

1 **Direct and correlated responses to laboratory selection for body melanisation in *D.***
2 ***melanogaster*: support for melanism- desiccation resistance hypothesis.**

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11 **Running title:** Melanism- Desiccation hypothesis revisited

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SUMMARY

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For *Drosophila melanogaster*, cuticular melanisation is a quantitative trait, varying from no melanin to complete dark. Variation in melanisation has been linked with stress resistance, especially desiccation, in *D. melanogaster* and other species. As melanism has a genetic component, we selected melanic and non-melanic phenotypes of *D. melanogaster*, in order to confirm the association of desiccation resistance and rate of water loss with cuticular melanisation previously reported for this species. A bidirectional selection experiment for dark (D1- D4) and light (L1- L4) body color in *D. melanogaster* was conducted for 60 generations. In 60 generations of selection for pigmentation, an increase of 1.6 fold in selected dark strain and decrease of 14 folds in selected light strain was observed as compared to control populations. Desiccation resistance increased significantly in the dark selected morphs as compared with control. The observed increase in desiccation resistance appeared as a consequence of decrease in cuticular permeability. Our results show that water balance related traits were significantly correlated with abdominal melanisation and were simultaneously selected bidirectionally along with melanisation.

Keywords: Artificial selection experiment, abdominal melanisation, correlated responses, desiccation resistance, *Drosophila melanogaster*

INTRODUCTION

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Several studies have shown evidences for the role of natural selection in maintaining phenotypic variation in body melanisation of diverse insect taxa (Majerus, 1998; True, 2003). In *D. melanogaster*, body melanisation is a quantitative trait and shows significant levels of both within and between population variations (Parkash et al., 2008). Geographical populations of *D. melanogaster* from Africa (Pool and Aquadro, 2007), India (Parkash et al., 2008) and Australia (Telonis- Scott et al., 2011) have shown clinal variation in abdominal or thoracic melanisation which suggest adaptations to local climatic conditions. In several other studies, clinal variation is evident for many stress related traits which covary strongly with latitude or altitude (Parkash et al., 2008). However, it is not clear whether various ecologically relevant quantitative traits show independent or correlated selection responses. For example, associations between body melanisation and desiccation related traits have been observed in latitudinal as well as altitudinal populations of *D. melanogaster* from India but these studies provide indirect evidence (Parkash et al., 2008a). If desiccation resistance evolves through changes in cuticular permeability in *D. melanogaster*, the target of selection might be cuticular components (cuticular melanisation and/or cuticular lipids). A possible link between body melanisation and desiccation resistance can be shown if laboratory selected strains for higher melanisation evidence increased desiccation but this hypothesis has not been tested so far in *D. melanogaster* as well as other *Drosophila* species.

For wild populations, ecophysiological and morphological traits might coevolve according to their combined influence on fitness (Angilletta, 2009). For example, tropical habitats on the Indian subcontinent select lighter body color phenotype as well as starvation

68 tolerance (Parkash and Munjal, 2000) but it is not clear whether these traits are under
69 independent selection or coevolve. Further, there are evidences in favor of coadaptation hypothesis
70 (Angilletta, 2009) e.g. behavioral thermoregulation and body coloration are coadapted traits in
71 pygmy grasshopper (*Tetrix subulata*; Forsman, 2000). Coadapted traits are also represented by
72 associations between body melanisation and desiccation related traits (Parkash et al., 2008a,
73 2010a) and thermo-resistance traits in *D. melanogaster* (Parkash et al., 2010b). Cuticular
74 hydrocarbons are also subject to natural selection, being important in providing desiccation
75 resistance for many insect species (Gibbs & Rajpurohit, 2010). Several insect taxa have shown
76 variable cuticular permeability due to changes in the composition or amount of cuticular lipids
77 (Edney, 1977; Toolson, 1984; Hadley, 1994; Rourke, 2000). There are clines of water balance
78 measures correlated with the amount of cuticular lipids (Rourke, 2000; Parkash et al., 2008a).
79 Seasonal changes in the composition or amount of cuticular lipids also affect water loss in
80 scorpions and tenebrionid beetles (Hadley, 1977; Toolson and Hadley, 1979; Hadley and
81 Schultz, 1987). In contrast, analysis of water balance mechanisms in diverse *Drosophila* species
82 have shown lack of changes in cuticular traits for reduced body water loss (Gibbs et al., 1998,
83 2003; Gibbs and Matzkin, 2001; Parkash et al., 2008a) Further, there is lack of differences in T_m
84 (melting temperature), composition and/or amount of surface lipids in laboratory selected
85 desiccation-resistant and sensitive strains of *D. melanogaster* (Gibbs et al., 1997). Within
86 species, Indian populations of *D. immigrans* differ in water-loss rate, but not in surface lipid
87 amounts (Parkash et al., 2008c). In a laboratory selection experiment, populations selected for
88 desiccation resistance lost water ~50% less rapidly than unselected controls, but the two groups
89 exhibited minor differences in lipid composition and T_m (Gibbs et al., 1997). Thermal
90 acclimation of the desert fly, *D. mojavensis*, results in substantial changes in HC composition,

