

**S003** Epigenetic programming of male gametes in flowering plants

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The male germ line in flowering plants is initiated by asymmetric division of uninucleate microspore leading to the formation of two unequal cells with the chromatin of the generative nucleus appearing more condensed than that of the vegetative nucleus. Histones crucially influence the structure and function of chromatin, and the incorporation of histone variants can lead to the generation of a histone code specific to the male germ line that combines both histone variants and their post-translational modifications. Our studies on lily, *Arabidopsis* and rice have revealed the presence of male germ line specific histone H3 variants. In lily the male germ cell chromatin is enriched with H3K4me2 modification, while the vegetative nucleus chromatin shows enrichment of H3K27me3 modification. Further, our genome wide transcriptional profiling of rice sperm cells points towards sperm cells being sites of most extensive epigenetic reprogramming events. The genes involved in modifying the chromatin state are among most up regulated set in sperm cells. RNA-interference (RNAi) pathways are implicated in post-transcriptional gene regulation events. Highly activity RNAi machinery in sperm cells is reflected through activation of an evolutionarily conserved family of proteins including argonautes (AGO), dicer-like (DCL) and RNA-dependent RNA polymerases (RDRs).