

Frequency Fingerprints. Genome-wide association analysis revealed a total of eight significant markers with a bias towards genic/expressed genomic regions. A number of candidate genes previously associated with abiotic stress response in plants were located on marker-tagged genomic scaffolds, while some of the tagged yet uncharacterized genes once validated might clarify the complex genetic mechanisms underlying FT in perennial ryegrass.

Acknowledgement: Funding provided by the Research Council of Lithuania (grant no. MIP-64/2015) and the the Nordic Council of Ministers.

P1135: Other Plant Species

Characterization of Imazamox Resistance in Jointed Goatgrass (*Aegilops cylindrica* Host)

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Wheat growers have limited herbicide options to manage jointed goatgrass (*Aegilops cylindrica* Host), with many relying on imazamox or mesosulfuron in combination with Clearfield™ winter wheat. Both imazamox and mesosulfuron inhibit acetohydroxyacid synthase/acetolactate synthase (AHAS/ALS). In 2015, a suspected imazamox resistant biotype of jointed goatgrass was found in eastern Washington. Due to a shared D genome, jointed goatgrass ($2n=CCDD=28$) may outcross and hybridize with wheat ($2n=AABBDD=42$). Jointed goatgrass may acquire *ALS* resistance by hybridizing with Clearfield™ wheat, but no Ser₆₅₃(Al)N mutation on the D genome of the resistant biotype of jointed goatgrass was identified. Sequencing efforts in the *ALS* gene indicate an Ala₁₂₂Thr substitution in the herbicide binding region of the *ALS* gene on the D-genome of jointed goatgrass. Increasing concentrations of imazamox were applied to both the resistant and a comparison susceptible jointed goatgrass biotype to test for resistance. The resulting dose-response data were fit using a 3-parameter log-logistic with GR₅₀ (50% growth reduction) as a parameter. The suspected resistant biotype had a GR₅₀ of 642 g ai ha⁻¹ that is 29 times more resistant to imazamox than the known susceptible biotype with a GR₅₀ of 22.21 g ai ha⁻¹. A field use rate of 12.3 times the recommended rate of 52.5 g ai ha⁻¹ would be necessary to achieve 50% reduction in biomass. Thus, the Ala₁₂₂Thr substitution on the D genome of jointed goatgrass appears to confer a high level of resistance to imazamox. Future work will exclude alternate mechanisms and inheritance of resistance.

P1136: Other Plant Species

Genetic Structure of Native and Exotic Reed Canarygrass Populations

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Reed canarygrass (*Phalaris arundinacea*) is a wind-pollinated, wetland grass, cultivated in temperate regions around the globe as a forage and ornamental crop. It is also used for soil stabilization, bioremediation and bioenergy. In North America, it exists as both native and introduced populations from Eurasia that became invasive in MN. Native populations were identified from plants collected prior to 1940 in herbaria. The purpose of this study is to examine populations (along rivers and transects) in MN for their native, invasive vs. hybrid status to aid in land management. Reed canarygrass populations for genetic studies includes a total of 1,110 genotypes for analyses: 3 forage; 3 ornamental; 76 wild populations of 863 genotypes sampled every 30 km along 6 rivers (Mississippi, Minnesota, St. Croix, Red, Des Moines, Roseau) where at each site, 3 genotypes were collected at 10m intervals along each river edge as well as perpendicular transects; 166 genotypes from 6 transects in 3 wet meadows or cultivated fields collected along perpendicular, intersecting transects and historic 13 University of Minnesota (UM) herbarium samples that are native genotype. Genetic variation among and within reed canarygrass populations will be assessed by genotyping by sequencing (~1000 SNP markers) with support from a shallow genome sequence of a selected low alkaloid cultivar. It is critical to identify the extent of native vs. exotic reed canarygrass populations in MN using genetic testing for better management of exotic invasive populations and preservation of native populations in state and Tribal lands.

P1137: Other Plant Species

Sorghum Hybrids and their Parental Genetic Differences in Diversity

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Objective. In order to further prove the diversity of genes in the leaves of hybrid and parental leaves of sorghum. **Method.** Four copies of the sorghum sterile lines and five types of Sudan grass for parents, according to the NC II design were formulated to 20 hybrid combinations. **Measuring** the cross combinations and field shape index and physiological and biochemical index of the parents. **Using** cDNA-AFLP differential display analysis of gene diversity difference. **Result.** The results of 29 sorghum hybrids and their parental cDNA-AFLP markers for the hybrids and their parental leaves were displayed: 12 pairs of primer combinations amplified 336 sites, including specific sites 276, accounting for 82.14% of the total, an average of primer combinations amplified specific sites 23. The number of alleles (No) was 1.8701, the effective number of alleles (Ne) was 1.7365, the Nei's gene diversity index (H) was 0.3898, and the Shannon's (I) was 0.5569, which indicated that the gene expression of the hybrid and its parents were complex. The results of cluster analysis show that the change of Genetic similarity coefficient between 29 sorghum sudanense materials is between 0.508-0.876, and the Genetic similarity coefficient 0.54 is the standard, and the 29 materials can be divided into 4 categories. The parental materials were mainly in I and the IV class, and the hybrids were mainly in the II and III. **Conclusion.** The reactive system of cDNA-AFLP differential display technique was constructed, and the genetic diversity of the leaves in the seedling stage was analyzed.

