Introducing Pitt-Hopkins syndrome-associated mutations of TCF4 to Drosophila daughterless

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ABSTRACT
Pitt-Hopkins syndrome (PTHS) is caused by haploinsufficiency of Transcription factor 4 (TCF4), one of the three human class I basic helix-loop-helix transcription factors called E-proteins. Drosophila has a single E-protein, Daughterless (Da), homologous to all three mammalian counterparts. Here we show that human TCF4 can rescue Da deficiency during fruit fly nervous system development. Overexpression of Da or TCF4 specifically in adult flies significantly decreases their survival rates, indicating that these factors are crucial even after development has been completed. We generated da transgenic fruit fly strains with corresponding missense mutations R578H, R580W, R582P and A614V found in TCF4 of PTHS patients and studied the impact of these mutations in vivo. Overexpression of wild type Da as well as human TCF4 in progenitor tissues induced ectopic sensory bristles and the rough eye phenotype. By contrast, overexpression of DaR580W and DaR582P that disrupt DNA binding reduced the number of bristles and induced the rough eye phenotype with partial lack of pigmentation, indicating that these act dominant negatively. Compared to the wild type, DaR578H and DaA614V were less potent in induction of ectopic bristles and the rough eye phenotype, respectively, suggesting that these are hypomorphic. All studied PTHS-associated mutations that we introduced into Da led to similar effects in vivo as the same mutations in TCF4 in vitro. Consequently, our Drosophila models of PTHS are applicable for further studies aiming to unravel the molecular mechanisms of this disorder.

KEY WORDS: Pitt-Hopkins syndrome, Drosophila melanogaster, Intellectual disability, Daughterless, bHLH, Nervous system

INTRODUCTION
Pitt-Hopkins syndrome (PTHS, OMIM #610954) is a rare human disorder characterised by severe developmental delay, autistic behaviours, absence of speech, distinct facial features, epilepsy, constipation and hyperventilation (Pitt and Hopkins, 1978; Whalen et al., 2012). PTHS is caused by haploinsufficiency of the Transcription factor 4 (TCF4, located at 18q21.1, OMIM #602272) (Amiel et al., 2007; Brockschmidt et al., 2007; Zweier et al., 2007). Large chromosomal deletions, partial gene deletions, frame shift, nonsense, splice site or missense mutations in the TCF4 gene have been found in PTHS patients. These mutations are usually sporadic, but in some cases children have inherited the mutant allele from a mosaic parent (reviewed in Sweatt, 2013). In vitro, PTHS-associated missense mutations result in hypomorphic, non-functional or dominant-negative TCF4 alleles (Sepp et al., 2012). It is unclear whether mutations causing PTHS impair development of the nervous system or functioning of the adult central nervous system (CNS), or both. In addition to PTHS, TCF4 is associated with several other human diseases such as schizophrenia, Fuchs’ corneal endothelial dystrophy and primary sclerosing cholangitis (reviewed by Forrest et al., 2014).

TCF4 (previously also known as ITF2, SEF2 or E2-2) belongs to the family of class I basic helix-loop-helix (bHLH) transcription factors (Massari and Murre, 2000) and should be distinguished from T-cell factor 4 (TCF4/TCF7L2) involved in the Wnt signalling pathway. The bHLH transcription factors form a large evolutionarily conserved family with important roles in numerous developmental processes including neurogenesis, myogenesis, haematopoiesis, and sex determination. The highly conserved bHLH region mediates interaction with other bHLH proteins and specific binding to DNA. Class I bHLH proteins, also called the E-proteins, comprise the mammalian TCF3/E2A, TCF4, TCF12/HEB and the Daughterless (Da) (Massari and Murre, 2000). They are widely expressed and form homo- or heterodimers with class II bHLH proteins to bind DNA at the Ephrussi box (E-box) sequence, CANNTG. Class II bHLH proteins (Achaete-Scute complex proteins, MyoD, Myogenin, Atonal family etc.) are expressed in a tissue-specific manner but are not capable of activating transcription without E-proteins. In this study, we used the only E-protein in Drosophila, Da, to study PTHS-related mutations in the fruit fly.

Being the sole E-protein in Drosophila, Da has multiple roles in development – in sex determination and oogenesis (Crommiller and Cummings, 1993; Smith et al., 2002), neurogenesis (Caudy et al., 1988; Hassan and Vaessin, 1997; Vaessin et al., 1994), eye development (Bhattacharya and Baker, 2011; Lim et al., 2008; Tanaka-Matakatsu et al., 2014), intestine stem cell maintenance (Bardin et al., 2010), and mesoderm development (Castanon et al., 2001). Da can both homodimerise or form heterodimers with class II bHLH proneural proteins and regulate the establishment of neural precursors (Cabrera and Alonso, 1991; Murre et al., 1998; Smith and Crommiller, 2001; Tanaka-Matakatsu et al., 2014; Troost et al., 2015; Zarifi et al., 2012). Both lack of Da and ubiquitous overexpression of Da result in embryonic lethality, showing the importance of proper dosage (Crommiller and Cline, 1987; Giebel et al., 1997).

