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Identification of genetic variation explaining variation in plasticity of cold tolerance using the *Drosophila Genetic Reference Panel* (34271)

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Genome-wide association studies (GWAS) have enabled associating variation in millions of genetic markers with phenotypic variation, thus identifying regions of the genome explaining variation in the phenotypic trait under investigation. Phenotypes are typically assessed in one environment and therefore the detected candidate genes may be restricted to this environment. Thus traditional GWAS do not account for genotype-by-environment interactions (GxE). We have used 169 inbred lines of *Drosophila melanogaster* from the *Drosophila Genetic Reference Panel* (DGRP) to investigate such G by E interactions across an environmental gradient consisting of five developmental temperatures from 17 to 29 °C. We assessed the cold tolerance of adult flies developed at these temperatures using the dynamic measure critical thermal minimum ($\mathrm{CT}_{\mathrm{min}}$), to determine the variation in the plasticity of cold tolerance in the DGRP population. We have focused on quantifying the slope and elevation of the norm of reaction curves for the lines and associating the phenotypic information with the publicly available genomic sequence information (~4 million mapped SNPs). We aim to detect genetic fingerprints of e.g. plastic and canalized genotypes. Additionally, we are associating variation in cold tolerance of flies from each developmental temperature with genetic variation to investigate whether the same genetic architecture or metabolic pathways are involved in basal cold tolerance across the thermal gradient. We found significant variation in the slopes of reaction curves and thus in the plasticity of cold tolerance within the DGRP population. Cold tolerance differed rather dramatically between flies from different developmental temperatures with $\mathrm{CT}_{\mathrm{min}}$ spanning from 1.7 to 11 °C in flies developing at 17 and 29 °C, respectively. A large variation in $\mathrm{CT}_{\mathrm{min}}$ between the lines within each developmental temperature indicates a strong genetic component to cold tolerance. Preliminary association analyses have identified several regions of the genome that explain differences in the plasticity of cold tolerance.