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Functional Analysis of a Putative Target of Spatially Varying Selection in the *Menin1* Gene of *Drosophila melanogaster*

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ABSTRACT While significant effort has been devoted to investigating the potential influence of spatially varying selection on genomic variation, relatively little effort has been devoted to experimental analysis of putative variants or genes experiencing such selection. Previous population genetic work identified an amino acid polymorphism in the *Mnn1* gene as one of the most strongly latitudinally differentiated SNPs in the genome of *Drosophila melanogaster* in the United States and Australia. Here we report the results of our transgenic analysis of this amino acid polymorphism. Genotypes carrying alternative *Mnn1* alleles differed in multiple phenotypes in a direction generally consistent with phenotypic differences previously observed along latitudinal clines. These results support inferences from earlier population genomic work that this variant influences fitness, and support the idea that the alleles exhibiting clines may be likely to have pleiotropic effects that are correlated along the axes favored by natural selection.

KEYWORDS

DNA damage
chill coma
recovery
local adaptation
latitudinal cline

One of the defining problems of empirical population genetics is determining the genetic and population processes that explain the abundance of genetic variation in natural populations. In addressing this difficult problem, the discipline of population genetics has developed multiple intellectual traditions. These include the analysis of random samples of genetic variation to infer population genetic processes, and the experimental analysis of defined genetic variants to discover the properties of alleles that may influence or explain their spatial or temporal patterns in nature. In some cases these two intellectual traditions have coalesced, as in the classic work on the population genetics of lethal mutations in natural *Drosophila* populations (reviewed by Simmons and Crow 1977), the ecological genetics of Mendelian

(or nearly Mendelian) traits (e.g., Ford 1965, Majerus 1998), or the ecological genetics of specific variants, including several that were identified via allozyme electrophoresis (e.g., Watt 1977, Hilbish and Koehn 1985, Chappell *et al.* 1988, Hochachka and Somero 1984). Population genomic analysis has occasionally been integrated with *in vivo* experimental work on specific candidate variants, however, such efforts have sensibly focused on genetically simple traits and alleles of large effect (e.g., Shindo *et al.* 2005, Schmidt *et al.* 2008, Chan *et al.* 2010, Nadeau *et al.* 2016). While there are good examples of candidate targets of selection identified from allele frequency data that were later subjected to transgenic analysis in *D. melanogaster* (e.g., Laurie-Ahlberg and Stam 1987, Catalán *et al.* 2016, Glaser-Schmitt and Parsch 2018, Yang and Edery 2018), the integration of population genomic inference with detailed *in vivo* functional analysis is still in its infancy.

Spatially varying selection is among the plausible selective mechanisms contributing to the maintenance of polymorphism in natural populations (e.g., Levene 1953, Slatkin 1975, Felsenstein 1976, Endler 1977, Hedrick 1986, Yeaman 2015). For example, *D. melanogaster* phenotypic and genomic variation appears to be strongly influenced by recent selection in latitudinal clines in the United States and Australia (reviewed in Hoffmann and Weeks 2007, Adrion *et al.* 2015). Putative selected variants revealed by population genomic analysis of clinal samples in *D. melanogaster* (and in most species) are typically interpreted in one of two ways (e.g., Turner *et al.* 2008,

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Kolaczowski *et al.* 2011, Svetec *et al.* 2011, Fabian *et al.* 2012, Reinhardt *et al.* 2014, Machado *et al.* 2016, Božičević *et al.* 2016). First, variants or associated genes are subjected to enrichment analysis to generate hypotheses on the classes of sequence or phenotypes generally influenced by selection. Alternatively, the possible functional effects of such variants are speculated on based on inferences of gene function (related to annotations and expression patterns) and ecology. The quality of both types of hypotheses, however, may be compromised because of uncertainty in the identity of the true targets of selection and because the putative effects of candidate selected variants typically reflect gene annotations derived from laboratory mutations, the effects of which may differ substantially from those of natural variants. These uncertainties raise the question of the general role of experimental analysis of candidate targets of spatially varying selection for a model system such as *D. melanogaster*.

In this report we present our work using transgenic analysis to investigate a strong candidate SNP target of spatially varying selection as revealed by our previous population genetic analysis of latitudinal differentiation in *D. melanogaster* (Kolaczowski *et al.* 2011, Reinhardt *et al.* 2014). Our focal variant is a non-synonymous SNP (nsSNP) in the *Mnn1* gene. The T/A (CAT to CAA) polymorphism at position 2L:7061538 (FlyBase, v6.0) codes for a predicted Histidine(H)/Glutamine(Q) polymorphism at amino-acid residue 703 (H703Q). *Mnn1* has three transcripts RA, RB and RC; RB is unaffected by the focal SNP. All remaining *melanogaster* subgroup species reference sequences carry a Q at this residue, strongly suggesting that H is the derived allele. Indeed, all publicly available *Drosophila* reference sequences that include this residue are Q, with the exception of *D. bipectinata*, and *D. ananassae*, which are predicted to carry the H allele. The neighboring serine at amino-acid position 704 in *D. melanogaster* is predicted to be a phosphorylation site according to the NetPhos 2.0 software (Blom *et al.* 1999). Two alternative MNN1 protein alleles that differ only at the focal variant at residue H703Q have predicted phosphorylation probabilities at Ser704 of 0.69 (His allele) and 0.13 (Gln allele).

