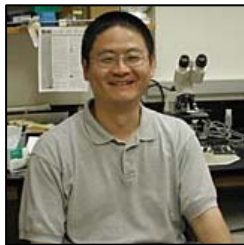


Current Topics in Plant Biology

Graduate Student Hosted Seminar Series – Fall 2005

TNS 132, 1:15-2:15



Monday, November 21 – contact ktplants@yahoo.com

Dr. Bo Liu, University of California Davis

Roles of the Microtubule-based Motor Kinesins in Plant Cytokinesis

In flowering plants, cytokinesis results in the formation of the cell plate. Dynamic microtubules form the framework of the cytokinetic apparatus of the phragmoplast, thus play essential roles in plant cytokinesis. Studies in our group are devoted to understanding how the phragmoplast microtubule array is organized, and how Golgi-derived vesicles are delivered to the division site. The microtubule-based motor kinesins are force generators for microtubule reorganization as well as transports along microtubule tracks. The model plant *Arabidopsis thaliana* contains 61 genes encoding kinesins. Members of the Kinesin-12 subfamily decorate the plus end of phragmoplast microtubules. Our work suggests that Kinesin-12 plays a role in linking anti-pa! rallel microtubules in the phragmoplast so that microtubule plus ends remain at the cell division site during cell plate formation. Several other kinesins are believed to drive vesicle transport along phragmoplast microtubules. We believe that in plant cells, orchestrated activities of kinesins provide driving forces for microtubule-based motile activities required for the formation of the cell plate in the right place at the right time.



Monday, December 5 – contact aleonard@udel.edu

Dr. Scott Poethig, University of Pennsylvania

Regulation of developmental timing in Arabidopsis by trans-acting siRNAs

The transition from juvenile to adult development is an important event in shoot morphogenesis, and is a pre-requisite for flowering. Screens for mutations that accelerate this transition have revealed that post-transcriptional gene silencing plays an important role in this process. Three genes required for post-transcriptional gene silencing-SGS3, RDR6 and DCL4-promote juvenile development by silencing genes that promote adult development. These three genes act in a pathway that generates siRNAs from transcripts cleaved by miRNAs, and thus function in an miRNA-initiated silencing cascade. Some of the siRNAs generated by this pathway target non-homologous transcripts (trans-acting siRNAs); others target the transcript from which they were derived. Endogenous targets of this silencing pathway have been identified by microarray analysis and genetic analysis. The function of these targets will be discussed.



Monday, December 12 – contact nissan@dbi.udel.edu

Dr. Antoni Rafalski, DuPont Agricultural Genomics

Evolution of DNA Sequence Diversity in Maize

We have analyzed the DNA sequence diversity of maize at multiple levels of resolution: Whole chromosome, gene organization level (100-300 kb range) and individual gene polymorphism. At all levels of resolution, intraspecific genetic diversity of maize is extremely high. As has been noticed by Fu and Dooner, maize inbred lines McC and B73 not only differ extensively in the repetitive DNA segments, but also in some cases genic sequences present in one allele are found missing in the other allele. We have extended these observations to other genetic loci and surveyed the occurrence of genic and intergenic non-colinearities in maize gene pool. Four genomic segments of ca 250 kb each have been sequenced from two inbred lines, B73 and Mo17. Intergenic non-homologies were common and frequently consisted or relatively recent insertions of retrotransposon-derived sequences. The differences between the two alleles ranged from 20% to nearly 50%, depending on the locus. Genic non-homologies were relatively rare and were usually pseudogenes, even though some of them are transcribed. Most of these occur as clusters of exonic insertions which were captured and transposed by *Helitron* transposable elements. Some *helitron*-generated clusters of exons are transcribed and may give rise to novel functionality over the course of evolution. We predict that more than 10,000 such genic polymorphisms exist in the maize genome, most of them carried on *Helitron* insertions. We have analyzed in detail a family of related *Helitrons* in maize and teosinte germplasm, and propose their evolutionary relationship. Candidates for the autonomous *Helitron* elements, as well as their transcripts, have also been identified. The consequences of these findings for evolutionary history of maize will be discussed.