

1 **Tweedle proteins form extracellular 2D-structures defining body and cell shape**  
2 **in *Drosophila melanogaster***

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14 **Abstract**

15 Tissue function and shape rely on the organisation of the extracellular matrix (ECM)  
16 produced by the respective cells. Here, we report on our study on the function of the  
17 extracellular Tweedle proteins (Twdl) in the fruit fly *Drosophila melanogaster* during  
18 shaping of the integument composed of the epidermis and its apical extracellular  
19 cuticle. We show that Twdl proteins form at least two adjacent two-dimensional  
20 sheets underneath the cuticle surface by self-assembly. Dominant mutations in two  
21 *twdl* genes *Tubby*<sup>1</sup> and *TwdlL*<sup>93</sup> cause ectopic spherical accumulation of Twdl  
22 proteins within lower cuticle regions. These aggregates recruit also non-mutated  
23 Twdl proteins. Thus, the mutated residues are needed for the plane arrangement of  
24 Twdl proteins and their localisation underneath the cuticle surface without affecting  
25 their ability to self-assembly. Depletion of Twdl proteins from the sub-surface region  
26 and their ectopic accumulation are associated with the disruption of the ridged profile  
27 of the plasma membrane-cuticle interface region and lateral instead of longitudinal  
28 stretching of epidermal cells. Based on these data, we propose that depletion of Twdl  
29 proteins from the sub-surface region entails weakening of the cuticle resistance  
30 against the internal hydrostatic pressure that according to Barlow's law in turn causes  
31 lateral expansion of the body. Interestingly, these changes do not provoke crawling  
32 defects suggesting that body shape and locomotion require separate cuticle  
33 properties.

34 **Introduction**

35 Extracellular matrices (ECM) contribute to the geometry and consistency of cells and  
36 tissues. Generally, the role of an ECM depends on its components and their  
37 interactions that ultimately define its organisation. Cartilaginous tissues, for instance,  
38 consist of a random distribution of the extracellular polysaccharide hyaluronic acid  
39 and associated proteins including collagen and aggrecan produced and secreted by  
40 embedded chondrocytes [1-4]. Tension applied on this kind of tissues in concert with  
41 swelling forces entail the arrangement of the components and, finally, the shape of  
42 the tissue.

43 A less well studied ECM is the cuticle of insects that outlines the shape of the  
44 organism. In some body regions such as the head capsule of caterpillars or the  
45 protective elytra of adult beetles, the hardness of the exoskeleton is sufficient to  
46 sustain the required shape. In some other body regions such as the ventral abdomen  
47 of many adult insects or the larval body, the respective shape does not only depend  
48 on the exoskeleton, but involves the inner hydrostatic pressure. Despite these  
49 differences the principal organisation of the cuticle is well conserved in different body

50 regions and among species. The prototype of the cuticle consists of three composite  
51 horizontal layers, the outermost envelope, the middle epicuticle and the inner  
52 procuticle [5, 6].

53 Like cartilaginous tissues, the procuticle is composed of an extracellular  
54 polysaccharide, namely chitin, and associated proteins. In the last few years, data  
55 accumulated underlining that the proteins binding to chitin and their partners together  
56 specify the physical properties of the cuticle. In the elytral procuticle of the red flour  
57 beetle *Tribolium castaneum*, for instance, the chitin-binding proteins Cpr27 and  
58 Cpr18 associate with chitin and interact with the cuticle protein CP30 probably over  
59 covalent N- $\alpha$ -alanyl-dopamine (NBAD) bridges that are catalysed by the  
60 phenoloxidase TmLaccase2 [7, 8]. This arrangement correlates with the stiffness of  
61 the elytral cuticle. In the fruit fly *Drosophila melanogaster*, proteins such as the chitin-  
62 binding and elastic protein Resilin in the contact region between the procuticle and  
63 the epicuticle are cross-linked to each other via dityrosine bonds [9]. The formation of  
64 this sub-layer involves the C-type lectin Schlaff (Slf) and a yet unknown peroxidase.  
65 The exact underlying molecular mechanisms are not understood. Besides its function  
66 as a barrier, the dityrosine sub-layer may also be important for cuticle elasticity.

67 In order to deepen our understanding of the mechanisms of cuticle ECM  
68 organisation, we have studied the function of several members of a class of cuticle  
69 proteins named Tweedle (Twdl) in the fruit fly *Drosophila melanogaster* [10]. Twdl  
70 proteins are characterised by an N-terminal signal peptide and a domain with four  
71 conserved blocks (DUF243), but do not display any homology to any other entry in  
72 protein databases. Deletions of stretches of amino acids of these domains provoke  
73 body shape changes in larvae and adult flies. In brief, we show that Twdl proteins  
74 localise to the epicuticle and assist the organisation of the epicuticle-procuticle  
75 interface, which we hypothesise to be responsible for defining the body shape.

76 Here, we show that Twdl proteins localise to the epicuticle forming at least two 2-  
77 dimensional sheets. In addition, we demonstrate that Twdl proteins with deletions in  
78 the DUF243 domain form ectopic aggregates within the procuticle. These aggregates  
79 recruit non-mutated Twdl proteins as well as proteins from the procuticle-epcuticle  
80 interface. We propose that this mis-organisation entails changes in the physical  
81 properties of the cuticle that as a consequence dilates laterally rather than  
82 longitudinally, thereby facilitating lateral growth and conferring squat larval shape.

83

## 84 **Materials & Methods**

### 85 *Fly husbandry*

86 Flies were kept in cages with apple juice agar plates with yeast, from which embryos  
87 and larvae were collected. Embryonic stages were recognized according to the gut  
88 morphology described by Hartenstein and Campos-Ortega [11]. Homozygous  
89 mutants non-carrying any GFP- or YFP- constructs were identified from the rest of  
90 the embryos that were heterozygous or homozygous for the balancer chromosome  
91 expressing GFP (Dfd:YFP or Kr:GFP). Collected embryos were dechorionated in  
92 chlorine bleach diluted 1:1 in tap water, manually freed from the vitelline membrane  
93 or left in the vitelline membrane, subsequently mounted in Voltalef 10S oil (VWR  
94 Chemicals) and observed by microscopy.

95 Transgenic flies harbouring constructs were generated by the BestGene Inc (USA)  
96 company. The constructs used are: *knkp:cpr67Fa-rfp* with the promoter of the *knk*  
97 gene [12] upstream of the coding region of *cpr67Fa* fused to the open reading frame  
98 of *rfp* in pW8; TwdlID-RFP-NLS with the coding regions of *twdlID* and *rfp-nls* fused

99 together and downstream of the *twdID* promoter [9] in pW8, Tb-GFP and TwdIS-GFP  
100 from the Flyfos library [13], Tb1-RFP [14], TwdIF-dsRed and TwdID-dsRed [10],  
101 UAS:Verm-RFP [15] and Obst-E-GFP [16]. The Gal4 line to drive UAS:*verm-rfp*  
102 expression was *daughterless:Gal4*.

### 103 *Molecular biology*

104 In order to identify a mutation in TwdIL gene standard PCR reaction and sequencing  
105 were performed.

### 106 *Genetics*

107 In order to down-regulate the activity of respective Tweedle proteins, RNAi technique  
108 and UAS:Gal4 system were used. Flies carrying respective UAS:RNAi constructs  
109 were crossed to the ones bearing ubiquitously expressed Gal4 (*daughterless:Gal4*).  
110 The larval and pupal phenotype of the progeny was observed.

111 For confirmation that Tb<sup>1</sup> and Tb<sup>93</sup> mutations are not alleles of the same gene we  
112 performed the complementation test by crossing them with each other, subsequently  
113 crossing the F1 females with the wild-type males and counting the number of the  
114 wild-type, non-Tb looking pupae.

### 115 *Microscopy and image preparation*

116 For live imaging, larvae were anaesthetised with ether, mounted in halocarbon 700 or  
117 50% glycerol and observed either by confocal laser scanning microscopy (CLSM,  
118 using Zeiss LSM 710, 780 and 880) or fluorescent binocular Leica M205 FA.

119 For imaging of the cuticle preparations, the larvae were mounted in Hoyer's medium  
120 (30 g gum arabic, 50 ml distilled water, 200 g chloral hydrate, 20 g glycerol, mixed  
121 1:1 with lactic acid), kept overnight at 65°C and observed on a binocular Leica M205  
122 FA. Transmission electron microscopy was performed following our extensive  
123 protocol published in 2010 [17]. For examination of the cuticular ridges, third instar  
124 larvae were digested in Hoyer's medium and their cuticles washed several times in  
125 the distilled water. Afterwards they were stacked to the metal plate and their inner  
126 side was scanned by the atomic force microscope (Innova AFM, Bruker).

127 For figures preparation Adobe Photoshop CS3 and Adobe Illustrator CS4 softwares  
128 were used without changing initial microscope settings. For cell measurements  
129 AxioVision Rel. 4.7 was used.

130

### 131 *Body length measurements*

132

133 Third instar larvae were placed on the agar plate and the movie of 10 steps (1 step =  
134 contraction and subsequent stretching) was made. Afterwards in every step the body  
135 in the most contracted and stretched state was measured and the difference between  
136 shortest and the longest measurement of all 10 steps of 5 wild-type, homozygous Tb<sup>1</sup>  
137 and Tb<sup>93</sup> larvae were counted and compared.

138

### 139 *Movement measurements*

140

141 100 third instar wild-type, homozygous Tb<sup>1</sup> and Tb<sup>93</sup> larvae were placed into the vials  
142 with agar food, 20 larvae of each kind to one vial. After pupariation of all larvae the  
143 distance between the pupae on the vial wall and the food level was measured and  
144 the average of measurements of 20 larvae was determined.

145

## 146 **Results**

### 147 *Twdl proteins are expressed at different time points during development*

148 To study the cellular function of Twdl proteins, we first determined the expression  
149 pattern of transgenic flies expressing fluorescent-tagged versions of the candidates  
150 TwdlA-GFP (Tb-GFP), TwdlD-dsRed, TwdlF-dsRed and TwdlS-GFP under the  
151 control of their endogenous promoters (Fig.1).

152 Tb-GFP starts to be expressed in the late embryo in patches in the lateral epidermis.  
153 Later, during larval development, its expression is detected in the entire epidermis.  
154 The TwdlS-GFP signal is barely visible in the cuticle of L2 larvae and becomes more  
155 intense in the whole cuticle of L3 larvae. TwdlF-dsRed is localized in the whole  
156 cuticle at all three larval stages. TwdlD-dsRed is expressed in the epidermis during  
157 the first two larval stages, but is excluded from the segmental grooves. At the third  
158 larval stage, only a very faint TwdlD-dsRed signal at the posterior part is detected.  
159 In summary, Twdl proteins are expressed at different time points during development  
160 in different, partially overlapping regions of the epidermis.

