Jeremy C Andersen, PhD

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WORK EXPERIENCE

2016-Present	USDA-NIFA Postdoctoral Fellow, Roderick Lab, University of California, Berkeley
2015-2016	Postdoctoral Researcher, Elkinton Lab, University of Massachusetts Amherst

EDUCATION

2015	University of California Berkeley, Ph.D.
2009	University of Massachusetts Amherst, M.S.
2006	University of Massachusetts Amherst, B.S. – Graduated with Honors.

AWARDS and FELLOWSHIPS

2016 – present	USDA-NIFA ELI Postdoctoral Fellowship ($137,637)
2013 - 2015	Robert van den Bosch Memorial Scholarship recipient ($35,000)
2013 - 2014	USDA/USFS Research Subaward ($21,640)
2010 - 2013	EPA STAR Fellowship ($111,000)
2010, 11 & 13	Margaret C. Walker Fund recipient ($3,000)

TEACHING EXPERIENCE

Spring 2017	Gest Lecturer on Invasive Insects, Insect Ecology, UC Berkeley
Fall 2013 & 14	Graduate Student Instructor, Urban Agriculture, UC Berkeley
Fall 2012 & 14	Guest Lecturer on Non-Target Effects of Biological Control, UC Berkeley
Fall 2009	Student Outreach at Cragmont Elementary School, Berkeley California
Fall 2008	Guest Lecturer on Biogeography, Introductory Ecology, UMass Amherst
2007 – 2008	Graduate Student Instructor, Introductory Biology Lab, UMass Amherst

INVITED PRESENTATION

2015	"Population genetics and applied evolutionary biology: cryptic species, host-associations, and the geographic mosaic of coevolution." Ecology and Evolutionary Biology Seminar Series, San Francisco State University.

RECENT PRESENTATIONS

2017	"Distinguishing invasive from indigenous species in terrestrial arthropod communities on Moorea, French Polynesia, through metabarcoding signatures. International Biogeography Meeting, Tucson, AZ.
2016	"Population genetics of winter moth: identifying the origins of invasive populations in North America." International Congress of Entomology, Orlando, FL
2016	"Population genetics of winter moth and the origins of winter moth populations in North America." USDA Research Forum on Invasive Species. Annapolis, MD.
2015	"Developing a SNP-array to measure pre- and post-introduction genetic diversity and levels of hybridization between two host races of knotweed psyllid, candidates for the biological control of Japanese knotweed. USDA Research Forum on Invasive Species. Annapolis, MD.
2014	"Landscape genetics and the biological control of walnut aphids in California" Ecology Meeting. Sacramento, California
2014	"Examining the presence of a geographic mosaic of coevolution in the walnut aphid biological control system" Evolution Meeting. Raleigh, North Carolina

PUBLICATIONS

Andersen JC, Havill NP, Broadley HJ, Boettner GH, Caccone A, & Elkinton JS. In Prep. Differential *Wolbachia* infection rates for two species of *Operophtera* (Lepidoptera: Geometridae) and their hybrids: a possible driver of asymmetric hybridization. *Journal of Applied Ecology*.

Andersen JC, & Mills NJ. Submitted. Post-release genetic surveys reveal a geographic mosaic of coevolution in the walnut aphid biological control program. *Evolutionary Ecology*.

Andersen JC, Havill NP, Caccone A, & Elkinton JS. 2017. Post-glacial recolonization shaped the genetic diversity of the winter moth (*Operophtera brumata*) in Europe. *Ecology and Evolution*. DOI: 10.1002/ece3.2860, p. 1-12.

Havill NP, Elkinton J, Andersen JC, Hagen SB, Broadley HJ, Boettner GJ, & Caccone A. 2017. Asymmetric hybridization between non-native winter moth, *Operophtera brumata* (Lepidoptera: Geometridae), and native Bruce spanworm, *O. bruceata,* in the northeastern United States, assessed with novel microsatellites and SNPs. *Bulletin of Entomological Research*. 107, p. 241-250

Andersen JC, & Mills NJ. 2016. Geographic origins and post-introduction hybridization between strains of *Trioxys pallidus* introduced to western North America for the biological control of walnut and filbert aphids. *Biological Control*. 103, p. 218-229.

Andersen JC, & Wagner DL. 2016. Systematics and biological control. *In*. Van Driesche RG, Simberloff D, Blossey B, Causton C, Hoddle MS, Wagner DL, Marks CO, Heinz KM, & Warner KD (eds.) Integrating Biological Control into Conservation Practice. *John Wiley & Sons, Ltd,* Chichester, UK. p. 105-129.

Andersen JC, Bourchier RS, Grevstad FS, Van Driesche R, & Mills NJ. 2016. Development and verification of SNP arrays to monitor hybridization between two host-associated strains of knotweed psyllid, *Aphalara itadori*. *Biological Control*. 93, p. 49-55.

Andersen JC, Gwiazdowski RA, Gdanetz K, & Gruwell ME. 2015. Armored scale insect endosymbiont diversity at the species level: genealogical patterns of *Uzinura diaspidicola* in the *Chionaspis pinifoliae – Chionaspis heterophyllae* species complex (Hemiptera: Coccoidea: Diaspididae). *Bulletin of Entomological Research*. 105, p. 110-120.

Andersen JC, & Mills NJ. 2014. iMSAT: a novel approach to the development of microsatellite loci using barcoded Illumina libraries. *BMC Genomics*. 15, 858.

