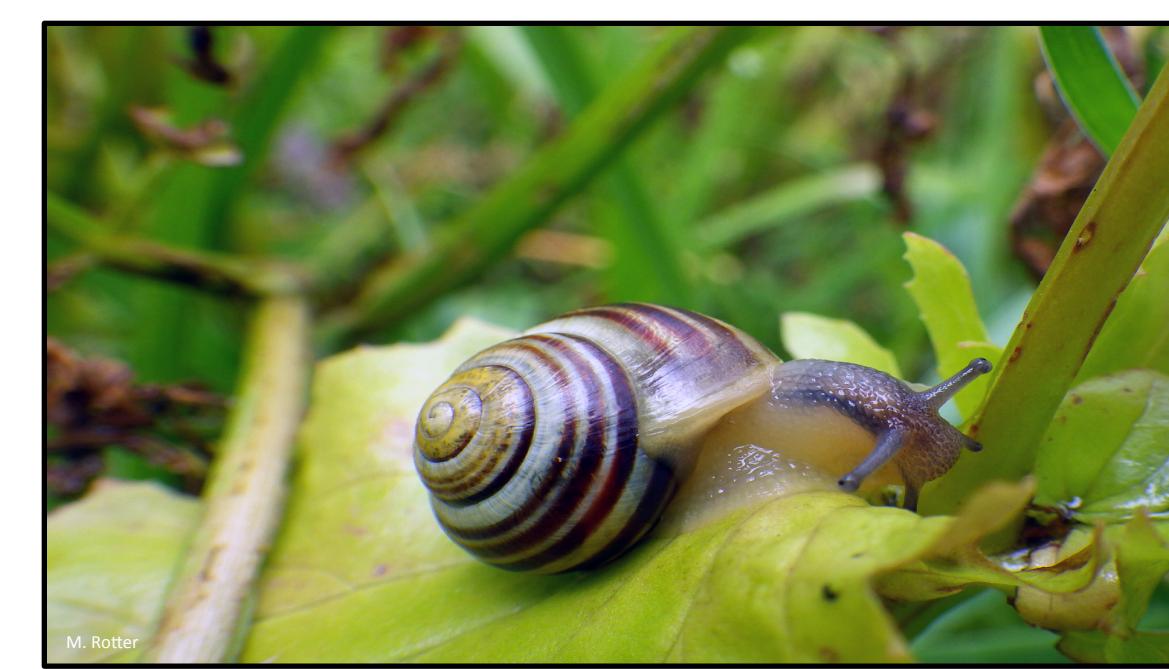




Ecology and genetic architecture of herbivory defense in yellow monkeyflower

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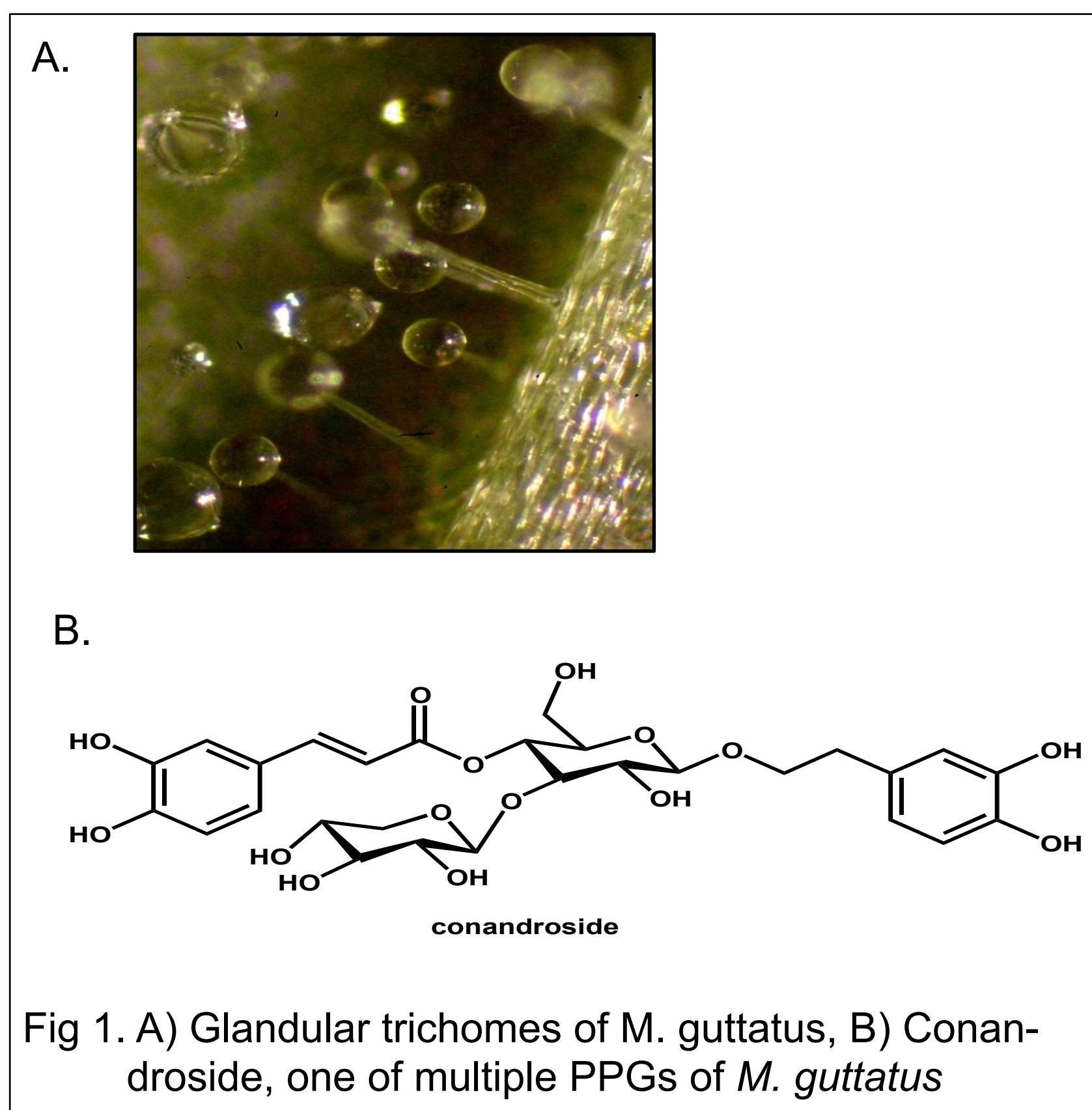
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Background

Yellow monkeyflower (*Mimulus guttatus*) inhabits mesic areas in western North America. It is a self-compatible, hermaphroditic plant that reproduces by outcrossing and self-fertilization. Local populations differ extensively in morphology, life history, selfing rate, and levels of herbivory.

Insect herbivory is a driving force of plant evolution. We used yellow monkeyflower as a model system to characterize 1) the ecological relationship between herbivores and plant defenses and 2) the genetic architecture of plant defense traits.

M. guttatus has substantial genetic variation for both physical and chemical defenses. Physical defenses include glandular trichomes, while a suite of phenylpropanoid glycosides (PPGs) are the signature foliar secondary compounds (Fig 1).



A wide variety of herbivores consume *M. guttatus*, including Lepidoptera larvae, beetles, xylem and phloem feeders, and molluscs (e.g., Fig 2).