### 161 *Twdl proteins mark the epicuticle*

162 In order to determine the sub-cuticular localization of Twdl proteins, we analysed the  
163 distribution of the three fluorescent-tagged Twdl proteins, i.e. Tb-GFP, TwdlF-dsRed  
164 and TwdlS-GFP in the cuticle of live L3 larvae by confocal microscopy (Fig. 2, 3, 4).  
165 We used the auto-fluorescence of the cuticle surface excited with a 405 nm laser and  
166 the tagged procuticle markers Cuticle Protein R&R 67b (CPR67b-dsRed) and  
167 Vermiform (Verm-RFP) as landmarks. GFP-conjugated TwdlS was located between  
168 the 405 signal and the broad CPR67b-dsRed or Verm-RFP region marking the  
169 procuticle (Fig. 2). TwdlF-dsRed was detected in layer above the TwdlS-GFP but  
170 below the 405-signal (Fig. 3). Tb-GFP overlapped with TwdlF-dsRed (Fig. 4). We  
171 conclude that these Twdl proteins belong to the epicuticle subdividing it into distinct  
172 horizontal domains.

173 To test this conclusion, we monitored the expression of TwdlF-dsRed in embryos  
174 deficient for ecdysone that we had previously shown to be necessary for epicuticle  
175 differentiation [12]. In wild-type embryos, TwdlF-dsRed is detected in the entire larval  
176 cuticle (Fig. 6). In embryos mutant for *phantom* (*phm*) that codes for a P450 enzyme  
177 acting in the ecdysone biosynthesis pathway, TwdlF-dsRed is hardly expressed.  
178 Sporadically, dots of an RFP signal are found within epidermal cells. This finding is  
179 consistent with our conclusion that Twdl proteins localise to the epicuticle. Moreover,  
180 this result also indicates that activation of the *twdlF* promoter depends on ecdysone  
181 signalling.

### 182 *Twdl proteins bind selectively to aggregates formed in Tb mutant larvae*

183 To unravel the role of Twdl proteins in epicuticle formation and structure, we  
184 analysed the distribution of the fluorescent-tagged Twdl proteins in *Tb* mutant i.e. *Tb*<sup>1</sup>  
185 and *Tb*<sup>93</sup> larvae. In *Tb*<sup>1</sup> larvae, TwdlS-GFP, Tb-GFP and TwdlF-dsRed are partially  
186 localized correctly in the epicuticle and partially aggregated in the procuticle (Fig. 2,  
187 3, 4). In the cuticle of *Tb*<sup>93</sup> larvae, the signal of aggregated TwdlS-GFP and Tb-GFP  
188 is weaker compared to the signal in the *Tb*<sup>1</sup> mutant larvae, whilst TwdlF-dsRed binds  
189 the aggregates very weakly or does not bind them at all (Fig. 2, 3, 4).

190 In order to find out whether the origin of the aggregates may be a mutated Tb protein,  
191 we compared the distributions of non-mutated, GFP-tagged and mutated, RFP-  
192 tagged versions of Tb, Tb-GFP and Tb<sup>1</sup>-RFP [14], respectively, in the cuticle of live  
193 L3 larvae (Fig. 4). Tb<sup>1</sup>-RFP formed aggregates in the cuticle of these larvae. Co-

194 expressed Tb-GFP was recruited to these aggregates. To test whether other Twdl  
195 proteins might be part of the Tb<sup>1</sup>-RFP aggregates, we co-expressed Tb<sup>1</sup>-RFP with  
196 TwdIS-GFP (Fig. 4). The TwdIS-GFP signal overlaps with the signal of the Tb<sup>1</sup>-RFP  
197 aggregates. We conclude that mutated Tb forms aggregates within the cuticle, which  
198 are able to recruit non-mutated Twdl proteins including Tb itself, TwdID, TwdIF and  
199 TwdIS.

#### 200 *The Tb<sup>93</sup> is a twdIL allele*

201 The differences in the localisation of TwdIF-dsRed, TwdIS-GFP and Tb-GFP in both  
202 *Tb<sup>1</sup>* and *Tb<sup>93</sup>* alleles suggest that this discrepancy may be a consequence of different  
203 mutations in the *Tb* gene. Indeed, the phenotypes caused by these two alleles differ  
204 also between the larval stages. *Tb<sup>1</sup>* larvae start to show the squat phenotype at the  
205 L2 larval stage, whilst *Tb<sup>93</sup>* already at L1 (supplementary data 1).

206 The *Tb<sup>1</sup>* allele carries a deletion removing six amino acids within the DUF 243  
207 domain [9]. Sequencing of the *Tb* gene in the *Tb<sup>93</sup>* genome revealed no changes in  
208 the Tb protein sequence (data not shown). We reckoned, therefore, that *Tb<sup>93</sup>* is not  
209 an allele of *Tb*. To test this notion, we sought to recombine the *Tb<sup>1</sup>* and *Tb<sup>93</sup>* alleles  
210 on one chromosome arguing that recombination would underline that these  
211 mutations affect different loci. For this purpose, in a population issued from a cross of  
212 *Tb<sup>1</sup>* and *Tb<sup>93</sup>* heterozygous flies segregating both mutations in trans, we screened for  
213 larvae that did not show the squat phenotype. We isolated four non-Tb larvae in a  
214 population of 5860 larvae suggesting that the mutations affect different loci and that  
215 these loci are roughly 0,1 cM apart. Based on this result, we sequenced other *twdl*  
216 genes in the *twdl* cluster on the right arm of chromosome 3 in *Tb<sup>93</sup>* animals in order to  
217 identify the mutation responsible for the phenotype. Indeed, we found a missense  
218 mutation in the sequence coding for a conserved amino acid of the DUF 243 domain  
219 in another *Twdl* gene, *TwdIL* (Supplementary fig.2). In order to confirm that the *Tb<sup>93</sup>*  
220 phenotype is caused by the mutation in the *TwdIL* gene, we expressed a hairpin RNA  
221 directed against the *twdIL* gene in the background of *Tb<sup>93</sup>*. The hairpin RNA  
222 abolished the squat phenotypes of *Tb<sup>93</sup>* larvae and pupae. In contrast, hairpin RNA  
223 against *TwdIL* did not cause any changes in the phenotype of *Tb<sup>1</sup>* animals. As a  
224 control, we also tested several hairpin RNAs against other *twdl* genes in the *Tb<sup>93</sup>*  
225 background. No phenotype changes were observed in any of these crosses. We  
226 conclude that *Tb<sup>93</sup>* is a dominant allele of the *twdIL* gene. Taken together, Tb and  
227 TwdIL are both needed for correct epicuticle formation.

#### 228 *Twdl aggregates constitute an ectopic epicuticle immersed in the procuticle*

229 The aggregates visible on optical cross-sections of the cuticle shown in figures 3 and  
230 4 do not localise to the expected region of the epicuticle just below the surface but  
231 scattered along the z-axis of the cuticle (Fig. 3, 4). To precisely localise these  
232 aggregates, we analysed the ultrastructure of the *Tb<sup>1</sup>* and *Tb<sup>93</sup>* larval cuticle by  
233 transmission electron microscopy. (data not shown). We observed electron-dense  
234 aggregates immersed within the procuticle.

235 To verify whether these inclusions might be the same structures as the aggregates  
236 identified by confocal microscopy, TwdIS-GFP was co-expressed with fluorescent-  
237 tagged chitin-binding proteins CPR67b-RFP and Vermiform-RFP (Fig.2) in *Tb<sup>1</sup>*  
238 mutant larvae. In both cases the TwdIS-GFP aggregates were surrounded by the  
239 respective red fluorescing procuticle marker.

240 Taken together, we conclude that Twdl proteins form an ectopic epicuticle within the  
241 procuticle of *Tb<sup>1</sup>* and *Tb<sup>93</sup>* larvae.

242

243 *Twdl function in hairs differs from their function in naked cuticle*

244 Organisation of the cuticle in dorsal hairs of wild type larvae is similar to the naked  
245 cuticle: Twdl proteins form layers under the blue auto-fluorescent layer (Fig. 5). The  
246 procuticle is located in the middle of a hair and reaches its tip. In the *twdl* mutant  
247 background Twdls accumulate at the tips of the hair. The procuticle still remains in  
248 the middle of the hair, except for the tip, so that these two layers (Twdl and  
249 procuticle) do not overlap.  
250

251 *Resilin associates with the margin of Twdl aggregates*

252 Recently, we showed that the contact zone between the epicuticle and the procuticle  
253 is marked by dityrosinylated proteins in *D. melanogaster* larvae [18]. In the *wild-*  
254 *type* third instar one-day-old larvae, Resilin-Venus representing the dityrosinylated  
255 layer localizes beneath the TwdlF-dsRed layer (Fig. 7). In the *Tb<sup>1</sup>* and *Tb<sup>93</sup>* mutant  
256 larvae at the same stage, Resilin-Venus is attracted to the aggregates and encases  
257 them. In the dorsal hairs of the young *wild type* third instar larvae just after hatching  
258 Resilin-Venus occupies the space below the TwdlF-dsRed layer in the dorsal hair,  
259 while in the hairs of the *Tb<sup>1</sup>* and *Tb<sup>93</sup>* mutant larvae, it accumulates also at the hair  
260 tips, where the aggregated Tweedle proteins occur. In one-day-old third instar *wild-*  
261 *type* larvae localization of Resilin-Venus is unchanged compared to young third instar  
262 larvae, whilst in one-day-old *Tb<sup>1</sup>* and *Tb<sup>93</sup>* mutant larvae Resilin-Venus is not  
263 localised at the hair tips anymore but encases the Twdl-aggregates the hair tip. Thus,  
264 Twdl proteins dictate the localization and the shape of the dityrosinylated layer  
265 between the epicuticle and the procuticle.  
266

267 *Non-cell autonomous localization of the aggregated Twdls in the cuticle*

268 In our live localization experiments, we noticed that, as reported, TwdlID-RFP was  
269 expressed in a striped pattern in wild-type larvae. Dorsal hairs were lacking TwdlID-  
270 RFP. In the cuticle of *Tb<sup>1</sup>* and *TwdlL<sup>93</sup>* larvae (Fig.8), the Twdl aggregates were  
271 visible in the areas of dorsal hairs including the tips of hairs. Two alternative  
272 scenarios may explain this observation. Either the expression pattern of *twdlID* was  
273 changed in *Tb<sup>1</sup>* and *TwdlL<sup>93</sup>* larvae, or, in addition to the vertical, the lateral mobility  
274 of the TwdlID within the cuticle was enhanced in these larvae. In order to distinguish  
275 between these two possibilities, we monitored the expression of a nuclear-binding  
276 RFP under the control of the *TwdlID* promoter (*TwdlID*>RFP-NLS) in wild-type, *Tb<sup>1</sup>*  
277 and *TwdlL<sup>93</sup>* larvae. In all three cases RFP-NLS was detected in a striped pattern in  
278 the epidermis of developing embryos and larvae. This finding indicates that there  
279 were no changes in the expression pattern of *twdlID*. Thus, the occurrence of the  
280 aggregates in the whole cuticle was due to the lateral spreading of the protein in the  
281 extracellular space.

