

Fig 1. Predation cues influence critical maximum temperature of *Daphnia pulicaria*. Means ± 1 S.E.M. of age at maturity (days), size at maturity (mm), average number of offspring of the first three clutches, intrinsic growth rate (r), and critical maximum temperature (CT_{max} , °C) of *Daphnia pulicaria* collected at Blue and Gardisky Lakes during summer 2017 in response to temperature (15° C and 25° C, x-axis) and predation cues treatments. Circles show response without fish cues (N) and triangles show response to fish cues (Y).

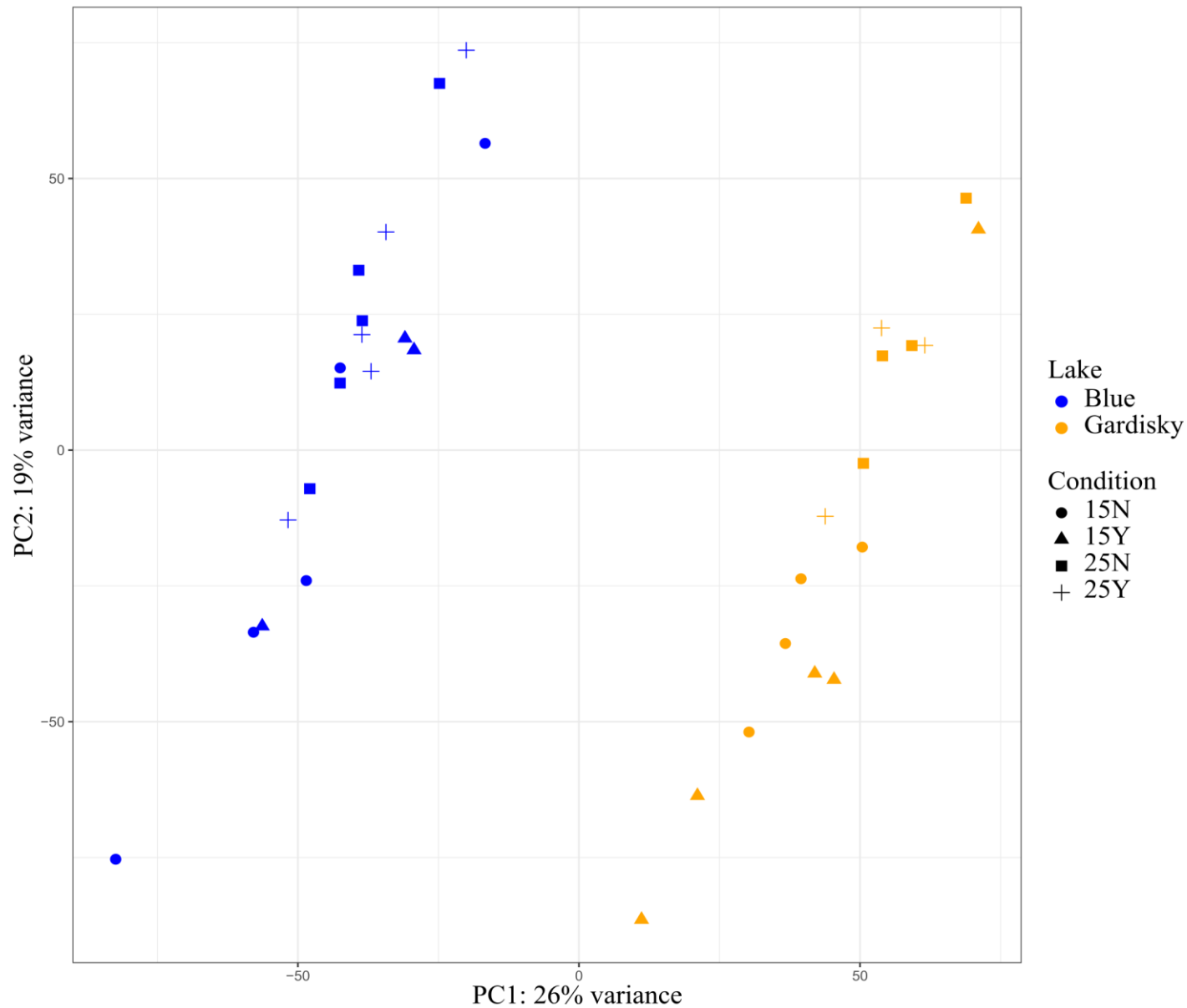


Fig 2. Genotype, not treatment group, is the dominant source of differential gene expression.

Principal component analysis of gene expression patterns generated through DESeq2 prominently separates individuals by clone along the first principal component.

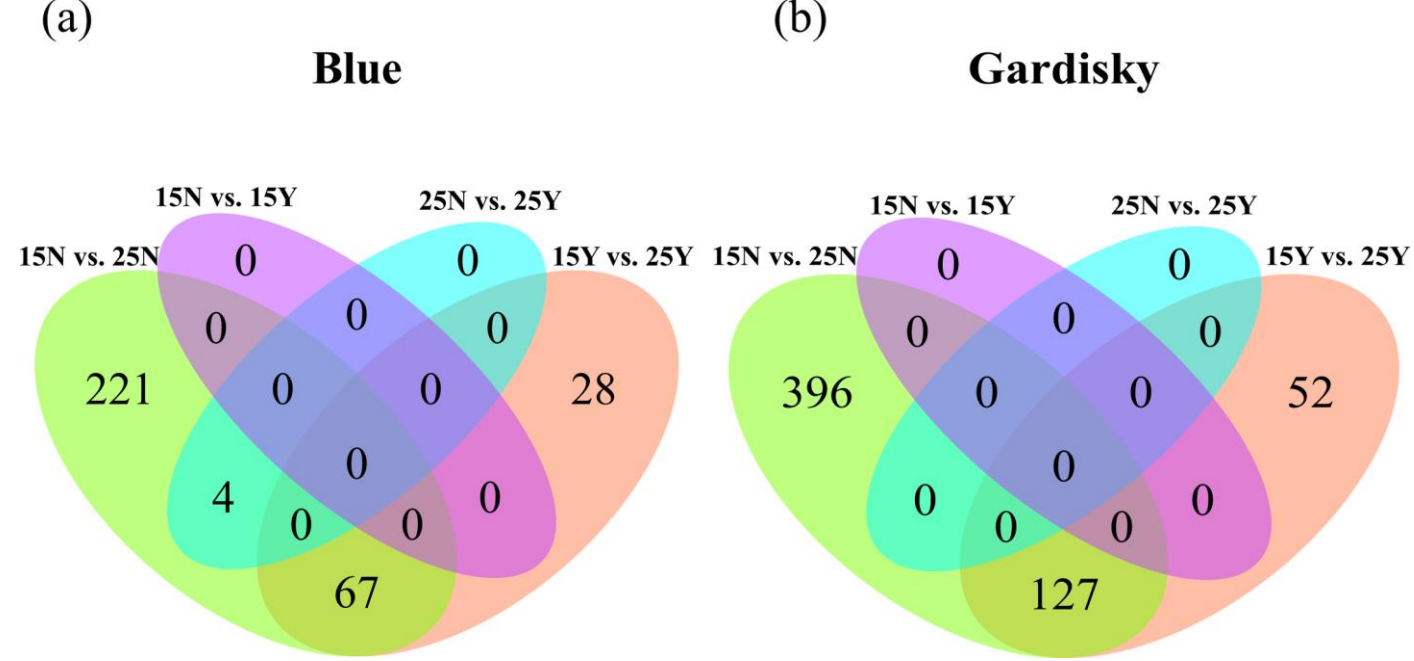


Fig 3. Many genes are differentially expressed in response to temperature changes, while kairomones have minimal observable effect at the level of transcript expression.