Key words: leaves of sorghum, cDNA-AFLP, heterosis, diversity of genes

P1138: Other Plant Species

Array-Based Comparative Study of Apomictic and Sexual *Eragrostis Curvula* Genotypes

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Apomixis is an asexual reproductive process that results in seeds containing maternal clones since meiotic reduction and egg cell fertilization does not occur. Apomixis is common in polyploid grasses, and poorly represented in crop species of economic interest. A key goal in understanding the molecular basis of apomixis is the possible transference of this trait to species of agronomic relevance. Weeping lovegrass (*Eragrostis curvula* [Schrad.] Nees) is a perennial grass native to Southern Africa that reproduces by diplosporous apomixis. A custom 60-mer spots Agilent array was designed with 970 k probes based on a reference transcriptome constructed from inflorescence of sexual and apomictic genotypes. Eight independent hybridizations were performed with one-color Cy3 labelled samples (four apomictic and four sexual *E. curvula* genotypes). Data preprocessing and analysis was performed using the GeneSpring software v. 14.5. Platform quality was verified by Agilent spike-in controls. Normalization procedures consisted on percentile shift 75, background correction, median as baseline and reproductive mode as parameter. Individual probes from the array were considered to be differentially hybridized under the log2 transformed Fold Change data > 1 and p-values > 0.01 using unpaired t-test and multiple Benjamini-Hochberg correction. From these analyses 138 differential 60-mer sequences were obtained and four candidate genes strongly expressed in apomictic plants were identified. These genes could have an important role in apomeiosis induction in weeping lovegrass and its relevance is currently being analysed through several complementary approaches, including in situ hybridization and obtention of Arabidopsis transformant.

P1139: Other Plant Species

A Genomic Approach to Study Apomixis using *Eragrostis curvula* as a Model Species

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Apomixis is defined as asexual reproduction by seeds, avoiding meiotic reduction and fertilization, being generally present in polyploid plant species. *Eragrostis curvula* is a perennial grass native to Southern Africa. This species can be taken as a model for the discovery of genes that govern pseudogamous diplosporic apomixis since its polyploid cytotypes (4x to 8x) may undergo sexual reproduction, facultative apomixis, or obligate apomixis whereas diploids are always sexual.

Here we present the first draft of a diploid version of the *E. curvula* genome. The cultivar selected was Victoria (~1200 Mb) originated from *in vitro* culture of inflorescences of the apomictic cv. Tanganyika (2n=4x=40). Two libraries were prepared with fragment lengths of 20 kb and 10 kb to get longer reads and to increase the coverage, respectively. The sequencing through PACBIO technology resulted in 6.223.627 and 3.309.811 reads respectively with 90X coverage. The assembly was performed using the software Falcon. The N50 was 380.026 bp with 3.118 contigs representing 95% of the haplotype length. The software BUSCO was used to find single copy orthologous genes, being represented 97% of the BUSCO genes. Dovetail Hi-rise software revealed the architecture of the complete genome chromosome-by-chromosome. The first draft of *E. curvula* genome showed high level of contiguity with a coverage of 95% of the diploid genome. The high proportion of annotated genes would allow the identification of those related to the reproductive mode. This draft represents the start point to obtain more complex tetraploid genomes, harboring the region/s involved in apomixis.

P1140: Other Plant Species

Molecular Characterization and Diversification Study in Wheatgrass Germplasm

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There is been a growing interest in improving native mono stands of Wheatgrass (*Triticeae trb.*) varieties in arid low nutrient marginal steppe lands. We have established two populations derived originally from unknown species of Mediterranean wheatgrass collections. Over the years of crossing within populations, final perennial hybrid cultivar “Enigma” was developed based on number of outperforming characteristics like drought tolerance, proliferation, persistence, biomass and forage quality. However, molecular characterization of the cultivar compare to other closely related known species and existing varieties is essential for enhanced improvement of the crop. A set of 48 SSRs previously reported in intermediate wheatgrass was used in this study. Phylogenetic analysis was done using free tree and tree view software's. Enigma was found closer to other advanced germplasm, while diversity of the population pool was wide. The population was characterized for flowering and leaf characteristics. Molecular characterization will be continued and markers will be analyzed for finding important trait association. Molecular characterization of the variety will accelerate the breeding program for further improvement of wheatgrass.

P1141: Other Plant Species

Genomic Selection in Timothy (*Phleum pratense* L.)

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Timothy (*Phleum pratense* L.) is a perennial, cross-pollinating hexaploid (2n = 6x = 42) species distributed naturally throughout Europe and parts of North Africa and Asia. It is one of the most important input factors in the Norwegian agriculture. New improved cultivars with high yield capacity and forage quality, which are well adapted to the future climate, are very important for an economically sustainable Norwegian milk and meat production. However, with traditional forage breeding methods it takes approximately 18-20 years to develop and release new cultivars on the market. Therefore, there is a great need for developing and implementing new breeding technologies in forage grass breeding. Genomic selection (GS) is a method that combines molecular markers with phenotypic and pedigree data for prediction of breeding values based on genome wide distributed markers. By selecting superior parents based on genomic information, the number of successful crosses increases and the breeding cycles shortens. In view of the recent developments in sequencing, molecular marker technologies and theoretical