Previously, Drosophila melanogaster has been successfully used to model human neurodegenerative diseases (Sang and Jackson, 2005). Recently efforts have been made towards exploiting fruit fly to model neuropsychiatric diseases and intellectual disability disorders (O’Kane, 2011; van der Voet et al., 2014). However, so far there are no fruit fly models of PTHS. Being the only E-protein...
in *Drosophila*, Da is a probable functional orthologue of all mammalian E-proteins. Here we prove that TCF4 is a true functional orthologue of Da capable of mediating neuronal development in *Drosophila*.

To recapitulate the PTHS in *Drosophila* we introduced four PTHS-associated mutations of TCF4 – R580W, R587H, R582P and A614V – into Da. Their transcriptional activation capability was compared and analysed in *vivo*. All these mutations caused similar defects as their counterparts in TCF4 in *vitro* compared and analysed.

PTHS mutations in adult lead to a reduced lifespan ranging from a few days to couple of weeks. These results implicate that in addition to their roles in development, expression of E-proteins has to be regulated in a spatially and temporally restricted manner also in adult flies.

**RESULTS**

**Daughterless is the only orthologue of human E-proteins in *Drosophila***

Amino acid sequence analysis showed that Da is about 35% identical to human E-proteins TCF3, TCF4, and TCF12 and has the highest identity with TCF4 (35.54%). Even though the entire amino acid sequence homology between human proteins and Da is below 50%, the amino acid identity of bHLH domains between Da and human E-proteins reaches 75% (Fig. 1) which allows extrapolation of mutations found in bHLH of TCF4 of PTHS patients into Da.

Seven out of nine PTHS-associated missense mutations in TCF4 are found in the bHLH region (Sepp et al., 2012). From these bHLH position conserved mutations we selected four R578H, R580W, R582P and A614V for introduction into Da (Fig. 1). We named all mutations after PTHS-associated mutations in TCF4, although the numeral positions in Da differ by 14 amino acids (R564H, R566W, R568P, and A600V respectively). Two additional mutations were generated in order to study the importance of amino acid position and specificity. The first of these is D515G (D501G in Da) in nonconserved region close to the basic region and R582 in the beginning of the first helix of Da bHLH domain is essential for activating E-box controlled transcription. The mutation A614V in the second helix shows diminished transcription activity which is completely consistent with the results obtained with TCF4 proteins carrying the same mutations (Sepp et al., 2012).

**TCF4 and Da, but not DaR578H**, DaR580W, DaR580L or DaR582P, activate E-box controlled reporter gene expression in wing disc and induce ectopic thoracic bristles in *Drosophila*

To analyse the functional consequences of Da mutations in *vivo*, we took the following approaches. First, we analysed the capacity of the overexpressed mutants to activate E-box dependent transcription in wing disc. Second, we tested the impact of the mutations on formation of ectopic sensory bristles induced by Da overexpression (Zarifi et al., 2012). To this end, transgenic *Drosophila* strains were generated expressing DaPTHS under GAL4 control element UAS (Brand and Perrimon, 1993). Additionally, we generated flies with two most widely expressed alternative

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**Fig. 1. Human E-proteins and *Drosophila* Da show high amino acid sequence conservation of bHLH domains.** The amino acid sequences of all three human E-proteins TCF3, TCF4, and TCF12 together with *Drosophila* Da bHLH domains with surrounding sequences are presented. The basic and loop regions are marked as light grey while the helices are coloured dark grey. Amino acid residues marked in red in TCF4 sequence are found mutated in PTHS patients and amino acid residues marked in red in Da sequence where mutations were introduced in this study.

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**Mutated Daughterless proteins have variable transactivation capabilities in HEK293 cells in comparison to wild type protein***

We and others have previously demonstrated that several PTHS-associated missense mutations impair the functions of TCF4 homodimers and/or heterodimers with ASCL1 in *vitro* (Zweier et al., 2007; de Pontual et al., 2009; Sepp et al., 2012; Forrest et al., 2012). Particularly, PTHS-associated mutations R578H, R580W and R582P abolish the DNA-binding and transactivation capacity of TCF4 homodimers and TCF4:ASCL1 heterodimers, whereas A614V mutation impairs the functions of TCF4 homodimer, but retains the activity of the TCF4:ASCL1 heterodimer (Sepp et al., 2012). To test the transcriptional capability of Da proteins carrying the same PTHS-associated mutations and two additional mutations (D515G and R580L), we used luciferase reporter assay in human embryonic kidney-derived cell line (HEK293). Three out of seven constructs tested – DaR580W, DaR580L and DaR614V – were capable of activating E-box controlled luciferase gene transcription (Fig. 2). DaR578 did not activate transcription from the reporter construct without E-boxes indicating that the transcriptional activation is E-box specific.