Our previous population genomic analyses of North America and Australia investigated allele frequency differentiation (F_{ST}) between higher and lower latitude populations on both continents (Florida vs. Maine, and Queensland vs. Tasmania) (Kolaczowski *et al.* 2011, Reinhardt *et al.* 2014). The goal of those analyses was to identify strongly differentiated variants potentially enriched for targets of spatially varying selection, in particular, those that showed substantial, parallel differentiation on both continents. Our focal nsSNP was among the more unusual variants as it was in the extreme tail of the nsSNP F_{ST} distribution of both continents (0.33% and 0.8% tails of the North America and Australia F_{ST} distributions, respectively), with the derived H allele occurring at higher frequency in higher latitude populations on both continents, consistent with strong, parallel selection. Other attributes of the SNP, such as the high degree of conservation of the corresponding residue and its location far from the breakpoints of any polymorphic cosmopolitan *D. melanogaster* inversions (the closest breakpoint, that of *In2R(NS)*, is more than 4 Mb away, Corbett-Detig and Hartl 2012) supported it as an attractive candidate target of spatially varying selection.

Mnn1 is widely expressed in multiple tissues and developmental stages (FlyBase) and codes for a protein that is predicted to have histone-lysine N-methyltransferase activity. Phenotypic analysis of laboratory mutations has suggested a contribution of the gene to multiple traits, including DNA repair, generalized stress resistance, and development (Busygina *et al.* 2004, Papaconstantinou *et al.* 2005, Papaconstantinou *et al.* 2010). The DNA repair function drew our

attention because of our work on the influence of spatially varying selection on embryo DNA repair (Svetec *et al.* 2016). Thus, we set out to use transgenic animals to investigate the influence of the focal SNP on an embryo DNA repair phenotype. However, unlike several of the candidate genes emerging from Svetec *et al.* (2016), most of which function specifically in DNA repair related phenotypes and were biased toward ovary or early embryo expression, *Mnn1* could plausibly affect many fitness components. Thus, this nsSNP was an interesting candidate not only to experimentally “validate” a population genomic outlier, but also to begin to estimate effect sizes and pleiotropic effects of such outliers. Therefore, to investigate the possible role of *Mnn1* variation in general stress response (Papaconstantinou *et al.* 2005), we also determined whether the focal variant influences response to physiological stressors (high and low temperature, starvation, and desiccation) that might be relevant in natural populations distributed along a latitudinal gradient.

MATERIAL AND METHODS

Fly lines

The double balancer stock with genotype *w; Kr[lf-1]/CyO; D[1]/TM3, Ser[1]* was obtained from the Bloomington Drosophila Stock Center (stock #7198). A stock carrying the *Mnn1* null allele, *Mnn1*^{c30} (Papaconstantinou *et al.* 2005) was a gift from André Bédard's lab. *D. melanogaster* Bloomington stock #9744 (genotype *y[1] w[1118]; PBac[y(+)-attP-9A]VK00027*) was used for the Pacman injections. All stocks were sib-mated for four generations prior to being used in crosses to reduce the amount of genetic variation segregating within balancer chromosome classes and on the X chromosome.

Transgenic line construction

We used the Pacman recombineering resources (reviewed in Copeland *et al.* 2001) and followed the strategy detailed by Biswas *et al.* (2012) to generate our transgenic constructs. We first obtained the CH322-167K14 BAC chromosome containing the *Mnn1* gene region (2L:7,045,627-7,065,515 in *D. melanogaster* reference sequence version 6). This BAC also contains complete copies of genes *CG31907* and *Sem1*, as well as the 3' end of *milt* upstream of *Mnn1*, and the 5' end of *Nuf2* downstream of *Mnn1*. We confirmed by Sanger sequencing that the BAC contained the H allele, thus, we used recombineering in *E. coli* to engineer the Q allele. The region of interest was first replaced by a *galK* positive cassette, allowing successful recombinants to grow on selective media. A *galK* positive colony was then electroporated with a repair template to exchange the *galK* cassette for the *Mnn1* Q allele. Positive events (successful exchanges) were isolated by screening for *galK* negative colonies on minimal media and confirmed by Sanger sequencing. As the BAC backbone already contains mini-white and an *attB* site, using *PhiC31* recombinase, both alleles (H and Q) of the BAC chromosome could be directly inserted at the same *attP* site on chromosome 3 at cytological band 89E11 in *D. melanogaster* line #9744. Embryos from line #9744 were injected following standard procedures (BestGene Inc, Chino Hills CA, USA) and surviving adults were screened for the presence of red eye color reflecting successful insertion of a BAC carrying the mini-white transgene. Homozygous, true-breeding stocks of each transgene (MQ or MH) were established and then both were introgressed into the same *Mnn1* homozygous null background (Supplementary figure 1). The resulting lines, which were designated MQ and MH, were validated at the focal SNP by Sanger sequencing. Lines MQ and MH are expected to be isogenic except for the *Mnn1* H703Q variant. While we cannot rule

out the possibility that low levels of balancer chromosome gene conversion resulted in other SNP differences between strains, such contamination should be random and unlikely to exhibit the large, directional effects on the phenotypes investigated here (below). Because experimental genotypes carried a non-functional endogenous copy of *Mnn1*, the transgenes were the only source of MNN1 protein for experimental animals.

