

Allelic strengths of encephalopathy-associated *UBA5* variants correlate between *in vivo* and *in vitro* assays

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Abstract

Protein UFMylation downstream of the E1 enzyme UBA5 plays essential roles in development and ER stress. Variants in the *UBA5* gene are associated with developmental and epileptic encephalopathy 44 (DEE44), an autosomal recessive disorder characterized by early-onset encephalopathy, movement abnormalities, global developmental delay, intellectual disability, and seizures. DEE44 is caused by at least twelve different missense variants described as loss of function (LoF), but the relationships between genotypes and molecular or clinical phenotypes remains to be established. We developed a humanized *UBA5* fly model and biochemical activity assays in order to describe *in vivo* and *in vitro* genotype-phenotype relationships across the *UBA5* allelic series. *In vivo*, we observed a broad spectrum of phenotypes in viability, developmental timing, lifespan, locomotor activity, and bang sensitivity. A range of functional effects was also observed *in vitro* across comprehensive biochemical assays for protein stability, ATP binding, UFM1 activation, and UFM1 transthiolation. Importantly, there is a strong correlation between *in vivo* and *in vitro* phenotypes, establishing a classification of LoF variants into mild, intermediate, and severe allelic strengths. By systemically evaluating *UBA5* variants across *in vivo* and *in vitro* platforms, this study provides a foundation for more basic and translational UBA5 research, as well as a basis for evaluating current and future individuals afflicted with this rare disease.

eLife assessment

The authors establish a *Drosophila* model to assess the severity of disease-linked alleles of Uba5 to study DEE44, a neurodevelopmental disease caused by UBA5 gene mutations. Using in vivo and in vitro experiments, this **valuable** study demonstrates that alleles fall into mild, intermediate, and severe classes, with **convincing** evidence to support their conclusion, which includes well-conserved relationships between UBA5 structure and function across humans and flies. This study establishes a model for further characterization of Uba5-related phenotypes in a powerful model system and will be used in the future to study the functional effects of these mutations on nervous system development.

Introduction

Variants in the human *ubiquitin like modifier activating enzyme 5* (UBA5) gene have been associated with three autosomal recessive disorders. In most reported cases, biallelic UBA5 variants cause developmental and epileptic encephalopathy 44 (DEE44, OMIM: #617132). The disease is characterized by early-onset encephalopathy, movement abnormalities, global developmental delay, and intellectual disability. Many individuals also have seizures, failure to thrive, and microcephaly. Delayed myelination, thinning of the corpus callosum, and white matter hyperintensities have also been documented with magnetic resonance imaging (MRI) (Colin *et al.*, 2016 [↗](#); Muona *et al.*, 2016 [↗](#)). Biallelic UBA5 has also been associated with spinocerebellar ataxia 24 (OMIM: #617133), which is characterized by a childhood-onset gait and limb ataxia (Duan *et al.*, 2016 [↗](#)). Another family has been reported with a rare homozygous missense variant in UBA5 that segregates with severe congenital neuropathy (Cabrera-Serrano *et al.*, 2020 [↗](#)).

UBA5 is a key component in UFMylation, a post-translational modification pathway mediated by a ubiquitin-like protein (UBL) ubiquitin fold modifier 1 (UFM1) (Millrine *et al.*, 2023 [↗](#)). UBL modifications play an essential role in eukaryotic biology by regulating protein stability and function via different enzymatic complexes (Cappadocia & Lima, 2018 [↗](#); van der Veen & Ploegh, 2012 [↗](#)). UFMylation is conserved in metazoans and plants (Figure 1A [↗](#)) (Millrine *et al.*, 2023 [↗](#)). In this pathway, UFM1 is first proteolytically processed by a UFM1 specific peptidase 1/2 (UFSP1/2) to expose a C-terminal Gly (Kang *et al.*, 2007 [↗](#); Komatsu *et al.*, 2004 [↗](#); Millrine *et al.*, 2022 [↗](#)). The ensuing conjugation process involves three steps. The first two steps are facilitated by UBA5, an E1 activating enzyme specific to UFMylation. UBA5 activates UFM1 through ATP-dependent adenylation of the UFM1 C-terminal Gly, which is then transferred onto the UBA5 active site Cys 250, forming a high-energy thioester intermediate. Next, the UFM1-specific E2 conjugating enzyme, UFC1, binds to the activated UBA5–UFM1 intermediate and receives UFM1 onto its active site Cys through a transthioylation reaction (Figure 1A [↗](#)) (Gavin *et al.*, 2014 [↗](#); Komatsu *et al.*, 2004 [↗](#)). The UFM1 activation and transthioylation processes are achieved by a trans-binding mechanism involving two molecules each of UBA5, UFM1, and UFC1, wherein one UBA5 protomer performs the enzymatic processes while the other provides essential UFM1- and UFC1-binding sites *in trans* (Figure 1B [↗](#)) (Kumar *et al.*, 2021 [↗](#); Mashahreh *et al.*, 2018 [↗](#); Oweis *et al.*, 2016 [↗](#)). Next, the E3 ligase UFL1 functions as a scaffold to bring the activated UFC1–UFM1 conjugate to the substrate protein and facilitate the conjugation of UFM1 to a substrate Lys residue (Peter *et al.*, 2022 [↗](#); Tatsumi *et al.*, 2010 [↗](#)).

UFMylation has been implicated in regulating many processes such as genome stability and receptor activation (Liu *et al.*, 2020 [↗](#); Qin *et al.*, 2019 [↗](#); Wang *et al.*, 2019 [↗](#); Yoo *et al.*, 2014 [↗](#)), but the principal role is believed to be in regulating proteotoxic stress at the endoplasmic reticulum

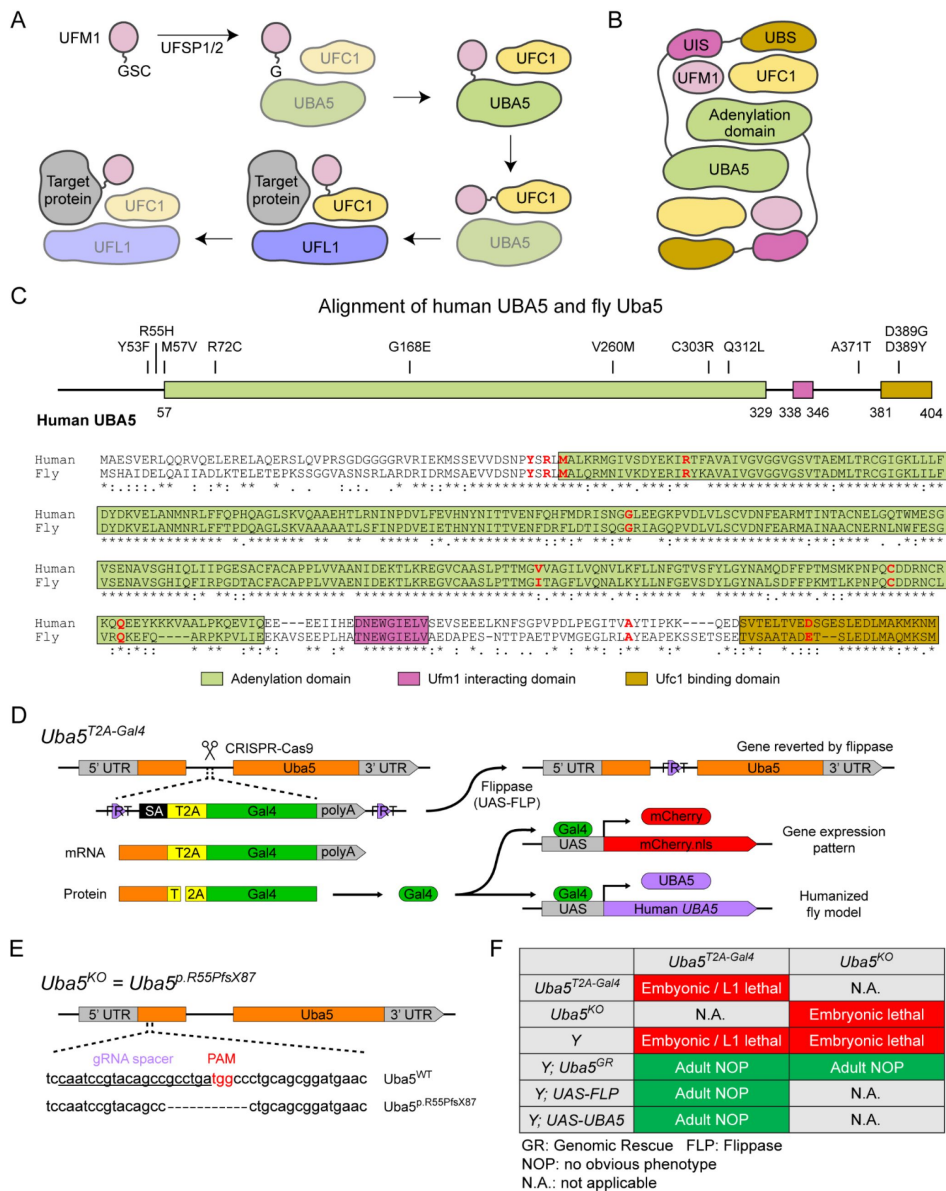


Figure 1.

UFMylation pathway, conservation of UBA5, and generation of fly *Uba5* LoF alleles

(A) A diagram showing the UFMylation pathway. Details of the biochemical processes in the pathway are described in the main text. In UBA5 proteins, only the adenylation domains are shown in the diagram.

(B) A diagram of the UBA5:UFM1:UFC1 complex. In the complex, two copies of UBA5 form a homodimer that interacts with UFM1 via a trans-binding mechanism. The activation of UFM1 requires the adenylation domain of one UBA5 subunit and the UFM1-interacting sequence (UIS) of the other UBA5 subunit in the complex. The opposing protomer of the UBA5 homodimer also contributes a UFC1-binding sequence (UBS) that is required for UFM1 transthiolation.

(C) Alignment of the human UBA5 and fly Uba5 protein sequences. The functional domains of UBA5 are marked in colored boxes. The DEE44-associated variants are marked in the protein topology diagram and the protein sequence alignment (letters in red).

(D) Generation of the *Uba5*^{T2A-Gal4} allele and the uses of the allele in flippase (FLP)-mediated conversion. The expression of the GAL4 to drive a fluorescent protein allows assessment of gene expression, and humanization of the flies by expression of human UBA5 cDNA.

(E) Generation of *Uba5* null allele by CRISPR-mediated indel formation.