The following mutations abolished reporter gene expression: R578H, R580W, R580L and R582P. In the case of DaR614V the luciferase signal was lower compared to Dawt whereas the control mutation D515G showed no effect on Da transactivation capability. These results indicate that arginines R578 and R580 in the basic region and R582 in the beginning of the first helix of Da bHLH domain are essential for activating E-box controlled transcription. The mutation A614V in the second helix shows diminished transcription activity which is completely consistent with the results obtained with TCF4 proteins carrying the same mutations (Sepp et al., 2012).

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splice forms of TCF4 — shorter TCF4-A isoform and the longer TCF4-B isoform (Sepp et al., 2011). In vivo lacZ reporter assay was performed using the transgenic flies with four E-boxes CATCTG upstream of lacZ reporter region as previously described (Culi, Modolell, 1998; Zarifi et al., 2012). UAS-transgenes were ectopically expressed under pannier-GAL4 (pnr-GAL4) in wing disc notum region (Fig. 3). Notum showed small spot-like areas of transgenic E-box activation by endogenous Da. Expression of GFP was used as a control showing no activation of reporter lacZ and mimicking transgenic E-box activation by endogenous Da (Fig. 3A). Importantly, this control did not induce ectopic bristles or thorax defects (Fig. 3F). Dawt (Fig. 3B), DaD515G (Fig. 3C), (Fig. 3A). Importantly, this control did not induce ectopic bristles and mimicking transgenic E-box activation by endogenous Da. Expression of GFP was used as a control showing no activation of reporter lacZ and mimicking transgenic E-box activation by endogenous Da (Fig. 3A). Importantly, this control did not induce ectopic bristles or thorax defects (Fig. 3F). Dawt (Fig. 3B), DaD515G (Fig. 3C), DaR578H (Fig. 3D), R580W (Fig. 3E), R580L (Fig. 3K) and R582P (Fig. 3L) abolished the ability of Da to activate reporter expression in the wing disc. Interestingly, DaR380W (Fig. 3J), DaR580L (Fig. 3P) and DaR582P (Fig. 3Q) reduced the number and size of thoracic bristles and caused malformation of the whole adult thorax indicating that these mutations share dominant-negative effects. Overexpression of DaR578H (Fig. 3I) resulted in no major defects on the thorax, but on several occasions formation of some ectopic bristles was observed. Taken together, these results demonstrate that TCF4 isoforms TCF4-A and TCF4-B, Dawt, DaD515G and DaR578H are capable of rescuing da null embryonic neuronal phenotype.

**Da, DaD515G, DaR578H, DaA614V, TCF4-A and TCF4-B are capable of rescuing da null embryonic neuronal phenotype**

Next we asked whether Dawt or any of the mutants used is able to rescue da null lethality or severe embryonic nervous system phenotype with total lack of peripheral nervous system (PNS) and disrupted CNS (Caudy et al., 1988). For this experiment transgenic fruit fly strains expressing Da wt, DaD188S, TCF4-A or TCF4-B under GAL4 responsive element were crossed to the GAL4 lines in da null background. First, we performed the rescue experiments using nervous system specific GMR12B08-GAL4 made of the only intron of da gene fused with Drosophila core synthetic promoter followed by GAL4 coding region (Pfeiffer et al., 2008). GMR12B08-GAL4 drives expression specifically in the nervous system in all developmental stages. This driver failed to rescue da null embryonic lethality with all our transgenes. The result obtained is consistent with known functions of Da outside the nervous system, for example in the mesoderm and muscle development (Castanon et al., 2001; Gonzalez-Crespo and Levine, 1993; Wong et al., 2008).

Subsequently, we repeated the rescue experiment with Da wt under ubiquitous daG122-GAL4 in da null background that led to embryonic lethality (Giebel et al., 1997; Smith and Cronmiller, 2001). Despite embryonic lethality, the severe nervous system phenotype i.e. peripheral nervous system absence was rescued. The nervous system of embryos from the rescue crosses with daG122-GAL4 was visualised by immunohistochemistry using neuronal marker Futsch (Drosophila homologue to mammalian Microtubule associated protein 1B). Embryos homozygous for null mutant allele da16 lack the entire PNS and have defects in CNS (Fig. 4B) compared to wt embryos (Fig. 4A). Expressing Da wt in da null background rescued the neuronal phenotype as reported before (Giebel et al., 1997; Smith and Cronmiller, 2001) (Fig. 4C). In embryos expressing DaD515G (Fig. 4D), DaA614V (Fig. 4I), TCF4-A (Fig. 4J) or TCF4-B (Fig. 4K) in da null background the neuronal phenotype was rescued as well. Interestingly, DaR578H that was unable to activate E-box controlled reporter expression in vitro (Fig. 2) and in the wing disc (Fig. 3D) rescued the development of the embryonic nervous system (Fig. 4E). DaR580W (Fig. 4F), DaR580L (Fig. 4G) and DaR582P (Fig. 4H) were unable to rescue the neuronal phenotype of da null mutants, which is consistent with their inability to activate da transcription from E-box.
Because rescue of da null mutants with expression of Da\textsuperscript{wt} using da\textsuperscript{G32}-GAL4 driver failed, other GAL4 strains with broad expression like tub-GAL4, 69B-GAL4 and ubi-GAL4 were used for rescue experiments. However, the rescue of da null embryonic lethality using these drivers was unsuccessful (data not shown). These results demonstrate that the exact dosage and spatial and temporal regulation of Da protein expression are highly important for Drosophila viability.

