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Cross-sex genetic correlations constrain the evolution of a behavioral syndrome

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In field crickets, males and female express genetically distinct behavioral syndromes, leading to diverging evolutionary responses

Cross-sex genetic correlations constrain the evolution of a behavioral syndrome

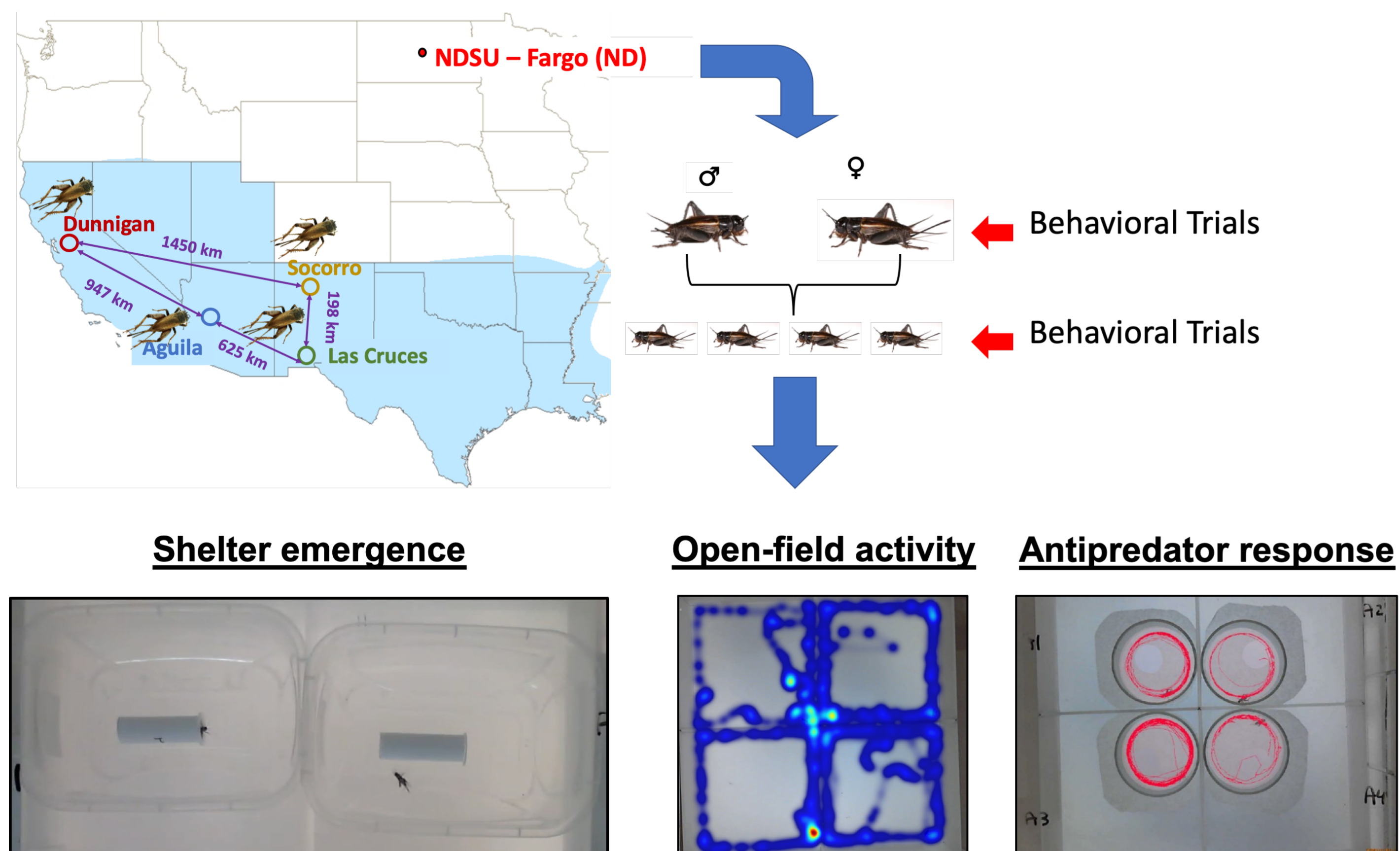
Raphaël Royauté¹, Ann Hedrick², Ned Dochtermann¹

CONTEXT

- Behaviors often integrated into syndromes & have genetic basis
- Sex-specific architecture unknown
- Implications for the evolution of behavioral dimorphism

METHODS

- Field crickets (*Gryllus integer*) collected from 4 populations
- Breeding design over 3 generations and behavioral phenotyping of 965 individuals