91 but relatively little change in water-loss rates (Gibbs et al., 1998). It must be noted that not all
92 studies result in negative findings (e.g. Toolson, 1982; Toolson and Kuper-Simbrón, 1989). If
93 ecophysiological traits and cuticular traits (body melanisation and/ or cuticular lipids) coevolve,
94 we may expect correlated responses between body color phenotypes and stress-related traits in
95 *D. melanogaster* but such traits associations have not been analyzed so far.

96 Several studies have focused on laboratory selection of desiccation resistance (Hoffmann
97 and Parson, 1989a, b; 1993; Gibbs et al., 1997; Chippindale et al., 1998; Djawdan et al., 1998;
98 Telonis- Scott et al., 2006); thermal sensitivity (Huey et al., 1991; Gilchrist and Huey 1999;
99 Anderson et al., 2005) and starvation resistance (Chippindale et al., 1996; Harshman et al., 1999;
100 Bublly and Loeschke, 2005). In contrast, a single study on laboratory selection of abdominal
101 spot number in *Drosophila falleni* has shown that selection exerted by nematode parasites may
102 influence pigmentation patterns (Dombeck and Jaenike, 2004). In most of the laboratory
103 selection studies, replicate lines at the end of selection protocol were investigated for changes in
104 the trait of interest as well as correlated selection responses but time course of evolutionary
105 response in the selected lines has not been investigated. A time course analysis is although time
106 consuming but can be helpful in better understanding the selected as well as correlated traits.

107 Experiments of artificial selection in *Drosophila* have recently been used as an
108 experimental evolutionary tool to identify the relevant traits that are most likely to be involved in
109 adaptation to environmental temperature in ectotherms (Hoffmann et al., 2003; Bowler
110 and Terblanche, 2008). One of the main advantages of artificial selection experiments is the
111 possibility to evaluate not only direct, but also the correlated responses to selection (Harshman
112 and Hoffmann, 2000). Artificial selection experiments have revealed moderate to relatively high
113 levels of heritability for resistance to high-temperature stress in *D. melanogaster* (Hoffmann et

114 al., 2003; Reusch and Wood, 2007). Remarkably, most artificial selection programs were mainly
115 performed in *D. melanogaster*, though recent studies have also addressed the question whether or
116 not results in *D. melanogaster* are consistent across species (Hoffmann and Willi, 2008). Further,
117 artificial selection on thermal-stress traits was generally performed in only a single direction
118 (mainly, for increased resistance), but studies have shown that selection for decreased resistance
119 to heat stress can also be informative as the selection response can often be asymmetrical for
120 thermal-stress traits (Gilchrist and Huey, 1999; Folk et al., 2006; Norry et al., 2007; Mori and
121 Kimura, 2008; Gomez et al., 2009; Bertoli et al., 2009).