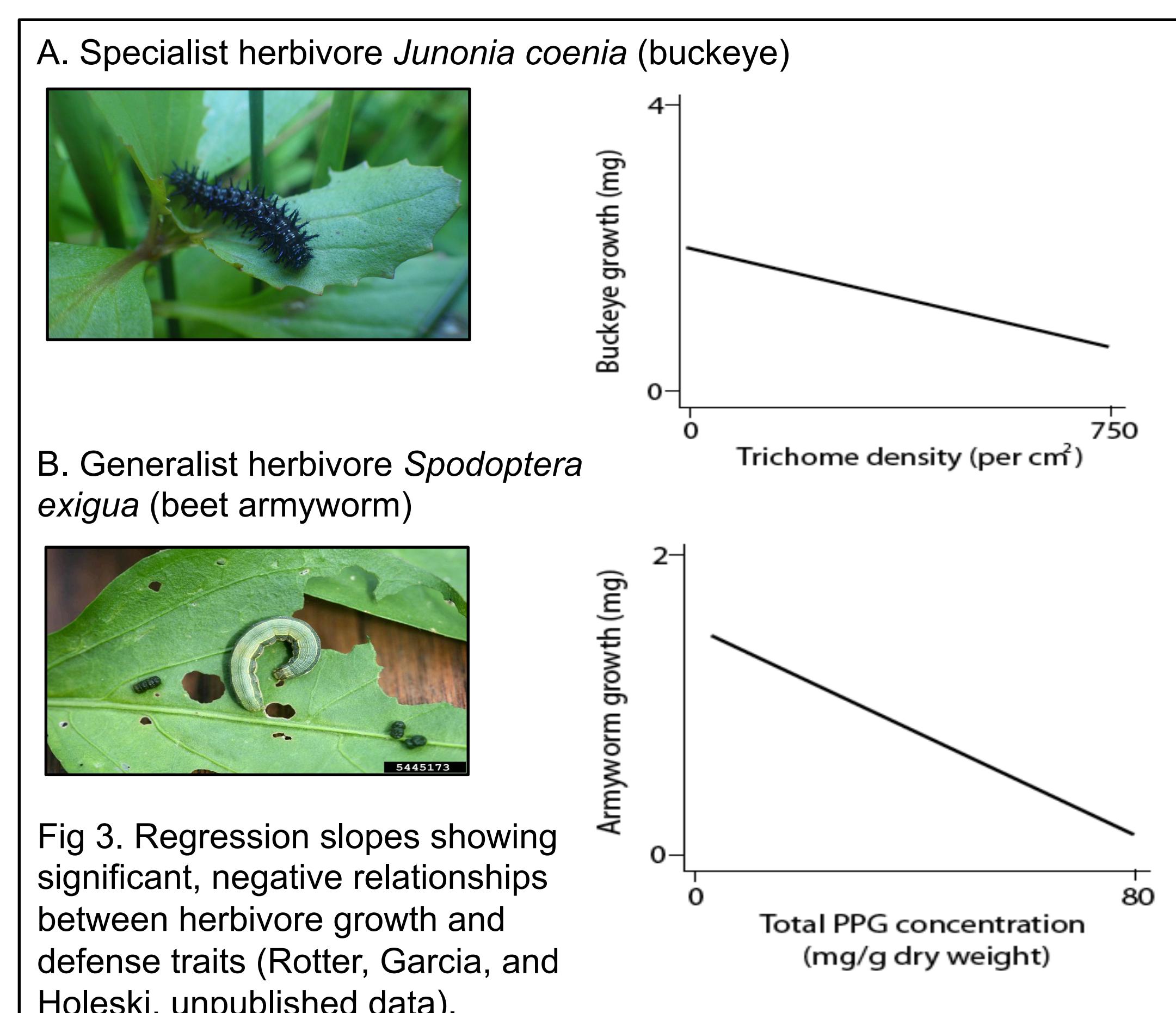


Fig 2. Herbivores of *M. guttatus*. Photos by M. Rotter and L. Holeski

Herbivores and plant defenses

Genetic variation in defenses affects herbivore performance: Generalist and specialist herbivores of *M. guttatus* are differentially affected by physical and chemical resistance traits (Fig 3).

In no-choice feeding trials using plants derived from multiple natural populations and encompassing natural variation in trichome density and PPG concentrations, specialist herbivores had reduced performance on plants with higher trichome densities (Fig 3A), while generalist herbivores performed best on plants with lower levels of PPGs (Fig 3B).



Genetic architecture of defense traits

I used recombinant inbred lines (RILs) derived from a cross between a plant from an annual alpine population (low ambient herbivory) and a plant from a coastal perennial population (high ambient herbivory) to assess genetic correlations between resistance traits and map underlying QTLs. PPGs were generally positively correlated with one another, while there was not a strong relationship between physical and chemical defense traits (Fig 4).

