

MEETING LINK: [CLICK TO JOIN MEETING](#)

Dear Faculty, Postdocs, Students, and Friends:

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



Dr. Steven Knapp
*Department of Plant Sciences
University of California, Davis*

Title:

**“Predictive Breeding in Octoploid Strawberry, a Species With
Complex Homoploid Hybrid Ancestry and a Highly
Diploidized Genome”**

DATE: Friday, November 20, 2020

TIME: 12:00 pm

MEETING ID: 929 1247 4758

PASSCODE: 644865

Host: Dr. Arthur Jia

Abstract: Cultivated strawberry (*Fragaria × ananassa*) originated in the early 1700s from spontaneous hybrids between non-sympatric cross-compatible wild allo-octoploid ($2n = 8x = 56$) species (*F. chiloensis* and *F. virginiana*). The global population has since steadily evolved and been reshaped by wild species introgression, admixture, directional selection, and population bottlenecks. Here, we highlight findings from studies undertaken in our laboratory to assemble phased octoploid reference genomes, understand and resolve sub-genome specific DNA variation and global population structure, shed light on gene flow and karyotypic evolution among the octoploid progenitors, and unravel the complex hybrid ancestry and domestication history of cultivated strawberry. The assembly of a high-quality reference genome enabled the development of sub-genome specific genotyping approaches that have been critical for applying genome-informed breeding approaches in octoploid populations. We developed phased chromosome-scale genomes from heterozygous individuals using trio-binning, third-generation DNA sequencing, and high-density genetic mapping of DNA variants identified by whole-genome shotgun genotyping-by-sequencing. We fully resolved the four sub-genomes, showed that the genomes of the wild octoploid progenitors lack chromosome

rearrangements, and discovered that domestication has not decreased genetic variation worldwide but has decreased genetic variation in locally adapted populations that have experienced the greatest genetic gains and been the source of numerous agriculturally important cultivars. Finally, we illustrate how the aforementioned advances have enabled the routine application of genome-wide association and genomic prediction approaches in octoploid strawberry.