Analysis of the relationships among gene imprinting, seed dormancy and reproductive barriers

Hikaru Sato[A,B], Wenjia Xu[A], Juan Santos-González[A], Heinrich Bente[A,C], Claudia Köhler[A,C]

[A] Swedish University of Agricultural Sciences, Uppsala BioCenter

[B] University of Tokyo, Dept. Integrated Sciences

[C] Max Planck Institute, Molecular Plant Physiology

Program theme: Genetics and Epigenetics

Oral

Abstract

The endosperm is a plant-specific reproductive tissue that regulates nutrient intake and seed dormancy. It is generated by fertilization of a diploid maternal central cell by a haploid paternal sperm cell. Epigenetic modifications established during gametogenesis render genes to be specifically expressed from the paternal or maternal alleles in the endosperm, referred to as paternally expressed genes (PEGs) and maternally expressed genes (MEGs), respectively. We found that the maternal-allele specific combination of trimethylation of histone H3 on lysine 27 (H3K27me3), dimethylation of histone 3 on lysine 9 (H3K9me2) and CHG methylation is highly associated with PEGs, causing the maternal alleles of PEGs to be continuously silenced. Meanwhile, genes with maternal-specific single H3K27me3 are associated with gene activation during germination, suggesting that different combination of epigenetic marks define different patterns of gene expression. Disruption of the enzyme establishing H3K9me2 causes higher seed dormancy, associated with the upregulation of *ABA INSENSITIVE 3* (*ABI3*). We recently found that the ABA pathway is also involved in the interploidy barrier where the parental-specific epigenetic regulation has a critical role. These findings suggest a connection between the pathways controlling seed dormancy and the interploidy barrier through parental-specific epigenetic regulation in the endosperm.