GENOTYPING BY SEQUENCING APPROACH FOR AUTOTETRAPLOIDY *UROCHLOA RUZIZIENSIS* GENETIC BREEDING

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Although Brazil is the major producer and exporter of beef in the world, the rangelands are cultivated with varieties obtained by selection on germplasm and conventional breeding. Only lately genomic information started to be used in the tropical forage breeding programs mostly because of the genome complexity and costs. *Urochloa ruziziensis* is a sexual autotetraploid forage that has a significant role in integrated systems that are currently important in the agribusiness in certain regions of Brazil and is essential as female parent in the other *Urochloa* spp. breeding programs. The objective of this work is to develop genetic information for genomic selection in the *U. ruziziensis* breeding program. A hundred and thirty individuals of a half-sib progeny and 50 progenies with bulked DNA of the first cycle of intrapopulation selection were sequenced using genotyping by sequencing (GBS). The reduction of the DNA complexity was made with two restriction enzymes, EcoT22I and MspI, and libraries were sequenced as 150-bp single-end reads on Illumina NextSeq 500 platform. A total of 727,616,969 sequence reads were obtained and processed by Tassel software, the tags created by the software were aligned using Bowtie2 to a draft genome of the specie, 15,97% of the tags aligned 0 times, 56,24% aligned more than 1 time and 27,78% aligned 1 time, only the tags that aligned 1 time were used in the genotyping, 154.467 SNPs were discovered by Tassel. SuperMASSA and Updog softwares estimated each tetraploid individual allele dosage by considering the general population model. This information enabled the construction of the first integrated genetic map for the species using tetraploid allele dosage. In addition, the SNPs markers and the phenotypic data of the 50 progenies of the first cycle of intrapopulation breeding will allow the prediction of the genomic breeding values using individual simulated best linear unbiased prediction (BLUPs) and estimate the markers genetic effects.

PRESENTER BIO: Mr. Martins is a PhD student that worked with sugarcane single copy genes in graduation and is currently researching on tropical forages for genetic breeding.