282 *Epidermal cell shape is altered in Twdl mutant larvae*

283 Compared to wild-type larvae, *Tb<sup>1</sup>* and *TwdlL<sup>93</sup>* mutant larvae are wider, but shorter.  
284 To study to what extent the body shape difference is reflected at the cellular level in  
285 *Tb<sup>1</sup>* and *TwdlL<sup>93</sup>* larvae, we examined the shapes of their epidermal cells visualised  
286 by the membrane bound CD8-GFP protein. In all larvae tested, the number of cells  
287 and their average area were unchanged, but the shape of the cells was significantly  
288 altered in *Tb<sup>1</sup>* and *TwdlL<sup>93</sup>* larvae (Fig.9, Supplementary fig.3). These cells were

289 shorter along the anterior-posterior axis and longer along the dorso-ventral axis of  
290 the animal as compared with cells of wild-type larvae.

291

292

293 *Cuticle stretchability and movement capabilities of the  $Tb^1$  and  $TwdIL^{93}$  larvae are*  
294 *unchanged*

295

296 An intact exoskeleton is a prerequisite for insect locomotion. To find out whether the  
297 altered body shape of  $Tb^1$  and  $TwdIL^{93}$  larvae affects crawling efficiency, we  
298 measured the ratio of the body length in the most stretched to the most contracted  
299 state of young third instar wild-type and  $Tb^1$  and  $TwdIL^{93}$  larvae (Suppl. Fig. 5). We  
300 observed there was no significant difference between the ratios of the wild-type and  
301  $Tb^1$  and  $TwdIL^{93}$  larvae.

302 We also investigated whether the barrel-like larval shape limits the crawling  
303 capabilities of the  $Tb^1$  and  $TwdIL^{93}$  larvae. For this purpose, we measured the height  
304 on which larvae formed pupae on the vial wall. We found that in all cases, the wild-  
305 type,  $Tb^1$  and  $TwdIL^{93}$  homozygous larvae, the average pupariation height was  
306 comparable (Suppl. Fig.5).

307 Taken together, we conclude that the stretchiness of the cuticle of the  $Tb^1$  and  
308  $TwdIL^{93}$  larvae and their movement efficiency are unchanged.

309 *Basal cuticular ridges are disorganised in  $Tb^1$  and  $TwdIL^{93}$  mutant larvae*

310 The cuticular protein Obstructor-E (Obst-E) is needed for ridge formation at the  
311 interface between the procuticle and the apical plasma membrane of epidermal cells  
312 [16]. These ridges are missing in *obst-E* mutant larvae that by consequence do not  
313 contract during pupariation. The question is whether these ridges are altered in  $Tb^1$   
314 and  $TwdIL^{93}$  mutant larvae. We analysed the basal site of the procuticle in wild-type,  
315 in  $Tb^1$  and  $TwdIL^{93}$  late third instar larvae by atomic force microscopy (AFM). The  
316 procuticle of wild-type larvae forms long convexities along the anteroposterior axis of  
317 the larva. The inner cuticular surface of in  $Tb^1$  and  $TwdIL^{93}$  larvae forms convexities  
318 that are comparably flat and disorganized (Fig. 10). Hence, Twdl proteins are needed  
319 for correct orientation of the procuticular basal ridges.

320 In these experiments, we also observed that the cuticular aggregates in Twdl mutant  
321 larvae influence the apical shape of the epidermal cells. We can therefore not decide  
322 whether the effect of Twdl on apical ridge formation is direct or indirect.

323 *Localisation of the Obst-E does not depend on Twdl function*

324 Both, Twdl and Obst-E proteins influence the formation of basal cuticular ridges. To  
325 test whether Twdl proteins may influence Obst-E localisation and function, we  
326 monitored Obst-E-GFP localisation in wild-type, in  $Tb^1$  and  $TwdIL^{93}$  late third instar  
327 larvae (Fig.10). In non-squat L3 larvae Obst-E-GFP is plainly localized in the  
328 procuticle. In  $Tb^1$  and  $TwdIL^{93}$  larvae Obst-E-GFP localisation is unchanged, and does  
329 not bind to the Twdl aggregates (Fig.10). We conclude that the localisation of Obst-E  
330 does not depend on the function of Twdl proteins.

331

## 332 **Discussion**

333 ECMs and the ECM-producing cells adopt a concerted shape that is potentially  
334 important for tissue function. The insect integument consisting of the epidermis and  
335 the apical cuticle, for instance, conceivably plays a key role in body shape

336 determination. The two *Twdl*-class cuticle proteins Tb and *TwdlD* have been shown  
337 to be involved in this process in *D. melanogaster* [10].

### 338 *Twdl* proteins form 2-dimensional sheets within the epicuticle

339 Live imaging experiments with fluorescent-tagged proteins using CLSM reveal that  
340 Tb, *TwdlF* and *TwdlS* proteins form two 2D-dimensional adjacent horizontal sheets i.e.  
341 the *TwdlF* and the Tb/*TwdlS* sheets underneath the surface and above the procuticle.  
342 This localisation indicates that *Twdl* proteins possibly the epicuticle. In agreement  
343 with this interpretation, in ecdysone biosynthesis mutants where the epicuticle is  
344 absent [12], *twdl* gene expression is strongly reduced. We also conclude that the  
345 uniform appearance of the epicuticle in electron-micrographs does not reflect the  
346 stratified organisation revealed by fluorescence CLSM. Thus, the epicuticle is a more  
347 complex structure than supposed by mere ultrastructure analysis.

348 Dominant mutations in *twdl* genes provoke mis-localisation of the mutated proteins  
349 and their accumulation as 3-dimensional aggregates within the procuticle. Non-  
350 mutated *Twdl* proteins are incorporated into these structures. Based on these data  
351 we assume that *Twdl* proteins interact with each other. These observations argue  
352 that the mutated *Twdl* protein sequence loses its ability to form a flat 2-dimensional  
353 ECM but recruits normal and mutated protein sequences to form ectopic 3-  
354 dimensional aggregates without losing the ability to self-assemble. The recruitment,  
355 however, is selective, i.e. not all *Twdl* proteins tested are attracted to these  
356 aggregates. In addition, mutant *Twdl* proteins attract di-tyrosinylated proteins from the  
357 epicuticle-procuticle interface. This supports the notion that *Twdl* protein polymers  
358 are responsible for the formation and orientation of the adjacent di-tyrosine sub-layer  
359 including Resilin that is assumed to confer elasticity.

360 In summary, the epicuticle consists of polymers of *Twdl* proteins that partition this  
361 layer into 2-dimensional horizontal sheets by self-assembly.

### 362 *Squat* body shape as a consequence of body wall tension changes

363 Our data underline that *Twdl* proteins play a key role in body shape determination or  
364 maintenance. This function might rely on their localisation and function within the  
365 cuticle. Alternatively, the dominant phenotype caused by *Twdl* mutations, however,  
366 suggests that the defects may be neomorphic, i.e. they might be unrelated to the  
367 normal function of these proteins. Together, three possible scenarios can explain the  
368 mechanism of *Twdl* protein function in body shape implementation: 1) the  
369 “cytoplasmic”, 2) “epidermal-cuticular interface” and 3) the “cuticle” scenario.

370 The “cytoplasmic” theory relies on mutated *Twdl* proteins that fail to be transported to  
371 the cuticle but accumulate in cytoplasmic structures, probably vesicles, during cuticle  
372 formation when massive secretion and vesicle sorting occur [5, 20]. Accumulation of  
373 *Twdl*-vesicles may perturb plasma membrane dynamics, and thereby cause loss of  
374 correct cell shape along the antero-posterior axis. The altered cell shape would, in  
375 turn, influence the body shape.

376 The alternative “epidermal-cuticular” theory relies on the extracellular *Twdl*  
377 aggregates that are in close contact with the apical surface of the epidermal cells.  
378 According to this theory, these aggregates in the procuticle are responsible for the  
379 dis-organisation of the regular ridges that run along the anteroposterior axis in the  
380 epidermal-cuticular interface [16]. These ridges have recently been shown to depend  
381 on the presence of the procuticular protein *Obst-E* that controls longitudinal  
382 contraction and lateral expansion of the L3 larvae during pupariation. The deletion of  
383 *obst-E* causes flattening of the ridges and formation of longer and thinner pupae. In  
384 *twdl* mutant larvae, *Obst-E* localisation appears to be normal. We therefore reckon



385 that body shape changes in *twdl* mutant animals are independent of Obst-E function.  
386 As a consequence of ridge mis-orientation in *twdl* mutant larvae, however, the  
387 epidermal cells lose their longitudinal antero-posterior direction and adopt a shape  
388 with random orientation. Accordingly, the change of orientation preference of  
389 epidermal cells may be responsible for the overall shorter but thicker body shape.  
390 The third, “cuticle” theory considers the depletion of either the epicuticle itself or the  
391 epicuticle-procuticle interface might be the reason for the aberrant body shape in *twdl*/  
392 mutant animals. In this view, the *Twdl* polymers and/or the dityrosynilated proteins of  
393 the epicuticle-procuticle interface confer the elastic forces resisting the internal  
394 hydrostatic pressure. A thin epicuticle and/or epicuticle-procuticle sub-layer may be  
395 insufficient to withstand these forces. According to the formula of Barlow, a  
396 weakened wall of a closed pipe or cylinder would allow radial rather than longitudinal  
397 expansion of the object (Fig. 11). In analogy, due to a weakened cuticle and  
398 assuming a normal hydrostatic pressure, *twdl* mutant larvae become thick and short.  
399 Epidermal cells would, in this scenario, passively follow cuticle stretching in the  
400 lateral direction.  
401 In any case, body shape change in *twdl* mutant larvae does not affect locomotion  
402 efficiency. Importantly, the *twdl* mutant phenotype enables us distinguishing body  
403 shape and locomotion as distinct functions of the cuticle that are not necessarily  
404 linked.

#### 405 *Twdl* evolution

406 The *D. melanogaster* genome encodes 27 *twdl* genes. Different combination of the  
407 respective proteins in different body regions allow establishment of different types of  
408 epicuticles, thereby, conform with our “cuticle” theory, probably influencing the  
409 physical properties of the cuticle. So far so good. In contrast to *D. melanogaster*  
410 some insects such as the bedbug *Cimex lectularius* or the honeybee *Apis mellifera*  
411 do only have two or three copies of *twdl* in their genome [21]. How is epicuticle  
412 complexity that we encounter in *D. melanogaster* achieved in these species? We can  
413 only speculate that, testified by the varying number of *twdl* genes, the epicuticle is a  
414 fast evolving structure and therefore reckon that other types of epicuticular proteins  
415 may contribute to its construction to accommodate its different functions in species  
416 with only a few *twdl* genes.