(F) Loss of *Uba5* causes lethality in early developmental stage. The lethality is rescued by a genomic rescue construct, the expression of FLP (*Uba5*^{T2A-Gal4} mutants only), and the expression of human UBA5 cDNA.

(ER), where UFMylation of stalled ribosomes initiates quality control measures (Liang *et al.*, 2020 [DOI](#); Scavone *et al.*, 2023 [DOI](#); Walczak *et al.*, 2019 [DOI](#); Wang *et al.*, 2020 [DOI](#)). So far, the only well-characterized *Uba5* mutant animal model is a mouse model in which removal of the gene causes embryonic lethality due to hematopoietic defects (Tatsumi *et al.*, 2011 [DOI](#)). Tissue-specific mouse knockouts of other genes within the UFMylation pathway support a role in regulating ER stress within secretory cells, as well as a critical developmental role within the central nervous system (Muona *et al.*, 2016 [DOI](#); Zhu *et al.*, 2019 [DOI](#)).

To date, 24 individuals from 17 families who have *UBA5*-associated DEE44 have been reported (Arnadottir *et al.*, 2017 [DOI](#); Briere *et al.*, 2021 [DOI](#); Colin *et al.*, 2016 [DOI](#); Daida *et al.*, 2018 [DOI](#); Low *et al.*, 2019 [DOI](#); Mignon-Ravix *et al.*, 2018 [DOI](#); Muona *et al.*, 2016 [DOI](#)). The genotypes (Table S1) and clinical features (Table S2) of the affected individuals are summarized in Supplemental Information. Prior functional studies using cultured cells or patient cells show that many reported *UBA5* variants cause various levels of loss of function (LoF). However, the study of the genotype-phenotype relationship is hampered by the limited number of affected individuals, incomplete description of clinical presentations and the heterogeneous genetic background. Variant-specific *in vivo* models are powerful tools for studying genotype-phenotype relationship, especially for rare diseases (Arnadottir *et al.*, 2017 [DOI](#); Goodman *et al.*, 2021 [DOI](#); Lu *et al.*, 2022a [DOI](#); Lu *et al.*, 2022b [DOI](#); Ma *et al.*, 2023 [DOI](#); Tepe *et al.*, 2023 [DOI](#)). However, systematic assessment of the effects of disease-causing variants *in vivo* is a challenge as it can be very labor intensive. Moreover, the *in vivo* assays should be compared to functional studies of the variant proteins, which typically relies on biochemical or other cell-based assays that are not available for most proteins/genes. By combining phenotypic studies and biochemical assays it should be possible to assess the severity of each variant, providing valuable information for the affected individuals and for assessing possible therapeutic interventions. In addition, genotype-phenotype relationships offer information about the molecular basis underlying variants LoF, paving the way for future therapeutic development.

In this study, we assess the genotype-phenotype relationship in *UBA5*-associated DEE44 variants by determining the phenotypes of variant-specific fruit fly models. In conjunction with the *in vivo* data, we also comprehensively assess the biochemical properties of each variant using assays that report on protein stability, ATP binding, UFM1 activation, and UFM1 transthiolation. The presence and severity of the phenotypes in flies are highly variant-dependent. Similarly, the enzymatic activities of the variants vary widely *in vitro*. Interestingly, both *in vivo* and *in vitro* assays produce a very similar allelic series for the variants, suggesting a correlation between specific enzymatic properties and the phenotypes in the animal models. Finally, combining our animal model work with available insights into *UBA5* enzymology provides us with a much better understanding of the structure- function relationship of the *UBA5* variants.

Results

Establishment of a variant-specific *UBA5*-associated disease model in fruit flies

To investigate the functions of *UBA5* variants *in vivo*, we utilized *Drosophila melanogaster* as a model organism. *Uba5* is the ortholog of human *UBA5* in flies (*UBA5* refers to the human gene; *Uba5* refers to the fly gene). The two proteins share 64% identity and 75% similarity in amino acid sequence, and the *Drosophila* Integrative Ortholog Prediction Tool (DIOPT) score between *UBA5* and *Uba5* is 15/16, indicating a high degree of homology (Figure 1C [DOI](#)) (Hu *et al.*, 2021 [DOI](#)). The *UBA5* protein has an adenylation domain, a UFM1-interacting sequence (UIS) and a UFC1-binding sequence (UBS), all of which are required for UFM1 activation and transthiolation (Bacik *et al.*, 2010 [DOI](#); Habisov *et al.*, 2016 [DOI](#); Kumar *et al.*, 2021 [DOI](#); Padala *et al.*, 2017 [DOI](#); Xie, 2014 [DOI](#)) (Figure

1C). Similarly, Uba5 has all three highly conserved functional domains, and all of the amino acid residues affected by the DEE44-associated variants reported so far are conserved in the fly protein (Figure 1C).

To study the variant-specific functions, we generated humanized fruit fly models in which the expression of the endogenous *Uba5* gene is removed or severely suppressed and a human *UBA5* cDNA is expressed under the control of the endogenous *Uba5* enhancer and promoter. If the human reference *UBA5* functions in flies and rescues the *Uba5* severe LoF phenotypes, the DEE44-associated variants can be expressed and their functions can be assessed by the phenotypes of flies. To achieve this, we generated a *Uba5^{T2A-Gal4}* allele using a CRISPR-Mediated Integration Cassette (CRIMIC) strategy (Lee *et al.*, 2018). In the *Uba5^{T2A-Gal4}* allele, an *FRT-Splice Acceptor (SA)-T2A-GAL4-polyA-FRT* cassette was inserted into a coding intron of the *Uba5* gene. The SA causes the inclusion of the cassette during transcription, while the polyA sequence arrests the transcription generating a truncated transcript. The translation of the transcript is arrested at the viral ribosomal skipping site (T2A) and reinitiated after the site, producing an untagged GAL4 protein (Figure 1D) (Diao *et al.*, 2015; Lee *et al.*, 2018). The *Uba5^{T2A-Gal4}* allele is likely a severe LoF allele (see below) (Lee *et al.*, 2018). In addition, this allele also results in the expression of GAL4 under the control of the endogenous *Uba5* enhancer and promoter, which enables the assessment of native gene expression pattern as well as the expression of human *UBA5* cDNA (Figure 1D). We also generated a *Uba5* null allele by CRISPR-induced indel formation (*Uba5^{p.Arg55Profs*87}*, named *Uba5^{KO}*) (Figure 1E).

We first tested the viability of the flies with the *Uba5^{T2A-Gal4}* and the *Uba5^{KO}* alleles. The fly *Uba5* gene is located on the X chromosome. For both alleles, homozygous female and hemizygous male flies are lethal at the embryonic stage, although a few *Uba5^{T2A-Gal4}* escapers survive to the L1 larval stage (Figure 1F). The lethality is rescued by a genomic rescue (GR) construct that carries the *Uba5* locus (P[acman] clone CH321-02B13) (Venken *et al.*, 2010), indicating that the lethality in both lines is caused by the LoF of *Uba5*. Moreover, expression of flippase (FLP) using *Uba5^{T2A-Gal4}* removes the insertion of the CRIMIC cassette and reverts the lethality of the *Uba5^{T2A-Gal4}* hemizygous males, showing that the lethality is indeed caused by the *Uba5^{T2A-Gal4}* allele (Figure 1F) (Lee *et al.*, 2018). Finally, expression of reference human *UBA5* cDNA using *Uba5^{T2A-Gal4}* rescues the lethality of the mutants, showing that the functions of the fly and human proteins are evolutionarily conserved (Figure 1F).

Uba5 is expressed in a subset of neurons and glia in the fly central nervous system

Next, we examined the expression pattern of *Uba5* by expressing a nuclear localized mCherry fluorescent protein (*UAS-mCherry.nls*) under the control of *Uba5^{T2A-Gal4}*. *Uba5* is expressed in multiple tissues in L3 larvae and adult flies (Figure 2A), consistent with high-throughput gene expression profiling results (Leader *et al.*, 2018). We next analyzed the expression of *Uba5* in the central nervous system (CNS). We stained the *Uba5^{T2A-Gal4}>mCherry.nls* larval CNS and adult brain with anti-Elav and anti-Repo antibodies to mark the nuclei of neurons and glial cells, respectively. In both larval CNS and adult brain, the mCherry.nls signals are found in a subset of neurons and glia (Figures 2B and 2C), suggesting that *Uba5* is expressed in the fly CNS but not in all cells. Intriguingly, *Uba5* is expressed more widely in the adult brains than in the larval CNS. In larval CNS, it is expressed in many fewer neurons than Elav (Figures 2A and 2B). The expression pattern resembles that of the *para* gene, which encodes the sole voltage-gated sodium channel in *Drosophila* which is only expressed in differentiated, actively firing neurons (Ravenscroft *et al.*, 2020). This suggests that *UBA5* may be required for the activity of neurons.