PREDICTIONS

Stronger selective pressure for ♀ to be active and for ♂ to guard burrows

- ♀ quicker to exit shelter and more active X ✓
- Less genetic variance in shelter emergence & activity in ♀ X ✓
- Stronger activity-antipredator response syndrome in ♀ ✓

RESULTS

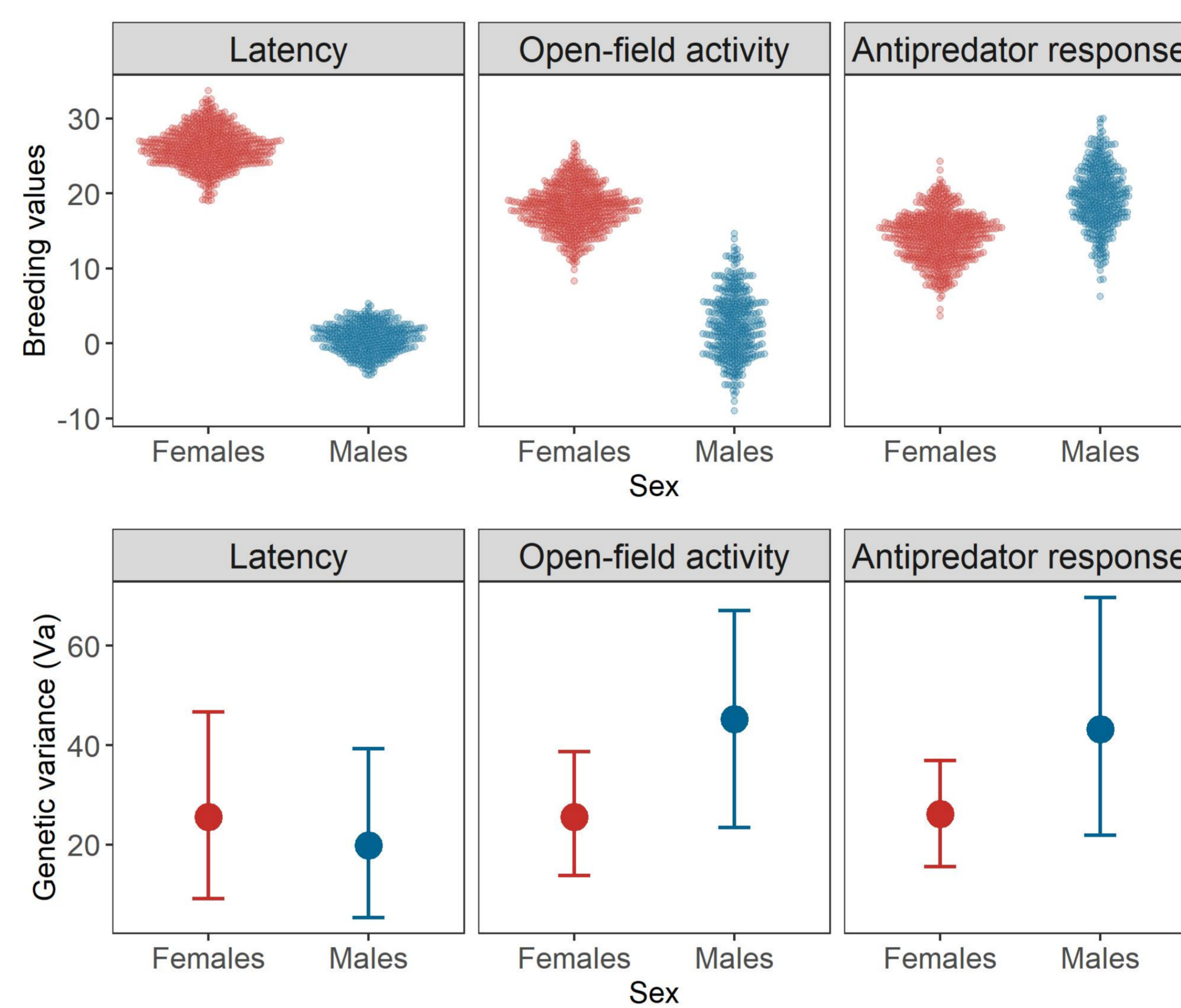


FIGURE 1. Males and females expressed diverging behaviors with females less prone to leave shelter ($Pmcmc = 0.95$) and more active than males ($Pmcmc = 0.90$). Males had more genetic variation in activity ($Pmcmc = 0.95$) and antipredator response ($Pmcmc = 0.92$). Shelter emergence had equal genetic variance among sexes ($Pmcmc = 0.68$).

