ABSTRACT SUBMISSION FORM FORMAT

**<TITLE/ALL CAPS/ARIAL/FONT 12PT>**

<Authors/Full Name, First, Lastx/Presenting author underlined and bold>/Arial/Font

12 pt

<xAuthor Affiliations/ Dept/Institution/City/Province or State/Country>

<Abstract text/Max 400 words/No Tables or Figures>

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***Recombination & Pollen Development***

***Development***

***Phenotyping***

***Below and Above Ground Processes***

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EXAMPLE

**Identifying induced mutations in barley meiotic genes**

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Barley is an important cereal crop having a non-random pattern of recombination which results in around 30% of the genes in the centromeric region not involved in the process of recombination. This is an impediment for both geneticists and likely also for breeders. Recombination occurs during meiosis as unresolved chromosomal crossover. One phenotype which can be observed by disrupting meiotic genes is semi-sterility. In a first attempt to identify genes involved in meiosis and therefore in recombination, we have identified semi-sterile mutants from two independent TILLING (Targeting Induced Local Lesions in Genomes) populations in the barley cultivars Optic and Golden Promise. Using our specific designed target exome capture array which contains baits for 46 meiotic genes we screened around 180 semi-sterile lines per population. We were able to identify mutations within most of our candidate genes from both populations. A first analysis was done using metaphase spread, which can highlight problems during meiosis, already identified some plant lines we would like to follow up. Future work will involve crossing the mutants to the barley cultivar Bowman, analysing if there are any changes in recombination but also trying to identify the exact function those genes might have in barley as transfer of function based on information from other species might not give the correct answers.