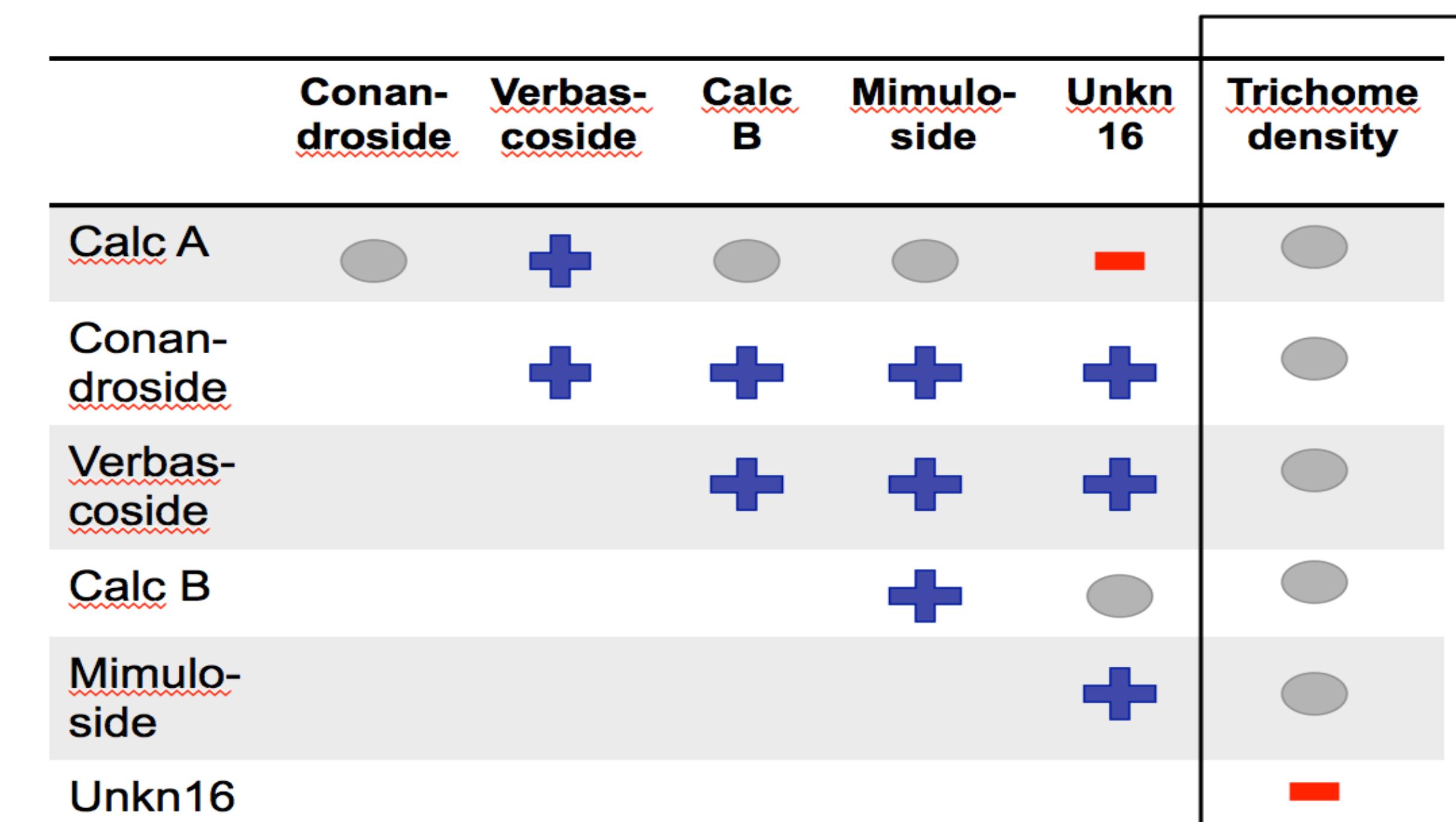


Fig 4. Genetic correlations between herbivore resistance traits in *M. guttatus*. Symbols indicate significant positive (+) or negative (-) correlations, or no significant correlation (●).

Multiple, non-overlapping quantitative trait loci (QTL) underlying trichome production and PPGs have been identified (Table 1).

Linkage group	Trait				
	CalCA	Conan-droside	CalcB	Unkn 16	Trichome density
3	11.4	8.8			
5		2.2			
6				9.2	
10					5.0 17.1
12					3.0
13					13.2
14					23.7

Table 1. Linkage groups and percent of phenotypic variance explained for QTL underlying defense traits. Traits with QTL on the same linkage group do NOT share positions for QTL. Data from Holeski, Monnahan, et al. 2014 and Holeski, unpublished data.

The absence of QTL that affect multiple PPGs detected thus far is surprising, given strong, positive correlations between some PPGs. Independent genetic control of individual PPGs and trichomes could increase the complexity and lability of suites of defense traits within *M. guttatus*.

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