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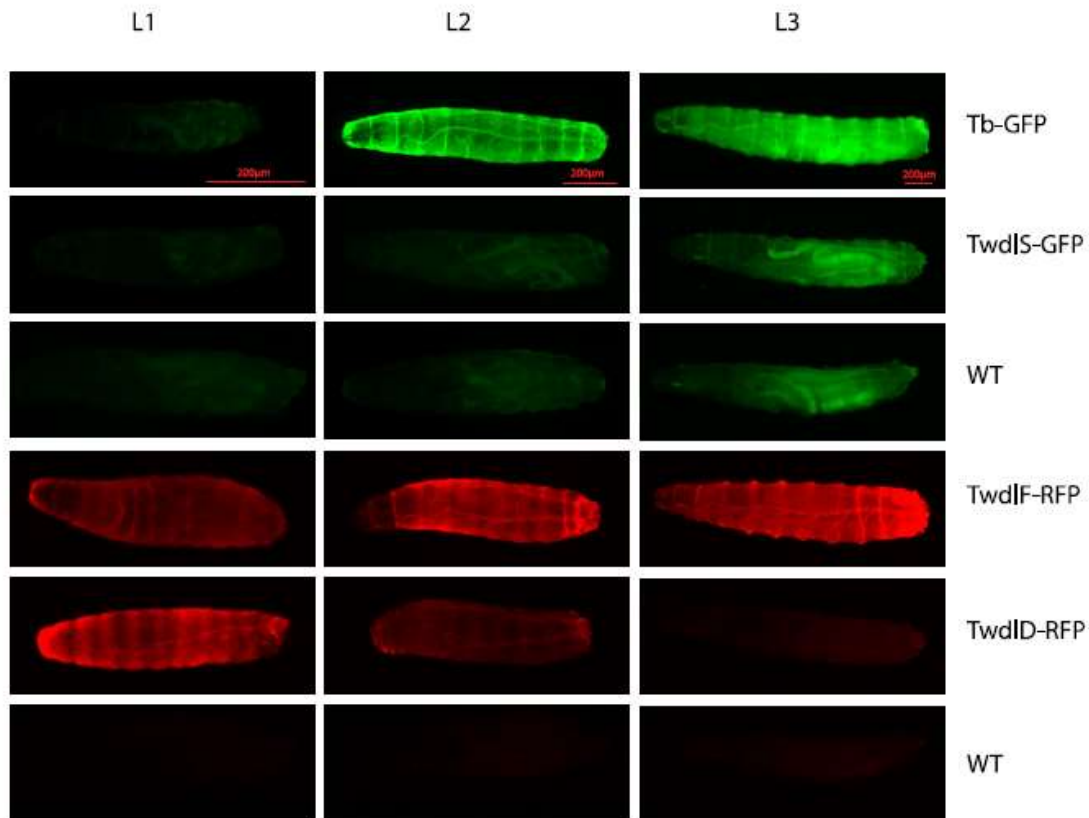
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506 **Figure legends**

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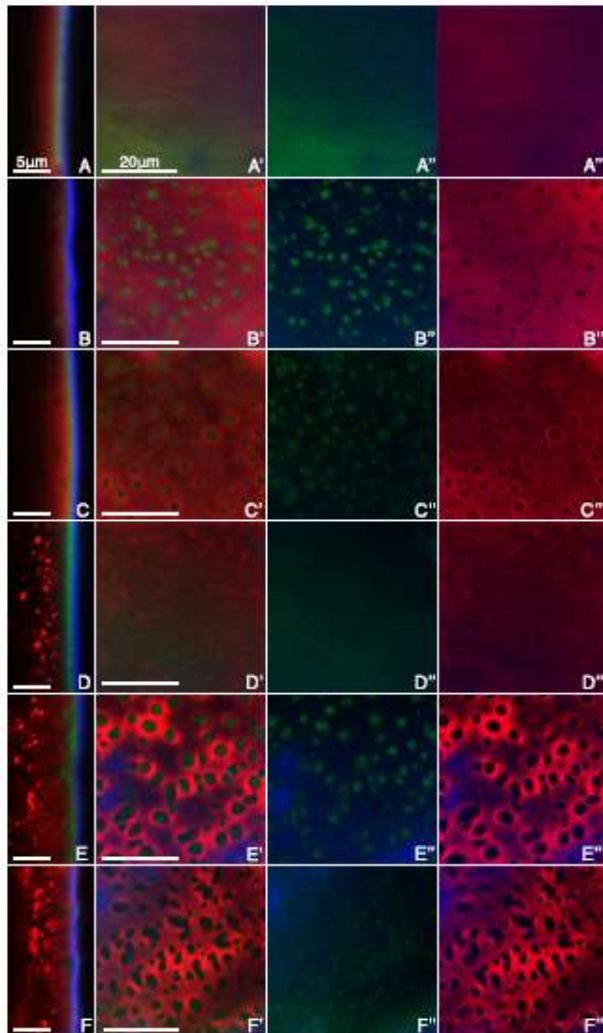


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509 *Fig. 1. Expression profile of GFP- and dsRed-tagged Twdl proteins at three larval*  
510 *stages.*

511 All four Twdl proteins localize to the larval cuticle. Tb-GFP is weakly visible at first  
512 larval stage (L1) as lateral patches, whilst at second (L2) and third (L3) larval stages  
513 is decently visible in the whole cuticle. The signal of TwdIS-GFP is very faint in the  
514 cuticle of L2 and weak in the whole cuticle of L3. TwdIF-RFP is observable in the  
515 entire cuticle at all larval stages. TwdID-RFP shows strong striped signal in the  
516 cuticle of L1, weaker in L2 and very faint signal in the posterior cuticle of L3 larvae.

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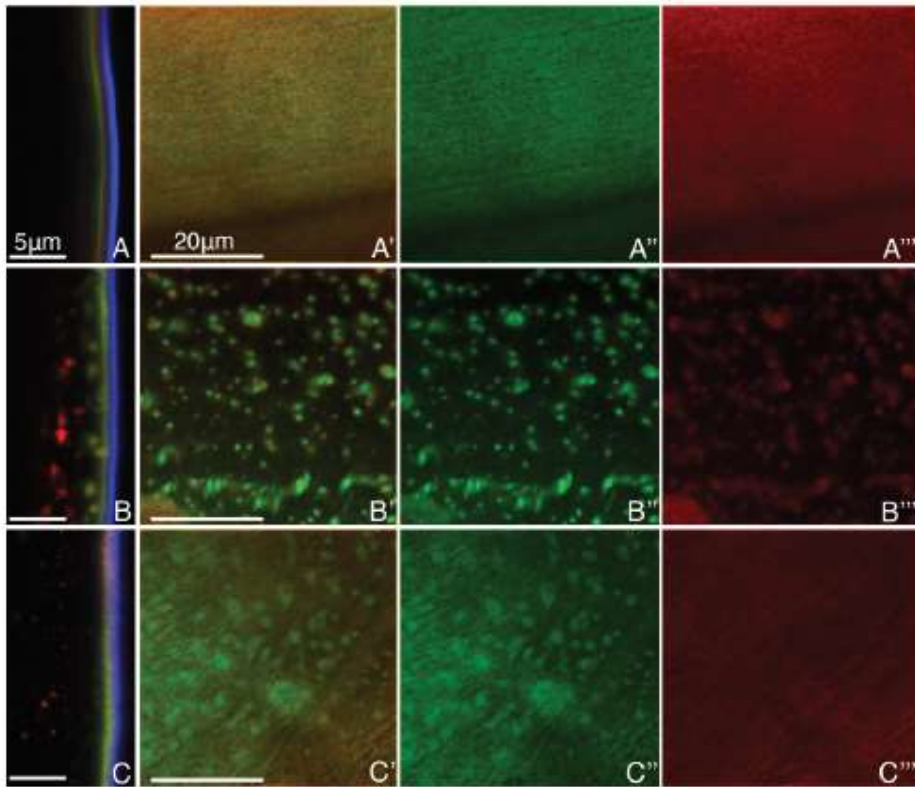


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520 *Fig. 2. Localisation of TwdIS-GFP, Cpr67b-RFP and Verm-RFP in the cuticle of non-*  
521 *Tb, Tb1 and Tb93 third instar larvae.*

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523 In the cuticle of non-Tb larvae, TwdIS-GFP (green) is uniformly distributed forming  
524 thin layer under the blue 405-induced autofluorescent line (A and D: lateral views; A'-  
525 A''' and D'-D''' top views with respective channels separation). dsRed-tagged chitin-  
526 binding Cuticular Protein 67b (Cpr67b-dsRed, red), expressed in the epidermis from  
527 the TwdIM promoter is plainly distributed in the thick procuticle under the TwdIS-GFP  
528 layer (A-A'''). Ubiquitously expressed Vermiform-RFP (Verm-RFP, red) is plainly  
529 distributed in the entire procuticle below the TwdIS-GFP layer and forms vesicle-like  
530 structures in the cells (D-D'''). In the cuticle of Tb1 larvae (B-B'''; E-E''') and Tb93  
531 larvae (C-C'''; F-F''') TwdIS-GFP partially localizes to the upper epicuticle, and  
532 partially binds to the aggregates immersed in the procuticle. It does not overlap with  
533 CPR67-dsRed (B-B'''; C-C''') and Verm-RFP (E-E'''; F-F'''), there are distinct borders  
534 between these proteins in the procuticle.



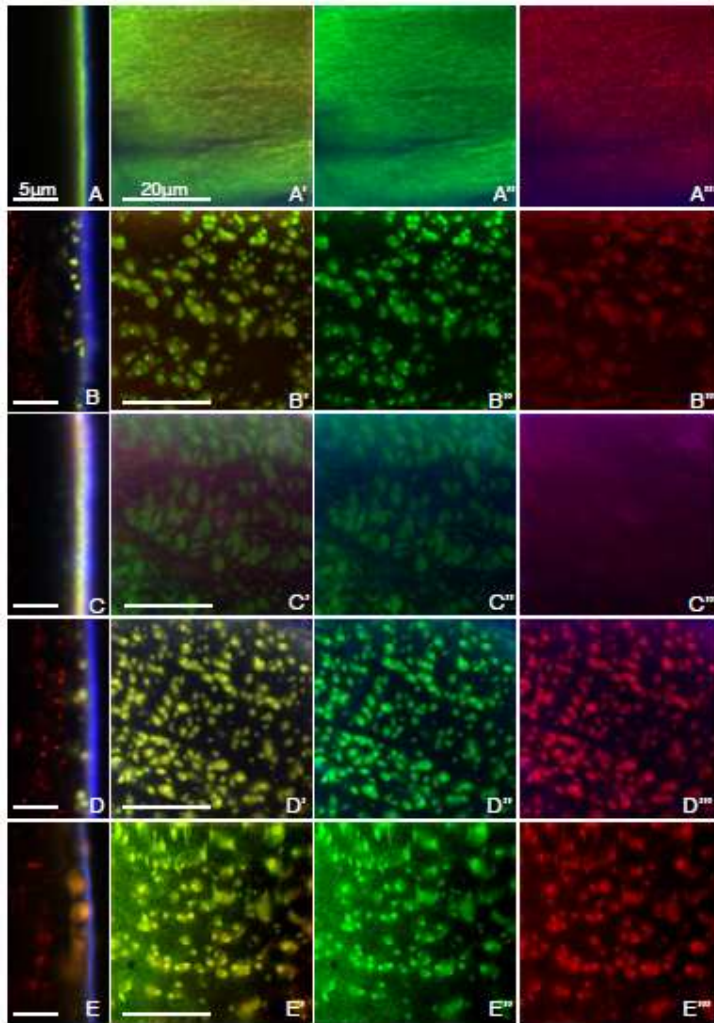
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537 *Fig. 3. Localisation of TwdIS-GFP and TwdIF-dsRed in the cuticle of non-Tb, Tb1 and*  
 538 *Tb93 third instar larvae.*

