

CRP: Livestock

Flagship: FP3 – Feeds and Forages

Cluster: 2 - Development of new feed and forage options

Activity: P1685 – Activity/Product Line 3.2.1: Improved feed & forage germplasm and new tools and technologies for breeding

Deliverable: D10520 - Report on the identification of ploidy of accessions for *Brachiaria*

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In cooperation with our UK partners, mainly from the University of Leicester, we took on the task of recognizing the genome structure and determining the genomic compositions of polyploid species from the genus *Brachiaria* (*Urochloa*) and related species. Prof. Pat Heslop-Harrison, Dr. Trude Schwarzacher and Dr. Paulina Tomaszewska from UoL integrated both sequencing, flow cytometry and molecular cytogenetic tools to study genomes of *Brachiaria ruziziensis*, *B. decumbens*, *B. brizantha*, and *B. humidicola*. Recognizing the levels of ploidy and finding genomic differences between related species is of applied importance and will assist in generating directed and successful hybrids to exploit biodiversity of wild and cultivated *Brachiaria* accessions to breed new varieties. Using flow cytometry on dried leaves exported to UK, the ploidy levels of almost 400 *Brachiaria* and *Panicum* accessions were established. Ploidy results were integrated with both RNA-seq and data found in previous reports for CIAT, including phenotyping and geographical distribution (analysis performed in Earlham Institute, UK by Dr. Jose de Vega). Using whole genomic DNA sequence data from nine *Brachiaria* and *Panicum* accessions, bioinformatic approaches (graph-based read clustering and analysis of abundant k-mer repeat analysis) were applied to identify repetitive motifs in *Brachiaria* genomes and to develop specific probes. The probes were tested on chromosomes of different polyploids (both CIAT and USDA accessions) using fluorescence *in situ* hybridization. Our results are promising, and can be used by breeders. Now, we are in the process of preparing a manuscript with a working title: "Polyploidy in an apomictic and sexual tropical forage grass group: Understanding of complex polyploid hybrids and determination of genomic compositions in *Urochloa* (*Brachiaria*) species using sequence and molecular cytogenetic data". Soon, this data will be publicly available.