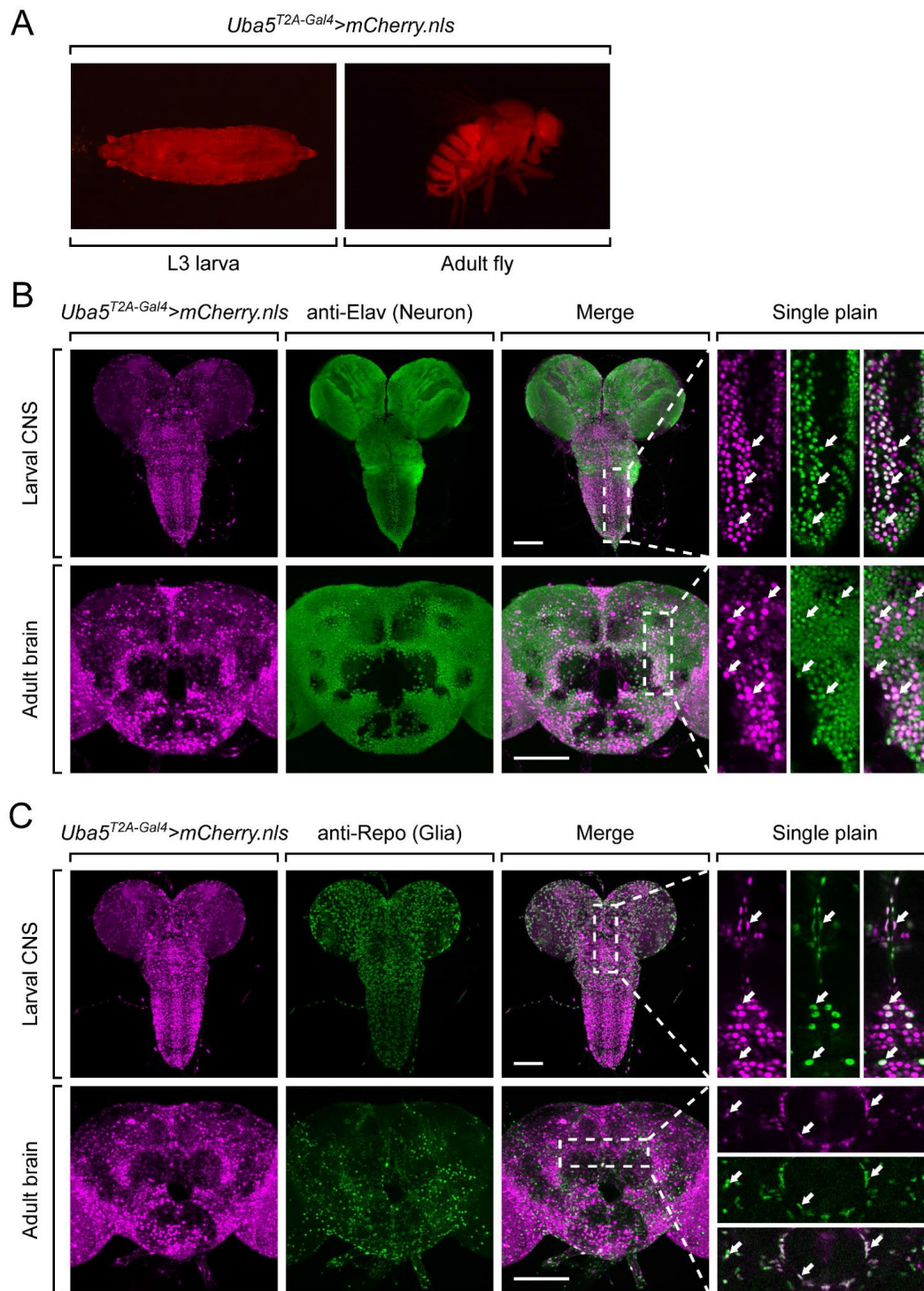


Figure 2.

***Uba5* is expressed in a subset of neurons and glial cells in fly CNS**

(A) The expression of nuclear localized mCherry (mCherry.nls) driven by the *Uba5^{T2A-Gal4}* allele (*Uba5^{T2A-Gal4} > mCherry.nls*) shows that *Uba5* is expressed in L3 larvae and adult flies.

(B and C) The larval CNS and adult brain of *Uba5^{T2A-Gal4} > mCherry.nls* animals were immunostained with a neuronal (Elav, Panel B) or glial marker (Repo, Panel C). Maximum projections of confocal z- stack images are shown. Single plane, high magnification images of the regions indicated by the dashed squares are shown on the right to visualize the colocalizations between mCherry and the immunostaining signals. Arrows indicate cells that colocalize both markers. Scale bar, 100 μ m.

DEE44-associated variants exhibit different rescuing abilities in flies

Next, we sought to evaluate the function of *UBA5* variants using the humanized fly model (Bellen & Yamamoto, 2015). We expressed reference or variant *UBA5* cDNA and DEE44-associated *UBA5* variants using *Uba5^{T2A-Gal4}* and measured phenotypes including survival rate, developmental timing, lifespan, locomotor activity, and seizure-like activity following mechanical stimulation in *Uba5^{T2A-Gal4}* hemizygous male flies. The variants we tested include all previously reported variants (Arnadottir *et al.*, 2017; Briere *et al.*, 2021; Colin *et al.*, 2016; Daida *et al.*, 2018; Low *et al.*, 2019; Mignon-Ravix *et al.*, 2018; Muona *et al.*, 2016), as well as a novel variant from an individual we report in this study. This individual has compound heterozygous variants in *UBA5*, p.Met57Val and p.Gln312Leu (Table S3), and presents with hypotonia, generalized dystonia, lower extremity spasticity, global developmental delay, and failure to thrive. However, this individual is so far seizure free. Further clinical details of the individual are summarized in Supplemental Information.

We first assessed the ability of the variants to rescue the lethality of *Uba5^{T2A-Gal4}* mutants. A synthetic enzyme-dead *UBA5* mutant p.Cys250Ala failed to rescue lethality (Figure 3A). Similarly, four DEE44-associated variants (p.Arg55His, p.Gly168Glu, p.Leu254Pro, p.Cys303Arg) failed to rescue the lethality, indicating that they are severe LoF. Two variants (p.Tyr53Phe, p.Met57Val) partially rescued and are therefore likely hypomorphic alleles (Figure 3A). However, six variants (p.Arg72Cys, p.Val260Met, p.Gln312Leu, p.Alc371Thr, p.Asp389Gly, p.Asp389Tyr) fully rescued lethality, suggesting they are mild LoF or do not affect protein function. We then raised the flies at 18 °C as this causes a decrease in GAL4 activity and hence lowers the expression level of *UBA5*. At this temperature, three variants (p.Tyr53Phe, p.Met57Val, p.Val260Met) partially rescued lethality. Based on these results, we stratified the variants into three groups according to the activity of rescuing lethality: Group I, full rescue; Group II, partial rescue; Group III, failure to rescue (Table 1, Group I was further divided into IA and IB according to the other phenotypes described below).

The variants that survive to adults were next tested for the time it takes for animals to eclose as adults, and lifespan. The variants in Group II exhibited significant developmental delay as well as a shortened lifespan, showing that they are partial LoF (Figures 3B and 3C). In contrast, some variants in Group I (Group 1A: p.Alc371Thr, p.Asp389Gly, and p.Asp389Tyr) caused neither defect. Other Group I variants (Group 1B: p.Arg72Cys and p.Gln312Leu) caused a shortened lifespan but did not affect the timing of development (Figures 3B and 3C), indicating that they are also partial LoF variants but could cause milder defects than Group II variants.

To determine if the flies display features that are associated with dysfunction of the nervous system, we measured locomotor activity using a climbing assay and assessed susceptibility to seizures using a bang sensitivity assay (Song & Tanouye, 2008). Flies with variants in Groups IB and II displayed reduced climbing activity at Day 7 and more severe defects by Day 30, showing a progressive worsening of the defects (Figure 3D). Moreover, the variants in Group II exhibited a bang-sensitive phenotype by displaying seizure-like behavior and paralysis following mechanical stimulation (Figure 3E). However, the Group IA variants displayed neither a climbing defect nor bang sensitivity (Figures 3D and 3E). These results are consistent with our classification of variants based on other assays: Group IA, no obvious LoF or benign; Groups IB and II, intermediate LoF; and Group III, severe LoF.

Structural analysis of *UBA5* variants

In order to link our findings in the fly model with functional changes in *UBA5*, we first analyzed the potential structural changes caused by the *UBA5* variants. Extensive structural analyses have been performed on *UBA5*, including its ability to bind ATP and homodimerize within the adenylation domain, its interaction with UFM1 in the process of activation, and its engagement of

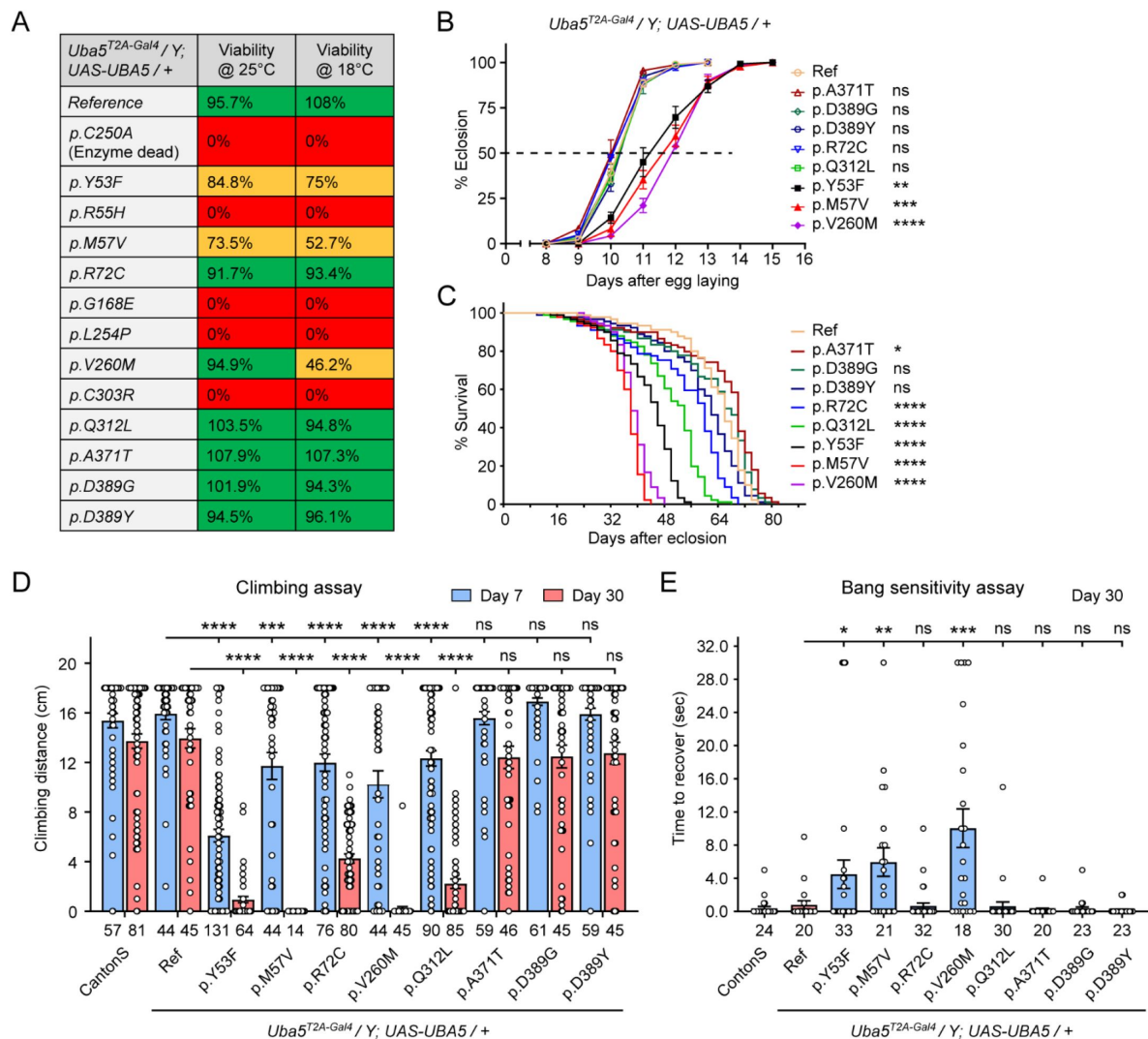


Figure 3.

