

**ADVANCES IN THE CHARACTERIZATION OF THE MOLECULAR BASIS OF
APOMIXIS IN SPECIES OF THE GENUS *Paspalum***

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Apomixis is an asexual mode of reproduction by seeds widely distributed in angiosperms. The manipulation of this trait can have an enormous benefit for agriculture. The transference of apomixis to important species would allow the perpetuation and multiplication of hybrids by seeds, the simplification of breeding programs, the generation of numerous intra- and inter-specific hybrids, the clonal propagation by seeds of plants which are currently propagated vegetatively and the one-step generation of transgenic cultivars. However, apomixis is not present in major crops or their close relatives. This condition required that studies in the field must be performed in wild species genetically poorly characterized and more recently in mutants of sexual model species. *Paspalum* is a large genus of the grass family that includes important forage resources for the tropical and subtropical regions of the Americas. Many *Paspalum* species reproduce by aposporous apomixis. Since the last 15 years our research group has been working on the genetic and molecular characterization of apomixis in species of genus. In this presentation I will summarize the latest results of this research directed to: *i*) localize and characterize the Apospory Controlling Locus (ACL) in species of the genus and establish syntenic relations with rice and maize, *ii*) identify genes up- or down-regulated in reproductive organs of aposporous plants in comparison with their sexual counterparts, *iii*) find out if some of these differentially expressed candidates were located within the ACL and *iv*) establish a plant transformation platform to investigate the role of candidate genes. Cytogenetic analysis in *P. notatum* showed that aposporous individuals had a genetic rearrangement affecting meiosis, that is absent in the sexual plants, and it is transmitted to the progeny associated with apomixis. The characterization of markers mapping at the ACL determined that protein-coding, repetitive and non-coding sequences are present in this genomic region. A comparative mapping analysis indicated that ACL in *P. notatum* is syntenic to segments of chromosomes 2 and 12 of rice and 3 and 5 of maize. Expression analysis in apomictic and sexual flowers allowed the identification of 65 transcripts with altered expression patterns between modes of reproduction. The analysis of one of them, led us to the identification of *P. notatum lorelei*-like genes, which might play a role in the final stages of the apomixis developmental cascade. Several other genes are still under analysis. On the other hand, the characterization and expression analysis of *P. notatum serk* genes revealed that *Pnserk2* displayed a spatially and chronologically altered expression pattern in reproductive organs of the apomictic genotype with respect to the sexual one. Therefore, apomixis onset in *P. notatum* seems to be correlated with the expression of *Pnserk2* in nucellar tissue. Additionally, we developed an *in vitro* plant regeneration protocol from mature embryos of *P. notatum* and a biolistic transformation platform by using the *bar* and *gfp* genes as selectable marker and reporter, respectively. Stable transformation of several plants was confirmed by molecular and expression analysis.