Andersen JC, Gwiazdowski RA, & Gruwell ME. 2014. Molecular evolution of sexual and parthenogenetic lineages of the armored scale insect *Aspidiotus nerii* (Hemiptera: Diaspididae) and its primary bacterial endosymbiont, *Uzinura diaspidicola*. *Annals of the Entomological Society of America*. 107, p. 954-960.

Andersen JC, & Mills NJ. 2012. DNA extraction from museum specimens of parasitic hymenoptera. *PLoS One*. 7, e45549.

Gwiazdowski RA, Vea IM, Andersen JC, & Normark BB. 2011. Discovery of cryptic species among North American pine-feeding *Chionaspis* scale insects (Hemiptera: Diaspididae). *Biological Journal of the Linnaean Society*. 104, p. 47-62.

Andersen JC, Wu J, Gruwell ME, Gwiazdowski R, Santana S, Feliciano NM, Morse GE, & Normark BB. 2010. A phylogenetic analysis of armored scale insects, based upon nuclear, mitochondrial, and endosymbiont gene sequences. *Molecular Phylogenetics and Evolution*. 57, p. 992-1003.

Andersen JC, Gruwell ME, Morse GE, & Normark BB. 2010. Cryptic diversity in the *Aspidiotus nerii* complex in Australia. *Annals of the Entomological Society of America*. 103, p. 844-854.

Rugman-Jones PF, Andersen JC, Morse JG, Normark BB, & Stouthamer R. 2010. Molecular phylogenetic placement of the recently described scale insect *Abgrallaspis aguacatae* and several congeners (Hemiptera: Diaspididae). *Annals of the Entomological Society of America*. 103, p. 30-38.

REVIEWER EXPERIENCE

Annals of the Entomological Society of the United States of America, Biological Control, Bulletin of Entomological Research, European Journal of Entomology, Evolutionary Applications, Insects, Journal of Insect Science, Public Library of Science (PLoS), Molecular Ecology, Molecular Ecology Resources

POSTDOCTORAL RESEARCH

Roderick Lab – University of California Berkeley

The continued introduction of invasive species has profound impacts on the sustainability and productive capability of American farmers, ranchers, and growers, in addition to threatening native wildlife and ecosystems. However, it is unclear when attempting to control for invasive species, whether it is more important to account for genetic or environmental variables. Yellow starthistle is one of the most economically damaging (~$1.4 billion in annual damages) and widespread invasive weed species in North America. I have developed a method to integrate ecological niche modeling with next-generation sequencing to determine the relative importance of genetic and environmental variables. My preliminary results indicate that there is a significant correlation between plant genetic diversity and the efficacy of the biological control agents. This research leverages the availability of extensive geographic sampling of yellow starthistle in California by the California Department of Food and Agriculture and recent breakthroughs in Next Generation Sequencing (NGS) technologies to examine the relative importance of landscape and genetic variables on the distributions, population structure, and rates of geneflow between populations of yellow starthistle. This USDA-NIFA Fellowship research is being supervised by Dr. George Roderick at the University of California Berkeley and Dr. Patrick Moran at the USDA ARS Western Regional Research Center in Albany, CA.

Elkinton Lab – University of Massachusetts Amherst

The biological control of winter moth (*Operophtera brumata*) in Nova Scotia represents a text-book example of a successful biological control program, however, winter moth has more recently invaded Oregon, British Columbia, and the northeastern United States and appears to be expanding its distribution. This expansion may be facilitated by hybridization with a native congener Bruce spanworm (*O. bruceata*). As a Postdoctoral Researcher in the lab of Dr. Joseph Elkinton, I used next-generation sequencing and microsatellite genotyping to uncover the historical biogeographic patterns for winter moth in Europe, and to identify hybrids in all of the invasive populations, and I am continuing to collaborate with Dr. Elkinton and Dr. Nathan Havill at the USDA Forest Service Northern Research Station to identify the geographic regions of origins of each invasive winter moth population.

DOCTORAL DISSERTATION RESEARCH

I examined the role of hybridization on the sustainability of the biological control of walnut aphids (*Callaphis juglandicola)* in California and filbert aphids (*Myzocallis coryli)* in Oregon by host-specific strains of the parasitoid wasp *Trioxys pallidus* introduced from Iran and Europe, respectively. Using microsatellite and Sanger sequencing I identified hybrid individuals in both crop systems, and found that measures of genetic diversity were significantly different between introduced and native populations. In addition, in California, I found evidence for a geographic mosaic of co-evolution in the walnut aphid biological control system, and found high levels of inbreeding within and low levels of dispersal among orchard populations. These results lead to me to recommend that *T. pallidus* individuals may need to be actively dispersed throughout the walnut growing region to maintain genetic diversity. In addition, I examined the utility of obtaining DNA from museum specimens, and developed a SNP array for post-release genotyping of two strains of the psyllid *Aphalara itadori* that are candidates for the biological control of Japanese and Giant knotweed.

REFERENCES

Dr. George K. Roderick, Department of Environmental Science Policy and Management, Mulford Hall, University of California Berkeley, CA 94720, Tel: (510) 643-4554, E-mail: roderick@berkeley.edu

Dr. Joseph S. Elkinton, Department of Environmental Conservation, University of Massachusetts Amherst, MA 01003, Tel: (413) 545-4816, E-mail: elkinton@ent.umass.edu

Dr. Nicholas J. Mills, Department of Environmental Science, Policy and Management, Wellman Hall, University of California Berkeley, CA 94720, Tel: (510) 642-1711, E-mail: nmills@berkeley.edu

Dr. Benjamin B. Normark, Department of Biology, Fernald Hall, University of Massachusetts Amherst, MA 01003, Tel. (413) 577-3780, E-mail: bnormark@bio.umass.edu

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