

**Dear Faculty, Postdocs, Students, and Friends:**

**You are cordially invited to attend a special seminar presented by the  
Institute for Integrative Genome Biology**



**Dr. Brandon Gaut  
Ecology & Evolutionary Biology  
University of California, Irvine**

**Title:  
“Evolutionary genomics of *Vitis*: Domestication, Sex  
and Introgression”**

**DATE: Friday, February 19, 2021  
TIME: 12:00 pm PST**

**MEETING ID: 929 1247 4758  
PASSCODE: 644865**

**Host: Dr. Arthur Jia**

**Abstract:** With collaborators at UC Davis, my lab has embarked on a delightful journey to address evolutionary questions in the genus *Vitis*. The genus is of special interest for many reasons, including that its ~70 species have radiated to inhabit a range of environments; that all species are inter-fertile and often grow in sympatry; that it contains a vital domesticate (*V. vinifera*); and that several wild species have the potential to be (or already are) agronomically important as rootstocks. Today I will talk about three distinct evolutionary questions that we have addressed within *Vitis*. The first examines the genomic effects of domestication and clonal propagation of *V. vinifera*. Clonal propagation allows structural variants to accumulate as deleterious recessive variants, leading to high genic hemizygoty. Some of these variants have phenotypic effects, with the berry color locus being a particularly dramatic example of convergent phenotypic due to complex inversions. The second topic is the evolution of sex. All members of the genus have separate sexes (dioecy) except for *V. vinifera*. Using comparative genomic data, we have disentangled features of the evolution of the sex determination locus and identified candidate male and female determining genes. Finally, we have been studying wild species from the American Southwest, which are useful for rootstock breeding due to their resistance to biotic and abiotic stresses. Our recent focus has been on the role of introgression in species' history. We find that introgression has shaped substantial portions of extant genomes and that introgressed regions are associated with climatic and biotic adaptation.