Population genetics

Allele frequencies from African and European samples were obtained from the Drosophila Genome NEXUS (Lack *et al.* 2015). Australian allele frequency estimates are from Kolaczowski *et al.* (2011). Allele frequency estimates from Maine and Panama are from Reinhardt *et al.* (2014) and Svetec *et al.* (2016). New data from US samples are from Morven, Georgia (latitude 30.56N), Media, Pennsylvania (latitude 39.55N), and Middlefield, Connecticut (latitude 41.31). These derive from isofemale lines established by Paul Schmidt (University of Pennsylvania) in 2009. For each population, a pool of females was generated, one per line, from each population. The number of female flies used to create each pool were 21, 100, and 70 for Georgia, Pennsylvania, and Connecticut, respectively. Roughly 5 µg of DNA was used for paired-end sequencing library construction following the Illumina protocol. Fragmentation was done by sonication using the Diagenode Bioruptor at high power for 15 cycles of 30 sec on/30 sec off. The adapter-ligation product was gel-purified to select molecules ~400 bp in length and then quantified using an Agilent Bioanalyzer. A total of 10 ng of size-selected ligation product was used as template for 10 cycles of library enrichment PCR. The enriched library was purified using Ampure XP beads (Beckman Coulter) and sequenced on a single lane of a flow cell with an Illumina GAIIx running Illumina software. Reads were aligned to version 6.04 of the *D. melanogaster* reference sequence using Bowtie2 with the--very-sensitive setting. Variants were called using bcftools (samtools.github.io/bcftools) requiring a read quality score of 30 for inclusion. The mean coverage of US samples from Georgia, Pennsylvania, and Connecticut were 26.8, 25.9, and 29.7, respectively. We required a minimum of 20× coverage at a site in all populations and at least two observations of an alternate base call to consider a SNP in the analysis as described in Svetec *et al.* (2016). Raw data for these three new population samples can be found at the NCBI Short Read Archive under BioProject PRJNA495885.

Egg hatch rate and UV sensitivity

UV sensitivity assays followed Svetec *et al.* (2016). For each transgenic line, we generated experimental animals by allowing groups of 10 to 15 parental flies to mate and lay eggs in a vial for 3–4 days. Those vials, which contained 4ml standard food, were placed into an incubator at 25° with 12:12 light/dark cycle and 50% humidity. The emerging offspring were anesthetized under light CO₂ and placed into a new empty vial containing a small plastic spoon with dyed standard fly food. The spoon was changed every 24 hr for two days for egg laying habituation. In the morning of the first collection day, a new spoon with a drop of fresh yeast-water paste was placed into the vial. Two hours later, this first spoon was removed to discard previously retained eggs and then replaced by another spoon. Two hours later, groups of eggs (25–40 per replicate) were collected with a clean needle and delicately placed on a new spoon with fresh food. All eggs were placed on their side on the food surface, not touching any other egg. Potentially damaged eggs were discarded. Egg collection lasted 1 hr, after which spoons with eggs were distributed into two treatment groups: a control group which was left 60s on the bench and an experimental group which was

immediately exposed to UV in an irradiator for 60s as described by Svetec *et al.* (2016). UVB incidence inside the irradiator was 201 µW/cm² and the temperature was maintained similar to the ambient temperature (23°; see Svetec *et al.* 2016 for details). Immediately after exposure, spoons were transferred to a vial with food, assigned a reference number so that scoring would be done blindly to genotype information, and then placed back into an incubator at 25° with 12:12 light:dark cycle and 50% humidity. Forty-eight hours later spoons were taken out of the vials and egg hatch was scored. UV sensitivity index was calculated as the difference between UV-exposed and UV-unexposed hatch rate. In other words, UV sensitivity is the reduction in hatch rate due to UV exposure (Svetec *et al.* 2016). UV sensitivity was calculated for each spoon and averaged for each genotype-by-treatment combination. Between 17 and 51 spoon replicates were used for each genotype and treatment for a total of 8392 embryos. Control hatch rate was measured for 3427 embryos.

Chill coma recovery assays

Four-day-old virgin flies (12 males and 12 females) from each transgenic line (total 192 flies, four flies per vial) were subjected to cold stress for four time-durations (2, 4, 6, or 8 hr). Vials containing flies were placed on ice for the specified time and then placed back on a laboratory bench at room temperature (25°). The time required for recovery for each fly (fly assuming a normal stance) was recorded, as was survival at 24 and 48 hr after treatment. These assays are a proxy for cold tolerance.

