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DEVELOPMENT OF SINGLE NUCLEOTIDE POLYMORPHISMS (SNP) MARKERS FOR GENETIC MAP SATURATION OF HEXAPLOID *UROCHLOA HUMIDICOLA*

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Large areas of Brazil are destined for the cultivation of pasture, where the purpose is to feed cattle. Among these, it stands out *Urochloa humidicola* (syn. *Brachiaria humidicola*), an apomictic polyploid species that tolerates waterlogged soils. The single sexual accession (H031) of the Germplasm Bank conserved at Embrapa is hexaploid (2n=6x=36). In the breeding program developed by Embrapa Gado de Corte, H031 was crossed with the commercial cultivar BRS Tupi, also hexaploid, generating 279 hybrids F_1, which were used in the construction of a genetic map. However, this map was based on single-doses marks from 124 microsatellites and has low resolution. It is known that high resolution in specific regions are fundamental for the identification of loci controlling relevant quantitative traits. Furthermore, little is known about the molecular basis of apomixis, whose understanding may also benefit from a saturated genetic map. In order to increase the density of markers on map, the main objective of this work was the development of single nucleotide polymorphism (SNP) by Genotyping-By-Sequencing (GBS). For this purpose, DNA was extracted from young leaves of each hybrid and the parents. Genomic libraries were constructed from the reduction of DNA complexity with two restriction enzymes, PstI and MspI, and were sequenced as 150-bp single-end reads on Illumina NextSeq 500 platform. After quality filters, we obtained a total of 1,732,628,260 sequence reads covering 260 Gb of sequence data, with an average greater than 5M reads per sample. SNP calling was performed using Tassel-GBS pipeline modified for polyploids, which allows the use of the total amount of reads available. We have used as reference the genomes of *Urochloa ruzizienses*, *Setaria italica*, *Setaria viridis*, *Panicum halli* and *Panicum virgatum*; and transcriptomes of *U. humidicola* and *Urochloa decumbens*. The *U. ruziziensis*'s genome provided the best alignment (30,81%), and 172,325 SNPs were identified. Dosage of each bi-allelic loci was estimated using the SuperMASSA software. Ploidy was fixed as 6, and after filtrations, 17,145 markers had the dose estimated with high reliability. The OneMap 2.0.6 software will be used to build an integrated genetic map using these SNP data and the SSR previously developed. As this software does not account for allele dosage, another map will be built with SNP markers considering dosage information using the polymapR. The proposal to construct a genetic map of high resolution and with genetic information relevant to *U. humidicola* will be of great importance for the breeding program in progress at Embrapa. From reproductive mode data previously phenotyped, apomixis can also be mapped on this population. The project will also develop a tool that in the future can be associated with other phenotypic traits of economic importance, raising the *U. humidico*la breeding program to high technology levels.

PRESENTER BIO: A. C. L. Moraes is a PhD student and Research Technician, and has been working with forage since 2012. She has experience with molecular genetic breeding of other tropical polyploids plants, and has been working on the improvement of several methodologies for polyploid studies.