DEE4-associated variants exhibit different rescuing abilities in flies

(A) The DEE4-associated *UBA5* variants rescued the lethality of *Uba5^{T2A-Gal4}/FM7* females were crossed with *UAS-UBA5* males and the viability of *Uba5^{T2A-Gal4}/Y; UAS-UBA5/+* progenies were measured by Mendelian ratio and indicated by color codes: red, zero viability; yellow, partial viability (< 90% of expected number); green, full viability (90% and above).

(B) Three variants caused developmental delay in *Uba5^{T2A-Gal4}/Y; UAS-UBA5/+* flies. The embryos were collected within 6 hours and the number of eclosed adult flies was counted at the same time every day. Three replicates were performed in each group.

(C) Five variants caused reduced lifespan in *Uba5^{T2A-Gal4}/Y; UAS-UBA5/+* flies.

(D) Five variants caused progressive climbing defects in *Uba5^{T2A-Gal4}/Y; UAS-UBA5/+* flies. Flies were tested on Day 7 and Day 30. The climbing activity of *CantonS* wildtype flies is shown as reference. Numbers of animals (n values) in each group are indicated under the bars.

(E) Three variants caused a bang-sensitive phenotype in *Uba5^{T2A-Gal4}/Y; UAS-UBA5/+* flies. Flies were tested on Day 30. The bang-sensitivity of *CantonS* wildtype flies is shown as reference. Numbers of animals (n values) in each group are indicated under the bars.

(B-E) Flies were cultured under 25 °C. The results of DEE4 variant-expressing flies are compared with the result of reference *UBA5*-expressing flies. Results are presented as means ± SEM. Statistical analyses were performed via two-sided, unpaired Student's t-test. ns, not significant;

*p<0.05; **p<0.01; ***p<0.001; ****p<0.0001.

	Variants	Survival rate	Dev. delay	Lifespan	Climbing defects	Bang sensitivity
Group IA	p.Ala371Thr	Normal	No	Normal	No	No
	p.Asp389Gly	Normal	No	Normal	No	No
	p.Asp389Tyr	Normal	No	Normal	No	No
Group IB	p.Arg72Cys	Normal	No	Decreased	Yes	No
	p.Gln312Leu	Normal	No	Decreased	Yes	No
Group II	p.Tyr53Phe	Decreased	Yes	Decreased	Yes	Yes
	p.Met57Val	Decreased	Yes	Decreased	Yes	Yes
	p.Val260Met	Decreased	Yes	Decreased	Yes	Yes
Group III	p.Arg55His	Lethal	N.A.	N.A.	N.A.	N.A.
	p.Gly168Glu	Lethal	N.A.	N.A.	N.A.	N.A.
	p.Lys254Pro	Lethal	N.A.	N.A.	N.A.	N.A.
	p.Cys303Arg	Lethal	N.A.	N.A.	N.A.	N.A.

Table 1.

Summary of phenotypes of humanized flies expressing *UBA5* variants

UFC1 prior to UFM1 transthiolation (Bacik *et al.*, 2010 [↗](#); Kumar *et al.*, 2021 [↗](#); Oweis *et al.*, 2016 [↗](#); Padala *et al.*, 2017 [↗](#); Soudah *et al.*, 2019 [↗](#); Wesch *et al.*, 2021 [↗](#)). This structural detail of UBA5 function offers a unique opportunity to visualize the location of variants and categorize their predicted effects. We compiled a series of UBA5 structures to create a composite model that illustrates a) UBA5 homodimerization, b) ATP coordination, c) UFM1 binding, and d) UFC1 binding (Figure 4A [↗](#)). Focusing on the UFM1 C-terminal Gly and the active site Cys residues of UBA5 and UFC1, the movements that occur during UFM1 activation and transthiolation can be mapped (Figure 4A [↗](#), yellow spheres).

With this structural model as a basis, we highlighted the location of all UBA5 variants (Figure 4A [↗](#), red spheres). Variants at positions Asp389 and Ala371 lie outside of the regions with determined structure, so their locations are modeled based on all available data. All Group IA variants localize in proximity of the UBS in protein sequence. The p.Asp389Gly and p.Asp389Tyr variants affect Asp389 which is two amino acids upstream of the structurally-resolved UBS. For p.Ala371Thr, although there is no structure of this region, previous biochemical and crosslinking data have demonstrated its proximity to the UFC1 active site (Kumar *et al.*, 2021 [↗](#)). Four variants, p.Tyr53Phe, p.Arg55His, p.Met57Val, and p.Arg72Cys, affect residues near the ATP-binding site (Figure 4B [↗](#)). The side chain of Arg55 makes direct contacts to the bound ATP, while Met57 and Tyr53 make secondary contacts behind this site, and Arg72 makes more distant tertiary contacts. Substitutions at these positions, therefore, may affect the affinity of UBA5 toward ATP. Residue Leu254 is four amino acids downstream of the active site Cys250, contained within a loop region that must undergo conformational changes to support UFM1 activation and subsequent transthiolation (Figures 4A [↗](#) and 4B [↗](#)). The Pro substitution within the p.Leu254Pro variant may constrain the required flexibility of the Cys250 loop, thus impacting ATP binding, UFM1 activation, and UFM1 transthiolation. Val260 is buried within the UBA5 homodimeric interface, opposing residue Val260 of the second protomer (Figure 4B [↗](#)). The increased size of the p.Val260Met variant may cause a steric clash that reduces UBA5 dimerization, which would decrease ATP binding, UFM1 activation, and UFM1 transthiolation as a result. Positions Cys303 and Gly168 are fully buried, making structural contacts to support the fold of the adenylation domain (Figure 4C [↗](#)). The increased size and charge associated with the p.Cys303Arg and p.Gly168Glu variants would most likely cause significant defects in UBA5 folding and stability. Lastly, the site of the novel p.Gln312Leu variant reported here is partially buried, making structural contacts to a loop region underneath the UFM1-binding site, and thus substitutions at this site may also cause structural instability (Figure 4C [↗](#)).

Generation and characterization of purified UBA5 variant proteins

To determine the functional capacity of the UBA5 variants, we expressed and purified reference and variant UBA5 proteins from *Escherichia coli* for biochemical assays. Two severe LoF (Group III) variants p.Gly168Glu and p.Cys303Arg were insoluble in the protein purification process, indicating that the variants influence the stability and/or folding of these proteins. We were able to obtain pure and homogeneous samples of all other UBA5 constructs (Figure 5A [↗](#)). For our first measure of UBA5 function, we measured the effects of each variant on protein stability using a thermal shift assay. Under our assay conditions, reference UBA5 demonstrated a melting temperature (T_m) of 46 °C. While most UBA5 variants exhibited little-to-no change in T_m , several showed a subtle destabilization by ≥ 1 °C, including p.Arg72Cys, p.Lys254Pro, p.Val260Met, and p.Ala371Thr (Figure 5B [↗](#)). Interestingly, the Group IB variant p.Gln312Leu exhibited a minor unfolding at 36 °C before fully melting at 48 °C. This could indicate destabilization in the local structure surrounding the Gln312Leu substitution, while leaving the remaining protein structure intact.

Ligand binding can stabilize protein structure and lead to a shift in T_m toward higher temperatures. This has been shown previously in the case of UBA5 binding to ATP, where it was determined to interact with a K_D of ~ 700 μ M (Mashahreh *et al.*, 2018 [↗](#)). The ATP-dependent stabilization of UBA5 allowed us to assess mutational effects on ATP binding using the thermal

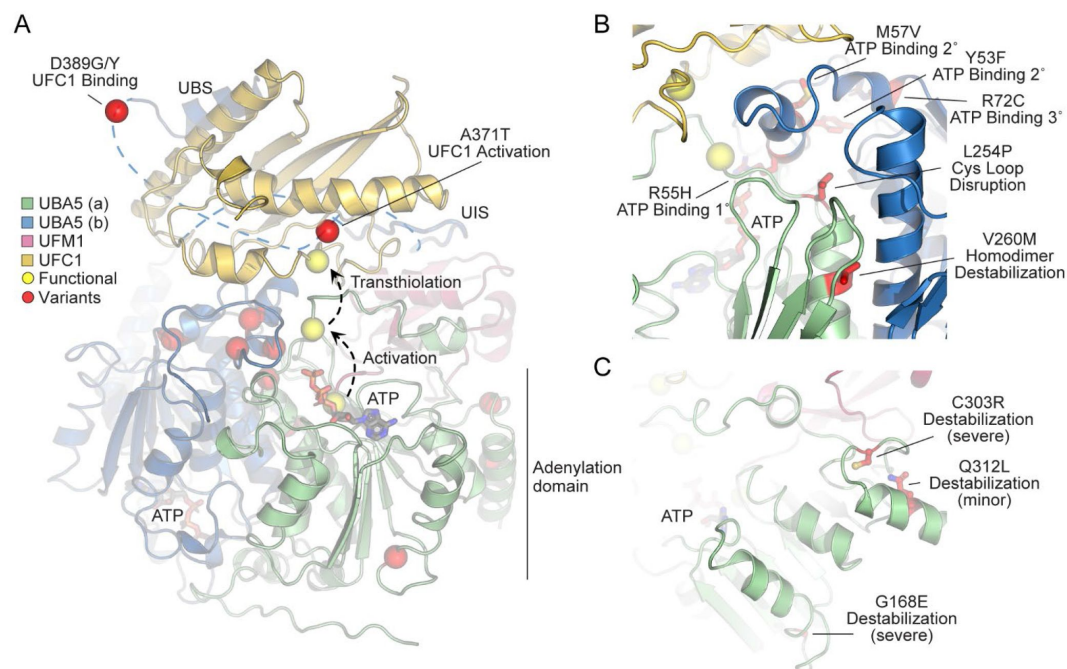


Figure 4.

Structural analysis of UBA5 variants

(A) Composite model of a UBA5 homodimer (green and blue) bound to ATP (grey sticks), UFM1 (magenta), and UFC1 (gold). The model was built using a series of UBA5 complex structures with UFM1 and UFC1 (PDB 6H77, 7NW1, and a modelled UBA5:UFC1 complex(Kumar *et al.*, 2021; Soudah *et al.*, 2019)). Functional residues comprising the active site cysteines of UBA5 and UFC1, as well as the C-terminus of UFM1 are shown in yellow spheres. UBA5 variants are shown in red spheres and are labeled with their predicted structural effects.

