BIOINFORMATICS APPROACHES TO STUDY CROP SPECIES WITHOUT REFERENCE GENOME

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New sequencing technologies (NSG) have greatly facilitated the generation of plant reference genome sequences, for instance, the genome draft of 49 different species has been published up to day. The genomics revolution of NSG technologies also brings promising perspectives for genetic diversity studies and crop improvement initiatives for species with and without an available reference genome. In this context, within the frame of the National Biotechnology Program at INTA, we are conducting genomics and computational genomics research lines to support different institutional projects that adopt NGT to solve problems in the field agro biotechnology. In this presentation, I will focus on same leading projects involving crop and forest crop species that lack a reference genome, where different genomics and functional genomics approaches are being developed.