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Marie-Laure Pilet-Nayel, Aurore Desgroux, Clément Lavaud, Angélique Lesné, Gilles Boutet, Gregoire Aubert, Rébecca Mcgee, Clarice J. Coyne, Virginie Bourion, Judith Burstin, et al.

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Legumes for a Sustainable World

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16:40-16:50 Oral – S6

Genetics of pea resistance to *Aphanomyces euteiches* in the genomics Era

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Common root rot, caused by the oomycete *Aphanomyces euteiches*, is a major soil borne disease of pea in many countries. The large pea genomic and plant resources recently developed have deepened the knowledge of genetics of partial resistance to *A. euteiches*. A dedicated panel of *Aphanomyces* genetic resources genotyped with a 13K-SNP array (Tayeh et al, 2015) was used in a genome-wide association study (GWAS) of partial resistance. Results identified a total of 52 small sized LD-based confidence intervals associated with the resistance, including 14 consistent QTL regions at which marker haplotypes were defined from the panel (Desgroux et al, 2016). This study validated six of the seven main resistance QTL previously identified, for which Near-Isogenic-Lines (NILs) were created by back-cross assisted selection (Lavaud et al, 2015). The fingerprint of the NILs using the 13K-SNP array showed that QTL introgressions could cover several smaller GWAS intervals, suggesting the presence of several linked genes or a single imprecisely located locus underlying a QTL. The genomic location of the major QTL Ae-Ps7.6, which effect was confirmed on slowing down symptom appearance and root colonization by the pathogen (Lavaud et al, 2016), was refined by GWAS and fine mapping. The unprecedented genomic resources recently developed in pea provide new markers closely-linked to *Aphanomyces* resistance loci, for accelerating progress in breeding future pea resistant varieties.