(B) Close-up view of variants (red sticks) within the UBA5 active site (yellow sphere), ATP binding pocket, and homodimerization interface.

(C) Close-up view of variants (red sticks) expected to impact UBA5 protein stability (results shown in the following figures).

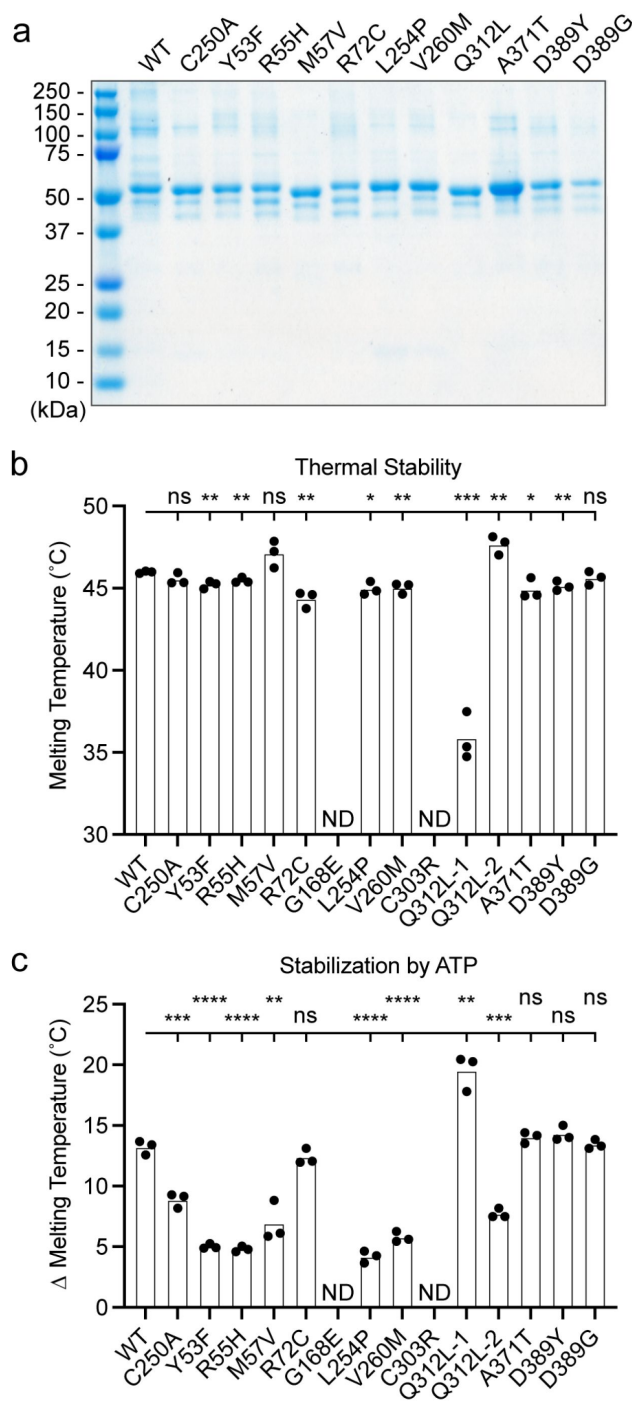


Figure 5.

Preparation and stability of UBA5 variant proteins

(A) Coomassie-stained SDS-PAGE analysis of all purified UBA5 variant proteins.

(B) Thermal shift assay measuring the melting temperature (T_m) of all UBA5 variant proteins, with the exception of p.Gly168Glu and p.Cys303Arg which could not be produced. The p.Gln312Leu variant displayed two melting curves. Experiments were performed in triplicate over three biological replicates.

(C) Change in melting temperature for all UBA5 variants in the presence of 5 mM ATP. Upon ATP addition, the p.Gln312Leu variant transitioned to a single melting curve. Experiments were performed in triplicate over three biological replicates.

(B-C) Statistical analyses were performed via unpaired Student's t-test. ns, not significant; * $p < 0.05$;

** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

shift assay. Whereas addition of 5 mM ATP led to a strong, 13 °C shift in the T_m of reference UBA5, many of the variants exhibited much weaker stabilization, indicative of a diminished capacity to bind ATP (**Figure 5C** [↗](#)). The other two Group III variants and one Group II variant p.Tyr53Phe showed the strongest defect, with only 4-5 °C shifts in T_m upon addition of ATP. The Group II variants p.Met57Val and p.Val260Met as well as one Group IB variant p.Gln312Leu showed a milder effect with a 6-8 °C shift in T_m . One Group IB variant p.Arg72Cys and all Group IA variants showed similar ATP-dependent stabilization to reference UBA5. Unlike the melting trend observed in the absence of ATP, in the presence of ATP the p.Gln312Leu variant displayed a single unfolding profile, suggesting that ATP binding corrected the local instability caused by the substitution.

These results show that not all tested variants strongly affect the stability of UBA5 protein. However, many variants impair the ATP binding capability of the protein. The levels of impairment correlate well with the phenotypic observations *in vivo* (**Table 1** [↗](#) and 2), suggesting that the defect in ATP binding is a major contributor to the LoF associated with the variants. Consistent with their severe LoF *in vivo*, variants p.Gly168Glu and p.Cys303Arg exhibited impaired protein folding and could not be included in our *in vitro* analyses.

Visualizing mutational effects on UFM1 activation and transthiolation

Previous functional characterization of UBA5 activity has relied upon gel-based assays that often lack kinetic information and are less sensitive to subtle changes. We sought to address this problem by developing a real-time, fluorescence polarization (FP) assay for UBA5 activity based upon a method we coined “UbiReal” (Franklin & Pruneda, 2019 [↗](#), 2023 [↗](#)). The approach leverages the large changes in molecular weight that occur as UFM1 is activated by UBA5 and transferred to UFC1 (**Figure 6A** [↗](#)), which are read out as changes in FP of fluorescently-labeled UFM1. Indeed, upon addition of UBA5 we observed a large shift in FP of Alexa488-labeled UFM1, which reached a plateau over the course of ~20 minutes under these conditions (**Figure 6B** [↗](#)). Addition of UFC1 to the reaction caused a concomitant downward shift in FP that reached a new plateau within ~5 minutes. To validate the molecular species observed in this assay, we ran samples from each stage of the reaction on non-reducing SDS-PAGE and were able to visualize free UFM1, UBA5~UFM1, and UFC1~UFM1 as predicted (**Figure 6C** [↗](#)).

With the UFM1 UbiReal assay in hand, we proceeded to assess the effects of UBA5 variant on the first step of the reaction: UFM1 activation. As anticipated, addition of reference UBA5 caused a rapid shift in FP over time, whereas the enzyme-dead p.Cys250Ala variant remained at baseline (**Figure 6D** [↗](#)). We quantified these kinetic data with Area Under the Curve (AUC) analysis using data collected just before addition of UBA5 to establish a baseline. The panel of UBA5 variants displayed a wide range of effects. The two Group III variants p.Arg55His and p.Leu254Pro remained near the baseline, indicating a severe impairment in UFM1-activating function. An intermediate, statistically significant effect was observed with the p.Val260Met variant (Group II), while the remaining variants showed mild or, in the case of p.Ala371Thr (Group IA), no decrease in the rate of UFM1 activation (**Figure 6E** [↗](#)). Similar trends were observed at both 22 °C and 37 °C, though interestingly the effect of p.Val260Met substitution was less severe at higher temperature (**Figure 6F** [↗](#)). The results show that a defect in UFM1 activation contributes to the LoF in all variants except for p.Ala371Thr. The severity of LoF in UFM1 activation correlates with our phenotypic observations *in vivo* (**Table 1** [↗](#) and 2 [↗](#)).

Having observed defects in UFM1 activation for many of the UBA5 variants, we next analyzed those that exhibited mild or no effect for their ability to complete the second enzymatic role of UBA5: UFM1 transthiolation onto UFC1. After forming the activated UBA5~UFM1 intermediates, we added UFC1 to the reactions and monitored the decay in FP over time (**Figure 6G** [↗](#)). Though many of the UBA5 variants showed similar trends for transthiolation, the p.Ala371Thr variant immediately stood out for having no effect on UFM1 activation (**Figures 6D** [↗](#)-**6F** [↗](#)), but a greatly