Desiccation resistance

Six-day-old flies (12 males and 12 females) from each transgenic line (four replicate vials of three flies each for each genotype and sex for a total of 48 flies) were subjected to desiccation stress (3 flies per vial). Vials were sealed with gauze and placed into a desiccation chamber containing silica beads. The chamber was sealed with petroleum jelly. The time until knockdown/death was recorded at hourly intervals until all flies had died.

Heat shock

Five-day-old virgin flies (12 males and 12 females) from each transgenic line (total 48 flies) were subjected to heat stress by immersing flies in individual vials into a water bath set to 39° (without temperature ramping). The vial positions in the water bath were randomized. The time until knockdown was recorded.

Starvation

Four-day-old virgin flies (12 males and 12 females) from each transgenic line were subjected to starvation stress (total 48 flies, 4 flies per vial). The flies were placed at 25° in a vial without media, sealed with gauze, and affixed end-to-end to a second vial containing wet cotton to provide moisture. The survival/death status was recorded at 4-hour intervals.

Statistical analyses of phenotypic data

Statistical analyses were performed using R. As the data were unbalanced and departed from normality, type III ANOVAs were performed on both the untransformed values and the rank-transformed values of UV sensitivity index and chill coma recovery time. The untransformed and transformed data gave the same results (Supplementary Table 1); here we only report the results of the ANOVAs on rank-transformed values. Wilcoxon tests, Mann-Whitney *U*-tests, or proportional hazards survival analyses were used for other phenotypes.

Data availability

New sequencing data from US *D. melanogaster* populations can be found in the NCBI Short Read Archive under BioProject

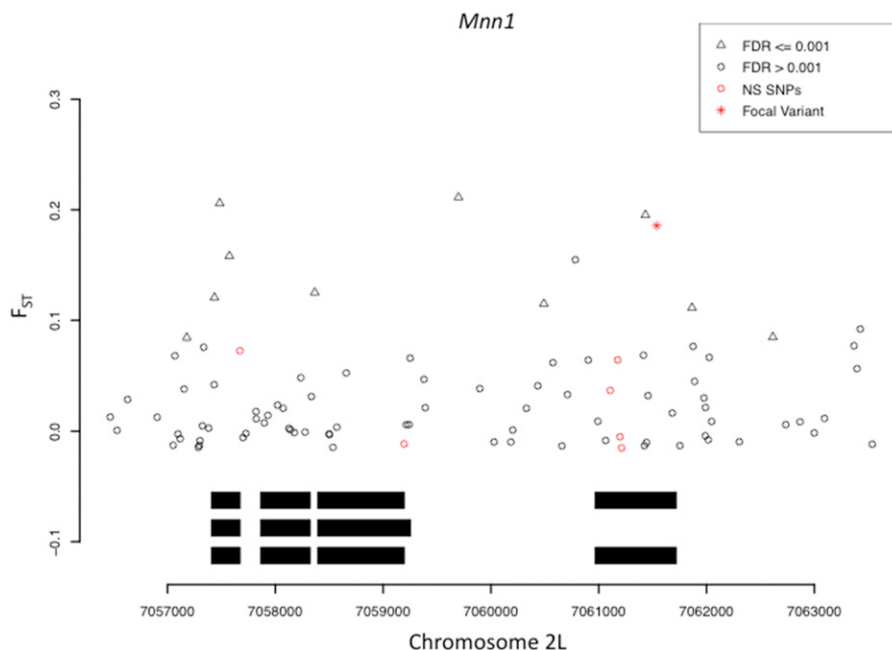


Figure 1 Estimates of genic SNP F_{ST} in Maine vs. Panama for *Mnn1*. Coding sequence represented by black boxes (three isoforms). F_{ST} estimates and false discovery rates (FDR) follow those from Svetec *et al.* (2016). The focal variant is the most differentiated nsSNP in the gene.

PRJNA495885. Supplemental material available at Figshare: <https://doi.org/10.25387/g3.7302002>.

RESULTS

Population genetics

As aforementioned, while our initial interest in this SNP was driven by our analysis of substantial, parallel geographic differentiation in the Americas and Australia, additional data, including more extensive sampling of the Americas and Africa have accumulated since that time. Thus, we carried out a population genetic analysis aimed at a more comprehensive characterization of allele frequency variation in the *Mnn1* gene region. Reinhardt *et al.* (2014) identified the focal SNP as an F_{ST} outlier in the US and Australia (Reinhardt *et al.* 2014). To compare those results with differentiation between Maine and a neotropical population, we estimated F_{ST} of the focal variant between Maine and Panama (Svetec *et al.* 2016) and found that it was in the 3% tail of the nsSNP distribution, consistent with our Maine vs. Florida estimate, though somewhat less differentiated. Figure 1 shows that the focal SNP, while not the only strongly differentiated *Mnn1* SNP between Maine and Panama, is substantially more differentiated than other nsSNPs in the gene. We extended these results by characterizing patterns of geographic variation in additional population samples from the US and from Africa and Europe.