**Overexpression of Da, Da\textsuperscript{PTHs}, TCF4-A, or TCF4-B by GMR12B08-GAL4 results in the rough eye phenotype**

Overexpression of Da\textsuperscript{wt}, Da\textsuperscript{PTHs}, TCF4-A or TCF4-B under ubiquitous da\textsuperscript{G32}-GAL4 driver resulted in embryonic lethality. Overexpressing these transgenes under the control of the nervous-system specific GMR12B08-GAL4 resulted in viable flies with the rough eye phenotype (Fig. 5). During eye development, this driver line is weakly expressed in larval eye discs and strongly in larval optic lobes (Pfeiffer et al., 2008 and our unpublished results). Overexpression of Da\textsuperscript{wt} (Fig. 5B,B'), Da\textsuperscript{D515G} (Fig. 5C,C'), Da\textsuperscript{R578H} (Fig. 5D,D'), TCF4-A (Fig. 5M,M') or TCF4-B (Fig. 5N,N') resulted in the rough eye phenotype only when GMR12B08-GAL4 driver was homozygous. Exceptionally, Da\textsuperscript{A614V} overexpression under GMR12B08-GAL4 driver was homozygous. Exceptionally, Da\textsuperscript{A614V} overexpression under GMR12B08-GAL4 led to the rough eye phenotype only in double homozygous state (Fig. 5K,K',L,L'). Da\textsuperscript{R580L} (Fig. 5J), Da\textsuperscript{R580W} (Fig. 5E,E') and Da\textsuperscript{R582P} (Fig. 5Q,Q') caused thorax malformation, Da\textsuperscript{R578H} (I) had no effect on thorax but induced occasional extra bristles. The expression pattern of pnr-GAL4 is shown in blue on panel U. Scale bar on A represents 100 μm and is applicable for A-E,K-O and U.
transgene in the X-chromosome making them double homozygous. Interestingly, the rough eye phenotype was also weaker in the males of other transgenic lines compared to females carrying arginine mutations (R580L and R582P) with transgene insertions in the second chromosome (Fig. 5H,H′,J,J′). These results demonstrate high sensitivity of eye development to da transgene dosage. A614V mutation yielded the most subtle rough eye phenotype and all three arginine mutations R580W, R580L and R582P produced the strongest rough eye phenotype. Our results also showed that DaR578H, DaD515G, TCF4-A and TCF4-B behave similarly to DaWT when overexpressed under GMR12B08-GAL4, indicating that all the mentioned proteins have transactivation activity during fruit fly eye development.

Overexpression of Da, TCF4-B and DaPTHS in young adult flies results in significantly altered survivorship

Next, we wanted to evaluate the impact of Da in adult flies. For this the temperature sensitive repressor of GAL4, GAL80ts was used. The overexpression of Da under the control of the ubiquitous daG32-GAL4 driver is lethal during embryogenesis (Giebel et al., 1997; Smith and Cronmiller, 2001). In order to overcome the lethality during development, we repressed GAL4 by GAL80ts. After the eclosion of adults, the collected virgin females were kept at restrictive temperature to inactivate GAL80ts. Activated overexpression of DaWT or DaD515G or TCF4 long isoform B lead to lethality in 2-3 days (Fig. 6). The flies initially lost their flight ability and most of locomotor activity and died soon afterwards. Also, the activation of Da carrying PTHS-related arginine mutations unable to bind DNA (R580W, R580L, and R582P) lead to lethality in median 3-4 days (Fig. 6). Flies overexpressing the Da with weaker mutations, DaR578H and DaA614V, resulted in median survival of 10-11 days while the control group flies overexpressing GFP survived generally 40 days (Fig. 6; Table S1). Surprisingly, the flies overexpressing the shorter TCF4-A isoform survived significantly longer than the flies overexpressing TCF4-B and were closer to the control group, with median survival of 30 days (Fig. 6; Table S1). All survivorship curves obtained were statistically significant by log-rank as compared to the GFP control curve (P<0.0001, Mantel–Cox test).

