



EvoLunch

Domestication selection and shifts in trait variability at the within-plant scale

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Since the advent of agriculture over 12,000 years ago, humans have been a powerful evolutionary force shaping the phenotypes of plants. While domestication selection is often considered a unique form of plant evolution, understanding how crops differ from their wild progenitors can shed light on basic evolutionary processes, and help us link plant traits to ecological outcomes. Thus far, the study of domestication syndromes has focused on changes in plant-level trait means. For example, crop plants often exhibit shifts in the average size of their seeds, sugar content of their fruit, or toxin concentration of their leaves. However, this focus on the average overlooks an important component of the plant phenotype: the magnitude of within-plant trait variability among plant reiterated organs. While this variability is often considered noise around a more meaningful mean, trait variance per se can affect critical biotic interactions, and evolve together with or independently of trait means. In the present study, we ask how levels of within-plant, among-leaf trait variability have changed with domestication in a key forage crop (alfalfa; *Medicago sativa*). To do this, we quantified and compared levels of trait variability between wild and domestic plants in a common garden, stratifying sampling within and among leaf age classes to explore the role of leaf ontogeny in shaping patterns of within-plant variability. We find frequent shifts in levels of within-plant variability with domestication, and conclude that within-plant variability is an underexplored component of the domestication syndrome and, potentially, of plant trait evolution more generally.

Wednesday, February 26, 2020 12:30pm - 01:30pm

Heinzel Seminar Room / Office Bldg West (I21.EG.101)



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