539 *TwdIF-dsRed (red) and TwdIS-GFP (green) form two separate layers in the cuticle of*  
 540 *WT larvae: TwdIF localizes just below the 405 layer and TwdIS-GFP under the TwdIF*  
 541 *layer (A: lateral view, A'-A''': top views with respective channels separation). In the*  
 542 *Tb1 larvae both proteins are partially mislocalised, forming aggregates in the lower*  
 543 *cuticular layer (B-B'''). In the Tb93 larvae only part of TwdIS-GFP binds to the*  
 544 *aggregates, but TwdIF-RFP does not (C-C'''). However, there is no decent*  
 545 *stratification of these two proteins in the lateral view of the naked cuticle visible (C).*

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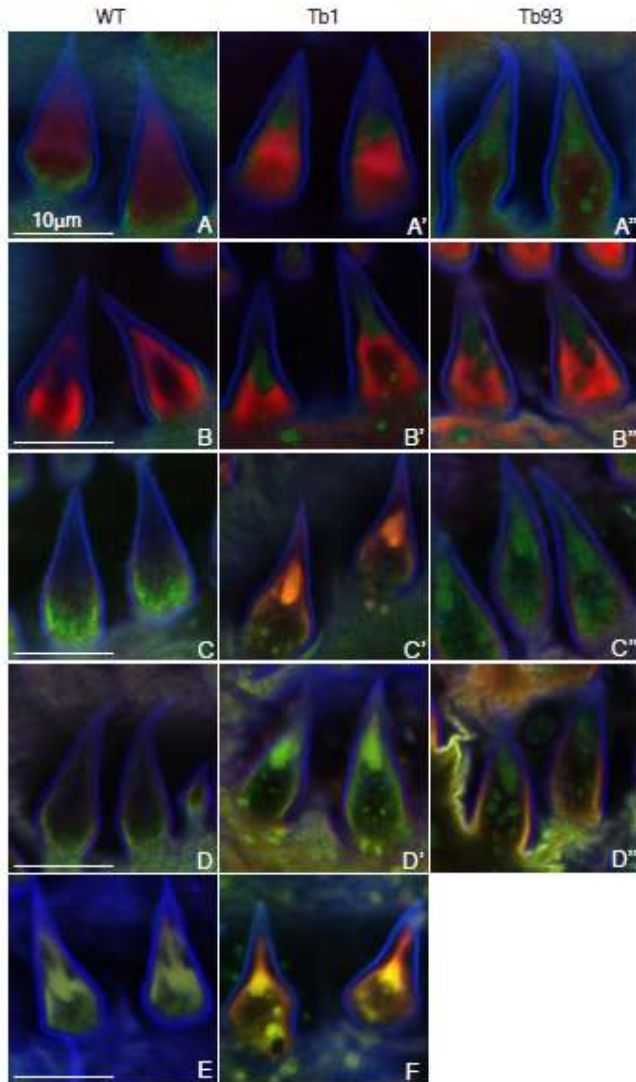


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*Fig.4. Localisation of Tb-GFP, TwdIF-dsRed and TwdIS-GFP in the cuticle of non-Tb and Tb mutant larvae.*

In the cuticle of WT larvae Tb-GFP (green) and TwdIF-dsRed (red) overlap (A: lateral view, A'-A''': the top views with respective channels separation). In the cuticle of Tb1 larvae both proteins are partially aggregated (B-B'''). In the cuticle of Tb93 larvae Tb-GFP forms aggregates, whilst TwdIF-dsRed does not or very weakly (C-C'''). In the cuticle of the larvae with two additional copies of RFP-tagged, mutated Tb protein (Tb1-RFP, red), the non-mutated Tb-GFP form (green) binds to the aggregates formed by Tb1-RFP (D-D'''). TwdIS-GFP protein (green) joins the Tb1-RFP aggregates as well (E-E''').





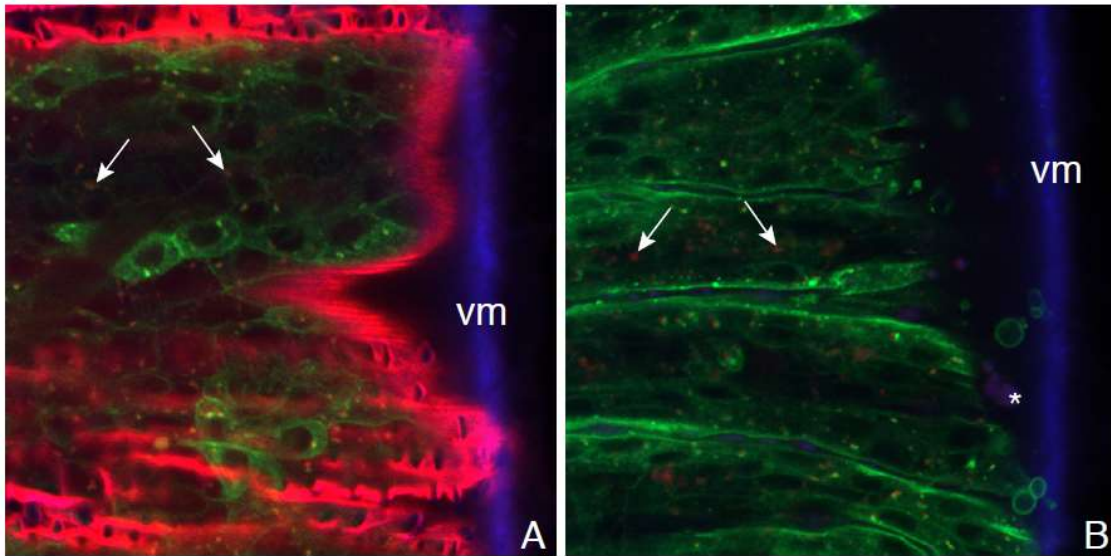
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*Fig. 5. Localisation of Twdl fluorescent proteins in the hairs of non-Tb and Tb mutant larvae.*

574 In the dorsal hairs of non-Tb larvae TwdIS-GFP forms a layer under the  
575 autofluorescent line (blue) at the bases of the hairs but does not reach their tip (A, B).  
576 Cpr67b-dsRed (A) and Verm-RFP (B) are localised in the center of hairs. In the hairs  
577 of Tb1 and Tb93 larvae, TwdIS-GFP accumulates at the tips and forms smaller  
578 aggregates in the middle of the hair, whilst Cpr67b-dsRed and Verm-RFP are  
579 localised in the center, excluding the TwdIS areas (A'-A''; B'-B''). TwdIF-dsRed (red)  
580 forms a layer between the autofluorescent layer and TwdIS-GFP layer (green) in the  
581 hairs of non-Tb larvae (C). In the hairs of Tb1 larvae stratification under the envelope  
582 seems to be retained, whilst at the hair tip and in the aggregates proteins overlap  
583 (C'). In Tb93 larvae stratification is retained and only TwdIS-GFP is mislocalized (C'').  
584 Localisation of Tb-GFP (green) in the hairs of non-Tb and Tb larvae is similar to  
585 TwdIS-GFP (D-D''). Mutated Tb1-RFP (red) form attracts unmutated Tb-GFP (E,



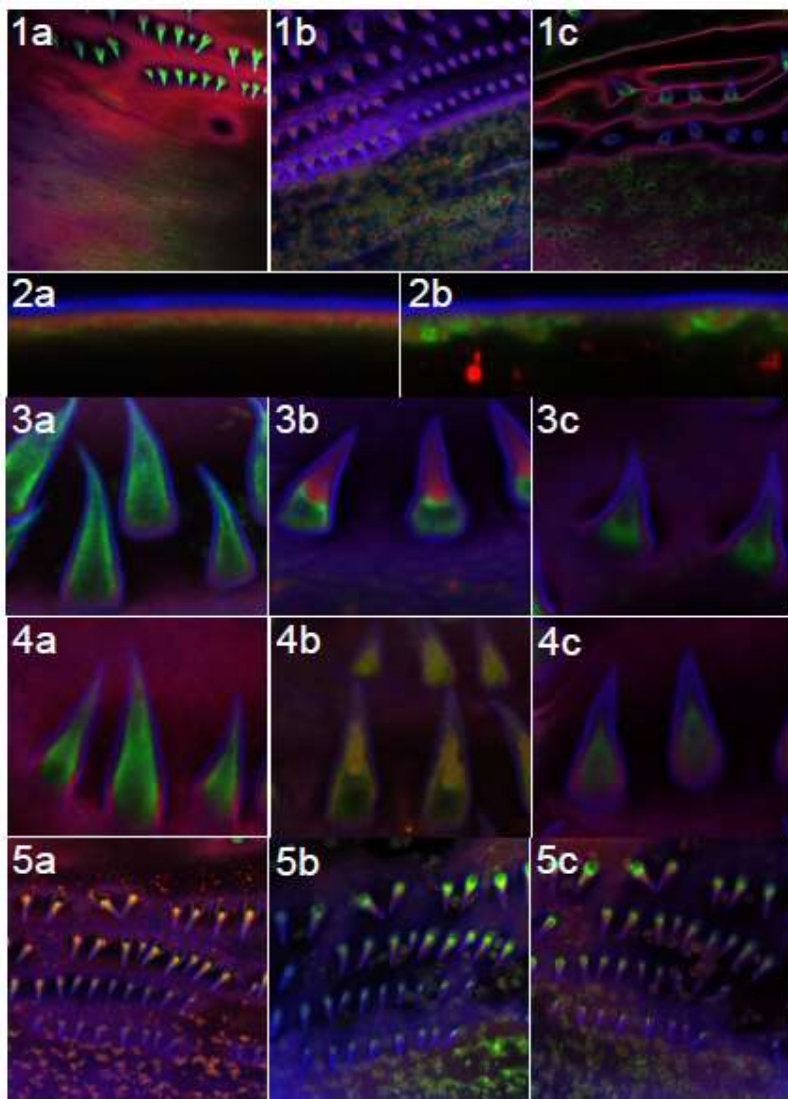
586 green) and TwdIS-GFP (F, green).  
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*Fig.6 Localisation of TwdIF-dsRed in WT and phm mutant larvae.*

