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PN_SCD1, VESICLE TRAFFICKING REGULATOR IS DEMETHYLATED AND OVEREXPRESSED IN FLORETS OF APOMICTIC PASPALUM NOTATUM GENOTYPES

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Apomixis (asexual reproduction through seeds) is considered a deviation of the sexual reproductive pathway leading to the formation of clonal progenies genetically identical to the mother plant. It has been suggested that apomixis might be a consequence of epigenetic alterations, such as interspecific hybridization and polyploidization, resulting in a wide deregulation of reproductive development. Studies on epigenetic are transforming our actual idea of the structural variation and diversity that prevails at key steps of plant female gametogenesis, with deep implications for understanding the evolutionary trends that model innovation in reproductive development and adaptation. Recent results have provided evidences indicating that epigenetic mechanisms are crucial to control events that distinguish sexual from apomictic development. Therefore, the epigenetic regulation of apomixis is an attractive theory as it potentially accounts for the facultative nature of apomixis as well as the ability of apomictic to revert back to sexuality. In this work we used the Methylation-Sensitive Amplification Polymorphism (MSAP) technique to characterize floral genome cytosine methylation patterns occurring in sexual and aposporous *Paspalum notatum* genotypes, in order to identify epigenetically-controlled genes putatively involved in apomixis development. A partial and rather divergent methylation reprogramming was detected in apomictic genotypes. From twelve polymorphic MSAP-derived sequences, one (PN_6.6, renamed *PN SCD1*) was selected due to its relevant annotation and differential representation in 454 floral transcriptome libraries of sexual and apomictic *P. notatum*. PN_6.6 encodes the DENN domain/WD repeat-containing protein SCD1, which interacts with RAB GTPases- and/or MAPKs to promote specialized cell division, functions in clathrin-mediated membrane transport and was defined as potential substrate receptor of CUL4 E3 ubiquitin ligases. Quantitative RT-PCR and comparative RNAseq analyses of laser microdissected nucellar cells confirmed *PN SCD1* upregulation in florets of apomictic plants and revealed that overexpression takes place just before the onset of apospory initials. Moreover, we found that several SCD1 molecular partners are upregulated in florets of *P. notatum* apomictic plants. Our results revealed a specific vesicle trafficking molecular pathway epigenetically modulated during apomixis. Results will be presented and critically discussed.