DISCUSSION

In this study we show that Da, the only E-protein in Drosophila with highly conserved bHLH domain, functions as human TCF4 orthologue. As the overall identity of a protein sequence between Drosophila and mammals is usually around 40% between homologues and 80-90% within conserved functional domains (Pandey and Nichols, 2011), Da can be considered the orthologue for all three human E-proteins. In all experiments conducted in this study, TCF4 acted in very similarly as Da (Table 1), proving the possibility of modelling PTHS in the fruit fly. The two human TCF4 isoforms, TCF4-A and TCF4-B, were able to activate E-box dependent lacZ expression in Drosophila, and more importantly, to induce ectopic bristle formation in the adult thorax, to rescue embryonic nervous system development in da null embryos, and to induce the rough eye phenotype when overexpressed in the nervous system identically to Da. Altogether these results show that TCF4 has comparable activity in the fruit fly as Da.
PTHS-associated arginine mutations R580W, R580L, and R582P abolished Da transactivation capability in luciferase reporter assays in HEK293 cells. DaR580W, DaR580L, and DaR582P behaved similarly to each other in both overexpression and rescue experiments in the fruit fly. The rescue by daG32-GAL4 driver of da null embryonic nervous system phenotype failed when using Da proteins with these arginine mutations. When Da carrying one of above mentioned mutations was overexpressed in flies under the control of the nervous system specific driver GMR12B08-GAL4, the strongest eye phenotype was observed. These flies had rough and partially unpigmented eyes with fused ommatidia consistent with Da having an important role in Drosophila eye development (Brown et al., 1996). In addition, overexpression of these arginine mutants under prn-GAL4 caused malformation of the thorax. Altogether, these results indicate that mutations R580W, R580L and R582P abolish the Da transactivation capability resulting in dominant-negative effects. This is in line with the previous data about the corresponding mutations in TCF4 having dominant-negative effects in vitro (Sepp et al., 2012).

R578H differed from the other three arginine mutations (R580W, R580L and R582P) in in vivo experiments. Although DaR578H was unable to activate reporter gene expression in luciferase assay carried out in mammalian cell line HEK293 and in lacZ assay in vivo, it caused rough eye phenotype similar to Da wild type when overexpressed by GMR12B08-GAL4. Furthermore, DaR578H rescued da null embryonic neuronal phenotype when expressed using daG32-GAL4. Also DaR578H showed weak induction of ectopic bristles. Taken together these results indicate that transactivation capability of DaR578H probably depends on its dimerisation partners, which could be lacking in mammalian cell line and weakly presented in the wing disc notum. Similarly, we have previously found that while TCF4 carrying the R578H mutation is unable to bind to E-box in vitro as a homodimer or in complex with either ASCL1 or NEUROD2, it does not act in dominant negative manner in reporter assays in mammalian cells (Sepp et al., 2012).

The A614V mutation positioned in the second helix of the bHLH domain showed the mildest effects. DaA614V was able to activate E-box-specific transcription in vitro and in vivo. Expressing DaA614V using daG32-GAL4 rescued da null embryonic neuronal phenotype. Overexpression using GMR12B08-GAL4 resulted in the rough eye phenotype only when both of the transgenes were homozygous, indicating that this mutation causes hypomorphic effects. This is consistent with our recent study which showed that the A614V mutation leads to lower levels of TCF4 because of reduced protein stability (Sepp et al., 2012).

The control mutation generated by us, D515G, did not reduce Da transactivation capability in vitro and behaved similarly to Da wild type in vivo. This shows that D515 positioned outside of the conserved bHLH is not required for Da transcriptional activity. The other control mutation generated by us, R580L, where the same arginine was mutated as in DaR580W, led to dominant-negative effects in vivo similarly to R580W. At least in the case of R580, the mutation specificity, whether it was mutated into tryptophan or leucine, made no difference in our study.

In rescue experiments with tested driver strains (69B-GAL4, tub-GAL4, ubi-GAL4, GMR12B08-GAL4, daG32-GAL4) all Da transgenes failed to rescue da null embryonic lethality. Apparently to our previous results obtained with human TCF4 (Sepp et al., 2012). Subsequently we studied PTHS-associated Da mutants in vivo in E-box lacZ reporter assay, and in both rescue and overexpression experiments.

PTHS-associated arginine mutations R580W, R580L, and R582P abolished Da transactivation capability in luciferase reporter assays in HEK293 cells. DaR580W, DaR580L, and DaR582P behaved similarly to each other in both overexpression and rescue experiments in the fruit fly. The rescue by daG32-GAL4 driver of da null embryonic nervous system phenotype failed when using Da proteins with these arginine mutations. When Da carrying one of above mentioned mutations was overexpressed in flies under the control of the nervous system specific driver GMR12B08-GAL4, the strongest eye phenotype was observed. These flies had rough and partially unpigmented eyes with fused ommatidia consistent with Da having an important role in Drosophila eye development (Brown et al., 1996). In addition, overexpression of these arginine mutants under prn-GAL4 caused malformation of the thorax. Altogether, these results indicate that mutations R580W, R580L and R582P abolish the Da transactivation capability resulting in dominant-negative effects. This is in line with the previous data about the corresponding mutations in TCF4 having dominant-negative effects in vitro (Sepp et al., 2012).