Figure 2 shows that the focal SNP exhibits strong latitudinal differentiation in Old World and New World samples. Linear regression of H703Q allele frequency vs. latitude led to $R^2 = 0.47$ ($P = 0.089$) and $R^2 = 0.67$ ($P = 0.025$) for the New World and Old World, respectively. Fisher's combined probability for the two regions rejects the null hypothesis of no correlation between allele frequency and latitude ($P = 0.016$). Linear regression on the combined data were also highly significant ($R^2 = 0.63$, $P < 0.001$). Overall, the data in Figure 2 strongly support the hypothesis that the H703Q polymorphism is clinal. Moreover, the presence of latitudinal clines in both Old World and New World populations supports the idea that the

clines result from selection in both the ancestral and recently established regions, rather than demographic processes in recently established populations.

UV sensitivity index

In Svetec *et al.* (2016) we presented several lines of evidence in support of the idea that natural populations of *D. melanogaster* experience spatially varying selection on embryonic DNA repair resulting from latitudinal variation in UV incidence. First, we demonstrated that lower latitude embryos tend to be more resistant to UV exposure than higher latitude embryos. We further demonstrated that embryo UV resistance is correlated with oocyte repair of damaged sperm DNA. Finally, we observed latitudinal differentiation for early embryo transcript abundance and SNPs associated with DNA repair genes. In spite of the strong correlational support for our hypothesis, our previous work presented no direct evidence of a strongly differentiated variant

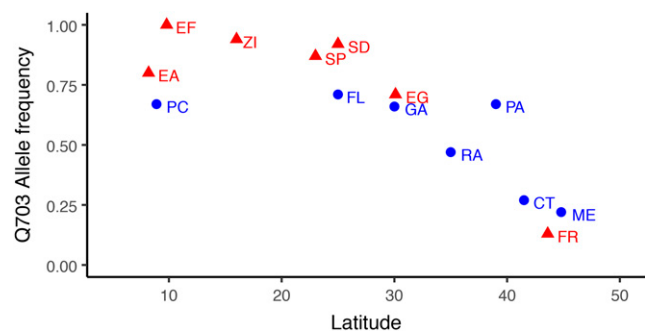


Figure 2 Frequencies of the *Mnn1* Q allele in Old World and New World samples: In blue is the New World cline: Panama (PC), Florida (FL), Georgia (GA), N. Carolina (RAL), Pennsylvania (PA), Connecticut (CT), Maine (ME). In red is the Old World cline: Ethiopia low altitude (EA), Ethiopia high altitude: 3070m (EF), Zimbabwe (ZI), South Africa low altitude (SP), South Africa high altitude: 2000m (SD), Egypt (EG), France (FR)

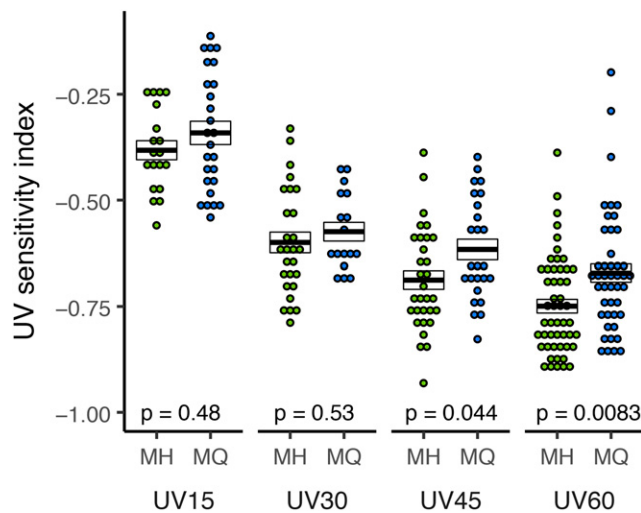


Figure 3 Early embryo UV sensitivity: The full model ANOVA with Genotype and UV treatment as factors was statistically significant ($df = 7, 233$; $F = 32.62$; $P < 0.001$). *Mnn1* (H703Q) contributes to variation in UV sensitivity as the Genotype factor was significant ($df = 1$; $F = 7.90$; $P = 0.005$). UV exposure also had a significant effect ($df = 3$; $F = 68.60$; $P < 0.001$); the interaction was not significant. UV sensitivity index (corresponding to the reduction in embryo hatch rate due to UV exposure) was measured for 1-3 hr. old embryos carrying either of the two *Mnn1* alleles. Embryos were exposed to UVB for 15, 30, 45, and 60 sec. Each data point represents the UV sensitivity index of a pool of 25 to 40 embryos. Sample size range is $17 \leq n \leq 51$ embryo sets. Crossbars represent mean $\pm$ SE and p-values correspond to a Wilcoxon test on MH vs. MQ for each UV treatment. UV15: $W = 363.5$; $P = 0.482$; UV30 $W = 256$; $P = 0.530$; UV45 $W = 510$; $P = 0.044$ UV60 $W = 1507$; $P = 0.008$. At the 60 sec dose the H allele reduces UV sensitivity by about 12%.

affecting embryo DNA repair. Figure 3 shows that the Q allele, which is more common in higher UV environments, consistently exhibits greater mean resistance to UV.