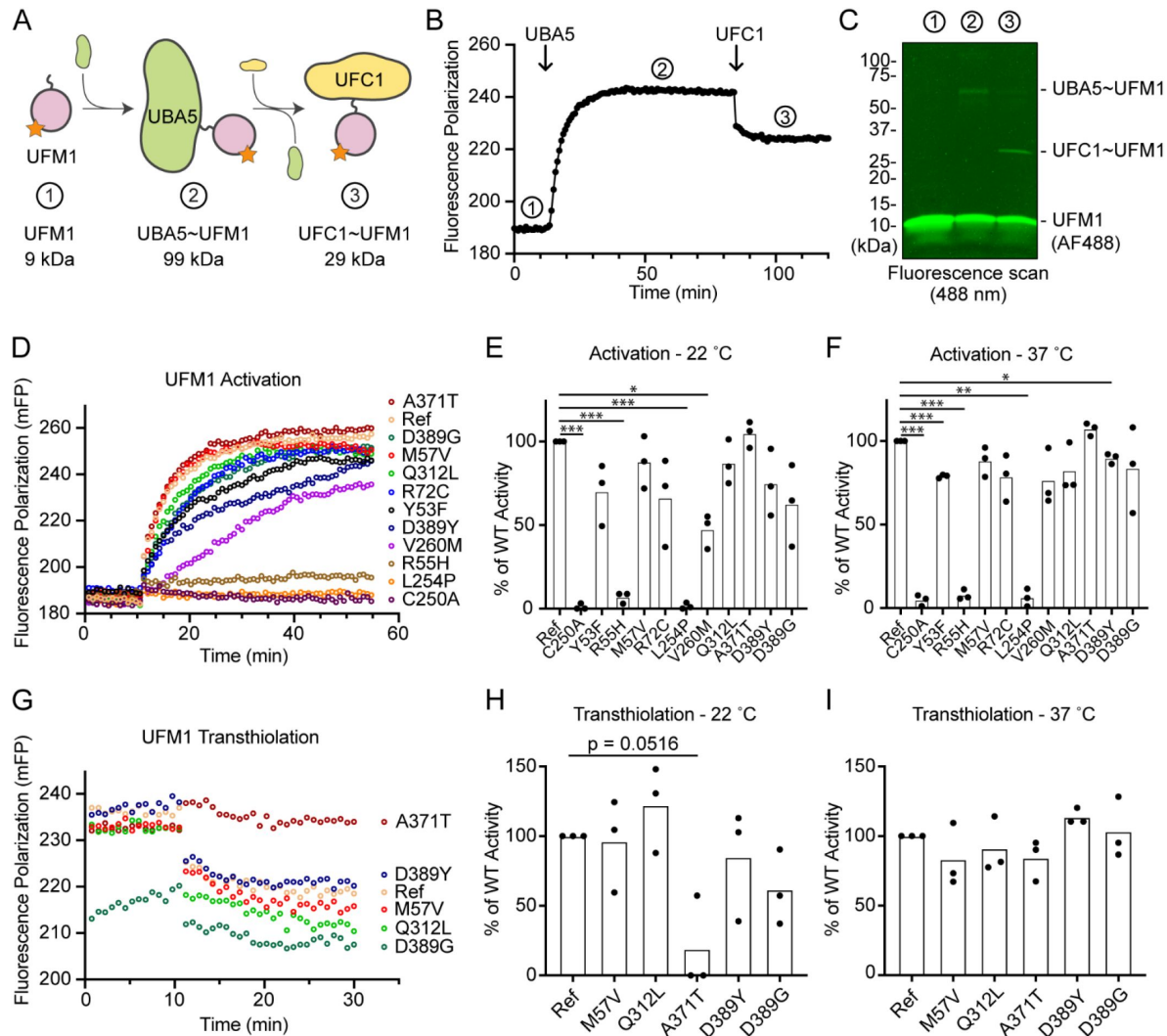


Figure 6.

Measuring UFM1 activation and transthiolation with UbiReal

(A) Cartoon schematic illustrating the complexes formed during UFM1 activation and transthiolation, as well as their expected molecular weights. The fluorescent group attached to UFM1 is denoted by an orange star.

(B) Proof-of-concept UbiReal assay monitoring the fluorescence polarization (FP) of Alexa488- labeled UFM1 alone (species 1), following addition of UBA5 (species 2), and following addition of UFC1 (species 3).

(C) Fluorescence scan of samples described in (B) separated by SDS-PAGE, illustrating the formation of activated UFM1 complexes.

(D) UbiReal assay tracking UFM1 activation by reference and variant UBA5 proteins over time.

(E) Area Under the Curve quantification of UFM1 activation performed at 22 °C. Experiments were performed in triplicate over three biological replicates. Statistical analyses were performed using a Welch's t test with comparison to the reference UBA5 data.

(F) As in (E), for reactions performed at 37 °C.

(G) UbiReal assay tracking UFM1 transthiolation for reference UBA5 and variants that showed little or no effect on activation.

(H) Area Under the Curve quantification of UFM1 transthiolation performed at 22 °C. Experiments were performed in triplicate over three biological replicates. Statistical analyses were performed using a Welch's t test with comparison to the reference UBA5 data.

(I) As in (H), for reactions performed at 37 °C.

(E-F, H-I) Statistical analyses were performed via Welch's t-test. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

impaired ability to transfer UFM1 onto UFC1 (**Figure 6G**). We quantified the kinetic data using AUC analysis of the inverted curve and observed a remarkable defect in the ability of the p.Ala371Thr variant to catalyze UFM1 transthiolation (**Figure 6H**). Interestingly, this defect is much more pronounced at 22 °C than at 37°C (**Figure 6I**). These results suggest that aside from a minor decrease in UBA5 stability (**Figure 5B**), UFM1 transthiolation is the only possible defect caused by the p.Ala371Thr variant. Transthiolation could be defective in other variants as well, such as p.Leu254Pro (Group III), but this effect is likely overshadowed by upstream effects on UBA5 stability, ATP binding, and/or UFM1 activation.

Discussion

In this study, we assessed the strength and properties of variants identified in individuals with DEE44 using a humanization strategy in fruit flies. Germline knockout of *Uba5* causes embryonic lethality in both flies (this study) and mice (Tatsumi *et al.*, 2011), and no individuals have been identified with biallelic null variants in humans. The lethality of *Uba5* knockout mice is caused by hematopoietic defects (Tatsumi *et al.*, 2011), however, the clinical presentations in DEE44 patients are predominantly related to the central nervous system (Arnadottir *et al.*, 2017; Briere *et al.*, 2021; Colin *et al.*, 2016; Daida *et al.*, 2018; Low *et al.*, 2019; Mignon-Ravix *et al.*, 2018; Muona *et al.*, 2016). These findings suggest that DEE44 is caused by partial LoF of *UBA5*, and that *Uba5* knockout models are not suitable to study disease pathogenesis. We generated a *Uba5*^{T2A-Gal4} allele that corresponds to a severe LoF allele but also leads to expression of GAL4 in the same spatial and temporal expression pattern of *Uba5*, which can then drive expression of the human *UBA5* cDNA (**Figure 1D**). Expression of reference *UBA5* cDNA fully rescues the loss of *Uba5*, showing that the proteins are functionally similar. This allowed us to assess the properties of the known *UBA5* variants and establish an allelic series *in vivo*. We measured an array of phenotypes in flies that relate to the phenotypes observed in affected individuals, including developmental delay, motor defects, and bang sensitivity (seizure-like behavior). Based on the *in vivo* data we establish groups of variants with different strengths from least severe to most severe: Groups IA, IB, II, and III (**Table 1**). To facilitate the discussion, hereafter we also refer to the deletion, nonsense, frameshift, and splicing variants observed in affected individuals as Group IV variants, although they were not functionally tested in this study.

To correlate the allelic strength with the functional defects caused by the variants, we first examined the stability of *UBA5* variants and assessed their activity in three key steps involved in *UBA5* enzyme function: ATP binding, UFM1 activation, and UFM1 transthiolation. Two variants were not tested due to instability during protein purification, while all remaining tested variants exhibited defects in at least one assay, suggesting that they cause protein LoF (**Table 2**).

Group IA includes three variants, p.Asp389Gly, p.Asp389Tyr, and p.Ala371Thr. The three variants fully rescued the defects caused by the loss of *Uba5* in flies, indicating that they do not affect *UBA5* function or only cause a mild LoF of *UBA5*. The biochemical assays show that p.Asp389Gly and p.Asp389Tyr only cause mild, but statistically insignificant defects in UFM1 activation, consistent with the complete rescue of the loss of *Uba5* in humanized flies (**Figure 3**). The other variant, p.Ala371Thr, has a minor allele frequency (MAF) of 0.0019 (517/274744 alleles) in general population and is more frequent in Finnish population (MAF=0.0059, 149/24996 alleles) in gnomAD v2.1.1. It is also the most commonly observed variant in affected individuals (Table S1). Individuals homozygous for this variant have been identified in the Finnish and Icelandic population but they do not present with obvious symptoms related to DEE44 (Arnadottir *et al.*, 2017; Colin *et al.*, 2016; Muona *et al.*, 2016), consistent with our observations in flies. Interestingly, although the biochemical assays showed no dramatic effect of Ala371Thr on *UBA5* stability, ATP binding, or UFM1 activation, the transthiolation of UFM1 onto UFC1 is impaired. While it may seem intuitive that defective UFM1 activation or transthiolation would be equally detrimental, formation of the activated *UBA5*–UFM1 intermediate is the rate-limiting step of the

	Variants	Thermal stability	ATP binding defect***	UFM1 activation	UFM1 transthiolation
Group IA	p.Ala371Thr	Decreased	No defect	Normal	Decreased
	p.Asp389Gly	Normal	No defect	Decreased	Decreased
	p.Asp389Tyr	Normal	No defect	Decreased	Normal
Group IB	p.Arg72Cys	Decreased	No defect	Decreased	Normal
	p.Gln312Leu	Local destabilization*	No defect	Normal	Normal
Group II	p.Tyr53Phe	Normal	Strong	Decreased	N.A.
	p.Met57Val	Normal	Intermediate	Normal	Normal
	p.Val260Met	Decreased	Intermediate	Decreased	N.A.
Group III	p.Arg55His	Normal	Strong	Near baseline	N.A.
	p.Gly168Glu	N.A.**	N.A.	N.A.	N.A.
	p.Lys254Pro	Decreased	Strong	Near baseline	N.A.
	p.Cys303Arg	N.A.**	N.A.	N.A.	N.A.

* See Results and Figure 5B

** Insoluble in protein purification

*** Strong, 4-5 °C in T_m shift; intermediate, 6-8 °C in T_m shift. Reference UBA5 shows 13 °C in T_m shift upon ATP addition.

Table 2.

Summary of protein stability and functions of UBA5 variants

reaction and hence more sensitive to perturbations (Gavin *et al.*, 2014). Importantly, the defect is observed at 22 °C but not at 37 °C *in vitro*, indicating that p.Ala371Thr is a very weak allele, consistent with all the *in vivo* and human genetics data.

Groups IB and II include variants that have an intermediate effect on the protein function *in vivo*. They rescued the lethality of *Uba5* mutant flies, but cause phenotypes of various levels of severity in adult flies. In biochemical assays, Group II variants exhibit a decreased capacity to bind ATP and a mild loss in the ability to activate UFM1, though the limitations of our assay precluded statistically significant effects among several variants. In Group IB, the p.Arg72Cys only causes a mild defect in UFM1 activation, consistent with it being near but not directly involved in ATP binding. The novel Group 1B variant reported herein, p.Gln312Leu, exhibited virtually no biochemical phenotype aside from signs of local instability in the UBA5 structure, which is stabilized in the presence of ATP. Among the sites of Group IB and II variants, only the Val260 residue lies at the homodimeric interface while no others lie immediately at a key interface for UBA5 function. This is consistent with p.Val260Met being the only variant among this set that exhibited severe activity defects *in vitro*. Despite this, all Groups IB and II variants caused phenotypes in flies. It is possible that the subtle effects of these substitutions are exacerbated in certain cellular conditions, such as ER stress.

Group III variants failed to rescue the lethality of the *Uba5* mutants, suggesting that they correspond to severe LoF alleles. This group includes four variants, p.Arg55His, p.Gly168Glu, p.Leu254Pro, and p.Cys303Arg. Two of the affected sites, Gly168 and Cys303, are buried in the UBA5 structure. Interestingly, neither of these variants are soluble when produced in *E. coli*, indicating compromised protein folding. The two remaining variants, p.Arg55His and p.Leu254Pro are in very close proximity of the UBA5 active site (Figure 4B) and may affect ATP binding and cause decreased conformational dynamics of the active site Cys. Both variants show a diminished capacity to bind ATP, and are incapable of activating UFM1, consistent with the observations that they are very severe LoF alleles in the fly. Hence, in Group III two alleles severely disrupt UBA5 protein stability while two others affect enzyme catalysis.