122 Body melanisation is one of the most common types of phenotypic variations in insects
123 (Majerus, 1998). Phenotypic variation of body melanisation in some lepidopterans and
124 coelopterans are represented by discrete morphs (melanic and non-melanic) consistent with a
125 major locus (da Cunha, 1949; Napp Martinez and Cordeiro, 1970). Several studies have shown
126 changes in the frequencies of two or more allelic variants in response to temporally or spatially
127 variable climatic conditions (Umina et al., 2005; Parkash et al., 2009; 2012). In contrast,
128 variation in body melanisation in a *D. melanogaster* population follows a bell shaped curve and
129 such a quantitative trait is expected to respond fast to laboratory as well as field selection. Such
130 pigmentation differences are polygenic and interact with abiotic factors of the environment
131 (Wittkopp et al., 2003). In *D. melanogaster*, melanisation varies continuously across
132 geographical gradients on different continents and such clines linked with body melanisation
133 reflect adaptations to local climatic conditions (David et al., 1985; Capy et al., 1988; Munjal et
134 al., 1997; Pool and Aquadro, 2007, Clusella Trullas et al., 2007; Telonis-Scott et al., 2011).
135 Several studies have considered plastic change in melanisation scores at different growth

136 temperatures in the laboratory populations of *D. melanogaster* (Das et al., 1994; Ottenheim et al.,
137 1999; Gibert et al., 1996, 2000; DeWitt and Scheiner, 2004).

138 Melanin patterns are involved in diverse aspects of insect ecology (Majerus, 1998, True
139 2003). For example, increased melanisation has been associated with higher fitness under
140 thermal as well as aridity stresses in *D. melanogaster* i.e. a darker cuticle may improve
141 thermoregulation as well as may reduce cuticular water loss (Parkash et al., 2008). Changes in
142 body melanisation are associated with thermal and/ or water stress related traits but the target of
143 selection is not clear. Laboratory selection of desiccation and starvation resistance show parallel
144 responses in *D. melanogaster* while field population show opposite clines. Such a mismatch
145 between field vs. laboratory selection may be due to selection acting on some other associated
146 trait which may impact resistance to starvation and desiccation in different ways. There is ample
147 empirical support for the thermal melanism hypothesis (Watt, 1969, David et al., 1985, 1990; de
148 Jong et al., 1996, Majerus, 1998, Rajpurohit et al., 2008). Several studies have demonstrated a
149 direct influence of melanization on body temperature, by increasing solar absorption under cool
150 conditions (de Jong et al., 1996; Ottenheim *et al.*, 1999; Ellers and Boggs, 2004). Furthermore,
151 the higher body temperature in more melanized females also increases egg maturation rate
152 (Ellers and Boggs, 2004) and, in ladybird beetles, dark-coloured individuals benefit from
153 increased mating success and earlier emergence in spring (Ellers & Boggs, 2004). In copper
154 butterflies, pupal and wing melanization increased with increasing altitude (Karl et al., 2009).
155 Conversely, lighter individuals may be better protected against overheating in warm
156 environments (Munjal *et al.*, 1997; Ellers and Boggs, 2002; Pereboom and Biesmeijer, 2003).
157 Accordingly, selection is expected to favour darker phenotypes in colder environments.
158 However, a longitudinal cline for body color in *D. americana* is not associated with desiccation

159 resistance (Wittkopp et al., 2011). Thus, it is not clear whether change in melanisation can play a
160 role in multiple abiotic stressors. If body melanisation is the target of selection, we may expect
161 changes in correlated traits consistent. Laboratory selected darker and lighter lines may clarify
162 whether such traits may coevolve or not.

163 The primary aim of the present study is to establish laboratory selected replicate lines
164 with high and low abdominal melanisation and to analyze change after every five generation in
165 abdominal melanisation due to direct selection response as well as correlated selection responses
166 in physiological traits related to water stress. We assessed traits related to water conservation i.e.
167 body water content, rate of water loss, hemolymph content and dehydration tolerance level in
168 dark as well as light selected replicate lines of *D. melanogaster*. We further tested whether
169 desiccation resistance show covariation with selected darker and lighter body color lines. We
170 also provide data on realized heritability based on laboratory selected lines. This paper presents
171 the results of a long-term artificial selection experiment having three major strengths: 1)
172 selection was maintained for 60 generations, a greater length than most experiments of this type;
173 2) the trait under selection varies clinally in the field, and a suite of correlated responses were
174 also measured, giving the work a good grounding in the biology of the organism in the field; and
175 3) the genetic variation in the trait was measured every 5 generations, a rarely implemented
176 addition to a selection experiment.

