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Detecting apparent competition by shared parasitoid enemies between a native and a range-expanding oak insect

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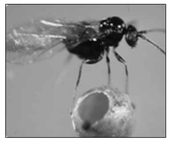
Introduction

- When a species' range expands due to anthropogenic change it leads to cascading effects in ecosystems. [1]
- As species expand their range, they may leave interacting species behind and form novel associations. Losing competitors and enemies results in **ecological release**. [2]



Canadian Forest Service

Fig. 1 *Neuroterus saltatorius* (NSA) is an oak gall wasp that is expanding its range poleward and outbreaking on its host plant *Quercus garryana*, causing leaf damage [3].

Fig 2. *Andricus opertus* (AO) is a common oak gall wasp that co-occurs with NSA on *Q. garryana* in the native and expanded range. It ***shares parasitoid wasp enemies with NSA***, and we investigate its role as an ***apparent competitor*** [4].

Methods

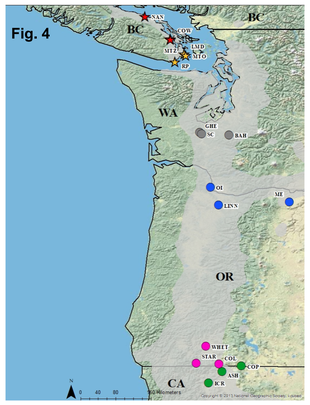


Fig. 3 Map of *Quercus garryana* ecosystems (grey) that is the dominant oak in western oak ecosystems. It is the host plant to oak gall wasps, which are insects that specialize on oaks. We performed systematic surveys at 18 sites in 6 regions (R1-6, different colors) in the native (circles) and expanded (stars) range in 2019, identifying **23 oak gall wasp species** [4]**.** We reared out **parasitoid enemy** wasps that attack and kill wasp hosts. Wasp emergents are collected biweekly and, we identified them using taxonomic keys to the lowest taxonomical level [5].

Does escape from ***apparent competition*** lead to outbreaks of range-expanding species?

Predictions

Apparent competition is *indirect* competition between prey species through shared enemies

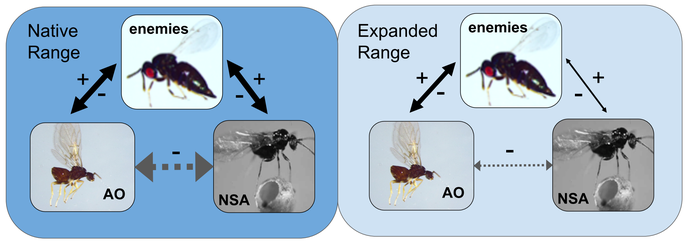


Fig 4. We predict strong apparent competition in the native range and weak apparent competition in the expanded range if shared enemies fail to follow NSA from the native range or switch from AO.

Results

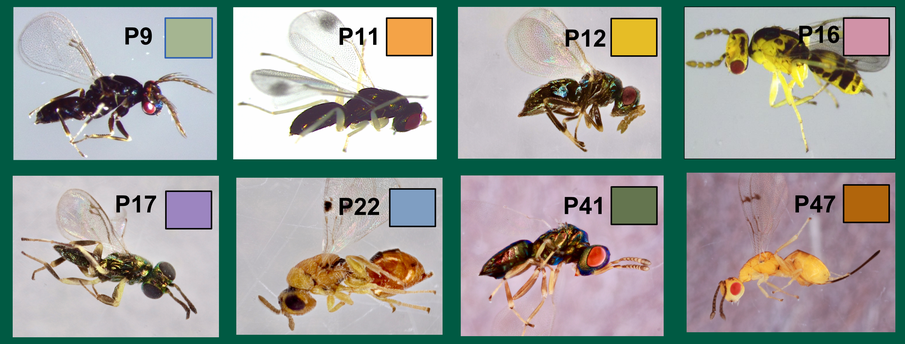


Fig 5. We identified 8 total shared parasitoids between AO and NSA. These parasitoids attack both species across the expanded and native region. All wasps are in the superfamily Chalcidoidea: P9 *Aprostocetus* sp. 1, P11 *Aprostocetus pattersonae,* P12 *Aprostocetus vericarri,* P16 *Tetrastichinae* sp. 2, P17 *Brasema* sp.1, P22 *Sycophila wilitzae,* P41 *Pteromalidae* sp. 1, and P47 *Bootanomyia dorsalis*