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the successful rescue of \( da \) null lethality closely mimics the endogenous \( da \) expression. \( da^{G32}-GAL4 \), comprising of 3.2 kb of \( da \) gene covering the promoter, the first intron, and the upstream noncoding region (Wodarz et al., 1995), is widely used as a ubiquitous driver line. Most probably the expression of this driver line is far too strong compared to the native expression of \( da \) gene as \( Da \) has been shown to positively autoregulate its own expression via a transcriptional feedback loop (Bhattacharya and Baker, 2011; Smith and Cronmiller, 2001). If \( da^{G32}-GAL4 \) expression is regulated by \( Da \) itself, then \( Da \) overexpression might drive even stronger GAL4 expression, resulting in a positive feedback loop. Furthermore, it has been hypothesised that \( da^{G32}-GAL4 \) lacks putative regulatory repressor elements since using a 15 kb genomic \( da \) transgene that has an additional 12 kb of downstream sequence rescues \( da \) null embryonic lethality (Smith and Cronmiller, 2001).

Little is known about the role of E proteins in adult nervous system. Here we show that exact temporal and spatial expression of \( Da/TCF4 \) remains vitally important during adulthood of fruit flies. We show that overexpression of \( Da/TCF4 \) in adults leads to lethality within 2-3 days. Surprisingly, TCF4 isoforms A and B lead to strikingly different outcomes when overexpressed in adult fruit flies. While the long isoform TCF4-B behaved identically to \( Da \), TCF4-A affected the survival only slightly compared to the control group. This could be related to the lack of interaction capability of much shorter N terminus of isoform A in fruit fly or different regulation of subcellular location and dimerisation of the alternative TCF4 isoforms (Sepp et al., 2011). Analysis of survival divided the PTHS related mutations into severe (R580W, R580L and R582P) and milder (R578H and A614V) according to survivorship. The severe mutants led to lethality within 3-4 days and the milder ones in

\[
\text{Survivorship Index} = \frac{\text{Surviving Flies at Time t}}{\text{Total Flies at Time t}}
\]

\[
\text{days} = 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30
\]

\[
\text{Survivorship Index} = 0.0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0
\]

\[
\text{GFP} \quad \text{TCF4A} \quad \text{da[A614V]} \quad \text{da[R582P]} \quad \text{da[R578H]} \quad \text{da[D515G]} \quad \text{da[R580W]} \quad \text{da[R580L]} \quad \text{da[wt]} \quad \text{TCF4B}
\]

**Table 1. Functional effects of transgenes used in this study**

| UAS construct | \( \text{In vitro activation of transcription} \) | \( \text{In vivo activation of transcription in wing discs} \) | Bristle induction by pnr-GAL4 | Eye phenotype by homozygous \( GMR12B08-GAL4 \) | Rescue of PNS of \( da \) null embryos | Adult median survival in days |
|----------------|-----------------------------------------------|-----------------------------------------------|---------------------------------|----------------------------------|-------------------------------|-----------------------------|
| \( da \)       | yes                                           | yes                                           | yes                             | rough                           | yes                           | 2                           |
| \( da^{D515G} \)| yes                                           | yes                                           | yes                             | rough                           | yes                           | 3                           |
| \( da^{R578H} \)| no                                            | no                                            | weak                            | rough                           | yes                           | 11                          |
| \( da^{R580W} \)| no                                            | no                                            | reduced bristles                | rough, partly discoloured       | no                            | 4                           |
| \( da^{R580L} \)| no                                            | no                                            | reduced bristles                | rough, partly discoloured       | no                            | 4                           |
| \( da^{R582P} \)| no                                            | no                                            | reduced bristles                | rough, partly discoloured       | no                            | 4                           |
| \( da^{A614V} \)| weaker                                        | yes                                           | yes                             | rough only when homozygous      | yes                           | 10                          |
| TCF4-A         | yes                                           | weaker                                        | yes                             | rough                           | yes                           | 30                          |
| TCF4-B         | yes                                           | weaker                                        | yes                             | rough                           | yes                           | 2                           |

