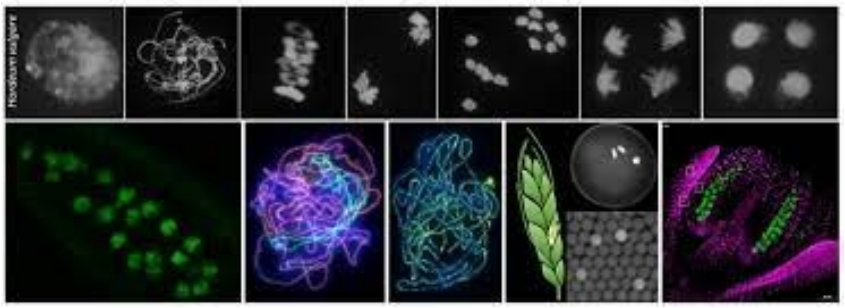
Special Seminar

To invite researcher from Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, we will hold a special seminar on plant meiosis.

Date and Time: October 16, 2023, 10:00-11:00
Place: Multipurpose room, ALRC



Dr. Stefan Heckmann

(Group leader of meiosis, Leipniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany)

TurboID-based identification of novel meiotic candidates in Arabidopsis to harness meiotic recombination in crops such as barley

Natural genetic variation harnessed during breeding is primarily assured by reciprocal DNA exchanges between homologous chromosomes (crossover, CO) during meiosis. CO formation occurs in the context of the meiotic chromosome axis, a proteinaceous structure along which sister chromatids are arranged in a loop-base array during meiotic prophase I. In plants including barley (*Hordeum vulgare*) tight CO regulation results in a limited number of CO that are skewed towards chromosome ends with large portions of the genome (particularly interstitial chromosome regions) kept untapped during breeding. Hence, new strategies and tools are needed to modify meiotic recombination outcome. To enable proteomic identification of (new) meiotic proteins, we used TurboID (TbID)-based proximity labeling in meiotic cells of *Arabidopsis thaliana* for two meiotic chromosome axis-associated proteins ASYNAPTIC1 (ASY1) and ASYNAPTIC3 (ASY3). Among 39 identified candidates most known axis-related and novel proteins were identified. After mutant screening, we identified (at least) four of the novel candidates with a meiotic mutant phenotype. Among them, one candidate was found to be part of the synaptonemal complex (SC). In its absence, SC formation is disrupted and chiasmata formation is reduced while CO levels are increased and CO interference is virtually abolished. To rapidly assesses and study meiotic genes in barley, we established barley stripe mosaic virus-induced gene editing (BSMVIGE) in Cas9 expressing plants and multiplex crystal digital PCR (dPCR)-based single pollen nucleus genotyping. BSMVIGE enables to isolate barley plants defective for meiotic genes without the need of stable genetic transformation and single pollen nucleus genotyping enables high throughput assessment of recombination rates without growing segregating offspring populations. The application of our setup is shown for various meiotic genes in barley demonstrating that the barley recombination landscape can be altered. Together, TbID-based proximity labeling enables the identification of protein proximate proteins in rare cell types such as meiotic cells and BSMVIGE together with single pollen nucleus genotyping enables rapid dissection of meiotic gene function in barley and likely also other crops.

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