



BIOLOGY COLLOQUIUM

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A Conserved Genetic Pathway Determines Inflorescence Architecture

by

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The architecture of inflorescences that bear flowers in space and time determines plant reproductive success through affecting fruit set and plant interaction with pollinators. Inflorescence architecture that displays great diversity across flowering plants depends on developmental decisions at inflorescence meristems. Here I discuss a novel genetic pathway determining inflorescence architecture in the model plant, *Arabidopsis thaliana*, and the economically important crop, *Oryza sativa* (rice). In *Arabidopsis*, four MADS-box transcription factors, *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1*, *SHORT VEGETATIVE PHASE*, *AGAMOUS-LIKE 24*, and *SEPALLATA 4* directly suppress *TERMINAL FLOWER 1 (TFL1)* to establish floral meristems on the flank of the inflorescence meristem. This is indispensable for the well-known function of *APETALA1* in specifying floral meristems, and is coupled with a conformational change in chromosome looping at the *TFL1* locus. In addition, the orthologs of these MADS-box genes in rice have also been revealed to determine panicle branching through regulating *TFL1*-like genes. These findings suggest a conserved regulatory pathway that determines inflorescence architecture in flowering plants.