\( Da^{wt} \), \( Da^{D515G} \), TCF4-A and TCF4-B share similar properties in most experiments conducted. \( Da^{R580W} \), \( Da^{R580L} \) and \( Da^{R582P} \) are incapable of transactivation but result in additional phenotypes in eye and thorax development, also the survivorship of adults is severely reduced. Both \( Da^{R578H} \) and \( Da^{A614V} \) have milder effects in survivorship assay and capable of rescuing embryonic nervous system development. The activity of \( Da^{R578H} \) may depend on the dimerisation partner present in the developing eye and which is weakly presented in developing thorax \( Da^{A614V} \) is a hypomorphic mutation allowing homodimerisation.
PTHS-associated mutations have been performed in the PTHS model flies. This gives valuable information about cognition and social behaviour of RNAi. Additional studies are needed to generate and compare viable flies and we were able to create stocks with each mutation. The dominance of TCF4 deletions would be to slightly mimic dosage loss by TCF4 deletions. In this study, we were able to create stocks with each mutation generated in this study. An alternative tactic to model PTHS and to generate stocks with each mutation generated in this study. An alternative tactic to model PTHS is to use the appropriate heterozygotes of the orthologous protein. However, in Drosophila there is a sole E-protein Da corresponding to all three mammalian E-proteins. In a way the heterozygous Da mutation corresponds to the heterozygous deletion of all three E-proteins in mammals. Accordingly, Da as the only binding partner of class II bHLH proteins has a large variety of roles outside nervous system. As TCF4 is highly expressed in the nervous system we have chosen here the approach to overexpress the mutated alleles specifically in the nervous system in a wild type background. Overexpression of Da under the nervous system specific GMR12B08-GAL4 led to viable flies and we were able to create stocks with each mutation generated in this study. An alternative tactic to model PTHS and to mimic dosage loss by TCF4 deletions would be to slightly downregulate Da expression nervous system specifically by RNAi. Additional studies are needed to generate and compare different PTHS models and to perform behavioural tests that would give valuable information about cognition and social behaviour of the PTHS model flies.

In conclusion, this study is the first where experiments with PTHS-associated mutations have been performed in vivo. We have verified Da as a functional TCF4 homologue, described similarities between Da and TCF4 carrying the same mutations, and obtained insights how PTHS-associated mutated Da genes could affect Drosophila embryonic nervous system development and thoracic bristle formation. The similarities between the effects of PTHS-associated mutations on Da and TCF4, ranging from hypomorphic to dominant-negative, prove that these proteins have similar functions and Da can be used for modelling of PTHS in Drosophila melanogaster. Our novel models of PTHS in Drosophila allow the design of further studies addressing the molecular mechanisms and treatment of PTHS.

MATERIALS AND METHODS

Drosophila stocks

All Drosophila stocks and crosses were kept on malt and semolina based food with 12 h light and dark daily rhythms at 25°C with 60% humidity unless otherwise noted. Drosophila strains used in this study were da^{G122-GAL4} (Wodarz et al., 1995), 69B-GAL4 (Brand and Perrimon, 1993), and tub-GAL4 provided by Riitta Lindström, ubi-GAL4 provided by Mari Teesalu, EE4-lacZ,pnr-GAL4/T(2,3)Sm6-TM6B kindly provided by Christos Delidakis, GMR12B08-GAL4 (Pfeiffer et al., 2008), da^{10,FRT40A} (BL5531), UAS-da^{44} (BL#37291), UAS-mCD8-GFP (BL#5137), and tub-GAL80° (BL#7019) from Bloomington Stock Center at Indiana University, USA. The following transgenic lines were generated in this study: UAS-da^{D135G}, UAS-da^{R579H}, UAS-da^{R580H}, UAS-da^{R580L}, UAS-da^{D552P}, UAS-da^{D515G}, UAS-TCF4-A, and UAS-TCF4-A.

Mutagenesis, cloning and transgenesis

The amino acid sequences were aligned and homology of human E-proteins and Da was calculated using Clustal Omega 2.1 (EMBL-EBI, Cambridge, UK). Site-directed mutagenesis was performed using the partial da cDNA construct GH10651-pOT2 as a template (Drosophila Genomics Resource Center, Bloomington, IN, USA). Primers were designed with that de novo restriction sites created next to the mutation with no change in amino acid sequence. The primer sequences are listed in Table S2. The constructs obtained by PCR were sequenced and subcloned into full-length da cDNA from Actin1-GAL4 (Drosophila Genomics Resource Center) using SphI and NruI restriction sites. Full-length da carrying appropriate PTHS-associated mutation together with TCF4-A(-) and TCF4-B(-) cDNAs from the respective pCDNA3.1 vectors (Sepp et al., 2011) were then subcloned into pUAST vector. Generation of transgenic flies with random insertions was ordered from Fly Facility (Clermont-Ferrand Cedex, France).

DNA transfection and luciferase assay

The transfection and luciferase assay was performed as described before (Sepp et al., 2011). Briefly, HEK293 cells obtained from ATCC (LCG Standards GmbH, Wesel, Germany) and routinely tested for contamination were transfected using Lipofectamine 2000™ (SignaGen Laboratories, Gaithersburg, MD, USA) with pCDNA3.1 based TCF4 or da constructs and firefly luciferase construct pGL4.29[luc2P/12µE5/Hygro] or pGL4.29[luc2P/min/Hygro] and Renilla luciferase construct pGL4.29[hRlucP/min/Hygro] for normalisation. Transfections were carried out as duplicates on a 48-well plate. After 24 h cells were lysed with 50 µl Passive Lysis Buffer (Promega, Madison, Wisconsin, USA). Dual-Glo Luciferase assay (Promega) was performed following manufacturer’s protocol and luminescence was measured with a luminometer. Renilla luciferase activity was calculated using Clustal Omega 2.1 (EMBL-EBI, Cambridge, UK). Site-directed mutagenesis was performed using the primers and TCF4-B(-) cDNAs from the respective pC DNA3.1 vectors (Sepp et al., 2011) were then subcloned into pUAST vector. Generation of transgenic flies with random insertions was ordered from Fly Facility (Clermont-Ferrand Cedex, France).