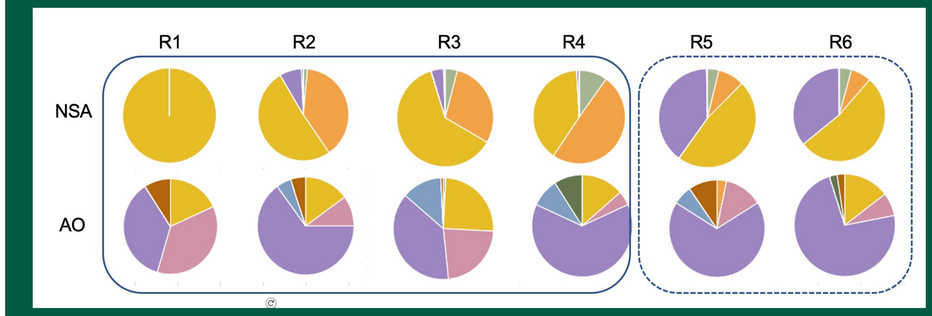
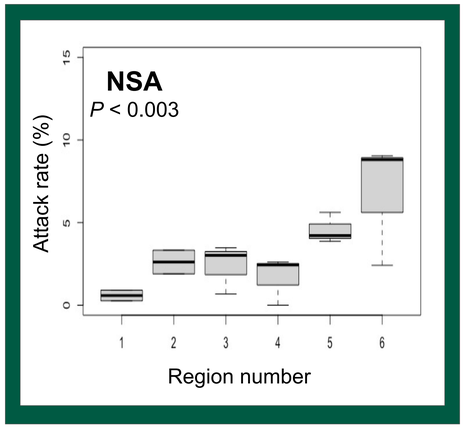


Fig 6. Each color represents the relative abundance of parasitoids reared out of each host pooled at sites among regions. Fig 5 serves as the legend with colors corresponding to parasitoids. Composition of parasitoids attacking hosts changes: P17 (purple) specializes on AO in the native range. P12 (yellow) is shared in both regions. P11 (light orange) specializes on NSA and is less abundant in the expanded range. NSA abundance was low in R1.



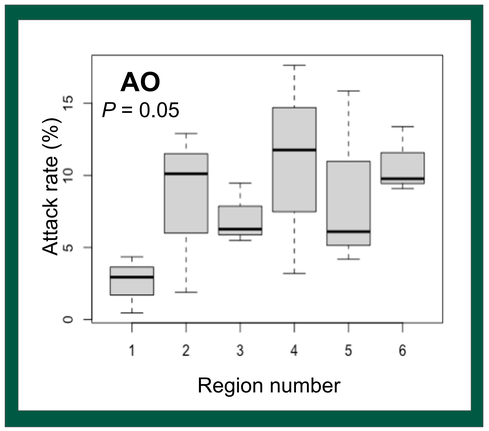


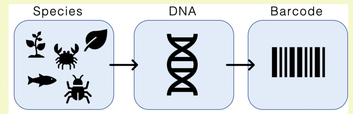
Fig 7. Attack rates are calculated as the number of parasitoids/collected galls. Attack rates of NSA differ among regions, being higher in the expanded range. Attack rates for AO are more similar among regions.

Discussion

- NSA and AO are apparent competitors, sharing 8 parasitoids out of 10 that attack NSA and 14 that attack AO.
- Changes in composition of shared parasitoids include: P17 (specialized on AO) replacing P12 (specializes on NSA). If P17 is less effective than P12 (as it specialized on AO) it could cause weak apparent competition.
- Higher attack rates of NSA in the expanded range do not suggest reduced apparent competition but estimating attack rates by bulk rearing is challenging and previous studies in this system show lower attack rates. [3].
- P47 is an introduced species
- These parasitoids might not actually be generalists as morphological delineation is challenging, and many studies find cryptic species from different hosts [6].

Current work: DNA barcoding

DNA barcoding is a method of species identification that uses universal gene regions as "barcodes" to identify species. A portion of the **cytochrome *c* oxidase I (CO1)** gene is used for animals. This tool is especially useful for cryptic organisms, like small parasitoid wasps.



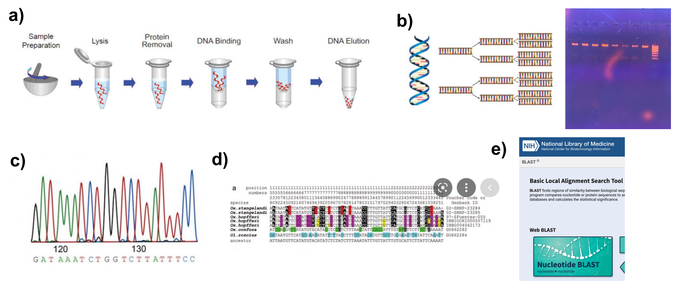


Fig 8. Current work includes DNA barcoding parasitoids of NSA and AO. We are barcoding multiple individuals from each region and each host. Steps include a) extracting DNA from parasitoid samples. b) Performing PCR using primers that amplify target regions of CO1. c) Sending off PCR products for Sanger sequencing, to obtain sequences of CO1 region. e) Aligning sequences to detect cryptic species in putative generalist groups (i.e., from P17 reared out of AO and NSA in different regions). e) Running sequences through databases (e.g., BLAST) to find potential matches to other sequences or identified species in databases.

Acknowledgements/References

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