Egg hatch rate

Sveteć *et al.* (2016) showed that in addition to a cline for UV sensitivity, there is a countervailing cline for embryo viability (in the absence of UV) such that lower latitude populations of *D. melanogaster* had reduced egg hatch rates compared to higher latitude populations. Sveteć *et al.* (2016) speculated that these countervailing clines might represent a DNA-repair related trade-off such that variants conferring increased embryo DNA repair capacity have reduced hatch rates in the absence of UV. Such trade-offs could, in principle, contribute to the maintenance of variation. Our direct test of the focal SNP supports this hypothesis (Figure 4), as the allele more common in high-UV environments exhibits a reduced intrinsic hatch rate (mean $\pm$ SE: 0.931 ± 0.007 ; $n = 55$ for the H allele and 0.855 ± 0.011 ; $n = 43$ for the Q allele; Mann-Whitney $U = 462$; $P < 0.001$). The H allele increases embryo viability by about 9%.

Chill coma recovery

The full model ANOVA with genotype, sex and treatment as factors was significant ($df = 15, 172$; $F = 39.48$; $P < 0.001$). The transgenic lines showed different response to cold treatment, as the Genotype factor was statistically significant ($df = 1$; $F = 20.47$; $P < 0.001$) with MH, the high latitude allele, recovering more quickly than MQ (Figure 5). The effect size varies considerably between sexes and among treatments, with the greatest effect sizes being 40% for males in the 2-hr. treatment

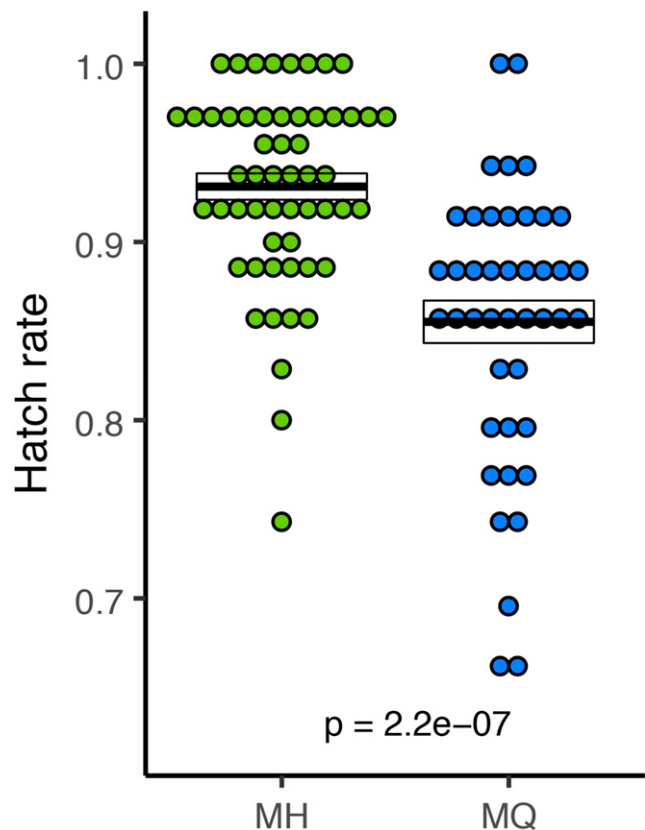


Figure 4 Egg hatch rate. Each point represents the hatch rate of a set of 25 to 40 embryos. Sample sizes are $n = 55$, $n = 43$ embryo sets, for MH and MQ respectively. Crossbars represent mean $\pm$ SE with p-value corresponding to a Wilcoxon test on MH vs. MQ.

and 31% for females in the 4-hr. treatment. Both Sex ($df = 1$; $F = 7.71$; $P = 0.006$) and Treatment ($df = 3$; $F = 183.56$; $P < 0.001$) terms were significant, with females recovering faster than males, and longer cold exposures correlated with longer recovery times. We observed no significant interactions between Sex and Treatment factors.

Desiccation and heat shock resistance

We used proportional hazards fit to analyze our measurements of desiccation resistance. As expected (*e.g.*, Hoffmann and Parsons 1989), females were significantly more tolerant to desiccation ($P < 0.001$) than males but we did not detect a significant effect of genotype (Figure 6A) ($P = 0.76$). Similarly, we found no significant differences between genotypes for heat tolerance (Figure 6B): MH vs. MQ: Males: Mann-Whitney $U = 48$; $P = 0.28$ and females: Mann-Whitney $U = 56.5$; $P = 0.57$.

