

BIOL 415: Key questions for quiz 5

Weed evolution (Coulatti & Barrett 2013)

- What is a weed? What categories do we include under “weeds”? *slides 3–6*
- How do founding events affect genetic diversity? Fitness? *slides 7–11*
- How does adaptation affect the probability of invasion *slides 12–17*
- What are the theories on how invasiveness evolves? *slides 19*
- How does invasive species compare to native? When does it do better, worse? *slides 20-36*
- General conclusions on weed evolution *slide 37*
- Case study of *Lythrum salicaria*, *paper discussion*

Plant domestication (Fuller et al. 2014)

- Where were plants domesticated? *slide 4*
- How fast does the domestication occur? *slides 6-7* (Fuller et al., 2014)
- How do domestication bottlenecks control for the certain genes and traits? *slides 8-9*
- What is a domestication syndrome? *slide 10, examples slides 11–13*
- The process of domestication *slides 14–18*
 - o Maize case study in understanding the domestication process *slides 19–21*
 - o What evidence supports single origin of Maize?
- Domestication genes *slides 22-25*
 - o *Don't need to know specific genes.*

Crop diversity (Voss-Fels & Snowdon 2015)

- Why is crop diversity important?
 - o The domestication bottleneck vs. later losses in diversity, *slide 4*
 - o Uses of crop diversity and examples *slides 5–14*
 - Why is it important to have crop diversity?
- What changes have occurred in crop diversity (over the last century)?
 - o The “modernization bottleneck”? *slides 15-17*
 - o Changes in national diets *slides 19-23*
- What are the major threats to crop diversity?
 - o Climate change projections *slide 10*
 - o Genetic erosion *slides 15-17*
 - o Crop replacement *slide 18, examples 21-23*
- What approaches do we have to solve these threats?
 - o Neglected and underutilized crop species *slides 25-27*
 - **No need to memorize the list on slide 26, especially the less clear points
 - o Conservation
 - What is *in-situ* vs. *ex-situ* conservation? *slide 27,*
 - *Ex-situ* conservation sites, Svalbard example *slides 28–29*

Population genomics (Siol *et al.* 2010)

- What are the two classes of approaches for understanding the genetic basis of important traits/adaptations? *slide 7*
 - o Phenotype to genotype (top down) *slides 8-15*

**For all of these, have a general idea of basic approach and benefits/drawbacks

- QTL mapping *slides 10 & 11*
- Association mapping *slides 12-14*
- Bulk segregant analysis *slide 15*
- o Genotype to phenotype (bottom up) *slides 16-43*
 - What is our null expectation (if not natural selection)? *slide 17*
 - What is a genomic signal of natural selection? *slides 17-21*
 - Commonly used methods *slides 22-43*
 - MacDonal-Kreitman type tests *slides 23-27*
 - o What do different values of K_a/K_s mean?
 - o What values of K_a/K_s are most common?
 - Site Frequency Spectrum *slides 28-35, example slides 36-39*
 - o What is the expected neutral distribution?
 - o How do selective sweeps differ from the neutral distribution?
 - Linkage disequilibrium *slide 40*
 - Population differentiation *slides 41*
 - o What can we do to reduce false positives?