Using our variant classification, we retrospectively analyzed the allelic combinations in reported DEE44 cases. The most severely affected individual is homozygous for a Group II variant p.Tyr53Phe. However, this individual was from a consanguineous family so other variants may correspond to the phenotypic presentation of this individual (Cabrera-Serrano *et al.*, 2020). Most (21/25) individuals are compound heterozygous for one allele from Group IA or IB and another allele from Group III or IV (Table S1). This strongly suggests that the pairing of a mild LoF with a severe

LoF allele is required to allow individuals to survive and manifest the disease. However, two individuals from a previous report (IA/II) and this study (IB/II) show that the disease is also associated with a combination of two partial LoF alleles (Table S1). Finally, no affected individual is free of alleles from Group II/III/IV, indicating that combinations of IA/IB alleles may not cause disease. This is also supported by the observation that homozygous p.Ala371Thr (Group IA) individuals are not affected (see above) (Arnadottir *et al.*, 2017; Colin *et al.*, 2016; Muona *et al.*, 2016). Our results provide compelling evidence for the interpretation of existing and future variants as well as the prediction of pathogenicity of allelic combinations in clinical genetic analyses, especially considering the very limited number of reported individuals and the partial LoF mechanism of the disease.

Three other genes in the UFMylation pathway are associated with diseases that share symptoms with DEE44. Variants in *UFSP2* (OMIM: #611482) cause another DEE (DEE106, OMIM: #620028) (Ni *et al.*, 2021). *UFM1* (OMIM: #610553) is associated with hypomyelinating leukodystrophy 14 (HLD14, OMIM: #617899) (Hamilton *et al.*, 2017; Nahorski *et al.*, 2018). Variants in *UFC1* (OMIM: #610554) cause a neurodevelopmental disorder with spasticity and poor growth (NEDSG, OMIM:

#618076) (Nahorski *et al.*, 2018 [DOI](#)). All these disorders cause global developmental delay, hypotonia, spasticity, seizures, delayed myelination, and microcephaly, consistent with them sharing a similar etiology. The UbiReal system developed herein can be easily adapted to test the variants in these other UFMylation genes in future work. In addition, given that the genes are also highly conserved in flies, the allelic strengths of the variants in these genes could also be established *in vivo* using our fruit fly model.

Material and Methods

Human genetics

The proband was recruited through the Doernbecher Children's Hospital and informed consent was obtained from legal guardians of the proband. The human study was approved by the Institutional Review Board at Oregon Health & Science University. The legal guardians of the proband consent to have the results of this research work published.

Trio exome sequencing was conducted by GeneDx using DNA extracted from blood. DNA was enriched using a proprietary capture system developed by GeneDx for next-generation sequencing. The enriched targets were simultaneously sequenced with paired-end reads on an Illumina platform. Bi-directional sequence reads were assembled and aligned to Human Genome Sequencing Center (HGSC) build 37, human reference genome 19. Reported variants were confirmed, if necessary, by an appropriate orthogonal method.

Drosophila strains and genetics

All fruit fly strains used in this study were cultured using standard fly food in a 25°C incubator unless a different culturing temperature was specifically indicated. The *Uba5*^{KO} mutant and the human *UAS-UBA5* transgenic fly lines were generated in the Bellen lab (for methods, see below). The *Uba5*^{T2A-Gal4} (#78928), *UAS-mCherry.nls* (#38424), *UAS-FLP* (#4540), *Uba5*^{GR} (#30359), *da-Gal4* (#5460), *Act-Gal4* (#4414), *elav-Gal4* (#8765), and *repo-Gal4* (#7415) lines were obtained from the Bloomington Drosophila Stock Center (BDSC).

Generation of *Uba5*^{KO} allele

The *Uba5*^{KO} allele was generated using CRISPR/Cas9 genome engineering technology as previously described (Port *et al.*, 2014 [DOI](#)). A TKO transgenic line expressing a *Uba5*-targeting single guide RNA (sgRNA) is available from the BDSC (BDSC #81448) (Zirin *et al.*, 2020 [DOI](#)). The sgRNA (CAATCCGTACAGCCGCCTGA) targets the coding region in the Exon 1 of the only *Uba5* transcript.

To generate indel variants, the TKO flies were crossed to *nos-Cas9* transgenic flies (BDSC #78781) and then the first generation (F1) female progenies carrying both sgRNA and Cas9 were crossed with 1st chromosome balancer flies. Single F2 females were crossed with balancer flies again to establish ~20 individual stocks with potential indel variants. Due to the lethality of *Uba5* mutants, the stocks without unbalanced flies were screened for *Uba5* indel variant by genomic PCR and Sanger sequencing. One mutant line with NM_132494.3 (*Uba5*):c.164_174del (p.Arg55ProfsTer87) variant was isolated and designated as *Uba5*^{KO} allele in this study.

Generation of *UAS-UBA5* transgenic stocks

Human *UAS-UBA5* transgenic fly lines were generated as previously described (Harnish *et al.*, 2019 [DOI](#)). In brief, the human *UBA5* cDNA sequences were cloned into the pGW-UAS-HA.attB vector (Bischof *et al.*, 2013 [DOI](#)) using the Gateway Cloning system (Thermo Fisher) and validated by sequencing. The cDNA vectors were then injected into fly embryos and inserted into the VK37 (BDSC #24872) docking site by ϕ C31-mediated transgenesis (Venken *et al.*, 2006 [DOI](#)). The human

UBA5 cDNA clone corresponding to Genebank transcript NM_024818.6 was obtained from the Ultimate ORF Clones library (Thermo Fisher). The *UBA5* variants were introduced into the reference cDNA using Q5 site-directed mutagenesis (NEB) before the cDNA was cloned into the pGW-UAS-HA.attB vector.

Immunostaining and confocal microscopy

Larval and adult flies were dissected in 1X PBS and the larval CNS and adult brain tissues were processed for immunostaining. Briefly, the tissues were fixed in 4% paraformaldehyde followed by normal horse serum blocking and incubation in the primary antibody (Rat anti-Elav, Developmental Studies Hybridoma Bank (DSHB) #7E8A10, 1:500; Mouse anti-Repo, DSHB #8D12 1:50). Cy5-conjugated secondary antibodies were used to detect the primary antibodies. Samples were mounted on slides using RapidClear (SUNJin Lab) and the images were captured using a confocal microscope (Zeiss 710).

Drosophila lifespan assay

For the measurement of lifespan, freshly eclosed flies were collected in separate vials and maintained at 25°C. Flies were transferred every day to fresh food in the first six days and every other day afterward. Survival was determined during every transfer. The results are represented as Kaplan-Meier curves.

Drosophila behavioral assay

To measure negative geotaxis, flies were transferred to a clean vial for at least 20 minutes prior to the experiment. During the test, flies were tapped to the bottom of the vial and their negative geotaxis climbing ability was measured. In each measurement, flies were allowed to climb for 30 seconds, after which the climbing distances were measured (18 cm is maximum). To perform bang-sensitive paralytic analyses, adult flies were transferred to a clean vial and vortexed at maximum speed for 10 seconds, after which the time required for flies to stand on their feet was counted (30 seconds is maximum).

Protein expression and purification

The reference *UBA5* gene and UFM1 cloned into pET15b and UFC1 cloned into pET32a were kind gifts from R. Wiener (The Institute for Medical Research Israel-Canada). The *UBA5* p.Met57Val and p.Gln312Leu substitutions were cloned into this background by Quikchange PCR using Phusion DNA polymerase. All other *UBA5* variant substitutions were subcloned into pOPIN-B using the constructs described above as templates. All of these constructs encoded N-terminal His-tags, and were purified in a similar manner. After plasmid transformation into *E. coli* Rosetta (DE3) cells, cultures were grown at 37 °C in Luria Broth containing 35 µg/mL chloramphenicol and 50 µg/mL of kanamycin. Once an optical density (600 nm) between 0.4-0.6 was reached, cultures were cooled to 18°C and protein expression was induced with 0.5 mM IPTG. Cells were harvested by centrifugation after 24 hours of expression and resuspended in 50 mM NaPO₄, 500 mM NaCl, 2 mM β-mecaptoethanol, pH 8.0 (Buffer A). The cell pellet was then subjected to a freeze-thaw cycle before adding DNase, PMSF, lysozyme and SigmaFAST Protease Inhibitor Cocktail (MiliporeSigma) and allowed to incubate on ice for 30 min. The cell pellets were then lysed by either french press or sonication, depending on the volume to be lysed. Lysates were then centrifuged at 35,000 xg, and the clarified lysate was added to a column containing HisPur Cobalt affinity resin (ThermoFisher), allowed to bind for 10 min, and washed with 1 L of Buffer A + 10 mM Imidazole. Proteins were then eluted with 5 mL of Buffer A + 350 mM Imidazole in a stepwise manner for a total elution volume of 25 mL. Purity of the fractions were analyzed via SDS-PAGE and those with highest purity were pooled and dialyzed overnight into 25 mM Tris, 100 mM NaCl, 2 mM DTT, pH 8.0 (Buffer B) at 4°C. After 24 hrs of dialysis, *UBA5* proteins were further purified on a RESOURCE Q (Cytivia) anion exchange chromatography column equilibrated in Buffer B. The protein was eluted over a 20 column volume gradient against Buffer B + 1 M NaCl. Peak protein fractions were

pooled and concentrated using Amicon centrifugal filters (MiliporeSigma) before being applied to a HiLoad Superdex 75 16/600 pg size exclusion chromatography column (Cytiva) equilibrated in Buffer B. Following affinity purification, the His-tags of UFM1 and UFC1 were removed by TEV cleavage during overnight dialysis into Buffer B at 4 °C. Proteins were then concentrated using Amicon centrifugal filters and applied to a HiLoad Superdex 75 16/600 pg as above. Peak fractions were evaluated for purity via SDS-PAGE, pooled, and concentrated before being quantified by absorbance at 280 nm and flash frozen above 10x their working stock concentration. All protein samples were stored at -80 °C.

