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Harnessing genetic diversity to improver key traits in red clover

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PLANT & ANIMAL GENOME CONFERENCE XXVIII
The Largest Ag-Genomics Meeting in the World.
January 11-15, 2020
San Diego, CA
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W440: Harnessing Genetic Diversity to Improve Key Traits in Red Clover

Saturday, January 11, 2020
08:40 AM - 09:00 AM
Pacific Salon 4-5 (2nd Floor)

Red clover (*Trifolium pratense* L.) is an important forage legume of temperate regions, particularly valued for its high yield potential and its high forage quality. Despite the significant progress achieved through systematic breeding in the last decades, continuous improvement of cultivars is crucial to ensure yield stability in view of newly emerging diseases or changing climatic conditions. The large amount of genetic diversity present in red clover ecotypes, landraces and cultivars provides an invaluable, but often untapped resource for the improvement of key traits such as yield, quality and resistance to biotic and abiotic stresses. In the framework of the EU funded Horizon 2020 project "EUCLEG" (
www.eucleg.eu
), a collection of 395 red clover accessions representing cultivars, breeding material, landraces and ecotypes of 25 countries from five continents has been established. All accessions have been genotyped using a pooled GBS (genotyping by sequencing) approach with 200 plants per accession. Field experiments have been established at five locations (United Kingdom, Czech Republic, Switzerland, Norway and Republic of Serbia) in 2018 and analysis of first full growing season phenotypic data (2019) revealed large variation for traits such as juvenile development, dry matter yield, vigour or flowering time. In addition, resistance to biotic and abiotic stress was evaluated in separate experiments. For example, resistance to southern anthracnose, caused by *Colletotrichum trifolii,* was assessed in the greenhouse by spray inoculation using a single spore isolate, followed by an additional inoculation of surviving plants with a mixture of seven additional isolates. Repeatability across three replicates ranged from r=0.62 to r=0.67 for both inoculations and a significant differences across accessions was observed. The mean survival rate for single and mixed isolate inoculation was 26.7% and 16.5%, respectively. Although some cultivars with considerable resistance to the disease were observed (survival rates >50%), this highlights the urgent need to improve resistance to southern anthracnose in red clover. However, these phenotypic results provide a valuable basis for GWAS and the identification of candidate resistance genes. Resistance screening in four unrelated bi-parental F_1 populations indicated resistance to be controlled by one or few resistance loci. GBS sequencing using resistant and susceptible pools from these populations revealed a number of candidate genes, which could valuably complement the resistance sources identified in the EUCLEG accessions.

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