$Pmcmc$: Bayesian probability for finding a difference among sexes.
 $Pmcmc < 0.7$: Poor evidence of difference
 $Pmcmc > 0.8$: Moderate evidence
 $Pmcmc > 0.9$: Strong evidence
 $Pmcmc > 0.95$: Very strong evidence

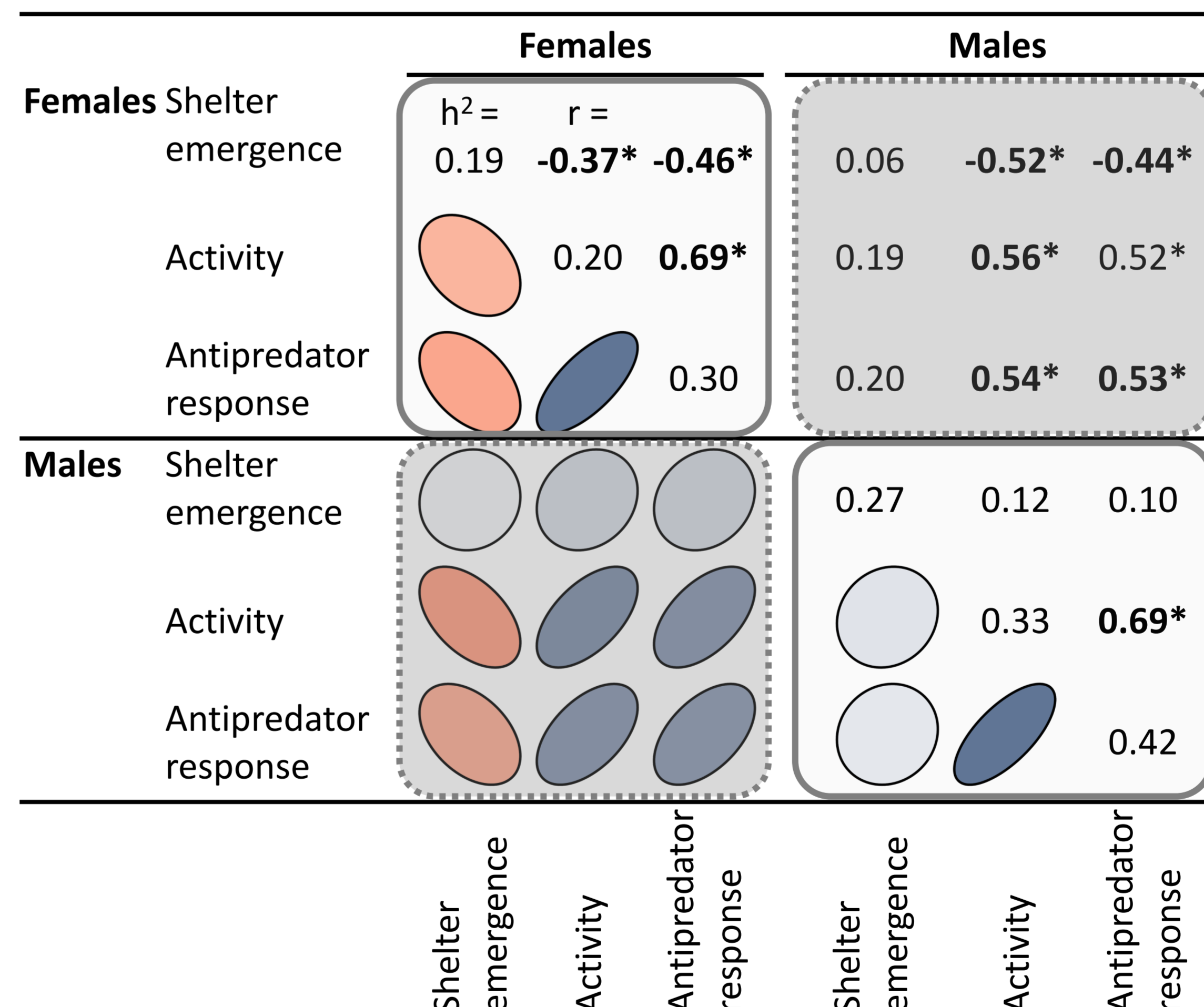


FIGURE 2. Genetic variance-covariance matrix. Heritabilities (h^2) are indicated on the diagonal and genetic correlations (r) on the off-diagonal elements. Shelter emergence was genetically uncoupled between sexes ($r = 0.07$, $Pmcmc = 0.61$). The activity-boldness syndrome had weaker correlations in males.

