Community Genetics

Genetic properties – and evolution/coevolution – of species affect community structure and function and can be placed in a multi-species context. These inter-relationships are now recognized in an important and new subfield → community genetics.

**Extended Phenotypes:** Genetic variation → phenotypics variation → changes interactions: genes affect both population and community-level processes.

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**Table 1** Summary of working definitions used in this paper (From Whitham et al. 2003)

<table>
<thead>
<tr>
<th>Term</th>
<th>Definition</th>
<th>Source</th>
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</thead>
<tbody>
<tr>
<td>Community</td>
<td>“An association of interacting species living in a particular area”</td>
<td>Molles (1999)</td>
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<tr>
<td>Community evolution</td>
<td>Natural selection leading to phenotypic change at the community level</td>
<td>sensu Wilson (1997)</td>
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<tr>
<td>Community genetics</td>
<td>The role of intraspecific genetic variation in affecting community organization and ecosystem dynamics</td>
<td>Antonovics (1992); this paper</td>
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<tr>
<td>Community heritability</td>
<td>“If the interactions among the members of the community are passed intact from the ‘parent’ community to the ‘offspring’ community, the interaction will be heritable at the community level.”</td>
<td>Goodnight (1990)</td>
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<tr>
<td>Dominant species</td>
<td>Species that “dominate community biomass and have total impacts that are large, but not disproportionate to their biomass”</td>
<td>Power et al. (1996)</td>
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<tr>
<td>Extended phenotype</td>
<td>The effects of genes at levels higher than the population</td>
<td>Senha Dawkins (1982)</td>
</tr>
<tr>
<td>Intraspecific genetic variation</td>
<td>Genetic variation found within a species or hybridizing complex (the largest unit with significant gene flow and heritable transmission of traits from one generation to the next)</td>
<td>this paper</td>
</tr>
<tr>
<td>Keystone species</td>
<td>A species “whose impact on its community or ecosystem is large, and disproportionately large relative to its abundance”</td>
<td>Power et al. (1996)</td>
</tr>
<tr>
<td>Minimum Viable Interacting Population (MVIP)</td>
<td>The size of a population needed to maintain genetic diversity at levels required by other interacting species in the community</td>
<td>this paper</td>
</tr>
</tbody>
</table>

Read:
1. Futuyma and Slatkin – a brief introduction to coevolution within communities
2. Mitton – a brief summary of recent ideas of Community Genetics
3. Whitham, TG. et al. 2003.(Abstract and Conclusions)
The March 2003 issue of Ecology has several papers (besides Whitham’s) that debate the usefulness of the concept of Community Genetics.

Examples of Cottonwoods and Pinyon Pines in this handout are from Whitham et al.’s paper.
Extended Phenotypes: The Genetic Basic of Interactions


![Graph showing latitudinal variation in predator-prey interaction](image1)

**Fig. 1.** Latitudinal variation in *N. canalicularata* predation on *M. californianus*. (A) Field data are mean density (+SEM) of drilled *M. californianus* in wave-exposed beds (*n* = 5 to 16 quadrats per site; nd, no data) (B) Mean drilling rate (+SEM) for whelks held in the laboratory with only *M. californianus* for 1 year (*n* = 4 containers x 16 sites)

![Graph showing variation in drilling by *N. canalicularata*](image2)

**Fig. 2.** Variation in drilling by *N. canalicularata* raised under common laboratory conditions from egg capsules collected at eight sites. Data are the percentage of whelks from each set of capsules that drilled *M. californianus* during a 124-day experiment.
2. In the overlap and hybrid zone (13 km long), plants are distinguished based on morphology (A) and also by the arthropod community that uses them (B).
3. Plant defenses (tannins) in cottonwood and consequences for communities...the VERY extended phenotypes.

In the field:
(But is this variation inherited?)

![Graph showing the relationship between proportion fremont markers and bark condensed tannins.](image)

Fig. 3 Concentrations of condensed tannin in cottonwood bark as a function of proportion of Fremont markers in the trees. A strong linear relationship exists between introgression of Fremont cottonwood markers and condensed-tannin concentration in the bark of cottonwood genotypes.

Genetic variation in tannins has other consequences.

Decomposition and N mineralization:

![Graphs showing aquatic decomposition and nitrogen mineralization.](image)

Fig. 3 Genetic variation in Populus hybrids results in differential expression of a condensed tannin QTL (Quantitative Trait Locus) that can be traced through ecosystem-level processes. (a) In a common environment, cross types express manyfold differences in the concentration of condensed tannins (Oribe and Whitham 2000). (b) The concentration of condensed tannins in different Populus cross types accounts for 63% of the variation in litter decomposition among cross types in a stream (Oribe and Whitham 2000). For panels (B) and (C), vertical lines represent 1 s.e., and different letters indicate significant differences among means (P < 0.05). (D) The concentration of condensed tannins also explains 37% of the variation in terrestrial net N mineralization rates between 12 stands that differ in cross type compositions (Schweitzer, unpublished manuscript).

Beaver preferences & activity

![Graph showing beaver preferences among cottonwoods.](image)

Fig. 1 Beaver preference among cottonwoods in the hybrid zone (Weber River, Utah, USA). In the wild, beaver selectively discriminated among related cottonwood species and their naturally occurring hybrids.
4 Other interactions of cottonwoods vary with genetic background:

**Bud Gall Mite (Aceria parapopulii)**

![Diagram of mite distribution](image1)

**Phenotype**

- Populus fremontii Zone
  - $X < 0.01$
  - $N = 250$
- Hybrids and Overlap Zone
  - $X = 0.12$
  - $N = 357$
- Populus angustifolia Zone
  - $X = 0.01$
  - $N = 138$

Fig. 4 On the Weber River drainage in northern Utah, USA, the geographical distribution of the eriophyid mite Aceria parapopulii is concentrated in the hybrid zone of Populus fremontii × P. angustifolia. Within the hybrid/overlap zone, where all tree classes grow in close proximity, mites are overwhelmingly concentrated on F₁-type hybrids. Leaf silhouettes illustrate the morphological differences among cottonwood species and their hybrids (bars indicate means ± 1 se).

**Birds**

![Diagram of bird distribution](image2)

Fig. 6 Within the hybrid and overlap zone of Populus fremontii and P. angustifolia, bird nests are significantly more abundant in F₁ hybrids than in adjacent backcross hybrids and cottonwood species. Similarly, bird nests are significantly more abundant in the hybrid zone than in nearby pure zones. Most of the nests belonged to Northern Orioles (Icterus galbula) and Black-billed Magpies (Pica pica); other common taxa included American Robin (Turdus migratorius) and Warbling Vireo (Vireo gilvus). Tree silhouettes illustrate the branch architectures characteristic of each tree type (adapted from Martinson and Whitham [1994]).
Other examples: community-level consequences of genetics: the Extended Phenotype:

a) Pinyon Pine (= Piñon Pine) [in a Whitham paper]

![Graph showing the ratio of resistant to susceptible abundance across different guilds.](image)

**Fig. 2** Genetic variation among pinyon pines (*Pinus edulis*, a community dominant) in resistance to a keystone herbivore (*Diorystria albovittella*, a stem-boring moth) affects bird, mammal, and rhizosphere microbe communities. The graph shows the ratio of the abundance of seven guilds on resistant trees relative to susceptible trees. Bars with values >1 indicate greater abundance of a guild on resistant trees than on susceptible trees; bars with values <1 indicate greater abundance on susceptible trees than on resistant trees. An asterisk above the bar denotes a statistically significant difference at $P < 0.05$. Data are adapted from Christensen and Whitham (1993), Brown et al. (2001), and Kuske et al. (2003).

b) White-tailed deer and meningeal worms [see: the Mitton paper in your assigned readings]
Extended phenotypes: how it might work → selection of traits and community effects.

Selection experiments: for the fastest beetles and population size

Selection experiments:
Select vials with particular traits to start next generation

(Flour beetles) [Goodnight 1990: Evolution]
*Tribolium confusum*: sp A
*Tribolium castaneum*: sp B

Responses to selection on traits ONLY in sp. A:

(i) Direct response of trait under selection

![Graph showing responses to selection on traits in *Tribolium confusum*](image)
ii). Indirect correlated response of a trait not under selection:

iii) Between-species correlated response: sp. B responds to selection in sp. A. = Extended phenotype
Four major points are raised in this section. (1) The issue of group selection vs. individual selection is outmoded; selection can operate simultaneously at multiple levels. (2) Due to the heritability of extended phenotypes and multiple levels of selection, community evolution is likely. (3) Realistic statistical methods and experiments allow us to measure the relative importance of selection acting at different levels. (4) To the extent that species interactions affect genetic covariances, species evolution must be placed in a community context.

Summary from Whitham et al 2003.

**Multi-level selection:** of individual and group-level traits (hugely debated, but many evolutionary biologists now agree that this is a real possibility)

**Genetic covariance:** traits under consideration vary together (in either positive or negative directions).