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**Oral Communication Abstract – 5.01**

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**REVERSE GENETIC TOOLS AND THEIR UTILIZATION TO DISSECT GRAIN  
YIELD COMPONENTS IN WHEAT**

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Wheat is a young polyploid species with a high level of functional redundancy among homeologs. As a consequence, the effect of many recessive mutations remain invisible to the breeders and natural selection. For many genes, combined mutation in all homeologs are required to determine gene function. In 2017, we developed a mutant database in tetraploid wheat Kronos and hexaploid wheat Cadenza including 10,000,000 sequenced EMS mutations. These mutations have been remapped to CS RefSeq v1.1 and are available in ENSEMBL wheat with their predicted effects on the encoded proteins. These mutants have been extensively used worldwide to study gene function in wheat. We recently developed a promoter capture database in Kronos including additional 5,000,000 sequenced mutations in the promoter regions of all annotated genes. In collaboration with Arbor Biosciences, we developed a second-generation regulatory capture for wheat combining promoter regions with open chromatin regions determined by ATAC-seq in leaves and roots, which is now commercially available. To complement these reverse genetic resources, we developed a new transformation technology (GRF4-GIF1) that improves regeneration of wheat transgenic plants, expands the range of genotypes that can be transformed, and facilitates the induction of CRISPR mutations in wheat. We have used these reverse genetic tools to study multiple genes that contribute to the regulation of the number of spikelets per spike, an important yield component. The talk will summarize our progress on the understanding of the effects of VRN1, FUL2, WAP01 and FT2 on the regulation of the number of spikelets per spike, and will discuss some useful alleles to improve this trait in wheat breeding programs.