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# JOHN WILLIS

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PARTICIPANT AT:

## EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS

**March, 17<sup>th</sup>-18<sup>th</sup>, 2015, Barcelona****John Willis**, Professor of Biology at Duke University, Durham, USA

John H. Willis is Professor of Biology at Duke University in Durham, North Carolina. Researchers in our lab work to further our understanding of the evolutionary dynamics of how species are formed, the origin of reproductive isolating barriers, mechanisms by which genetic variation is maintained in populations, and the underlying genetic basis of locally adaptive traits. We focus our experiments on wildflowers in the *Mimulus guttatus* species complex, a group of ecologically divergent populations and species with varying levels of reproductive isolation and local adaptation. We have developed genomic and experimental resources for these plants to help us in our research, including an annotated reference genome sequence and methods for stable transformation. Before moving to Duke University in 2000, John was hired as a faculty member of the Department of Biology at the University of Oregon in Eugene, Oregon in 1993, after a postdoc with Michael Lynch in the same department. He received his Ph.D. in Ecology and Evolutionary Biology from the University of Chicago in 1991, with Doug Schemske and Deborah Charlesworth as his dissertation advisors, and his A.B. in Biology with Honors from Brown University in 1985, with Annie Schmitt as his Honors advisor.

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ABSTRACT

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### **Genetic Analysis of Parallel Local Adaptation to Serpentine and Mine Soils in *Mimulus***

A major challenge in 21st century biology is to understand how organisms adapt to complex and often unpredictable environments. Evolutionary ecologists have studied plant adaptation to extreme edaphic environments such as serpentine soils and heavy metal contaminated mine tailings for decades and this classic work provides some of our best examples of “natural selection in action.” These extreme soils impose such strong selection that plant populations occurring on serpentine/mine soils and adjacent “normal” soils are often locally adapted over a scale of meters despite substantial gene flow. Throughout western North America local populations of the yellow monkeyflower *Mimulus guttatus* have repeatedly adapted to patches of serpentine soils or toxic copper mine tailings. Using a combination of reciprocal transplants in the field and lab, QTL mapping, physiological experiments, and population genomic approaches, we are beginning to identify the most important evolutionary genetic changes that have enabled this plant species to survive and reproduce on serpentine soils or mine tailings throughout its range. Serpentine soils and copper mine soils are patchily distributed and vary substantially in their physiochemical properties, and it is not known whether widespread species, such as *M. guttatus*, repeatedly adapt to different patches via the same or different molecular mechanisms. Even if the same gene is repeatedly used, is this due to new mutations or repeated use of standing variation? Are serpentine or Cu mine adapted alleles and pathways selectively equivalent on soils from different serpentine or mine regions, or uniquely suited to each particular habitat? This talk will highlight some of our initial discoveries that answer some (but not all!) of these basic questions about evolutionary plant solutions to ecological challenges.

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