
KIRSTEN BOMBLIES

CV

PARTICIPANT AT:

EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS



March, 17th-18th, 2015, Barcelona

Kirsten Bomblies, Thomas D. Cabot Associate Professor, Harvard University, Boston, USA

Kirsten Bomblies was primarily interested in genetics and mechanisms of evolution. She studied Genetics for her PhD at the University of Wisconsin - Madison, studying the genetics of maize domestication and received her degree in 2004. Kirsten was a postdoctoral fellow in Detlef Weigel's group at the Max Planck Institute for Developmental Biology in Tuebingen, Germany, studying genetic incompatibility in *Arabidopsis thaliana* from 2004-2009. She received a MacArthur Fellowship in 2008 and has been on the faculty of Organismic and Evolutionary Biology at Harvard University since 2009. Summer 2015 she was moving to the John Innes Center in Norwich, UK to start a new group, continuing to focus on the evolution of meiosis in polyploids and diploids.

B-DEBATE IS AN INITIATIVE OF:



KIRSTEN BOMBLIES

ABSTRACT

PARTICIPANT AT:

EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS

**March, 17th-18th, 2015, Barcelona**

Kirsten Bomblies, Thomas D. Cabot Associate Professor, Harvard University, Boston, USA

Meiotic Adaptation to whole Genome Duplication

Whole genome duplication (WGD) is a major factor in evolution, adaptation and speciation, and WGD events predate some of the major radiations in eukaryotes. Yet by doubling the number of homologous chromosomes that can pair and recombine, WGD challenges reliable meiotic chromosome segregation. Neopolyploids often show defects in meiotic chromosome segregation and low fertility. However, numerous polyploid species in nature, particularly among plants, and most of these have stable, often diploid like chromosome segregation, showing that evolution can overcome the early problems that face polyploids. The molecular basis of this stabilization remains mysterious. We use *Arabidopsis arenosa*, an outcrossing relative of *A. thaliana* with extant diploid and polyploid populations, to better understand the genic basis of adaptation to WGD. Using a genome scan, we find eight functionally interacting meiosis genes, γ which encode proteins that together coordinate chromosome pairing, synapsis, and the number and distribution of chiasmata. We show evidence for one gene that the derived allele has a strong functional consequence in tetraploid meiosis. We hypothesize that these genes represent a polygenic solution to WGD-associated chromosome segregation challenges, and that likely the derived tetraploid alleles condition increased reduced crossover numbers, perhaps by increasing crossover interference.

B-DEBATE IS AN INITIATIVE OF:

