Epistasis among clustered lineage-specific adaptive amino acid substitutions in the Drosophila *Trio* protein.

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Abstract

Intramolecular epistasis is increasingly recognized as a key factor shaping patterns of evolutionary rate variation among protein sites and constraining adaptive evolution. While genome-wide analyses have revealed that intramolecular epistatic interactions can drive the spatial clustering of amino acid substitutions, direct empirical evidence for such interactions and their evolutionary consequences remains limited. Using a statistical screen for lineage-specific clustering of adaptive substitutions in *Drosophila*, we systematically identify experimentally tractable candidate proteins with evidence for spatially-clustered adaptive amino acid substitutions for functional genetic analysis. As proof of concept, we focus on the Trio protein, which exhibits three spatially-clustered adaptive amino acid substitutions in along the *D. melanogaster* lineage. Through systematic reconstruction of evolutionary intermediates *in vivo*, we find that intermediate states exhibit reduced fitness, providing strong evidence for epistatic constraints on evolutionary trajectories. Notably, we find that the deleterious effects of intermediates are recessive, suggesting that intermediate combinations of epistatically interacting amino acid substitutions can arise and be maintained in heterozygotes before fixation. Our findings provide a rare empirical window into the fitness landscape shaped by intramolecular epistasis and establish a framework for broader investigation of constraints adaptive protein evolution in diploid multicellular organisms.

Introduction

The rate of protein evolution varies substantially among species, among proteins and among sites within proteins. This rate variation has historically been interpreted in terms of "neutral", or "nearly neutral" models of protein evolution, which depend on the proportion of newly arising amino acid altering mutations that are neutral with respect to protein function or effectively neutral due to genetic drift (Kimura 1968; Ohta 1973). While nearly neutral models can account for several important aspects of protein evolution (Wright and Andolfatto 2008), a debate raged for decades about the relative contribution of positive selection to protein evolution. The development and application of the McDonald-Kreitman test (McDonald and Kreitman 1991) and similar frameworks (Fay et al. 2002; Smith and Eyre-Walker 2002; Sawyer et al. 2003) suggested that protein divergence is well in excess of that predicted under neutral models of protein evolution in Drosophila and other species (Fay et al. 2002; Sella et al. 2009; Slotte et al. 2010; Charlesworth and Eyre-Walker 2006; Booker and Keightley 2018; Booker et al. 2017; Galtier 2016). While the McDonald-Kreitman and similar tests suffer from uncertainty of the population size over time (Eyre-Walker 2002; Soni et al. 2022), amino acid substitutions also exhibit genetic hitchhiking signatures at closely linked neutral sites, confirming an important role for positive selection in protein evolution (Andolfatto 2007; Macpherson et al. 2007; Elyashiv et al. 2016; Liang et al. 2022; Booker and Keightley 2018; Williamson et al. 2014). Rate variation within proteins has largely been interpreted in terms of differences in the intensity of purifying selection, associated with protein domain function. The finding that positive selection contributes significantly to protein divergence changes how we might interpret evolutionary rate variation within proteins.

Protein evolution is not only shaped by selection on individual sites but also by interactions among amino acids. Because protein function and three-dimensional structure depend on networks of interactions, the effect of any new mutation often depends on the history of prior substitutions. This principle was formalized early in the covarion model, which proposed that only a subset of codons is free to vary at any given time, and that this set shifts as substitutions occur (Fitch 1971; Fitch and Markowitz 1970; Miyamoto and Fitch 1995). If substitutions frequently compensate or permit one another, they are expected to occur more often near each other, either in the coding sequence or in the folded protein as spatially close amino acids are more likely to interact directly.

Consistent with this prediction, genome scale studies have revealed that amino acid substitutions tend to be spatially clustered in proteins, and this clustering signature is stronger in more highly conserved proteins and protein domains (Callahan et al. 2011; McFerrin and Stone 2011; Yu and Thorne 2006; Adams et al. 2017; Taverner et al. 2020; Chaurasia and Dutheil 2022).

Evolutionary rate variation (and spatial clustering) within proteins is expected due to variation in selective constraint among functional domains of proteins (Echave et al. 2016). However, several studies have noted that positively-selected amino acid substitutions also tend to be spatially clustered in proteins (Ridout et al. 2010; Wilson et al. 2011; Zhao et al. 2017; Adams et al. 2017; Slodkowicz and Goldman 2020). Additionally, several have highlighted the fact that spatially proximate amino acid substitutions exhibit signatures of epistasis and compensatory evolution dynamics (Davis et al. 2009; Callahan et al. 2011; Taverner et al. 2020; Chaurasia and Dutheil 2022; Stolyarova et al. 2022; Ragsdale 2022). Together, these findings suggest that intramolecular epistasis could shape protein evolution, leaving a distinct footprint of clustered substitutions.

Experimental work has further confirmed the central role of intramolecular epistasis in protein evolution. A landmark study by Weinreich et al. (2006) showed that interactions among five mutations in β-lactamase dramatically constrained the number of mutational paths to antibiotic resistance. Similarly, Ortlund et al. (2007) demonstrated that the glucocorticoid receptor evolved new hormone specificity in vertebrates via stability-mediated epistasis, in which nearly neutral permissive mutations fixed stochastically and stabilized local structures, enabling subsequent adaptive substitutions to fix. Later studies using ancestral protein reconstruction, viral evolution experiments, and large-scale mutational scans have confirmed that epistatic interactions can strongly influence evolutionary trajectories (Biswas et al. 2019; Hochberg et al. 2020; Gong et al. 2013; Sarkisyan et al. 2016; Harms and Thornton 2014). Furthermore, a few studies provide evidence of epistatic substitutions occurring in close spatial proximity, echoing the clustering patterns predicted from statistical analyses. For example, compensatory mutations have been observed near adaptive substitutions conferring toxin resistance in the poison frog nicotinic acetylcholine receptor (Tarvin et al., 2017), and similar patterns appear along the evolution of vertebrate proteins like p53, hemoglobin, lysozyme and Na, K-ATPase (Mateu and Fersht 1999; Weber et al. 2013; Storz 2018; Mohammadi et al. 2021; 2022).

While experimental work increasingly demonstrates that epistasis is central to protein evolution, most of these studies have been restricted to microbial or *in vitro* systems. In these systems, epistatic dynamics are typically modeled based solely on protein activity and stability, leaving a gap in our understanding of how interacting substitutions accumulate in diploid multicellular organisms where dominance, pleiotropy, and interactions across multiple phenotypic levels can strongly influence evolutionary outcomes.

To our knowledge, Na^+,K^+-ATPase (NKA) resistance to cardiotonic steroids (CTS) in insects is the only case where epistasis in protein adaptation has been directly demonstrated *in vivo* in a

multicellular organism (Karageorgi et al. 2019; Taverner et al. 2019; Yang et al. 2023). In CTS-adapted insects, adaptation frequently targets a highly conserved domain of the NKA alpha-subunit. The most common resistance-conferring substitutions—at positions 111 and 122—almost always occur after a permissive substitution at position 119 (A119S), which reduces the negative pleiotropic effects of these resistance mutations (Karageorgi et al. 2019; Taverner et al. 2019). Moreover, *in vivo* engineering of firefly CTS-resistance substitutions into Drosophila revealed similar deleterious pleiotropic effects, which were alleviated by additional background substitutions within a span of 12 amino acid residues, but not directly related to CTS resistance (Yang et al. 2023). Further, it was shown that the deleterious effects of CTS-conferring substitutions appear to be recessive, potentially explaining how they might persist in populations long enough to allow secondary compensating substitutions to arise and allow their fixation. This work highlighted the use of *in vivo* models in revealing pleiotropic effects on higher order phenotypes that are more closely related to organismal fitness (e.g viability, fertility, and behavior) and would be missed in *in vitro* assays.

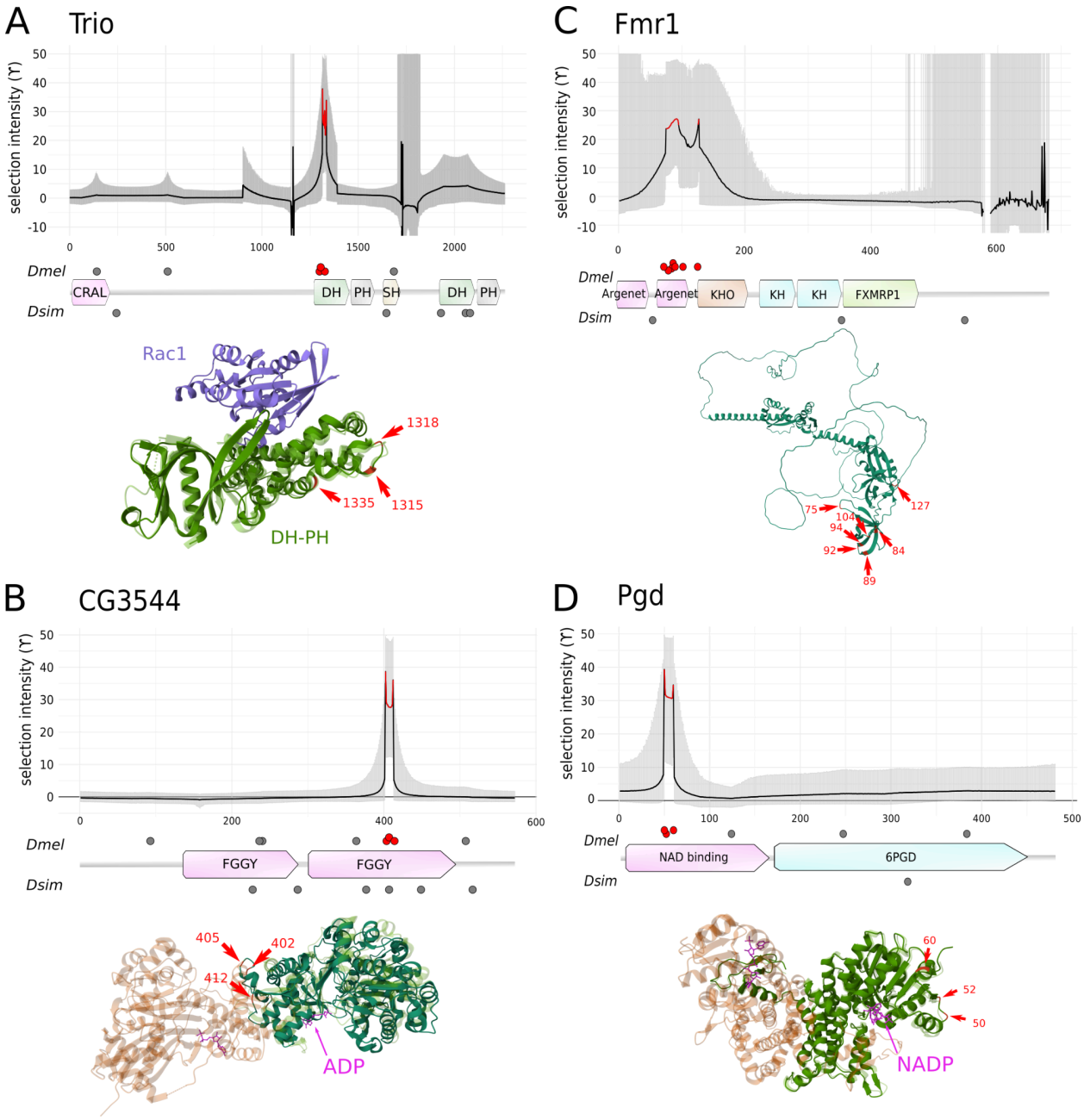
The case of CTS-resistant NKAs is a striking example of the role of epistasis in protein adaptation, but it remains unclear how broadly these findings apply to other proteins. To better understand how pleiotropy, epistasis, and dominance shape protein evolution during adaptation, new diploid *in vivo* models are needed. To this end, we systematically searched the *Drosophila melanogaster* genome for proteins that, like NKA, are highly conserved yet contain lineage-specific clusters of positively-selected amino acid substitutions. As a case study, we focus on one such cluster in the conserved protein Trio. Using scarless CRISPR-Cas9 genome editing, we engineered Drosophila strains carrying all possible intermediate combinations of substitutions in this cluster, enabling us to dissect the epistatic and dominance interactions involved.

Results

To identify candidate clusters under selection in *D. melanogaster*, we applied the Model-Averaged Site Selection with Poisson Random Field (MASS-PRF; Zhao et al. 2017). MASS-PRF estimates a site-by-site scaled selection coefficient (g = 2Ns) based on polymorphism and divergence clustering models. While the McDonald-Kreitman test is typically applied to whole proteins, MASS-PRF is designed to quantify variation in intensities of selection across a protein sequence, highlighting potentially localized targets of adaptive protein evolution. Applying this approach to

9137 proteins, we were able to identify 919 proteins containing at least one cluster of adaptive substitutions specific to the *D. melanogaster* lineage (Fig1, Fig S1, See Methods). The identification of spatially-clustered adaptive amino acid substitutions provides the opportunity to investigate potential epistatic interactions among individual substitutions within such clusters. We estimated that 679 proteins contain experimentally tractable clusters consisting of 2 or 3 substitutions located less than 20 amino acids away from each other.

As proof of concept, we decided to focus on the identified cluster of amino acid substitutions in the protein Trio (Fig 1A) as a tractable example. Trio is a Rho-guanine nucleotide exchange factor (GEF) that regulates several signaling pathways involved in functions such as neuronal migration, axonal outgrowth, axon guidance, and synaptogenesis in *D. melanogaster* (Bateman et al. 2000; Iyer et al. 2012), *C. elegans* (Wu et al. 2002) and in humans (Barbosa et al. 2020; Linseman and Loucks 2008). Missense and nonsense mutations in *Trio* can cause neurodevelopmental diseases such as intellectual disability and autism spectrum disorders in humans (Barbosa et al. 2020). In *D. melanogaster*, *trio* mutants show specific neurodevelopmental disorders resulting in locomotion behavior, leg and wing formation defects but also more general phenotypes such as prepupal lethality and sterility (Awasaki et al. 2000; Liebl et al. 2000).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FXMRP1
127
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104
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92
84
89
B
CG3544
FGGY
FGGY
405
402
412
ADP
D
Pgd
NAD binding
6PGD
60
52
50
NADP

Figure 1. Examples of Drosophila proteins exhibiting lineage-specific clusters of adaptive amino acid substitutions. Plotted are profiles of selection intensity (γ = 2Ns) across four *D. melanogaster* proteins inferred with MASS-PRF (Zhao et al., 2017). The black line corresponds to the model-averaged γ and the grey areas indicate 95% model uncertainty interval. Red lines indicate regions for which the 95% lower bound of γ > 4, which corresponds to a false positive rate of <0.1 (see Methods). Protein structure models are represented below each selection intensity plot. Functional domains are represented by colored boxes with their names in black. Lineage-specific amino acid substitutions are represented by dark gray dots and red for the cluster of interest (*D. melanogaster* above and *D. simulans* below, respectively). AlphaFold predictions of the 3D structure of the proteins are represented to the right of individual plots. The prediction has been superimposed with the crystallized structures of the homologous proteins (transparent) with ligands and in oligomerized form, when available. The positions of clustered adaptive amino acid substitutions are highlighted with red arrows. (A) Fragile X messenger ribonucleoprotein 1 (Fmr1); (B) Phosphogluconate dehydrogenase (Pgd). The alpha-fold structure prediction is represented in green and is superimposed onto the dimerized structure of the human Pgd (transparent orange and green) in complex with NADP (pink) (PDB 2JKV). (C) Trio, a Rho guanine nucleotide exchange factor. The alpha fold prediction of the first DH-PH domain of Trio is represented in green and is superimposed onto the the human trio DH-PH structure (transparent green) in complex with Rac1 (blue) (PDB 7SJ4, Bandekar et al., 2022). (D) CG3544, a xylulokinase. The Alpha-fold prediction is represented in green and is superimposed on the xylulokinase structure of *Chromobacterium violaceum)* (PDB 3KZB) (transparent orange and green) in complex with ADP (pink).

The *D. melanogaster* and *D. simulans* Trio proteins differ by 11 amino acid substitutions, six of which occur along the *D. melanogaster* lineage (Fig 1A). One cluster of three amino acid substitutions (V1315A; N1318S; R1335K), exhibiting lineage-specific positive selection in *D. melanog*aster, is located in the first GTPase binding domain DH-PH of the protein and constitute the only amino acid changes observed across the *D. melanogaster–D. yakuba* species group in this domain (Bandekar et al. 2019; Chhatriwala et al. 2007) (Fig 1C; Fig S2). These three substitutions appear to be fixed since these sites are monomorphic among 960 wild-derived *D. melanogaster* genome sequences from 30 populations worldwide (Lack et al. 2015). The amino acid substitutions in this cluster appear to be relatively conservative, preserving both polarity and charge properties (Fig S2), though there is a trend towards incorporation of smaller functional groups. Prediction tools assessing the impact of single substitutions on protein stability did not identify any substitutions predicted to strongly destabilize the DH-PH domain, with all predicted ΔΔG values ranging between −1 and +1 kcal/mol (Dynamut2, ACDC-NN, ThermoNet; Table S1). However, the absence of a *D. melanogaster* crystal structure limits the reliability of these predictions.

Using a scarless CRISPR-cas9/piggyBAC genome editing approach (see Methods), we created *D. melanogaster* strains representing all possible combinations of substitutions in the Trio protein from the ancestral state "VNR" (1315 Val; 1318 Asn; 1335 Arg) to "ASK" (1315 Ala; 1318 Ser; 1335 Lys), corresponding to the current state in *D. melanogaster* (Fig 2C). To avoid effects due to

variation in the genomic background, all the lines had their genomic background homogenized (see Methods and Fig S3).

To identify potential epistatic interactions among the three substitutions of this cluster, we first investigated homozygous effects of substitutions at these three sites on two fitness-related traits (viability and locomotion). Interestingly, most of the intermediate haplotypes showed severe defects in larval and adult viability. In particular, VSR, VNK, ASR and ANK flies are homozygous lethal and most individuals do not reach pupal stage (Fig 2A). For VSR, the few homozygous individuals that reach adulthood are sterile (6 males and 1 female out of 113 adults). Only ANR, VSK and the ancestral haplotype VNR showed viability similar to the current ASK haplotype of *D. melanogaster*. Additionally, while the intermediate haplotypes ANR and VSK did not show viability defects, they do exhibit defects in adult locomotion (Fig 2B). Thus, it appears that all three amino acid substitutions are involved in epistatic interactions, and it is apparent that all possible paths from ancestral to the current *D. melanogaster* state would involve transiting through a less fit intermediate state (Fig 2C).

Motivated by these findings, we next asked about the dominance of the deleterious effects associated with intermediate states. To examine dominance effects, we created heterozygotes carrying one intermediate state (x) and one ancestral haplotype (VNR). We found that all intermediate states have viabilities that are not distinguishable from that of the homozygous VNR or ASK haplotypes (Fig 2A). Similarly, all the intermediate haplotypes lacked locomotion defects when heterozygous (Fig 2B). Together, these results suggest that all deleterious effects associated with intermediate states are recessive. The finding that the deleterious effects of substitutions are recessive has important implications for how we expect this cluster of adaptive substitutions to have become established in the *D. melanogaster* lineage. Notably, all paths involving sequential substitution of amino acid substitutions would be deleterious, however, each of these substitutions may have persisted as polymorphisms in the population for some time, assembled into a favorable haplotype and fixed concominantly (Fig 3).

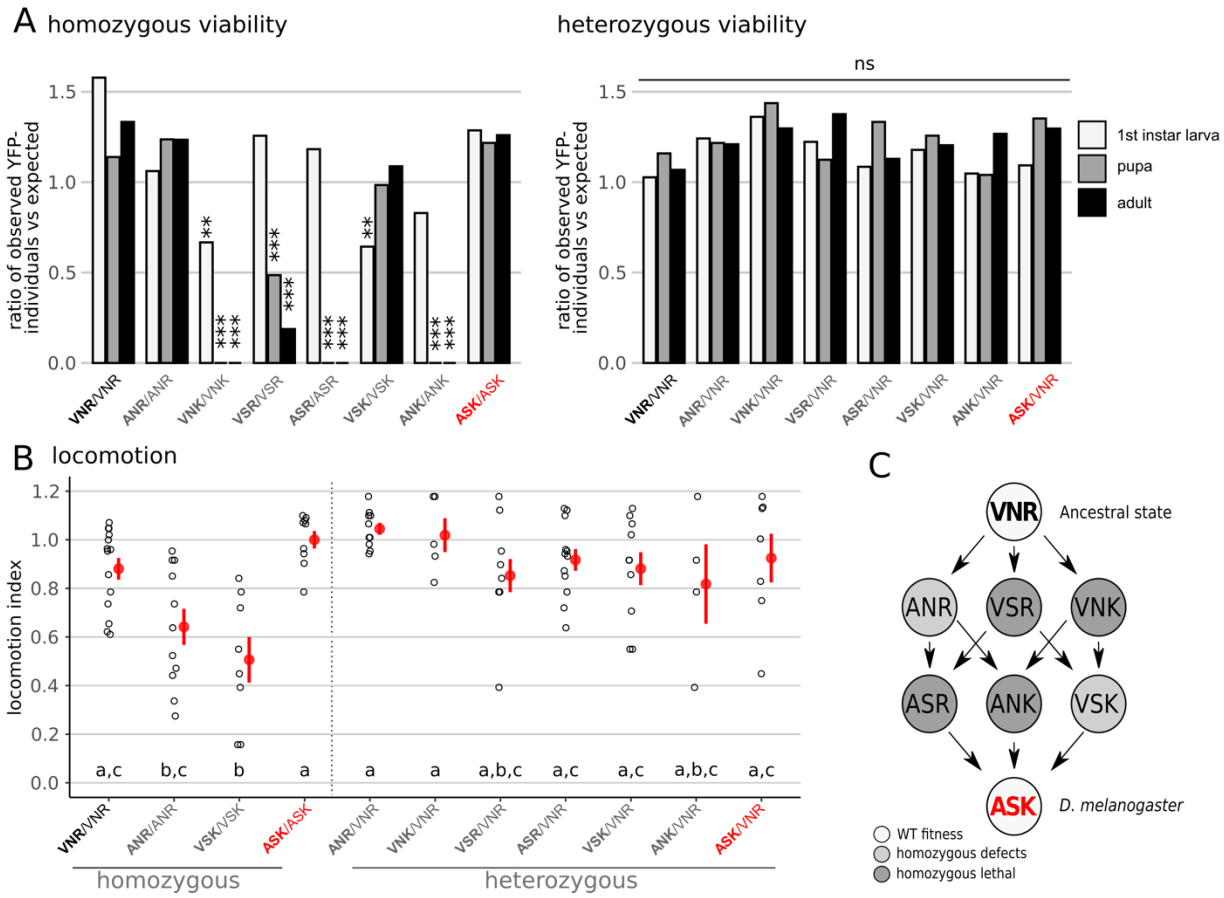

Figure 2. Evolutionary intermediates in the path from ancestral to extant *D. melanogaster* Trio sequences exhibit recessive deficits in fitness related phenotypes. (A) Viability of homozygous and heterozygous first instar larvae, pupae and adults. Plotted is the ratio of the observed proportion of YFP-individuals relative to expected proportions (see Methods). Asterisks indicate adjusted p-values (*** p<0.001; ** p<0.01; * p<0.05) determined by Fisher's Exact tests. (B) Locomotion defects in homozygous and heterozygous individuals. A locomotion index (y-axis) is assayed using a negative geotaxis assay and normalized relative to the ASK/ASK genotype (see Methods). Each dot represents a group of 5-10 males. The red dot and whiskers represent the mean and standard error, respectively. Two strains that share a letter are not significantly different from each other (Kruskall-Wallis followed by Dunn test, p<0.05). (C) Diagram representing all available genetic paths from the ancestral haplotype VNR to the extant *D. melanogaster* haplotype ASK. Colors represent the fitness of each haplotype based on viability and locomotion results.

As this cluster of substitutions is inferred to be positively selected (Fig 1C), we might expect the ASK haplotype to confer a fitness advantage relative to the ancestral haplotype VNR in *D. melanogaster* flies. However, homozygous VNR flies were not distinguishable from ASK flies for viability and locomotion. We also find that the level of fertility of the VNR and ASK strains is not distinguishable (Fig S4). This implies that either a fitness benefit occurs for a phenotype (or in an environment) that we have not investigated, the ASK haplotype is neutral relative to the VNR

haplotype, or that ASK may have had a fitness advantage in the context of the ancestral *D. melanogaster* genomic background.

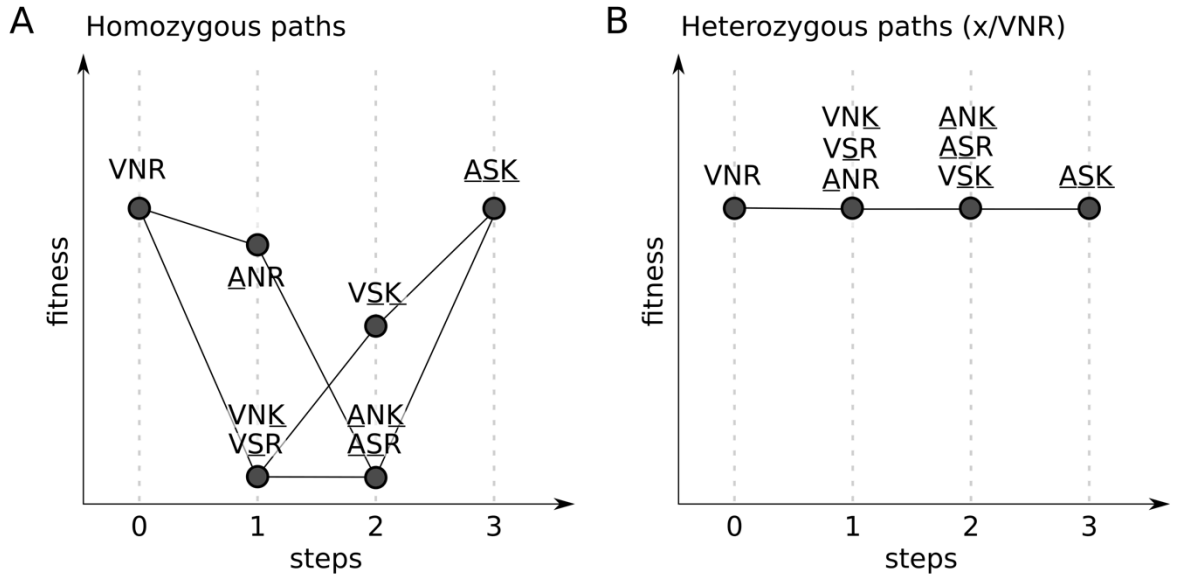

Figure 3. Adaptive paths are only accessible via heterozygous states. Shown is a schematic representation of the fitness landscape for the adaptive amino acid substitutions in Trio. The x-axis represents the number of mutational steps from the ancestral haplotype (VNR) to the extant *D. melanogaster* haplotype (ASK). The y-axis represents fitness based on viability and locomotion phenotypes of each haplotype in (A) homozygous *D. melanogaster* flies or (B) heterozygous flies carrying one ancestral VNR haplotype.

Discussion

Adaptive protein evolution is widespread in plant and animal genomes and has a major impact on levels of genome-wide variability. Most inferences about this process rest on the assumptions that amino acid substitutions act independently and that the intensity of selection on them remains constant. Increasing evidence, however, suggests that interactions among substitutions—especially those in close physical proximity—may be common. These interactions raise an unresolved question: are clusters of closely linked amino acid substitutions, whether adaptive or not, typically fixed sequentially or simultaneously within a species? Despite its importance, direct empirical evidence for such epistatic interactions among spatially clustered

substitutions remains scarce, particularly in multicellular eukaryotes, where most reports have been anecdotal.

To address this gap, we systematically searched for proteins with experimentally tractable clusters of adaptive amino acid substitutions and identified Trio as a promising test case. Our analyses suggest that a cluster of three adaptive amino acid substitutions in Trio did not fix sequentially along the *Drosophila melanogaster* lineage. Instead, negative epistatic interactions among residues, together with the recessive deleterious effects of the derived variants, make it more likely that all three substitutions became fixed together as a single haplotype. This work provides one of the few direct demonstrations that spatially clustered adaptive substitutions in a multicellular eukaryote can interact epistatically and have measurable effects on whole-organism phenotypes relevant to fitness.

The utility of *in vivo* assays

Most experimental studies of epistasis have been performed *in vitro,* typically in microbial systems. These approaches are powerful because they allow systematic exploration of epistatic interactions within a protein. Deep mutational scanning can be applied efficiently to map the interactions among different sites of a protein and reconstruct the full fitness landscape of that protein (Olson et al. 2014; Sarkisyan et al. 2016; Starr and Thornton 2016). Such studies have been invaluable for uncovering principles of protein structure–function relationships and for providing quantitative descriptions of higher-order epistasis. However, the phenotypes measured *in vitro*—such as enzymatic activity, ligand binding —are tied to the specific function of the protein being studied and may not accurately reflect the overall organismal fitness. Moreover, *in vitro* assays cannot easily be generalized to proteins whose functions are not amenable to straightforward biochemical assays.

In contrast, *in vivo* provides the opportunity to measure more complex, higher-order phenotypes—such as development, reproduction, or behavior—that can be more directly interpreted in terms of fitness. They also provide a way to investigate amino acid substitutions in proteins that are otherwise difficult to assay biochemically, thereby broadening the range of proteins for which epistatic interactions can be experimentally explored. In this study, we tested the effects of amino acid substitutions on viability, fertility, and locomotion using an *in vivo* framework. This work offers a template for future research, making it possible to systematically explore epistatic interactions in a broad range of proteins while considering their impact on overall fitness.

Implications for the dynamics of adaptation

Although epistasis is recognized as an important factor of protein evolution (Lunzer et al. 2010; Riffis et al. 2025; Storz 2018), it remains poorly understood how groups of interacting amino acid substitutions can reach fixation in functional regions of proteins without compromising fitness. In principle, epistasis can allow sets of mutations that are individually deleterious or neutral to confer a benefit when combined, yet the evolutionary paths by which such groups of substitutions become established are often opaque. Studies that have directly investigated the timing and dynamics of epistatic mutation fixation (Harms and Thornton 2014; Gong et al. 2013; Sideraki et al. 2001; Wang et al. 2002; Levin et al. 2000) generally support a sequential fixation model. In this model, mutations fix in a stepwise manner, with each substitution either being neutral or slightly deleterious until the beneficial combination is assembled. However, such investigations remain rare, and this question is largely unexplored in diploid organisms.

Here, we showed that individual amino acid substitutions in the Trio cluster, as well as pairs of substitutions, are deleterious when present in the homozygous state. This means that any evolutionary trajectory involving the stepwise, sequential substitution of these amino acids would pass through strongly deleterious intermediate states (Fig 3), making such paths highly unlikely. These results therefore provide strong evidence that the cluster did not arise through a process of sequential fixation. Instead, since these deleterious effects are recessive, we propose that the cluster was likely to have assembled at the polymorphic phase, with all three substitutions eventually fixing concomitantly. This scenario contrasts with previous findings in microbial protein adaptation and highlights that dominance effects may fundamentally alter the dynamics of protein evolution—whether adaptive or compensatory—in diploid eukaryotes.

Implications for the interpretation of population genetic inferences

Over the past several decades, population genetics has undergone a paradigm shift in how we understand the role of positive selection in protein evolution and its impact on genomic variation in plants and animals (Sella et al. 2009; Booker et al. 2017). In Drosophila, estimates suggest that 50–90% of amino acid divergence exceeds neutral–deleterious model predictions and is therefore attributed to positive selection, though the exact proportion varies depending on datasets and methods (Sella et al. 2009; Wilson et al. 2011; Eyre-Walker and Keightley 2009; Messer and Petrov 2013). Independent support for adaptive substitutions comes from hitchhiking signatures near individual amino acid substitutions (Elyashiv et al. 2016), but these analyses tend to yield somewhat lower estimates of the proportion of divergence that is adaptive.

If, however, epistasis among amino acid substitutions—such as that observed for Trio—is common in protein evolution, then the McDonald–Kreitman framework may overestimate the proportion of adaptive divergence (Fay 2011). This is because the framework assumes independence among sites

and a constant direction and strength of selection over time, both of which are violated when substitutions interact epistatically. Although this issue has been raised conceptually, the consequences of pervasive epistasis for interpreting McDonald–Kreitman results remain largely unexplored.

More broadly, widespread non-independence among amino acid substitutions could alter how we interpret their effects on genome-wide diversity. For example, if several closely linked substitutions fix simultaneously rather than sequentially, the apparent average strength of selection per substitution would be underestimated, since its impact would be distributed across multiple fixed sites. How such non-independence—particularly in light of the dominance and epistasis uncovered in the case of Trio—affects inferences of population genetic parameters is an important open question for future research.

Conclusions

By studying a cluster of adaptive amino acid substitutions in the *D. melanogaster* protein Trio, we uncovered strong epistatic interactions among residues of this cluster. Because these substitutions exhibit recessive deleterious effects, they are more likely to have persisted at low frequencies in the population as polymorphisms before combining into a beneficial haplotype that eventually became fixed in the species. This phenomenon may be common in adaptive protein evolution and has important implications for how we interpret its associated population genetic signals. This case study lays the groundwork for more systematic *in vivo* studies of amino acid substitution clusters in diploid organisms, where the effects of mutations can be measured at the whole-organism level. Such studies will help clarify how epistasis, pleiotropy, and dominance interact to shape protein evolution, deepening our understanding of the evolutionary constraints that govern adaptive trajectories.

Methods

Identification of adaptive clusters

We created groups of homologous proteins using *D. melanogaster* ISO1 (GCA_000001215.4), *D. simulans* w501 (GCA_016746395.2), *D. yakuba* NY73PB (GCA_016746365.2), *D. santomea* STO CAGO 1482 (GCA_016746245.2) and *D. teissieri* GT53w (GCA_016746235.2) Homologous proteins were identified using a reciprocal best-hit exonerate approach (Slater and Birney 2005) following Taverner et al., (2020). ISO1 *D. melanogaster* proteins were aligned to each genome sequence to extract candidate proteins, and each extracted protein was subsequently realigned to its corresponding *D. melanogaster* protein. *D. melanogaster*'s longest transcript was used to represent each protein and multispecies alignment was created

using PRANK (-codon parameter, v.170427; Löytynoja and Goldman 2008). Ancestral sequences were inferred based on this alignment and the species tree using PAML's baseml function (v 4.9; Yang 2007) with the following parameters: model=7, kappa=1.6, RateAncestor=2. MACSE (-max_refine_iter 1 parameter, v. 2.07; Ranwez et al. 2011) was then used to align sequences from the *D. melanogaster* Zambia population (n = 82; Lack et al. 2015) with the reconstructed *D. melanogaster–D. simulans* ancestral sequence.

To infer selection on protein sequences, we applied Model Averaged Site Selection via Poisson Random Field (MASS-PRF), which relies on both polymorphism and divergence data (Zhao et al. 2017). In this framework, sequences from the Zambia population served as polymorphism data, while the reconstructed *D. melanogaster–D. simulans* ancestral sequence was used as divergence (outgroup) data.

To prepare the input files required for running MASS-PRF (Zhao et al. 2017), we generated consensus sequences capturing polymorphism and divergence changes for each protein, as follows. To create the polymorphism consensus sequence, monomorphic codons were replaced by "*", synonymous codons by "S" and non-synonymous changes were replaced by "R". To create the divergence consensus sequence, outgroup codons that were present in the ingroup sequences were replaced by "*", outgroup codons were replaced by "S" or "R" if the ingroup codon was fixed and the outgroup codon was synonymous or non-synonymous to it respectively. If the ingroup codon was polymorphic and the outgroup codon was different from both of these, the codon was replaced by "-". For proteins longer than 900 amino acids, Consensus sequences were split into fragments of 900 codons or smaller.

MASS-PRF was run on each consensus sequence using parameters –ic 1 –sn 82 -o 1 -r 1 -ci_r 1 -ci_m 1 -s 1 -exact 0 -mn 30000 -t 2. Out of 10573 sequences (corresponding to 9137 unique proteins), MASS-PRF run successfully 5743 sequences (4082: too little substitution information to run; 748: out of memory). Successful runs were screened for positive selection. A site was estimated to be under positive selection if the lower 95% confidence bound for gamma > 4, which corresponds to a false positive rate <0.1 (Zhao et al. 2017). Out of the 5743 successful runs (corresponding to 5355 proteins), 1144 had at least one site under positive selection and 970 more than one, with 940 forming a cluster (at least two sites less than 20 codons apart). We found that 679 proteins contain at least one potential experimentally tractable cluster. We defined a cluster as experimentally tractable if exactly 2 or 3 sites that show divergence and positive selection are less than 20 codons apart from each other.

For Fig 1 and Fig S1, predicted functional domains were found in FlyBase.org and alpha-fold predictions were found in the AlphaFold Protein Structure Database (EMBL-EBI). Superimposition

of the alpha-fold prediction and the crystal structure (when available) was performed using mol* Viewer (Sehnal et al. 2021).

Plasmid assembly

Genomic DNA was isolated from ywISO8 flies using a "squish prep" protocol (Gloor et al. 1993). Homology arms were amplified with PCR from this genomic DNA using Q5 polymerase from NEB . The plasmid backbone and dsRed were amplified from plasmid: pScarlessHD-DsRed, a gift from Kate O'Connor-Giles (Addgene #64703). The four fragments were combined at an equimolar concentration (150 fmoles each) and assembled using NEBuilder HiFi DNA assembly kit. To verify that assembly was successful, PCR was performed using primers that spanned multiple fragments. The NEBuilder HiFi DNA assembly kit result was used to transform NEB 5-alpha competent E. coli. To verify that the transformation was successful, colony PCR was performed on individual bacteria colonies using pairs of primers that spanned multiple fragments using LongAMP or regular Taq. Final plasmid assembly was verified by a Tn5 tagmentation-based Illumina sequencing protocol (Picelli et al. 2014) followed by *de novo* assembly. Plasmid was extracted using Qiagen's QIAprep Spin Miniprep kit.

Site-Directed Mutagenesis

Starting from a base plasmid sequence representing the current *D. melanogaster* haplotype (ASK), we used site-directed mutagenesis (SDM) to create all possible intermediates leading back to the ancestral A1315V/S1318N/K1335R (VNR) haplotype. To do this, we used the Agilent QuikChange Lightning Multi Site-Directed Mutagenesis Kit in two reactions: one containing three primers: 1) A1315V, 2) S1318N, and 3) K1335R, and one containing two primers: 1) A1315V, S1318N and 2) K1335R. The standard Agilent kit protocol was followed. First, PCR was performed without the addition of QuikSolution, as it was not necessary. This was followed by DpnI digestion (provided) and transformation into the provided competent cells. Colony PCR using Taq polymerase was performed on 48 bacterial colonies from each reaction. Amplicons form each sample were barcoded with a unique combination of Illumina-compatible i5 and i7 adapters and sequenced to assess the presence of the desired mutations. Plasmids were extracted using the Qiagen Plasmid Midi Kit for CRISPR injection. The design for mutation 3 (K1335R) is completely scarless. All the other combinations introduce a single synonymous single nucleotide polymorpjhism that is naturally present within *D. melanogaster* populations. Plasmids were obtained for the following combinations: A1315V (VSK), A1315V/S1318N/K1335R (VNR), A1315V/S1318N (VNK), S1318N (ANK), K1335R (ASR), S1318N/K1335R (ANR). One additional haplotype, A1315V/K1335R (VSR) was generated using a second SDM reaction starting from A1315V plasmid to introduce K1335R.

CRISPR injections and post-injection processing

gRNAs were created from the shared tracrRNA and a site-specific crRNA, ordered as two separate Alt-R® CRISPR-Cas9 RNA fragments from IDT. For each gRNA, tracrRNA and crRNA were annealed by adding 2ul of crRNA at 100 µM, 2ul of tracrRNA at 100µM, and 2ul of IDT nuclease-free duplex buffer and incubating at 95°C for 5 minutes, then allowing the mixture to come to room temperature on the benchtop. gRNA were loaded into the Alt-R® S.p. Cas9 Nuclease from IDT to make the ribonucleoprotein (RNP) complex: First, stock Cas9 solution was diluted into an equivalent volume of IDT nuclease-free duplex solution. Then 2.68 mL of both annealed gRNAs and 1.8 mL of the diluted Cas9 protein were mixed and incubated at room temperature for 5 minutes. Finally, 7.5 mg of donor plasmid was added and the volume was increased to 30 mL with water. CRISPR-cas9 injections were done in line "ywISO8" to facilitate ease of fluorescent screening. Injected flies were crossed to a double balancer line (BL#2537: w[*]; TM3, Sb[1] Ser[1]/TM6B, Tb[1]). Progeny of the crosses were screened for red fluorescent eyes and mated with siblings with the same balancer chromosomes to establish a stable line. pBac excision was performed following (Stern et al. 2017): DsRed embryos were injected with 250ng/mL phsp-pBac plasmid (Handler and Harrell 1999), heat shocked 1 hour after injection for 1 hour at 37 C. Injected flies were then crossed with a balancer line (Bloomington #23232: w[*]; ry[506] Dr[1]/TM6B, P{Dfd-GMR-nvYFP}4, Sb[1] Tb[1] ca[1]). Progeny of the crosses were screened for non-fluorescent eyes and sib mated to establish mutant lines.

Background homogenization

In order to fully control for genomic background effects, two balancer lines with a fully homozygous genome were created using the inbred line RAL386 (BL#28192 (Huang et al. 2014)) and the chromosome balancer of respectively BL#23232 (w[*]; ry[506] Dr[1]/TM6B, P{Dfd-GMR-nvYFP}4, Sb[1] Tb[1] ca[1]) and BL#35524 (w[1118]; DCTN1-p150[1]/TM3, P{w[+mC]=sChFP}3, Sb[1]). RAL386 males were crossed with virgin females of either balancer line BL#23232 or BL#35524. An F1 male was then backcrossed with a RAL386 virgin female. Resulting fluorescent male progeny were then backcrossed to RAL386 virgin females. Several days after the crosses, the father of each cross was collected and genotyped for chromosome 2 by PCR and Sanger sequencing of a region with a known diagnostic single nucleotide polymorphism. Crosses for which the father was homozygous for RAL386 haplotype for chromosome 2 were kept. Fluorescent virgin female progeny from this cross were then backcrossed to a RAL386 male. The balancer chromosomes in the established lines were maintained by screening for fluorescence every 2-3 weeks. *Trio* mutant lines and yw-ISO8 line, used as the control ASK, were crossed

alternatively with the two RAL386 balancer lines following the same crosses scheme as described below so the final lines could be balanced with TM6B, P{Dfd-GMR-nvYFP}4, Sb[1] Tb[1] ca[1].

Drosophila rearing

All fly strains were reared in bottles or vials at 21°C, 50% in day-night cycle of 12hr-12hr unless specified.

Viability assays

Viability of homozygous strains was measured as the relative survival of homozygous YFP-progeny relative to YFP+ progeny produced by parents balanced with TM6B, P{Dfd-GMR-nvYFP}4, Sb[1] Tb[1] ca[1]. For 1st instar larva, virgin males and females [YFP+, Sb+, Tb+] were crossed and allowed to lay eggs on grape-juice agar plates with yeast paste for 24hr. After 48hr, the yeast past was washed out through a cell strainer to collect and count fluorescent and non-fluorescent 1st instar larvae. For pupal and adult stage, females were allowed to lay eggs on regular fly food vials for 7 days. [Tb+] and [Tb-] pupae were counted after about 10 days. [Sb+] and [Sb-] adults were counted after about 20 days. We measured the viability of heterozygous individuals the same way except that homozygous VNR virgin females were crossed to males balanced with TM6B, P{Dfd-GMR-nvYFP}4, Sb[1] Tb[1] ca[1]. 60 to 300 larvae, 100 to 200 pupae and 100 to 150 adults were counted for each haplotype. For VSR, we obtained 6 adult homozygous males and 1 adult homozygous female. To estimate the fertility of those homozygous adult individuals, males were crossed individually with one homozygous VNR virgin female and the female was crossed with one heterozygous VSR male. No progeny was observed after 21 days.

Locomotion performance assay.

We quantified locomotor performance by quantifying startle-induced negative geotaxis, an innate behavior where flies tend to climb against gravity after being mechanically agitated (Ali et al. 2011). Ten 1-day-old males were grouped with ten females into vials for 7-10 days. Before the assay, the males were transferred into ethanol-cleaned assay tubes, consisting of two tubes attached with tapes with a line set at 4.5 cm from the bottom of the tube. Flies were let to recover for 40 to 60min before the start of the experiment. The assay tube was taped 5 times on a fly pad so that all flies fell to the bottom of the tube, and the flies that reached the line in the following 10 sec were counted. Each group of flies were assayed three times, with 5 min recovery between each time, the average of the three replicates was used. The same assay tubes were then assayed the same way after 10 min recovery but counting flies that reached the line in the following 5 sec instead of 10. Four to 14 replicates were performed for each haplotype.

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Supplementary

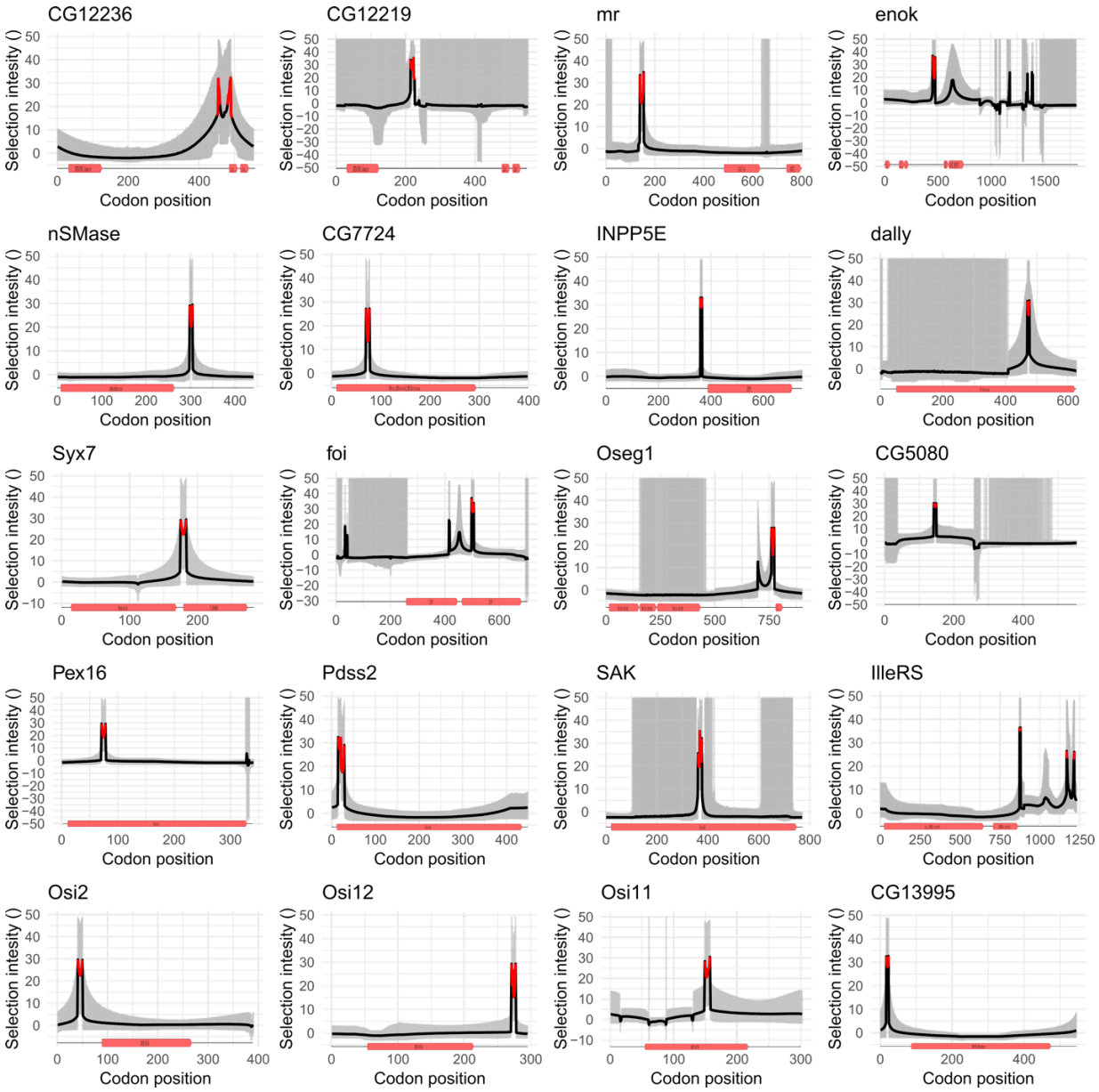

Figure S1. Clusters of mutations in 20 *D. melanogaster* genes. Profiles of selection intensity for four D. melanogaster proteins using MASS-PRF (Zhao et al., 2017). The x-axis indicates codon position and y-axis indicates selection intensity (γ= 2Ns). The black line corresponds to the model-averaged γ and the grey area indicates 95% model uncertainty interval. Red lines indicate regions for which the 95% lower bound of γ > 4, which corresponds to a false positive rate of <0.1. T. Protein models are represented below each selection intensity plot. Functional domains are represented by red boxes with their names in black.

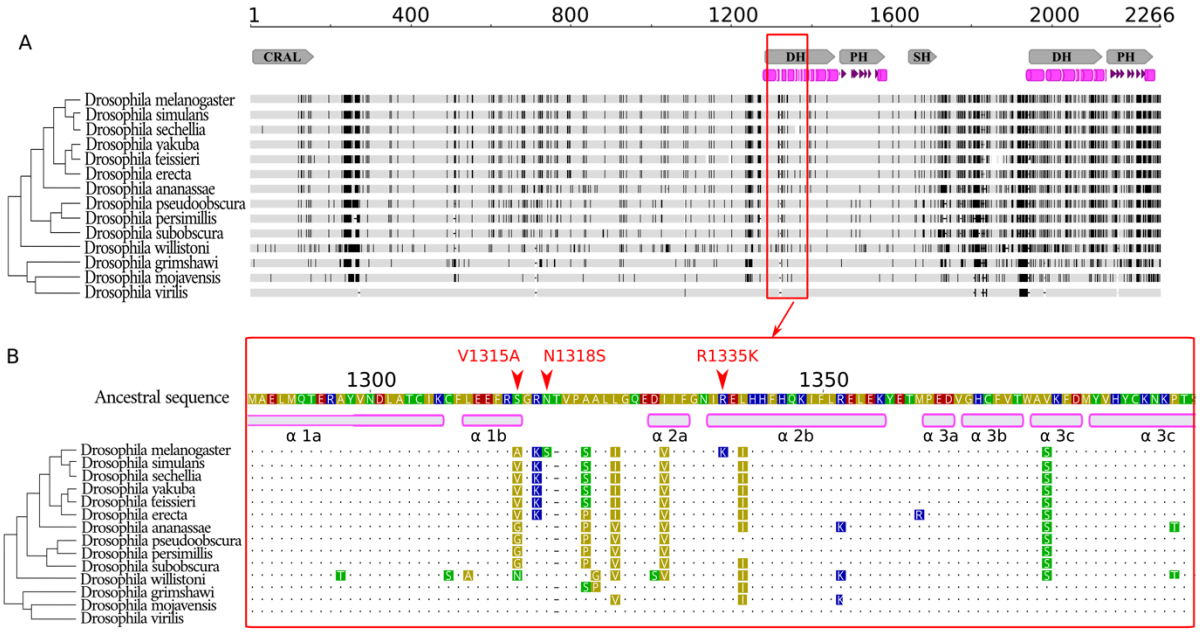

Figure S2. Trio protein alignment within Drosophila genus. multiple protein alignment of Drosophila species trio. A) entire alignments with large indels removed. B) Focus on the trio cluster region. Amino acids are colored according to their polarity (yellow: non-polar; green: polar; red: polar, acid; blue: polar, basic). Dot represents agreements to the ancestral sequence (see below). Positions of the helix are based on the human structure (PDB 7SJ4, Barbosa et al., 2020). Species tree from (Clark et al., 2007; Suvorov et al., 2021). Branches are not at scale. Muscle alignment (v 3.8.425) implemented in geneious prime (v 2019.0.4). Trio ancestral sequence has been estimated using codeml function of PAML (v 4.9; Yang 2007) using protein sequences of *D. melanogaster, D. simulans, D. yakuba, D. ananassae, D. pseudoobscura, D. willistoni, D. virilis* and the corresponding species tree.

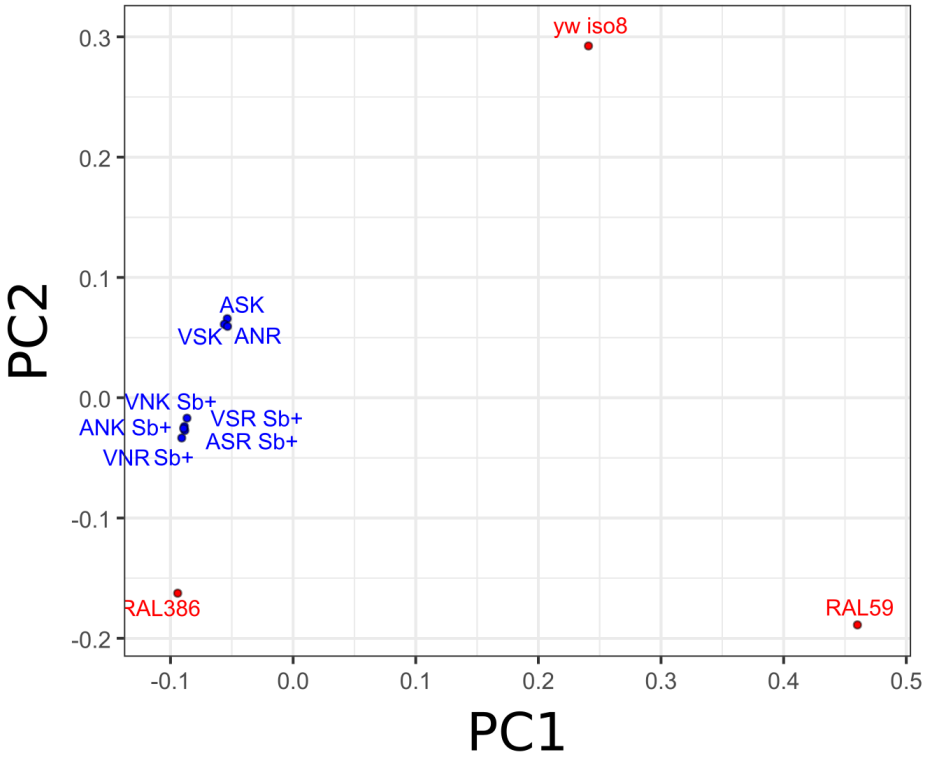

Figure S3. Sequencing confirmation of engineered lines. To confirm the genomic background of engineered lines, 10 female individuals were collected from each line and frozen at -20°C. Whole DNA was extracted from each fly individually using Quick-DNA 96 Kit (Zymo research). DNA from each fly from the same line was then pooled. Tn5-tagmentation libraries (Picelli et al. 2014) were prepared and indexed with one specific index for each line and enriched by 12 PCR cycles (HS One Taq, NEB). Libraries were then pooled and size selected for fragments around 500nt using AMPure XP (Beckman Coulter) following manual. The pooled libraries were then sequenced with paired-end 150nt on NovaSeq X Plus 10B Illumina 2x150 (Admera Health). Illumina adapters were trimmed using trim-galore (-q 0, -e 0.1) (v 0.6.7) and reads were aligned to the *D. melanogaster* reference genome (GCA_000001215.4) using bwa mem (v 0.7.17-r1188). Duplicates were marked with picard (v 2.18.29) and reads were re-aligned with gatk3 (v 3.8-1-0). Variants were called and pseudo references were made with samtools (v 1.6) and bcftools (v 1.9) using scripts available on github (https://github.com/YourePrettyGood/PseudoreferencePipeline). ANGSD (v 0.935) was run on the re-aligned bam files.

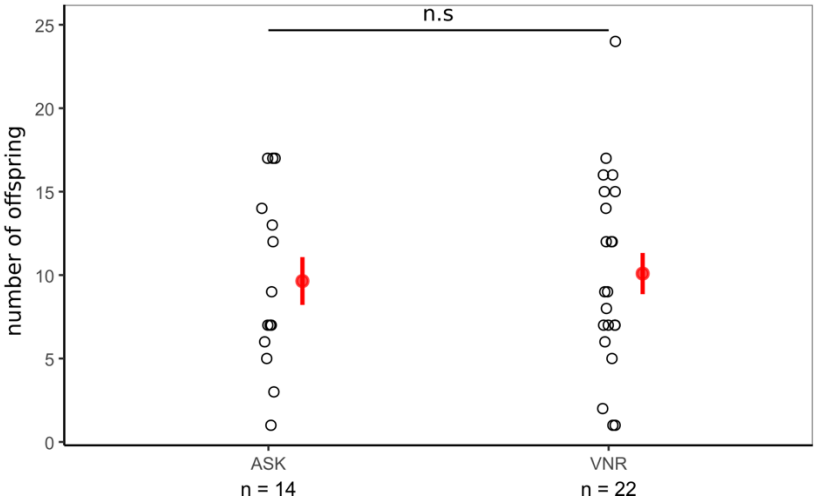

Figure S4. Fertility of homozygous ASK and VNR strains. Single 1-3 day-old virgin females were crossed with single 1-3 day-old virgin males from the same line and allowed to mate for 24hr. Males and females were removed and adult offspring were counted 20 to 27 days later. Each dot represents the number of progeny for one fertile cross. Red circles and bars represent the mean and standard error, respectively. The two haplotypes do not show a significant difference (Wilcoxon-Mann-Whitney, p=0.8961).

Table S1. Predicted effects of single mutations on protein stability. The DH-PH domain of the D. melanogaster Trio as well as the ancestral and all the intermediate versions of the domain were predicted using ColabFold v1.5.5 (AlphaFold2 using MMseqs2) (Mirdita et al., 2022) with default parameters. The effects of all single mutations on stability were predicted using Dynamut2 (Rodriguez et al., 2020), ThermoNet based on Rosetta modules (Li et al., 2020; Tika et al., 2011; Cooper et al., 2011; Maguire et al., 2020) and ACDC-NN (istruct function) (Pancotti et al., 2021). ΔΔG (kcal/mol) = ΔG(mutant) – ΔG(wild-type) (so positive means destabilizing, negative means stabilizing).

Change	Dynamut2	ACDC-NN (istruct)	ThermoNet
VNR -> ANR	0.30	0.20	0.73
VNR -> VSR	-0.27	-0.0015	-0.014
VNR -> VNK	1.00	0.36	-0.058
ANR -> ASR	-0.28	-0.019	-0.11
ANR -> ANK	0.87	0.40	-0.20
VSR -> ASR	0.27	0.20	0.24
VSR -> VSK	-0.86	0.40	-0.18
VNK -> ANK	0.33	0.20	0.70
VNK -> VSK	-0.27	0.40	0.22
ASR -> ASK	0.85	0.36	-0.13
ANK -> ASK	-0.29	-0.0069	0.044
VSK -> ASK	0.47	0.20	0.75