

Dissertation Committee Meeting Spring 2012

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Contents

1	Meeting Outline (Max 2hrs)	2
2	Dissertation Goal	3
3	Requirements	3
3.1	Forms/Paperwork	3
4	Projects	4
4.1	REVIEW – Ecological and evolutionary interaction network exploration	4
4.2	CHAPTER I – Network architecture and the evolution of ecological communities	4
4.3	Chapter II – A Genes to Ecosystems simulation framework	5
4.4	CHAPTER III – Genotypic variation in a foundation tree species structures lichen co-occurrence networks	6
4.5	CHAPTER IV – Inter-species hybridization and genotypic variation influence the structure of plant-herbivore networks	8

4.6	rENA: Tools for Ecosystem Network Analysis in R	9
4.7	Phylogenetic structure influences co-occurrence network architecture in alpine plant communities	9
4.8	Phenotypic variation in a foundation tree species directs lichen com- munity composition	9
4.9	Plant mediated indirect genetic effects of scale herbivory reduce diver- sity and alter arthropod community networks on a foundation tree . .	10
4.10	Directional selection by a non-native herbivore alters arthropod com- munity composition and co-occurrence network structure	10
4.11	Intraspecific variation in a foundation tree species influences endo- phyte community composition and interactions	10
5	Time-line	11

1 Meeting Outline (Max 2hrs)

- Overview of dissertation goal
- Requirements
- Projects
- Time-line
- Discussion

2 Dissertation Goal

Interactions among species contribute to both ecological and evolutionary dynamics in ecosystems. Community genetics, which seeks to identify the community-wide influence of genetic variation, has primarily focused on the effects of focal species, typically foundation species (i.e. dominant and keystone species). This dissertation will aim to expand this scope to a larger number of species in the community primarily through the integration of network theory and community genetics.

3 Requirements

3.1 Forms/Paperwork

- **May 2012** Assessment, prospectus review and course plan approval

Bio form 5 - PhD Program Form

Bio form 10 - Progress/Funding Assessment

Bio form 13 - Teaching requirement documentation

Bio form 14 - Scientific paper presentation documentation

- **October 2012** Prospectus defense and oral exam

Bio form 7 - Written exam results

Bio form 10 - Progress/Funding Assessment

Bio form 8 - Oral exam results REPORT

Bio form 8.11a - Oral exam assessment/questionnaire

Bio form 9 - Prospectus approval form

Bio form 11 - Oral exam results

Bio form 10 - Progress/Funding Assessment

- **May 2013** Final dissertation defense

Dissertation draft

Dissertation Defense Scheduling Form

Graduate college final oral exam form (can only be accessed by advisor)

4 Projects

4.1 REVIEW – Ecological and evolutionary interaction network exploration

- Summary: interactions in ecological communities generate complex dynamics. By applying a community genetics approach combined with network modeling and statistics to move beyond pairwise studies in community dynamics, community ecology can move toward a better predictive framework.
- Current Status: COMPLETED [1]

4.2 CHAPTER I – Network architecture and the evolution of ecological communities

- Main Question: how does network architecture influence community-wide evolutionary dynamics?
- Summary:

- Pascual and Dunne (2006) [2]
 - Individual based modeling [3]
 - Genotype -> Phenotype -> Interactions (Networks) -> Fitness -> Reproduction
 - Networks will be observed as an emergent property of interactions and selection
 - Salas and Borrett (In Prep) [4]
 - Lonsdorf et al. (In Prep) [5]
 - Monitor the architecture of interactions among networks as individuals evolve in response to fitness consequences of interactions
- TARGET: Evolution
 - Current Status:
 - Currently developing software in R
 - Plan to run on quad-core bioinformatics server
 - May require faster server or programming in lower level language (e.g. C or C++)

4.3 Chapter II – A Genes to Ecosystems simulation framework

- Main Goal: build a framework and write software for simulating evolution in a community context.
- Summary:

- A set of functions that will facilitate the exploration of evolution in a community context
- Genotype -> Phenotype -> Interactions (Networks) -> Fitness -> Reproduction
- Genotype = a list containing allelic information
- Phenotype = a function operating on the allelic information of genotypes
- Interactions = a function that determines the fitness outcomes based on trait matching among individuals
- Fitness = determined by the interaction function
- Reproduction = function that operates on the fitness value for individuals, species boundaries, mutation and recombination to produce offspring genotypes
- The package will be built in R (possibly supported with C)
- TARGET: Ecological Modeling and Software
- Current Status:
 - Concept stage
 - Currently doing more extensive literature review
 - Beginning to outline functions

4.4 CHAPTER III – Genotypic variation in a foundation tree species structures lichen co-occurrence networks

- Main Question: does genetic variation in a foundation species influence the network of co-occurrences among associated lichen species?

- Summary:
 - Co-occurrence patterns arise from interactions among species, similar ecological responses or demographic patterns of species [6, 7]
 - Multiple studies have shown that genetic variation in one species (e.g. foundation species) can affect the outcome of interactions among associated species [8, 9]
 - Araújo et al. 2011 [10]
 - Lichen represent a good model community for studying community dynamics [11]
 - Cottonwoods are a good model species for studying community-wide genetic effects [12]
 - Collect replicate observations of bark lichen communities from individual cottonwoods in two common gardens and one wild population
 - Also collect potential important tree traits (e.g. bark roughness, tree size)
 - Model co-occurrence patterns using Araújo et al. 2011 method
 - Analyze co-occurrence using network approach focusing on structural properties (e.g. degree, connectance and centralization)
- Target: PLoS One
- Current Status:
 - Common garden data collected (Ogden Nature Center and Pit Common Gardens)
 - Wild stand data collected
 - Currently running final analyses

4.5 CHAPTER IV – Inter-species hybridization and genotypic variation influence the structure of plant-herbivore networks

- Main Question: how does genetically based variation in a foundation tree species influence the structure of plant-herbivore networks?
- Summary:
 - Plant-herbivore interaction networks have been shown to have an architecture that is distinct from other ecological networks (e.g. mutualistic networks) [13]
 - This structure arises through both ecological (e.g. assembly) and evolutionary processes
 - Previous work has shown the intraspecific variation in both a hybridizing complex and pure species contribute to the composition of arthropod communities [14, 15]
 - This study will focus on examining the contribution of genetic variation to the structure of plant-herbivore networks
 - Data from Wimp et al. 2007 and Keith et al. 2010 will be re-analyzed from a network analytical perspective, primarily a modularity analysis [16]
 - New data from the Ogden Nature Center common garden will be collected to examine leaf modifying arthropod co-occurrence patterns
- Target: Oecologia
- Current Status:

- Re-analyzing Wimp et al. 2007 and Keith et al. 2010 data
- Collected leaf material for co-occurrence study, currently processing samples

4.6 rENA: Tools for Ecosystem Network Analysis in R

- Main Goal: generate software for the analysis of ecological networks.
- Target: Ecological Modeling and Software
- Current Status:
 - Currently in beta-testing
 - Populating help files and debugging

4.7 Phylogenetic structure influences co-occurrence network architecture in alpine plant communities

- Main Question: how are co-occurrence patterns of alpine plant communities influenced by phylogenetics?
- Analysis of global dataset of alpine plant species
- Target: Ecology Letters
- Current Status: waiting on final phylogenetic analysis from B. Butterfield

4.8 Phenotypic variation in a foundation tree species directs lichen community composition

- Lead Author: R.R. Næsborg (M.K.Lau)

- In Prep

4.9 Plant mediated indirect genetic effects of scale herbivory reduce diversity and alter arthropod community networks on a foundation tree

- Lead Author: A.C. Stone
- In Submission

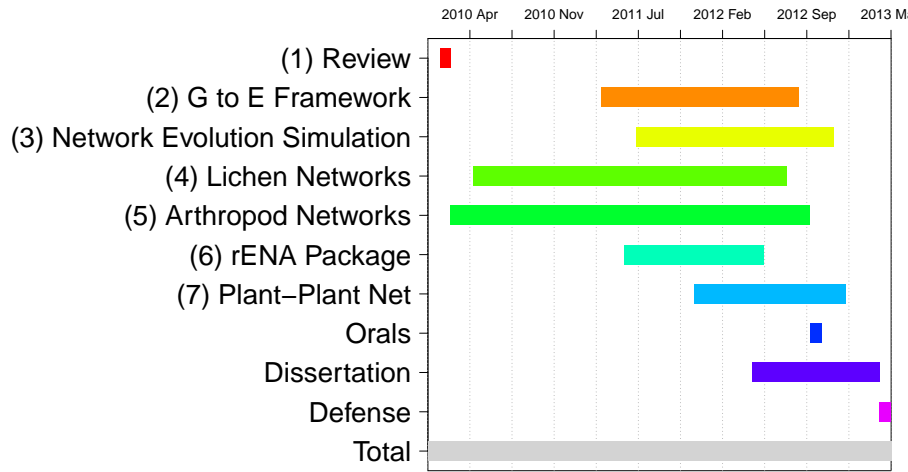
4.10 Directional selection by a non-native herbivore alters arthropod community composition and co-occurrence network structure

- Lead Author: D.S. Smith
- In Prep

4.11 Intraspecific variation in a foundation tree species influences endophyte community composition and interactions

- Lead Author: L.J. Lamit
- In Prep

5 Time-line



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