

## Plenary Lectures

**Lecture 1 Chairperson: Prof. Kiyotaka Okada (Kyoto University, Japan)**

### **The Evolutionary Genomics of Plant Adaptations: From Arabidopsis to Crop Species**

Michael Purugganan

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The ability to infer evolutionary histories and determine the nature of evolutionary forces has been aided tremendously by the application of new genomics technologies. We will discuss two on-going studies - on the evolutionary ecology of flowering time in *Arabidopsis thaliana* and the spread of barley in Eurasia - to illustrate what we can learn from the application of nucleotide sequence data to evolutionary questions of speciation and adaptation.

**Lecture 2 Chairperson: Prof. Kentaro K. Shimizu (University of Zurich, Switzerland)**

### **The Regulatory and Evolutionary Consequences of Ploidy Changes on Hybridization**

Luca Comai<sup>1</sup>, Brian Dilkes<sup>1</sup>, Caroline Josefsson<sup>2</sup>, Isabelle Henry<sup>2</sup>, Margaret Woodhouse<sup>1</sup> and Harkamal Walia<sup>1</sup>

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Speciation in plants depends on the establishment of reproductive barriers that allow populations to diverge from each other and, in certain cases of mechanisms that allow diverged species to reunite in the formation of allopolyploids. Species divergence may involve protein sequence, copy number or expression changes resulting in dosage- dependent effects. We use *Arabidopsis thaliana* and *A. arenosa* to explore the genetic and molecular basis of hybrid incompatibility.

Hybridization between these two species can fail or succeed depending on the genomic dosage of the parents. In addition, *A. thaliana* accessions differ in efficiency of hybridization to *A. arenosa*. We are mapping and characterizing the loci underlying this variation and characterizing the global regulatory changes involved. Discovery and testing of candidate loci suggest at least two dosage-sensitive mechanisms. The first is the one responsible for coordination between seed-mother sporophyte and zygotes. We have found that genes acting sporophytically affect this response. The second is chromatin regulation. Consistent with this hypothesis, in incompatible crosses, the normally silenced and heterochromatic element *ATHILA* was expressed from the paternal, but not maternal, chromosomes. Three Polycomb regulated genes, *PHERESJ*, *MEIDOS* and *MEDEA*, were also induced. At *PHERESJ*, maternal imprinting of the promoter was disrupted. The rate of hybrid seed lethality was sensitive to parental genome dosage and gene activation was proportional to the dosage of parental genomes. A causal link was established between *PHE1* and hybrid seed failure as a transposon-induced disruption of *PHE1* significantly improved fertility. We propose that the dosage-dependent developmental regulation of sporophytic tissues associated with the seed, and dosage-dependent regulation of chromatin could be universal phenomena affecting lethality in interspecies hybrids.

**Lecture 3 Chairperson: Dr. Ian M. Dworkin (North Carolina State University, USA)**

## **Footprints of Adaptation in the Genome**

Wolfgang Stephan

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I will discuss the results of several studies of adaptation at the genome level. These studies are based on the identification of molecular signatures of positive Darwinian selection. I will explain how such footprints can be found in the genome and will estimate the frequency of these adaptive events. Using examples from various organisms (including humans and fruit flies), I will also describe the "targets" of selection, i.e., the genes involved in adaptation.