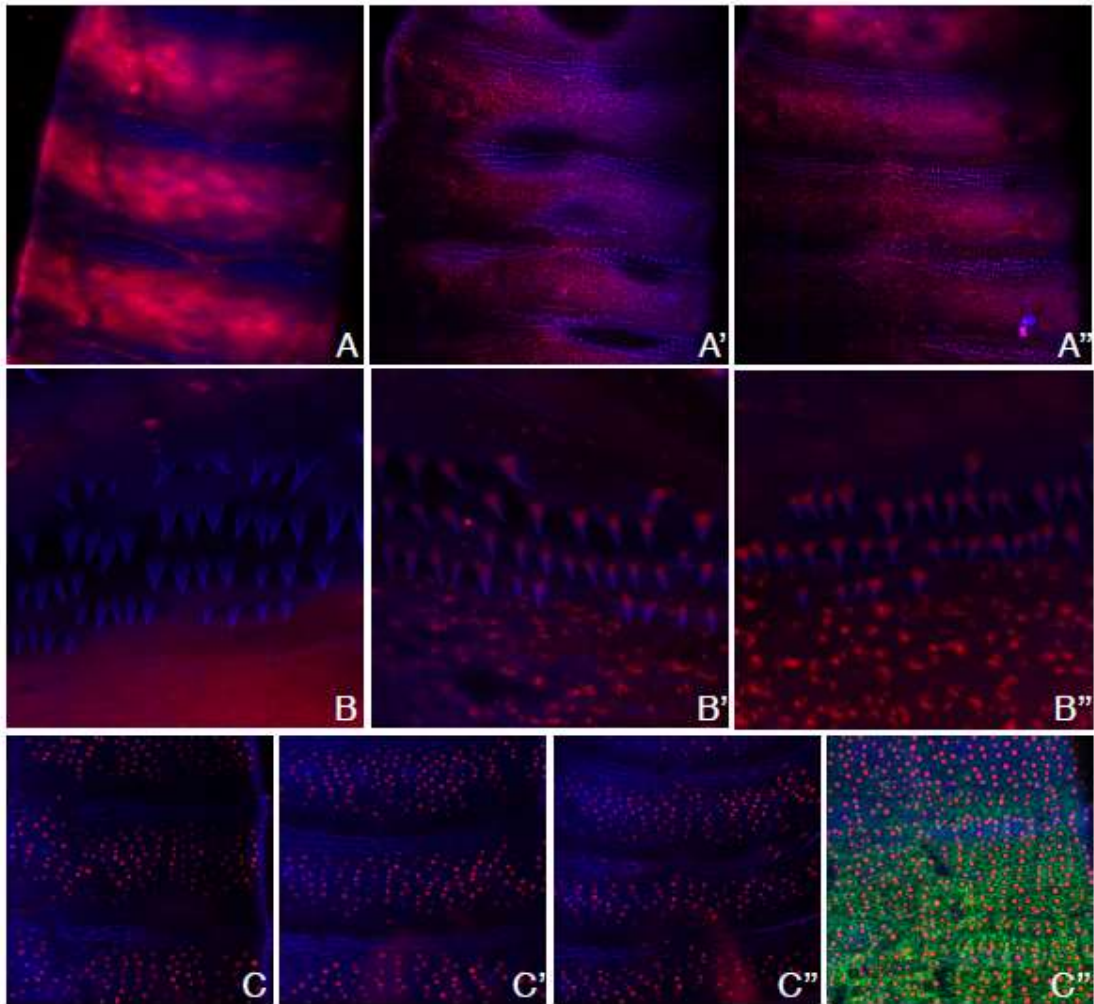
In the wild type first instar larvae before hatching the signal of TwdIF-dsRed (red) is strong in the entire cuticle and in the round-shaped cellular structures (shown by arrows), probably vesicles (A; green: ubiquitously produced membrane-binding CD8-GFP; blue: 405-induced cuticle and vitelline membrane (vm) autofluorescence). In the phantom mutants expression of TwdIF-dsRed is very low, there is weak red signal corresponding to the cellular vesicles and unusual structures outside the epidermis, not attached to the body surface (shown by asterisks), containing also the 405-induced material (B). In this case, the 405-induced autofluorescent signal is also strongly diminished in the whole cuticle.



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Fig. 7. Localisation of Resilin-Venus in wild type, *Tb1*, *Tb93* larvae.

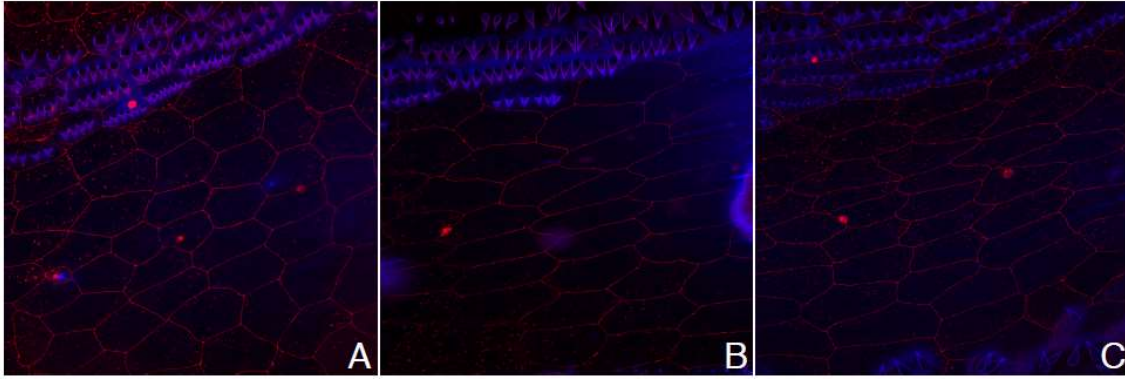
In the *wild-type* third instar larvae Resilin-Venus localizes beneath the TwdIF-dsRed layer (1a, 2a). In the *Tb<sup>1</sup>* (1b, 2b) and *Tb<sup>93</sup>* (1c) mutant larvae Resilin-Venus is attracted to the aggregates and encircles them. In the dorsal hairs of the young *wild-type* third instar larvae just after hatching Resilin-Venus occupies the space below the TwdIF-dsRed layer (4a), whilst in the hairs of the *Tb<sup>1</sup>* and *Tb<sup>93</sup>* mutant larvae (4b and 4c, respectively), it accumulates also at the hair tips, overlapping with the aggregates. In one-day-old third instar *wild-type* larvae Resilin-Venus localisation is unchanged compared to young third instar larvae (3a), whilst in one-day-old *Tb<sup>1</sup>* and *Tb<sup>93</sup>* mutant larvae (3b and 3c, respectively) Resilin-Venus is not localised at the hair tips but encases the TwdI-aggregates at the hair tip. Changes of Resilin-Venus localization occurring with time can be visualized in one region of a living L3 *Tb1* larva just after hatching (5a), 24 hours after hatching (5b) and 48 hours after hatching (5c).



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*Fig.8 Non-cell autonomous localization of the aggregated TwdIDs in the cuticle.*

On the dorsal side of the non-Tb L2 larvae TwdID-dsRed is visible in striped domains of the naked cuticle, excluding the domains with hairs (A; B: magnification of the hair region). In the cuticle of Tb1(A', B') and Tb93 (A'', B'') mutant larvae the aggregates of the TwdID-dsRed are observable in the whole cuticle, also in hairs. Red Fluorescent Protein with attached nuclear localisation signal, expressed from the TwdID promoter (TwdID>RFP-NLS) in the background of the non-Tb(C), Tb1 (C') and Tb93 (C'') larvae, in all three cases shows a striped pattern of red nuclei. In control larvae expressing Red Fluorescent Protein with an NLS signal in the whole cuticle, all epidermal red nuclei are visible (C'''; green: ubiquitously expressed membrane-binding CD8-GFP marks the cell borders).



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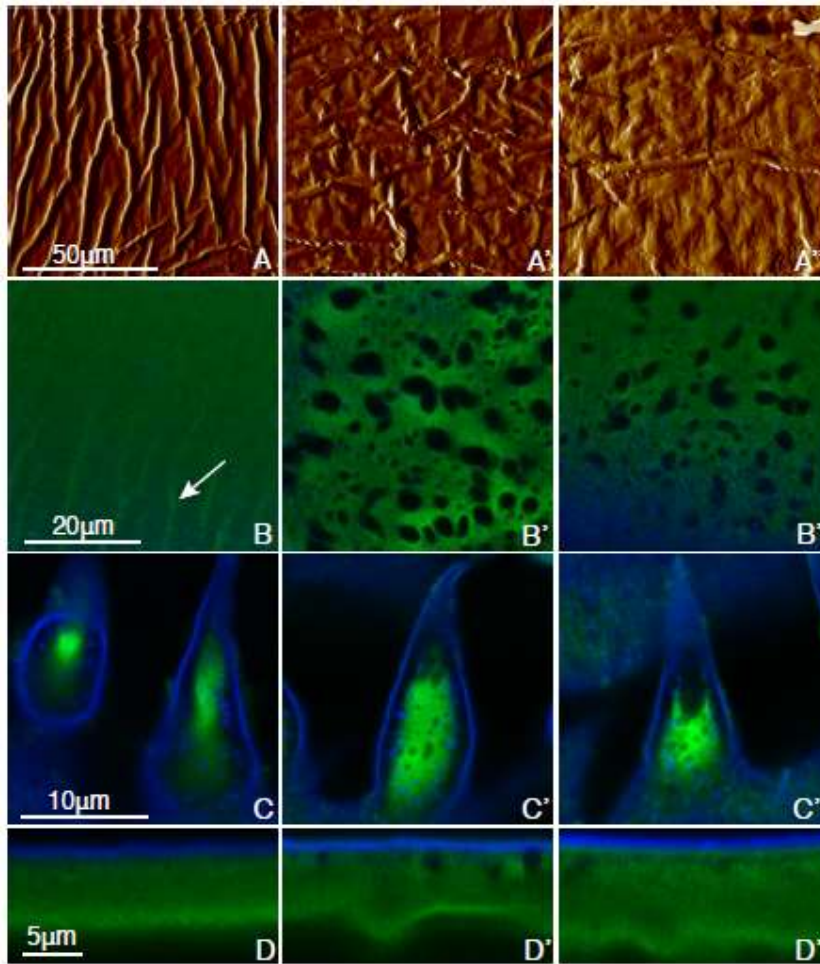
637 *Fig. 9 The differences in the cell shape and cuticular internal surface of the non-Tb*  
638 *and Tb mutant larvae.*

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640 The expression of the fluorescent-tagged E-Cadherin (E-Cadherin-mCherry, red),  
641 accumulating at the borders of epidermal cells shows that the cells of the third instar  
642 Tb1 (A) and Tb93 (B) larvae are more flat longitudinally and more broad laterally  
643 compared to the wild-type epidermal cells (A). The signal strength of E-Cadherin is  
644 comparable at all cell borders, anterior, posterior and the lateral ones in the non-Tb  
645 and Tb mutant larvae.