In vivo lacZ reporter assay

For expression of transgene in wing discs, ubiquitous temperature-sensitive tub-GAL80° repressor was used to avoid larval lethality caused by pnr-GAL4-UAS-da. Vials with 3rd instar larvae were transferred from permissive temperature at 18°C to restrictive temperature at 30°C for 24 h before dissection of wing discs and afterwards moved to 25°C until adults emerged. Each da mutant strain under UAS was crossed to EE4-lacZ, pnr-GAL4/T(2,3)Sm6-TM6B. 3rd instar wing discs of their progeny were dissected and the X-gal staining was performed. Expression of transgene in wing discs and X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside) histochemistry was performed as described before (Zarifi et al., 2012). For imaging, Olympus BX61 microscope (Tokyo, Japan) with UPPlanApo 20×/0.75 objective was used.

RNA isolation and RT-PCR

Total RNA was isolated from embryos using RNeasy Micro Kit (Qiagen, Hilden, Germany) and treated with Turbo DNase (Ambion, Thermo Fisher Scientific, Waltham, MA, USA). First strand cDNA was reverse transcribed from 1 µg of RNA using oligo(dT)20 primer and Superscript III Reverse Transcriptase (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA). PCR was performed using FirePol DNA polymerase (Solis Biodyne, Tartu, Estonia). Primer annealing temperature was 55°C and
primer sequences are presented in Table S2. After PCR, restriction analysis was performed using restriction sites created during mutagenesis (Fig. S1).

**Immunohistochemical staining of embryos**

The following primary antibodies and dilutions were used: rabbit EGFP anti-serum (provided by Andres Merits, Tartu University, 1:2000; mouse monoclonal 22C10 anti-Futsch antibody (deposited by Benzer, Seymour/Colley, Nansi, obtained from the Developmental Studies Hybridoma Bank, University of Iowa, IA, USA), 1:20. The following secondary antibodies and dilutions were used: goat anti-mouse Alexa 594, 1:1000; and goat anti-rabbit Alexa 488 (both ImmunoResearch Laboratories, Inc., West Grove, PA, USA), 1:1000. Drosophila embryos were dechorionated using 2% sodium hypochlorite (Sigma-Aldrich, St. Louis, MO, USA) and fixed using 4% formaldehyde (AppliChem GmbH, Darmstadt, Germany) in PEM buffer (100 mM PIPES, 1 mM EGTA, 2 mM MgSO₄, pH 7.4) and stored in methanol at −20°C until used. Primary antibody labelling was performed overnight on overhead rotator at 4°C. Secondary antibodies were preadsorbed to wt embryos before use. Incubation with secondary antibodies was performed for 3 h on overhead rotator at room temperature. All staining procedures and washes were performed in Vectashield mounting medium with DAPI (Vector Laboratories, Burlingame, CA, USA). For image collection, Zeiss LSM 510 Meta

Light microscopy and imaging of adult flies

Flies were euthanased using chloroform (Sigma-Aldrich). For capturing eye and thorax images, Zeiss Stereo Discovery V8 microscope and Zeiss Axioscan MRc camera were used. For scanning electron microscopy, Zeiss Evo LS15 (Carl Zeiss Microscopy) was used.

Evaluating the lifespan of da transgenic flies

w−; tub-GAL80Δ; da352-GAL4 flies were crossed to da transgenic flies with insertions in second chromosome (lines UAS-daΔD315G1, UAS-daΔR75H1, UAS-daΔR136D1, UAS-daΔR532P2, UAS-daΔG164F3, UAS-TCF4-B4) or in third chromosome (lines UAS-daΔD3150F1, UAS-daΔB7, UAS-mCD8-GFP, UAS-TCF4-A4) and raised in permissive temperature 18°C where GAL80Δ represses the activity of GAL4. The progeny – eclosed virgin females – were collected and transferred to restrictive temperature 30°C where GAL80Δ is inactive and GAL4 is produced. Altogether, on average 200 flies (from at least 79 up to 314) were collected from each cross, maintained in uncrowded vials, counted on daily bases, and changed to new vials at three-day intervals. Survivorship index was calculated by dividing the survivors with the starting number of flies. Comparison of survival curves and P-value calculations were performed using Mantel–Cox log rank method with Prism 6.0 GraphPad Software (La Jolla, CA, USA).

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Competing interests

The authors declare no competing or financial interests.

Author contributions

L.T., M.S., M.P. and T.T. conceived and designed the experiments. M.P. and T.T. provided research tools. L.T. and M.P. performed the experiments. L.T. and M.P. analysed the data. L.T. and M.P. wrote the paper. All authors commented and edited the manuscript.

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Supplementary information

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