

Seminar/Talk

Heritable in trans silencing at the maize b1 locus: a story about distal cis-regulatory sequences, RNA-directed DNA methylation and unexpected epigenetic profiles.

Maike Stam

University of Amsterdam

Host: Xiaoqi Feng

Paramutation, the transfer of heritable silencing information between two homologous alleles, results in the silencing of a susceptible allele (1,2). Paramutation requires multiple components of the RNA-directed DNA methylation (RdDM) pathway, which is characterized by 24nt siRNAs and CHH methylation (H=A,T, or C). With paramutation at the maize b1 gene, affecting plant pigmentation, the low expressed, inducing B' epiallele heritably changes the high expressed, sensitive B-I epiallele into B' with 100% frequency. A hepta-repeat 100kb upstream of the b1 gene is required for paramutation and high b1 expression (3). High B-I expression correlates with histone acetylation, nucleosome depletion, and a multi-loop chromatin structure at the b1 locus, whereas low B' expression correlates with DNA hypermethylation, the repressive histone modifications H3K9me2, H3K27me2, and a single-loop chromatin structure (4-6). However, surprisingly, paramutation at the b1 locus appears associated with more RdDM activity at the sensitive allele than at the inducing allele. I will discuss the hypothesis why this may be in the seminar. I will furthermore discuss results obtained with mutants in the RdDM pathway that indicate a role for RdDM components in maintaining H3K9me2 and H3K27me2 independent of their role in establishing (6). References:1. Hövel et al. (2015) Sem. Cell 10.1016/j.semcdb.2015.08.012.2. Hollick (2017) Nat Rev. Genetics doi: 10.1038/nrg.2016.115.3. Stam et al. (2002) Genes & Dev doi: 10.1101/gad.1006702.4. Haring et al. (2010) Plant J. doi: 10.1111/j.1365-313X.2010.04245.x 5. Louwers et al (2009) Plant Cell, doi/10.1105/tpc.108.064329 6. Hövel et al. (2024) Plant Physiology, doi: 10.1093/plphys/kiae072.

Wednesday, October 22, 2025 10:30am - 11:30am

Office Bldg West / Ground floor / Foyer seminar room



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