Fluorescence-based UBA5 activity assays

UFM1-Alexa 488 substrates were prepared using an Alexa Fluor 488 TFP ester (ThermoFisher). Labeling was performed at room temperature for 1 hr in 0.1 M sodium bicarbonate buffer at pH 7.5, which directs labeling toward the N-terminus. Following labeling, excess fluorophore was quenched with addition of 150 mM Tris pH 7.4 and separated by size exclusion chromatography on a HiLoad Superdex 75 16/600 pg as above. Transfer and activation of UFM1 onto UBA5 and further transthiolation to UFC1 was monitored by fluorescence polarization (FP) based on published methods from the ubiquitin system (Franklin & Pruneda, 2019 [DOI](#), 2023 [DOI](#)). FP was measured using a BMG LabTech CLARIOstar plate reader at an excitation wavelength of 482 nm, an LP 404 nm dichroic mirror, and an emission wavelength of 530 nm. Free UFM1 was used as a reference with a target FP of 190. All assays were performed in black Greiner 384-well small-volume HiBase, low protein-binding microplates. UFM1 and UBA5 stocks were prepared at 2X assay conditions in 25 mM NaPO₄, 150 mM NaCl, 10mM MgCl₂, pH 7.4 (Buffer C). UFM1 was prepared at 100 nM in Buffer C + 20 mM ATP (pH 7); UBA5 variants were prepared at 1 μM in Buffer C. UFC1 was prepared at 3 μM (10X assay concentration) in Buffer C. Final assay conditions in 20 μL volumes were 50 nM UFM1, 500 nM UBA5 variants, and 300 nM UFC1 in Buffer C + 10 mM ATP. FP data was first collected for the substrate only to establish a baseline before addition of UBA5 variants at 1:1 ratio to reach the described assay conditions. FP values were collected in 45-second intervals until the reference UBA5 readings plateaued, at which point UFC1 was added at 1:10 ratio to achieve final assay conditions. Reactions were performed in triplicate for each of three experimental replicates, both at 22 °C and 37 °C. AUC calculations were performed using Prism 9.5, with baseline values calculated from data collected prior to addition of UBA5/UFC1.

Gel-based UBA5 activation and transthiolation assay

Conditions for the gel-based assay were identical to those described above for the 22°C FP assays. Parallel reactions were prepared, one to be read out by FP using the CLARIOstar plate reader and the other was left in a low light environment at room temperature. After 15 minutes of establishing a baseline FP reading for UFM1 alone, a 20 μL sample was taken from the parallel reaction and quenched using non-reducing sample buffer. FP readings were paused and reference UBA5 was added to both reactions before continuing FP data collection. The FP values were allowed to plateau before another 20 μL sample was collected from the parallel reaction and quenched with non-reducing sample buffer. FP readings were then paused and UFC1 was added to both reactions before continuing FP data collection. The FP values were allowed to plateau before taking a final 20 μL sample from the parallel reaction and quenching with non-reducing sample buffer. Gel samples were run on a TGX 4-20% SDS-PAGE gradient gel (Bio-Rad). The resulting gel was imaged using a Sapphire Biomolecular Imager (Azure Biosystems). This experiment was performed in triplicate.

Thermal shift assay

The thermal shift assay was conducted in MicroAmp Fast 96-Well Reaction Plates (Applied Biosystems) with SYPRO Orange Protein Gel Stain (MiliporeSigma) using a QuantStudio 3 Real-Time PCR system (Applied Biosystems). Assays were performed in 20 μL volumes containing 5 μM UBA5 variants and 20X SYPRO dye (diluted from a 5000X stock) in 25 mM NaPO₄, 150 mM NaCl, 10

mM MgCl₂, pH 7.4 with or without 5 mM ATP. The protocol ramped temperature from 22 °C to 99°C over a gradient of 0.1 °C every 5 seconds, and fluorescence was monitored using an excitation wavelength of 580 ± 10 nm and an emission wavelength of 623 ± 14 nm.

Statistical analysis

Statistical analyses were carried out using the Student's unpaired two-tailed t test for comparison of two groups or the Welch's t test for data normalized to reference UBA5. Multiple comparisons within the group were tested against the corresponding control. Kaplan-Meier survival curves were analyzed using Gehan-Breslow-Wilcoxon test and log-rank test. Calculated p values of less than 0.05 were considered significant. All statistical analyses were performed using GraphPad Prism, version 9.5.0 (GraphPad Software).

Data Availability

All data produced in the present study are available upon reasonable request to the authors.

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Declaration of interests

The authors declare no competing interests.

Web resources

OMIM, <https://omim.org/>

DIOPT, https://www.flyrnai.org/cgi-bin/DRSC_orthologs.pl/ 

gnomAD, <https://gnomad.broadinstitute.org/> 

CADD, <https://cadd.gs.washington.edu/> 

SIFT, <https://sift.bii.a-star.edu.sg/> 

PolyPhen2, <http://genetics.bwh.harvard.edu/pph2/> 

MutationTaster, <https://www.mutationtaster.org/> 

PROVEAN, <http://provean.jcvi.org/> 

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Editors

Reviewing Editor

Murim Choi

Seoul National University, Korea, the Republic of

Reviewer #1 (Public Review):

Summary:

In this study, the authors generate a *Drosophila* model to assess disease-linked allelic variants in the UBA5 gene. In humans, variants in UBA5 have been associated with DEE44, characterized by developmental delay, seizures, and encephalopathy. Here, the authors set out to characterize the relationship between 12 disease-linked variants in UBA5 using a variety of assays in their *Drosophila* Uba5 model. They first show that human UBA5 can substitute all essential functions of the *Drosophila* Uba5 ortholog, and then assess phenotypes in flies expressing the various disease variants. Using these assays, the authors classify the alleles into mild, intermediate, and severe loss-of-function alleles. Further, the authors establish several important *in vitro* assays to determine the impacts of the disease alleles on Uba5 stability and function. Together, they find a relatively close correlation between *in vivo* and *in vitro* relationships between Uba5 alleles and establish a new *Drosophila* model to probe the etiology of Uba5-related disorders.

Strengths:

Overall, this is a convincing and well-executed study. There is clearly a need to assess disease-associated allelic variants to better understand human disorders, particularly for rare diseases, and this humanized fly model of Uba5 is a powerful system to rapidly evaluate variants and relationships to various phenotypes. The manuscript is well written, and the experiments are appropriately controlled.

Reviewer #2 (Public Review):

Relative simplicity and genetic accessibility of the fly brain make it a premier model system for studying the function of genes linked to various diseases in humans. Here, Pan et al. show that human UBA5, whose mutations cause developmental and epileptic encephalopathy, can functionally replace the fly homolog Uba5. The authors then systematically express in flies the different versions of the gene carrying clinically relevant SNPs and perform extensive phenotypic characterization such as survival rate, developmental timing, lifespan, locomotor and seizure activity, as well as *in vitro* biochemical characterization (stability, ATP binding, UFM-1 activation) of the corresponding recombinant proteins. The biochemical effects are well predicted by (or at least consistent with) the location of affected amino acids in the previously described Uba5 protein structure. Most strikingly, the severity of biochemical defects appears to closely track the severity of phenotypic defects observed *in vivo* in flies. While the paper does not provide many novel insights into the function of Uba5, it convincingly establishes the fly nervous system as a powerful model for future mechanistic studies.

One potential limitation is the design of the expression system in this work. Even though the authors state that "human cDNA is expressed under the control of the endogenous Uba5 enhancer and promoter", it is in fact the Gal4 gene that is expressed from the endogenous locus, meaning that the cDNA expression level would inevitably be amplified in comparison. The fact that different effects were observed when some experiments were performed at different temperatures (18 vs. 25) is also consistent with this. While I do not think this caveat weakens the conclusions of this paper, it may impact the interpretation of future experiments that use these tools, and thus should be clearly discussed in the paper. Especially considering the authors argue that most disease variants of UBA5 are partial loss-of-functions, the

amplification effect could potentially mask the phenotypes of milder hypomorphic alleles. If the authors could also show that the T2A-Gal4 expression pattern in the brain matches well with that of endogenous RNA or protein (e.g. using HCR-FISH or antibody), it would help to alleviate this concern.

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Variants in the UBA5 gene are associated with rare developmental and epileptic encephalopathy, DEE44. This research developed a system to assess *in vivo* and *in vitro* genotype-phenotype relationships between UBA5 allele series by humanized UBA5 fly models and biochemical activity assays. This study provides a basis for evaluating current and future individuals afflicted with this rare disease.

Strengths:

The authors developed a method to measure the enzymatic reaction activity of UBA5 mutants over time by applying the UbiReal method, which can monitor each reaction step of ubiquitination in real time using fluorescence polarization. They also classified fruit fly carrying humanized UBA5 variants into groups based on phenotype. They found a correlation between biochemical UBA5 activity and phenotype severity.

Weaknesses:

In the case of human DEE44, compound heterozygotes with both loss-of-function and hypomorphic forms (e.g., p.Ala371Thr, p.Asp389Gly, p.Asp389Tyr) may cause disease states. The presented models have failed to evaluate such cases.

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We thank the reviewer for pointing out this limitation.

Regarding the humanization strategy we used in the study, we agree that this is a binary system which may lead to overexpression of the target protein. However, as the

reviewer also points out, this temperature-sensitive system also enables us to flexibly adjust the expression level of the target protein, which is especially useful to study

partial LoF variants such as the UBA5 variants in this study. In our study we have successfully compared the relevant allelic strength of most of the variants, which

supports the use of our system in future studies. However, we do agree that the gene dosage effect could vary widely, so it is difficult to directly predict the effects of one variant in humans based upon results obtained in a model organism.

We agree with the reviewer that a masking effect may exist in our system due to its gene overexpression nature. However, we cannot conclude that this masking effect

really affects the interpretation of Group IA variants in our tests. The three variants are mild LoF, which is also supported by the biochemical assays. Hence, the variants may not cause any phenotype even when they are expressed at a physiological level.

Regarding the temporal and spatial expression pattern of the T2A-GAL4, the Bellen lab has generated T2A-GAL4 lines for more than 3,000 genes. The expression pattern of the vast majority of these GAL4 lines faithfully reflects the expression pattern of the endogenous

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We agree with the reviewer that our model did not reflect the situation of the individuals who are compound heterozygous for a Group IA variant (p.Ala371Thr, p.Asp389Gly, or p.Asp389Tyr) and a strong LoF variant. However, we argue that our results do show that the Group IA variants alone do not cause disease. As discussed in the manuscript, individuals homozygous for the p.Ala371Thr variant are healthy and do not present with obvious phenotype. This is consistent with our findings in flies, and shows that the p.Ala371Thr variant is a mild LoF variant.