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178 *MATERIALS AND METHODS*

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180 *Selection of lines for dark and light body color*

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182 Wild living flies of *Drosophila* species (n = 150- 200 flies per site) were collected from
183 six localities, two lowland: 500-600m (Kalka and Parwanoo); two midland: 1200- 1400m
184 (Kandaghat and Solan); and two highland localities: 2000- 2200m (Kasauli and Shimla) along an
185 altitudinal transect in the western Himalayas. On an average, about 40 % were *D. melanogaster*
186 out of each sample of wild caught flies. From each population, thirty pairs of wild caught flies
187 were pooled to make a mass bred population which was grown for seven generation (two week
188 cycle on standard *Drosophila* media) at a constant growth temperature of 21 ± 0.05 °C and 65 ± 1
189 % relative humidity in a thermo as well as humidity controlled incubator. This mass-bred
190 population was maintained in a population cage (n = 5000- 6000 flies) in the laboratory for seven
191 generations before onset of selection protocol. Four stocks (P₁- P) each with randomly chosen
192 500- 600 flies were derived from this mass-bred population. For each stock, two replicate lines
193 (control and selected) were established. Thus, we had four control and their respective four
194 selected (S₁- S₄) lines, each with about 300- 350 pairs of flies.

195 For the selection regime, from each of the four selected (S₁- S₄) lines, forty dark and forty
196 light female flies were selected to initiate the next generation while remaining flies were
197 discarded. Each generation, about 300 emergent female flies per replicate were aged for 7 days
198 prior to establishment of the next generation. It was observed that melanisation of flies did not
199 change after two days. The flies with > 45 % and < 30 % body melanisation were sorted as
200 darker and lighter flies for the first generation of selection. In the selection regime, each
201 generation forty dark and forty light female flies were selected to initiate the next generation
202 while remaining flies were discarded. These selected female flies correspond to selection
203 intensity of about 1.40 (Falconer, 1981), this selection intensity depends only on the proportion

204 of the population included in the selected group and, provided the distribution of phenotypic
205 values is normal. This selection procedure was followed independently for each of the mass bred
206 five stocks. Selection protocol was followed for 60 generations resulting in dark selected line
207 (D₁, D₂, D₃ and D₄) and light selected line (L₁, L₂, L₃ and L₄).

208 A replicate of each selected line (D₁, D₂, D₃, D₄ and L₁, L₂, L₃, L₄) was maintained
209 without further selection after 60th generation i.e. from 61st through 65th generation. These
210 replicate lines were maintained with the same number of flies without any further selection
211 regime. For relaxed lines i.e. 61st through 65th generation, a sample of 100- 150 flies of each dark
212 and light selected line was again scored for changes in abdominal melanisation, if any.

215 **Quantification of melanisation: direct response to selection**

216 **(a) *General scoring method***

217 Body melanisation was estimated under a stereo zoom microscope (Olympus,
218 www.olympus.com) from a lateral view of the female and male abdomen giving values ranging
219 from 0 (no melanisation) to 10 (complete melanisation) for each of the six visible (2nd to 7th)
220 abdominal segments (David et al., 1990). Since the abdominal segments differ in size, relative
221 sizes (i.e. 0.86, 0.94, 1.0, 0.88, 0.67 and 0.38 for 2nd to 7th segments respectively) were
222 multiplied with segment wise melanisation scores. Abdominal melanisation scores were
223 weighted to the relative sizes of the respective segments. The abdomen of each fly minus viscera
224 was mounted on a slide and total body melanisation per fly was also estimated through
225 Biowizard image analysis software, - Dewinter Optical Inc. - (www.dewinterindia.com). Data on

226 percent melanisation were calculated as (Σ observed weighted melanisation scores of six
227 abdominal segments per fly/ Σ relative size of each abdominal segment x 10 per fly) x100.

