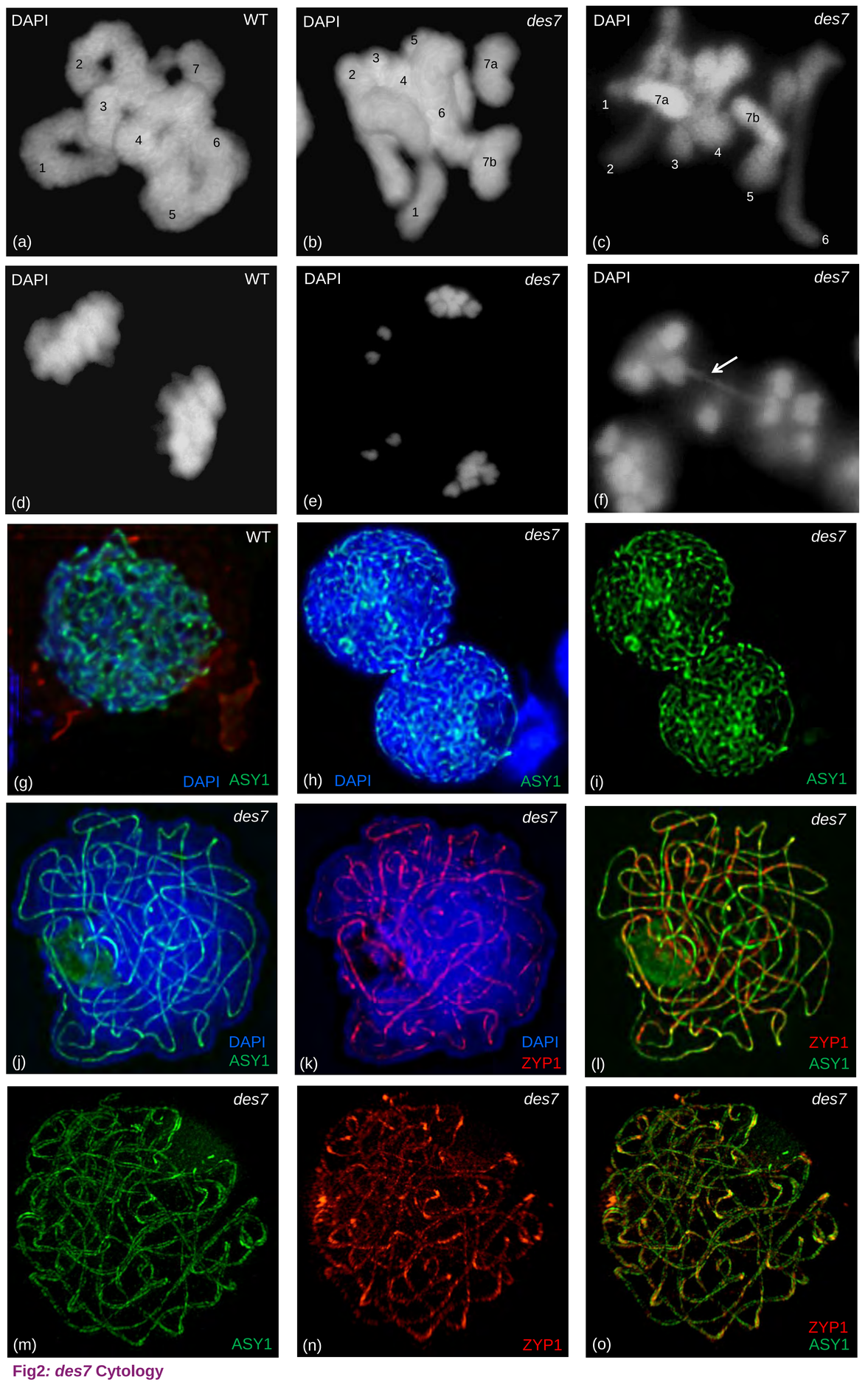

Fig2*: des7* Cytology

Conclusions

The EU FP7 project MeioSys, brings together nine participants and combines approaches in genomics and systems biology with the aim of obtaining a detailed understanding of the factors that control recombination. An important strand of the project is the utilization of knowledge derived from Arabidopsis to provide a basis for the development of strategies to modify recombination in barley.

The transfer of knowledge to the crop will involve the development of novel resources with altered meiotic phenotypes. These will provide the means of improving our understanding of chromosome pairing, synapsis and recombination in cereals and allow manipulation of the frequency and distribution of recombination to enable breeders to access variation in these low-recombinogenic regions of the genome.

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MeioSys
SEVENTH FRAMEWORK PROGRAMME