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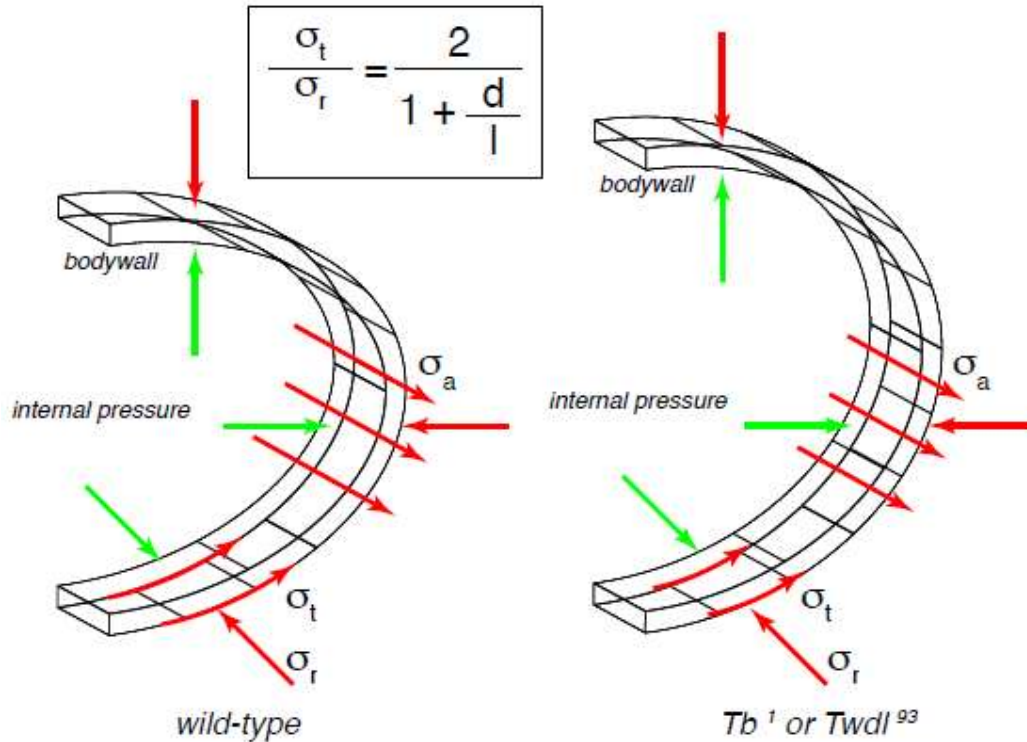


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*Fig.10 The structure of procuticular ridges but not the localisation of Obstructor-GFP is changed in Tb mutant larvae.*

The internal cuticular surface of the non-Tb L3 larvae scanned by the atomic force microscope shows longitudinal ridges running parallel to the anterior-posterior axis (A). In the Tb1 (A') and Tb93 mutants (A'') the structure of the ridges is disrupted, they run in different directions and seem to be flatter.

GFP-tagged chitin binding protein Obstructor E (ObstE-GFP, green) is plainly distributed in the whole procuticle of the naked cuticle (B: the top view of the dorsal cuticle; D: the lateral view; blue: autofluorescence of the external cuticular envelope) and in the center of the dorsal hairs of wild type larvae (C). On the top view the cuticular ridges are discernable (B, marked with arrow). In the Tb1 (B'-D') and the Tb93 larvae (B''-D'') it is still plainly distributed in the procuticle, excluding the epicuticular aggregates.

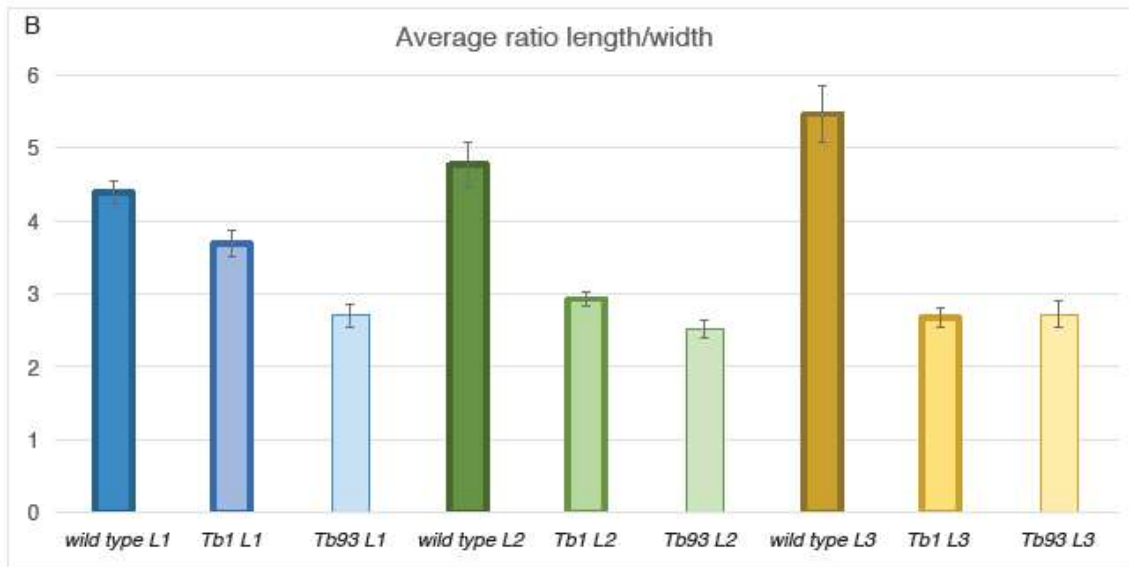
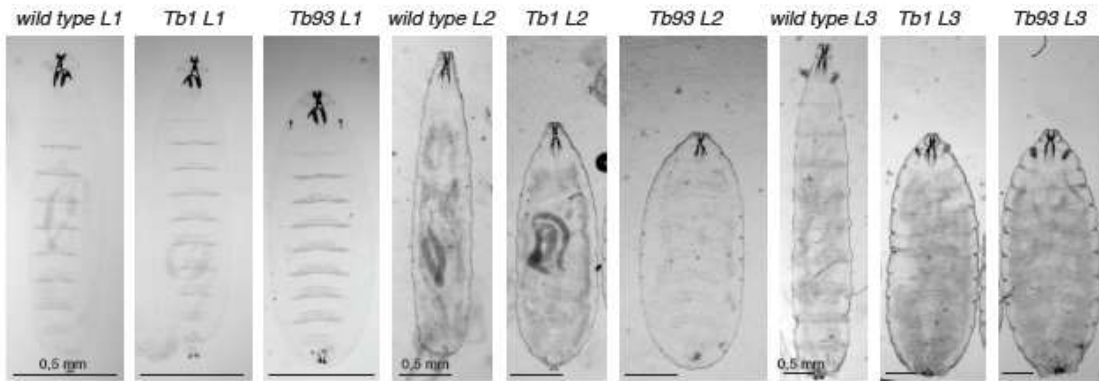


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*Fig. 11 Explanation of a growth of mutated Tweedle larvae according to Barlow's law.*

According to the law of Barlow, an object of the shape of a closed pipe or cylinder with a weakened wall will expand rather radially than longitudinally. In analogy, the Tweedle mutants with depleted epicuticle will become thicker and shorter during growth than the wild type larvae.  $d$  = diameter of the object,  $\sigma_a$  = axial tension (longitudinal direction) in the wall,  $\sigma_t$  = tangential tension in the wall,  $\sigma_r$  = radial tension,  $l$  = length of the object.

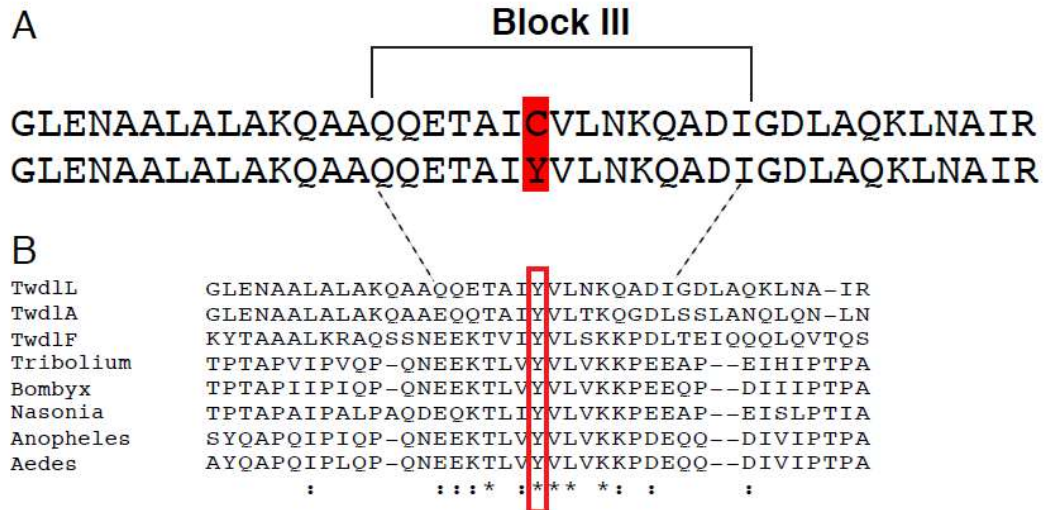
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Suppl. Fig.1 Comparison of the shape of the wild type, Tb1 and Tb93 three larval stages.

Hoyer's preps of the larval cuticles reveal that the the first, second and third instar Tb93 larvae are decently shorter and thicker than the wild type larvae (A). Second and third instar Tb1 larvae are clearly shorter and thicker, but the first instar larvae are only a little bit shorter than the wild type larvae (A). The shape differences between Tb and wild type larvae become more visible at every subsequent stage. B: The average ratio of length to the width of measured cuticle preps of the wild type, Tb1 and Tb93 first, second and third instar larvae.