228

229 **(b) Response to selection**

230 The selection response was measured at each fifth generation. Selection of abdominal
231 melanisation was done on female flies only, but in the time course of selection males were also
232 analyzed. For both sexes and each replicate line of control as well as selected dark and light flies
233 60 flies were scored for abdominal melanisation at each 5th generation.

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236 **Correlated responses to selection: analysis of stress resistance/assay**

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238 We analyzed correlated changes in body water content, hemolymph content, desiccation
239 resistance, rate of water loss and dehydration tolerance in selected darker and lighter replicate
240 lines of *D. melanogaster*. We further analyzed changes in epicuticular lipids in control and
241 selected replicates, if any. For analysis of stress resistance and epicuticular lipids, we analyzed
242 ten replicates from each of the control (C₁ to C₄), dark selected (D₁ to D₄) and light selected (L₁
243 to L₄) lines of *D. melanogaster*.

244

245 **a) Desiccation resistance**

246 Desiccation resistance was measured as time to lethal dehydration effect under dry air in
247 ten replicates of female and male individuals of each of the control (C₁ to C₄), dark selected (D₁
248 to D₄) and light selected (L₁ to L₄) lines. 10 male and female individuals were isolated in dry

249 plastic vials which contained 2 g of silica gel at the bottom of each vial and was covered with a
250 disc of plastic foam piece. Finally, such vials with foam plugs were placed in a desiccator
251 chamber (Secador electronic desiccators cabinet; www.tarson.com) which maintains 6-8%
252 relative humidity. Number of immobile flies was counted at every 1h interval. The time period to
253 lethal desiccation (LT_{100}) effect in dry air was recorded.

254

255 ***b) Basic measures of water balance***

256 In order to estimate total body water content, rate of water loss and dehydration tolerance
257 (%), 10 flies of each of the C, D and L (10 replicate each) were used. First, the flies were
258 weighed on Sartorius microbalance (Model- CPA26P; with precision 0.001 mg) and then
259 reweighed after drying at 60 °C overnight. Total body water content was estimated as the
260 difference between masses before and after desiccation stress of 8h at 6- 8% relative humidity,
261 and water loss was calculated as: (initial body mass- body mass after 8h desiccation stress)/
262 initial body mass x 8; and the values were given in $\mu\text{g h}^{-1}$. Dehydration tolerance was estimated
263 as the percentage of total body water lost at death due to desiccation (until death) and was
264 calculated by the formula (wet body mass – mass at death) / (wet body mass – dry body mass) x
265 100.

266 To measure hemolymph volume, blotting assays were conducted. Ten replicates of 7 days
267 old male and female individual were anesthetized and weighed as a group. The abdomen of each
268 was gently torn with surgical forceps, and hemolymph was blotted from the opening with a piece
269 of Kimwipe® slightly moistened with isotonic saline. Within a maximum of 10 min, 10 blotted
270 flies were reweighed as a group and dried for 1h at 60 °C and weighed a third time. Hemolymph
271 volume was estimated from the reduction in mass following blotting.

272

273 ***c) Response of cuticular lipids to selection***

274 For estimation of cuticular lipid mass per fly, individual flies in ten replicates per
275 replicate line were dried overnight at 60 °C to get constant dry mass i.e. devoid of body water.
276 Such dried flies were kept in HPLC-grade hexane for 1h; thereafter the flies were removed from
277 the solvent and were again dried at room temperature and finally reweighed. The sartorius
278 microbalance (CPA26P, www.sartorius.com) with precision upto 0.001mg ensured accuracy.
279 For each individual fly, cuticular lipid mass in mg was estimated per unit surface area (surface
280 area scales to 2/3 power of the wet body mass) as: difference between initial dry weight and dry
281 weight after solvent treatment / initial dry weight*surface area (where area was expressed in cm²
282 and wet body mass in mg).

