AN INTEGRATED APPROACH TO IDENTIFY APOMIXIS GENES IN *PASPALUM SIMPLEX*

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Apomixis reproduction in *Paspalum simplex* is controlled by a single dominant locus embedded on a non pericentromeric and heterochromatinic-poor chromosomal region that is characterized by a strong repression of recombination and synteny with the distal part of the long arm of the chromosome 12 of rice. To overcome the drawbacks of recombination repression, a multi-sided approach was undertaken to isolate genetic determinants of apomixis in this species. Screening a 3x coverage genomic BAC library with apomixis-specific SCARs allowed us to isolate 15 BACs spanning in total 1,3 Mbp. Four apomixis-linked SCARs showed one recombination event over 85 individuals indicating that a gradient of recombination repression is also present in the close nearness of the ACL. Out of the BAC selected, three resulted positive to more than one SCAR suggesting that the ACL of *P. simplex* might be shorter than those reported for other species. Sequence analysis showed that most part of the sequence of the isolated clones was formed by repetitive and non coding sequences. Only very few genes were recognized. Based on the assumption that the effect on the reproductive system of the genes located on the ACL is likely related to their transcription, we undertook a comparative transcription analysis to identify apomixis-related polymorphisms at the level of mRNA in the perspective to isolate transcriptionally active genes that are also apomixis-linked. Some of these genes were identified on an comparative cDNA-AFLP analysis of apomictic and sexual developing flowers. Several differentially expressed genes showed heterochrony of gene expression between sexual and apomictic flowers. Epigenetic mechanisms connected with sexual gene silencing was also investigated on an apomixis candidate gene identified on the basis of the above approaches and used as case study. Finally, a possible role on rice reproductive phenotype of the same candidate gene was hypothesized on the basis of a reverse genetics approach. Results were puzzled together to discuss a possible model of interaction of genes located on the ACL with their sexual homologues in relation to the de-regulation of sexual development.