Starvation resistance

We used a proportional hazards fit analysis to compare the starvation resistance of the MQ an MH genotypes. We found a significant effect of Genotype ($P < 0.001$ for both sexes), but no effect of Sex or Genotype-by-Sex. This result was consistent with a re-analysis using Wilcoxon tests on the same data sorted by sex (Figure 7). The MH allele increased survival under starvation by 20% and 18% for females and males, respectively ($P < 0.001$ for both sexes).

DISCUSSION

Given the polygenic nature of fitness variation, one might reasonably expect that the functional analysis of individual candidate selected

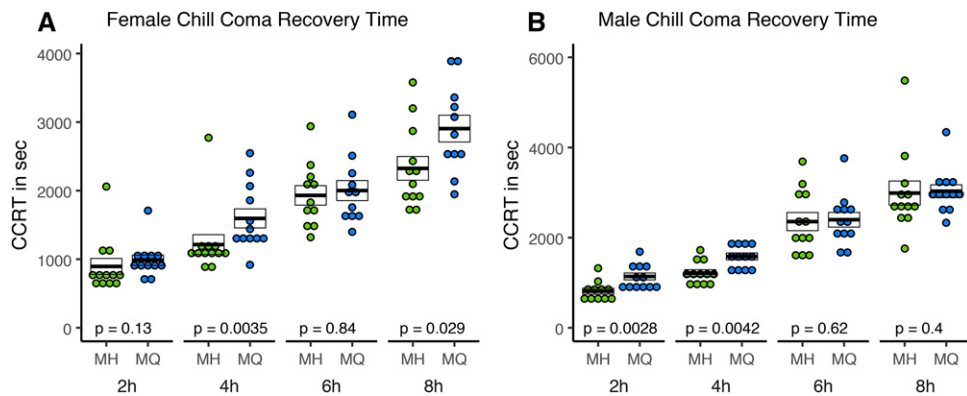


Figure 5 Chill coma recovery time: Phenotypes were measured for adult female (A) and male (B) flies exposed to cold for 2, 4, 6, and 8 hr. Each point depicts the recovery time (stand up) from cold shock. Crossbars represent mean $\pm$ SE, with p-values corresponding to a Wilcoxon test on MH vs. MQ for each cold treatment. Sample sizes are $n = 11$ or $n = 12$ vials.

variants inferred from population genetic data may often fail to yield experimental evidence of phenotypic effects as a result of low power. An alternative hypothesis for negative experimental results on such candidates is that they are population genetic false positives or that the appropriate phenotypes have not been measured. The positive experimental results reported here are cause for a somewhat more optimistic view, in support of other similar work on *Drosophila* (Laurie-Ahlberg and Stam 1987, Catalán *et al.* 2016, Siddiq *et al.* 2017, Glaser-Schmitt and Parsch 2018, Yang and Edery 2018). We compared two genotypes that differed for a single amino acid variant and found that four of six assayed phenotypes were different: embryo UV sensitivity, embryo hatch rates, chill coma recovery, and starvation resistance (Table 1). Importantly, for embryo UV sensitivity, hatch rates, and chill coma recovery, the direction of the observed allelic effect was consistent with general patterns of phenotypic differentiation between high and low latitude populations and with the frequency differences of alternative alleles at the focal SNP. Thus, the pleiotropic effects of the alleles appear to generally be in the same direction as the mean population differences (Lovell *et al.* 2013). For starvation resistance, however, we observed that the high latitude allele was more resistant, while an analysis of Australian populations (Hoffmann *et al.* 2001) revealed that low latitude populations were slightly, though significantly, more starvation resistant. However, there are few studies of geographic variation in starvation resistance for *D. melanogaster* (Goenaga *et al.* 2013, Božičević *et al.* 2016) and the relationship between geography and starvation resistance may be weak (Brown *et al.* 2018).

An apparent puzzle generated by these data is that the effect sizes seem surprisingly large. For example, focusing on UV sensitivity index at the 60 sec dose, which was the same treatment used in our earlier experiments (Svetec *et al.* 2016) and assuming the genetic background used for the recombineering experiments was more temperate-like than tropical-like, we observe that the MH genotype has a UV sensitivity index (-0.74) nearly identical to the mean value for the Rhode Island + Maine populations (-0.76). However, introducing the focal amino acid change leads to a phenotype (UV sensitivity index = -0.67) that is similar to the mean value previously observed for Florida + Mexico (-0.67), corresponding to a genotypic effect of H703Q on UV sensitivity of about 0.035 units. While this effect is substantial, it does not imply that the influence of the focal SNP explains most of the mean population difference. For example, given the frequency differences for the Q allele between Rhode Island and Florida in Figure 2 and assuming additivity, the contribution of the frequency difference of the H703Q polymorphism to the difference in population means is about 0.015 UV sensitivity units (Falconer 1989). This is consistent with a complex, though not highly polygenic basis for population differences in UV sensitivity.