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Statistical analyses

286 The response to selection was analyzed by computing realized heritability over every
287 fifth generation of selection in both darker and lighter selected replicate lines. The realized
288 heritability for cuticular melanisation was calculated for each line by plotting the mean
289 melanisation score for each generation against the cumulative selection differential. The
290 expected selection differential was calculated as the deviation of the mean cuticular melanisation
291 score of the selected individuals in each generation from the population mean before selection.
292 This was then summed each generation to give the cumulative selection differential. The realized
293 heritability (h^2) was then calculated from the slope of the regression of mean color score (R)
294 against the cumulative selection differential (S), as $h^2 = R/S$ (Falconer and Mackay, 1996). To

295 compare control and selected dark and light replicate lines analysis of variance (ANOVA) was
296 used, with replicate line (4 replicate each control, dark and light group x 10 replicate each).
297 Mean \pm s.d values of replicates were used for tabular and figure illustrations. Statistica (Statsoft
298 Inc., Release 5.0, Tulsa, OK, USA) was used for calculations as well as illustrations.

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300

301

RESULTS

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Response to selection: changes in abdominal melanisation in dark and light selected lines

304

305 Selection was initiated from mass-bred populations having high variability for abdominal
306 melanisation ($m \pm$ s.d. = 41.39 ± 13.12 , Fig. 1A). Selection for abdominal melanisation in *D.*
307 *melanogaster* for 60 generations resulted in a decrease of around 14 fold (ANOVA; females: $p <$
308 0.0001 ; males: $p < 0.0001$; Table 1) in light selected strains; and 1.6 fold increase in D selected
309 strains (ANOVA; females: $p < 0.0001$; males: $p < 0.0001$; Table 1). A plot of the response to
310 selection as a function of cumulative selection differential (Fig. 1B) indicated that the response
311 was asymmetric: divergence from unselected controls was faster and greater in lighter selected
312 lines than dark selected lines.

313 Realized heritabilities were estimated from the regression of selection response on
314 cumulative selection differential. The regression of cumulative selection differential on response
315 was highly significant for each of the dark and light selected lines giving heritability estimates
316 ($h^2 \pm$ SE) for cuticular melanisation 0.46 ± 0.03 for dark selected lines (mean value of five

317 replicates) and 0.39 ± 0.02 for light selected lines (Fig 1B). For abdominal melanisation, females
318 responded quickly to selection. The laboratory selection was done on females only but males
319 were also found to respond to selection for changes in abdominal melanisation (Fig 2A). Dark
320 selected females showed ~87 % melanisation, while males exhibited ~88 % melanisation (Fig.
321 2A). However, in light selected strains, females and males were very light (about 3%
322 melanisation only, Fig 2A). The replicate selected lines reached significantly different final %
323 melanisation, and the complete lack of response to relaxed selection. Further, the variability in
324 each D and L selected strains was quite low (dark: $m \pm s.d = 87.12 \pm 0.79$; light = 3 ± 0.21).

325

326 *Physiological assays*

327

328 Male and female flies were tested for changes in body water content (Table 1) and the
329 analysis showed a significant line term in the ANOVA ($p < 0.001$). Darker selected lines have
330 around 10.0 % more water content, whereas in light selected replicates body water content
331 reduced by ~13.0% as compared with their unselected control. Figure 2 (B-D) illustrates a
332 comparison of desiccation-related traits in selected darker and lighter body color strains as
333 compared with unselected control lines. For control and selected strains of *D. melanogaster*,
334 grown at 21° C, there is lack of differences in cuticular lipid mass. In contrast, we found
335 significant difference in the desiccation resistance of these two selected darker and lighter strains
336 (Table 2, Fig. 2B) and significant difference in their rate of water loss i.e. 0.3% / hr (1.5% / hr in
337 darker versus 1.8% / hr in lighter strains; Fig. 2C). However, the level of dehydration tolerance is

338 much higher in darker (~82.32%) than lighter strains (~22%) as compared with control lines
339 (~50%; Table 2; Fig. 3D).