Venn diagram of differentially expressed genes for *Daphnia pulicaria* clones **(a)** Blue and **(b)** Gardisky in response to temperature and predation cues. Cyan and purple sections illustrate differential expression from the introduction of predator cues (Y vs. N for the presence and absence of fish cues), while the green and orange sections illustrate differential expression due to temperature change. Treatment abbreviations: 15Y, 15° C with kairomones; 15N, 15° C without kairomones; 25Y, 25° C with kairomones; 25N, 25° C without kairomones.

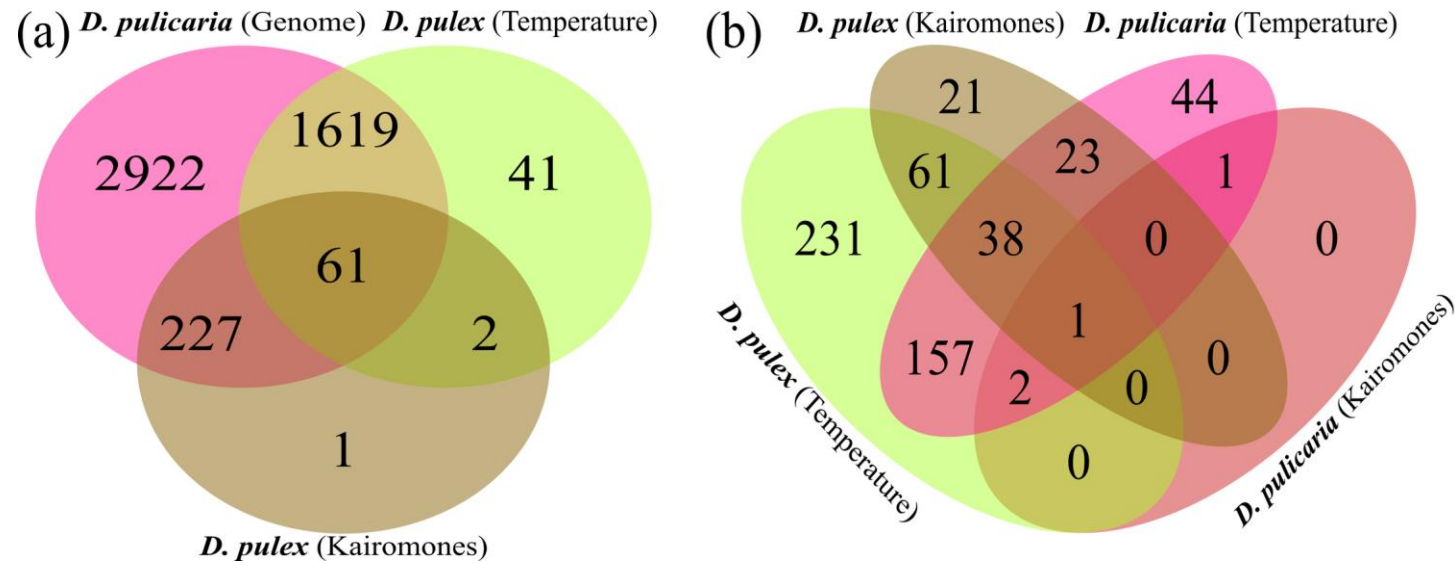


Fig 4. Gene orthology analysis reveals similarities between stress-responsive genes in *D. pulicaria* and *D. pulex*.

Venn diagrams of orthologous gene clusters between *D. pulex* DEGs from the *Daphnia* Stressor Database and **(a)** the *D. pulicaria* genome or **(b)** DEGs from *Daphnia pulicaria*. Numbers indicate protein families with at least two members, excluding "singletons" that have no orthologous or paralogous matches. Gene identifiers for orthologous clusters and singleton genes are available in **(a)** Supplementary File 1 and **(b)** Supplementary File 2.