Our results support the view that the transgenic analysis of major population genomic outliers, which are expected to be among the most strongly selected variants in the genome, will be a valuable approach for integrating studies of effect size and pleiotropic effects on specific phenotypes, with estimates of fitness effects indirectly inferred from population genetic analysis. Whether such an

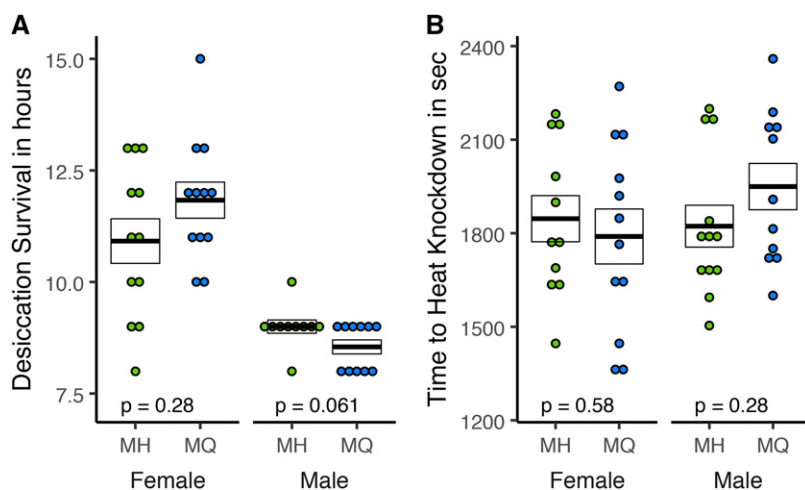


Figure 6 Desiccation and heat shock resistance were measured for adult female and male flies. For desiccation resistance (A) each data point represents the time in hours until death. For heat shock resistance (B), each data point represents the mean time in hours until death of all individuals in a vial. For both traits, sample sizes are $10 \leq n \leq 12$, crossbars represent mean $\pm$ SE and p-values correspond to a Wilcoxon test on MH vs. MQ for each sex.

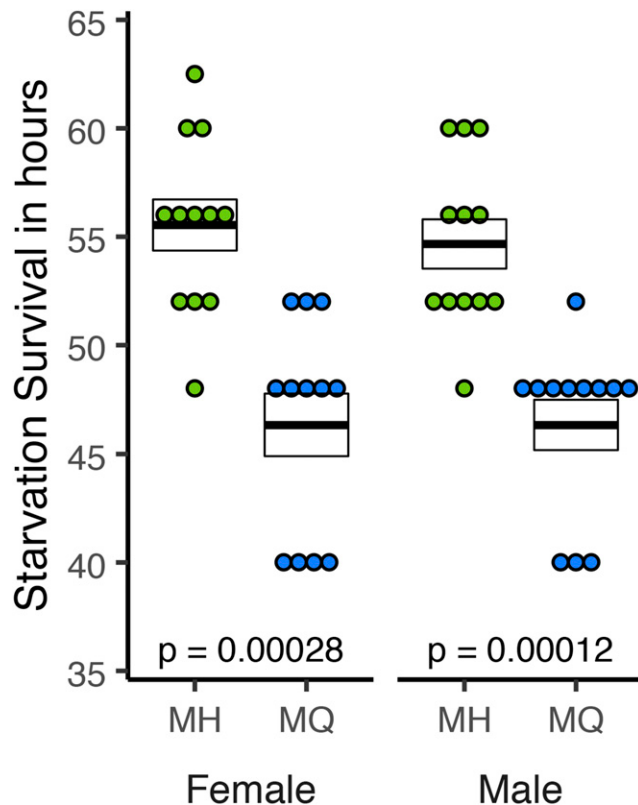


Figure 7 Starvation resistance was measured for adult female and male flies. Each point represents the time in hours until the death of one individual. Crossbars represent mean $\pm$ SE; p-values correspond to a Wilcoxon test on MH vs. MQ for each sex. Sample sizes are all $n = 12$.

experimental program can succeed on a substrate of less extreme population genomic outliers is an open question. A longstanding and remaining problem for *Drosophila* population genetics (and empirical population genetics in most organisms) is that while fitness effects can be indirectly estimated from population genetic data and effects of individual variants on particular phenotypes can, in principle, be estimated in the laboratory or in semi-natural populations (e.g., Mitrovski and Hoffmann 2001), the measurement of fitness effects of individual variants in a manner that reflects their properties in natural genotypes in natural populations is difficult, if not impossible. It is plausible that even variants with major phenotypic effects in laboratory experiments, such as the focal SNP investigated here, may have small fitness effects in natural populations, either because of their distributions of pleiotropic effects on both measured and unmeasured traits, or because of the properties of interactions between natural genotypes and natural biotic or abiotic variation.

Table 1 Summary of phenotypic effects of the H (high latitude) and Q (low latitude) alleles of *Mnn1*

Life stage	Phenotype	MH	>	MQ
Embryo	Control hatch rate	MH	>	MQ
	UV sensitivity index	MH	<	MQ
Adult	Chill coma recovery	MH	>	MQ
	Heat shock tolerance	MH	=	MQ
	Starvation resistance	MH	>	MQ
	Desiccation resistance	MH	=	MQ

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