340

341 *Correlated responses to selection*

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343 For any trait, consistent bidirectional changes in selected lines relative to their unselected
344 control lines are due to the effect of selection (Lynch, 1980) and indicate that abdominal
345 melanisation and the co-responding traits are influenced by some of the same genes (i.e. show
346 genetic covariance; Falconer 1981). 60 generations of artificial selection on abdominal
347 melanisation produced consistent bidirectional selection, correlated response in body water
348 content, desiccation resistance, rate of water loss, dehydration tolerance (Table 1; Fig 2 B-D) and
349 mean trait values increased significantly for body water content, desiccation resistance and
350 dehydration tolerance in dark selected replicate lines, whereas rate of water loss showed a
351 negative correlated response. However, in light selected replicate lines body water content,
352 desiccation resistance and dehydration tolerance decreased significantly; and rate of water loss
353 showed a positive correlated response (Table 1; Fig. 2 B-D).

354 Direct selection of cuticular melanisation impact desiccation resistance significantly (Fig.
355 2). Comparison of direct and indirect selection responses provide a clearer view of melanism –
356 desiccation correlation hypothesis. Replicates selected for higher melanisation showed higher
357 desiccation resistance and reduced rate of water loss, whereas desiccation survival decreased and
358 rate of water loss increased significantly in replicates selected for low cuticular melanisation as
359 compared with control (Table 2). Selection for cuticular melanisation had a significant effect on

360 water balance and desiccation resistance. Darker lines had significantly higher desiccation
361 resistance ($p < 0.0001$) than control flies, whereas lighter ones have 2 fold decreases in
362 desiccation survival. Similar effects were observed for rate of water loss ($p < 0.0001$). For body
363 water content, there were non significant changes in selected vs. control replicates ($p < 0.23$).
364 Further, we observed no changes in wing length (as a measure of body size) due to selection (F_7 ,
365 $\eta^2 = 5.01$ ns).

366 Flies were analyzed for cuticular lipids in control as well as selected replicates to
367 examine their response towards selection and relation with desiccation resistance. Cuticular
368 lipids do not change in response to selection (Fig. 3D, Table 2). There was a non significant
369 difference for cuticular lipids between the control lines ($p < 0.07$) and also between the selected
370 lines ($p < 0.20$) when tested by ANOVA. Changes in desiccation and changes in water loss rate
371 are significantly correlated with selection in cuticular melanisation (Fig. 4, Table 3). Cuticular
372 lipids do not respond to selection and were not correlated with increasing desiccation resistance
373 and water balance (Table 3).

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DISCUSSION

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378 *D. melanogaster* exhibits considerably high variation in abdominal melanisation in
379 natural populations. Laboratory selected dark and light body color strains of *D. melanogaster*
380 differ significantly in abdominal melanisation. Our study shows that there is a great deal of

381 genetic variation in abdominal melanisation in *D. melanogaster*, as evidenced by consistent,
382 rapid and substantial response to selection for high and low melanisation phenotypes. For body
383 melanisation, we found a rapid response to laboratory selection. Interestingly, selection produced
384 both light females as well as light males, in contradiction with the well known sexual
385 dimorphism of body melanisation in *D. melanogaster*. The replicate selected lines reached
386 significantly different final % melanisation, and the complete lack of response to relaxed
387 selection suggests that different combinations of alleles affecting abdominal melanisation may
388 have become fixed in the different selected lines. Although, the external appearance of our
389 selected strains is different from typical wild populations, we detected no statistically significant
390 effects of melanisation on basic morphometric traits such as wing length, thorax length and wing
391 width ($p < 0.12ns$). However, dark and light selected strains differ significantly in wet body mass
392 ($p < 0.001$).