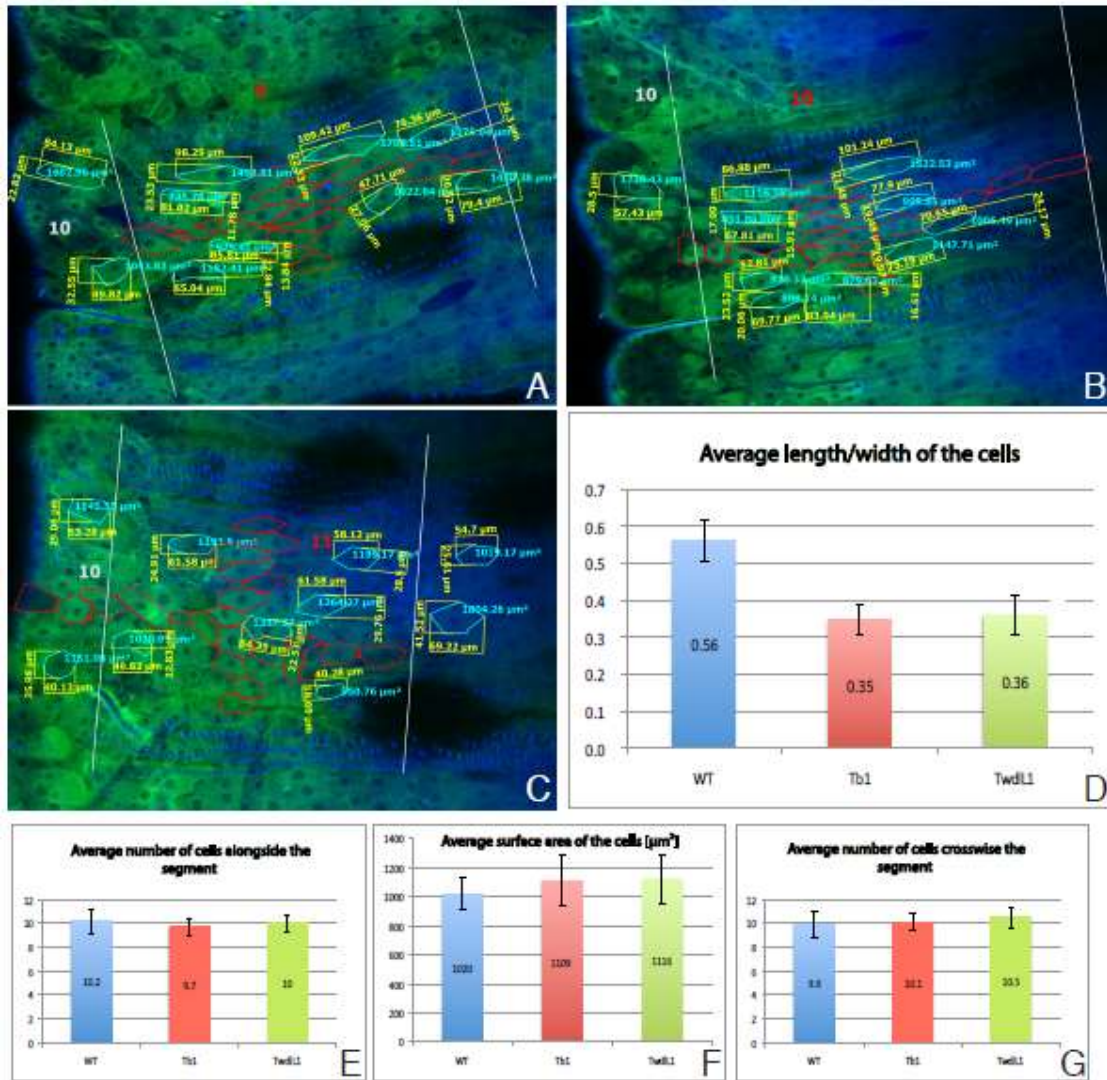


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*Suppl. Fig. 2. Tb93 allele is a TwdLL allele.*

In a conserved block III of a DUF 243 domain of the TwdLL protein in Tb93 larvae there is a missense mutation changing tyrosine into cysteine (A, mark on red). This tyrosine is conserved in the Twdl proteins of many insect species (B, conserved tyrosine marked with red frame).

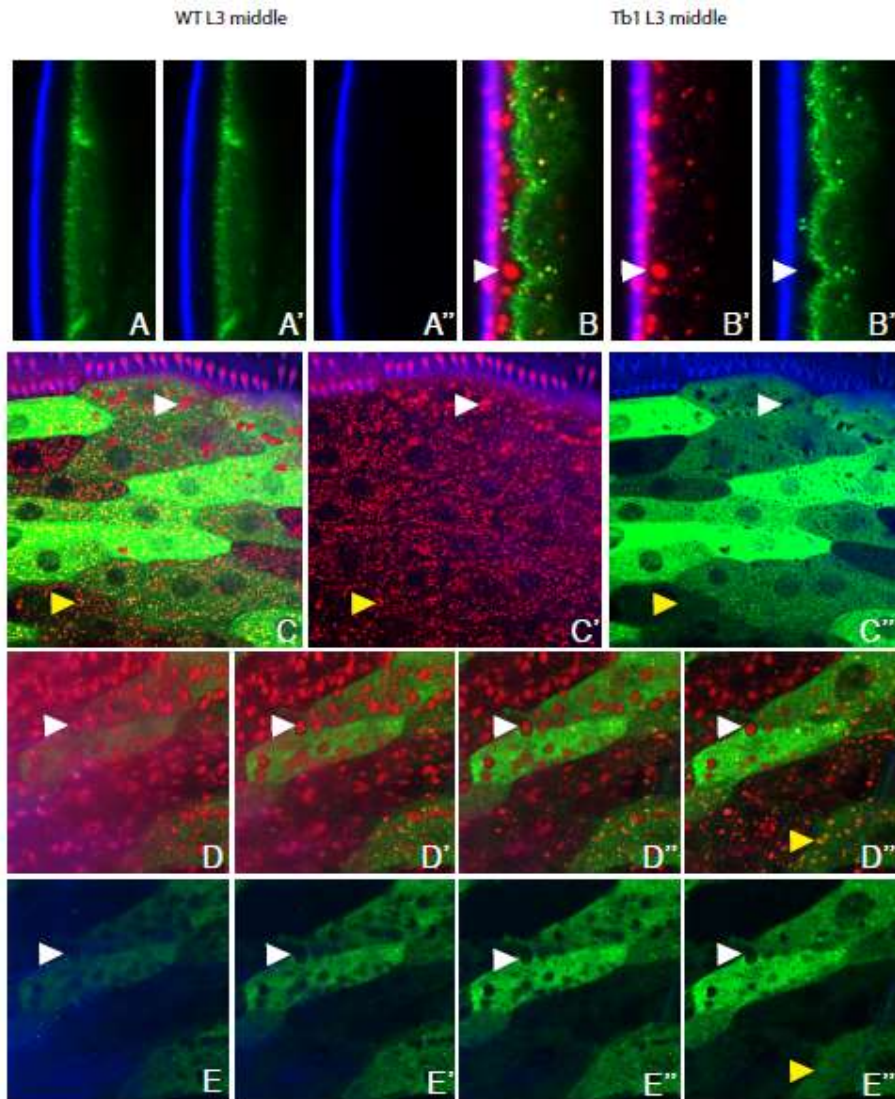




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Suppl. Fig. 3. Comparison of the cell shape and the cell number in wild type, *Tb1* and *Tb93* third instar larvae.

In the larval third abdominal segment the average cell number along the whole segment (between the two apical areas with hairs) and across half of the segment is comparable in the apical epidermis of the wild type, *Tb1* and *Tb93* mutant larvae (A, B and C, respectively; Borders of counted cells marked on red. Green: ubiquitously expressed membranous CD8-GFP, blue: 405-induced cuticle autofluorescence; E, G). The average cell area also does not differ between all three cases (A-C: borders of the cells with measured area and the outcome marked on blue; F). The ratio of the length to the width of the epidermal cells of the *Tb* larvae is significantly lower compared to the ratio of the non-*Tb* epidermal cells (A-C: measurements of the length and the width marked on yellow; D).



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*Suppl. Fig.4 Influence of the ectopic Twdl aggregates on the epidermal apical surface*

The apical epidermal surface in wild type third instar larvae is even (A-A'', green: ubiquitously expressed membranous CD8-GFP marking the apical cell surface, blue: autofluorescent 405-induced envelope; A': without red channel; A'': without green channel). Tb1-RFP aggregates (red) accumulating ectopically in the procuticle cause the convexities in the epidermal cell surface (B-B''; without red (B') and green channel (B'')); convexity shown by a white arrow). C-C'': the top view, convexities in the epidermal apical surface shown by a white arrow, whilst the cellular Tb1-RFP aggregates shown by a yellow arrow. D-D'': Z-stack of the epidermal cells from the top view with higher magnification, showing procuticular aggregates and the cellular aggregates inside the cell. E-E'': Z-stack without a red channel, revealing holes in the epidermal surface in the places of the procuticular aggregates.

	WT1	WT2	WT3	WT4	WT5	Tb1 1	Tb1 2	Tb1 3	Tb1 4	Tb1 5	Tb93 1	Tb93 2	Tb93 3	Tb93 4	Tb93 5
longest	190.43	188.4	187.97	186.75	180.35	117.69	117.89	101.32	98.08	96.57	108.47	103.77	106.45	116.25	107
shortest	163.23	163.32	167.29	162.53	160.59	98.08	102.83	91.21	87.01	90.25	98.62	89.94	95.41	107.79	91.92
% shortest/longest	85.72	86.69	89.00	87.03	89.04	83.34	87.23	90.02	88.71	93.46	90.92	86.67	89.63	92.72	85.91
	87.50					88.55					89.17				
SD	44.47373					3.714186					2.862643				

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	WT					Tb1					Tb93				
	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
1	3	10	43	22	4	13	7	26	16	15	20	0	0	0	0
2	18	28	5	18	23	23	13	27	20	14	8	0	0	0	0
3	17	13	11	11	33	32	15	5	35	33	17	15	0	0	0
4	18	23	32	13	3	25	4	8	41	37	35	33	1	49	34
5	24	24	32	27	22	31	17	13	25	30	45	43	23	22	34
6	26	3	20	3	10	20	33	16	30	5	18	43	28	12	26
7	27	15	21	15	19	10	28	6	12	7	41	47	40	25	23
8	42	30	26	10	27	7	28	10	30	30	41	13	41	1	23
9	28	6	2	43	5	12	20	20	46	38	3	13	10	25	48
10	43	10	8	47	18	26	1	28	2	44	3	13	18	16	15
11	3	32	13	25	20	10	5	30	25	10	24	4	24	1	40
12	8	6	26	5	42	6	8	35	28	17	23	21	10	7	36
13	34	5	28	14	27	12	15	35	3	22	13	45	27	7	19
14	36	22	10	3	27	18	17	20	8	13	35	5	21	35	21
15	27	5	14	7	18	35	26	6	13	28	16	20	8	46	28
16	32	5	23	9	22	18	40	25	50	37	16	22	22	1	48
17	45	7	35	46	34	17	38	45	27	17	19	42	48	10	54
18	42	53	59	41	54	2	31	12	22	13	33	28	32	33	32
19	33	12	6	14	17	26	55	28	12	25	33	53	19	52	40
20			23	4	33	34	58	36	51			45	18	42	41
average	26.63	16.26	21.85	18.85	22.90	18.85	22.95	21.55	24.80	22.89	23.32	25.25	19.50	19.70	28.10
average from SD			21.30					22.21					23.17		
			3.96					2.21					3.68		3.91

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Suppl. Fig. 5 *Cuticle stretchability and movement capabilities of the wild type, Tb<sup>1</sup> and TwdIL<sup>93</sup> larvae.*