393 We found an asymmetric response to selection, in lines selected for dark and light
394 abdominal melanisation in *D. melanogaster* (Fig 1B). Asymmetric responses to selection are a
395 common finding in selection experiments. The reasons given by Falconer and Mackay (1996)
396 involve experimental artifacts (random drift, inbreeding depression and unmeasured natural or
397 sexual selection acting during the experiment) as well as a multitude of potential genetic causes
398 (genetic asymmetry, presence of major genes, scalar asymmetry). Random drift is unlikely to
399 explain the present results because of the consistency of response between replicates. Inbreeding
400 depression is also unlikely because the mean of the unselected control line did not decline.
401 However, we can not at this point rule out the genetic causes (major genes, directional
402 dominance or genetic asymmetry); it is possible that the asymmetric response is explained by
403 scalar asymmetry: high phenotypic values might be particularly subject to environmental

404 influence (e.g condition-dependency, rearing conditions) and the extreme values an artifact of
405 laboratory rearing. One interesting possibility is that the asymmetry results from the previous
406 action of selection in the base population. Favorable alleles are expected to have frequencies
407 above their symmetrical points (Falconer and Mackay, 1996).

408 Artificial selection experiments are longer in duration and correlations are limited to the
409 trait being selected, but they have the advantage of directly revealing patterns of responses and
410 co- responses to a specified selection regimen. Thus, they can provide an independent test for the
411 presence of significant patterns of genetic variation and co- variation in a given environment.
412 Due to the physiological relationship between melanisation and desiccation resistance, we
413 predicted that selection for melanisation would result in a correlated increase and decrease in
414 desiccation resistance of *D. melanogaster*. We found that desiccation resistance was higher in
415 dark selected strains and was significantly low in light selected strains (Fig 1C). For adaptations
416 to drier habitats, the function of cuticular lipids in reducing cuticular water loss is well known in
417 different insect taxa from deserts (Hadley, 1994). However, some studies have shown the role of
418 melanisation in reducing cuticular water loss in *Drosophila* species (Parkash et al., 2008b,c).
419 Associations between pigmentation and desiccation resistance was initially proposed by Kalmus
420 (1941). Fraenkel and Rudall (1940) and Pryor (1940) concluded that the darkening and
421 hardening of the cuticle are due to the same biochemical processes, which may involve cross-
422 linking of proteins with melanin. In the present work, we have investigated effects of
423 bidirectional selection of body melanisation selection on correlated traits. For *D. melanogaster*,
424 rapid response to direct selection of melanisation confirms the existence of substantial additive
425 genetic variation for this trait. Populations of *D. melanogaster*, therefore, have the potential to
426 undergo rapid genetic changes when they are exposed to one or the other selective environment.

427 The correlated responses to selection indicate that at least some of the genes which contribute to
428 variation in abdominal melanisation have pleiotropic effects on other traits. Specifically, body
429 melanisation shares positive additive genetic covariance with body water content, hemolymph
430 content desiccation resistance and dehydration tolerance and it shares negative genetic
431 covariance with rate of water loss. Epicuticular lipids, however, do not respond to selection.

432 Another problem is to differentiate water proofing role of cuticular melanisation versus
433 cuticular tanning (hardening) in *D. melanogaster*. Different cuticular components may affect
434 cuticular transpiration in insects (Chapman, 1998). Darker cuticle achieves its color due to
435 deposition of melanin granules (polymers of dopa and other tyrosine derivatives; True, 2003).
436 Like cuticular lipids, melanin is also hydrophobic and therefore may reduce cuticular
437 permeability. It has been suggested that the darkening and hardening of cuticle result due to
438 cross-linking of cuticular proteins with melanin (Pryor, 1940; Fraenkel and Rudall, 1940;
439 Hopkins and Kramer, 1992). Thus, melanisation and sclerotization pathways (tanning) could be
440 related because in the insects, harder body parts are generally darker. In the present study, we
441 have not considered the role of sclerotization. However, further studies are needed to
442 differentiate the effects of cuticular melanisation and cuticular tanning for waterproofing
443 function in *Drosophila* species and in insects in general.

444 Insect cuticle is a complex structure and its components vary greatly between populations
445 and species (Rajpurohit et al., 2008). Changes in body melanisation have been shown to affect
446 cuticular permeability in some *Drosophila* species (Parkash et al., 2008b,c). According to
447 melanisation–desiccation hypothesis, darker flies of *D. melanogaster* are abundant in cooler
448 uplands while lighter flies are predominant in foothills (Parkash et al., 2008c). The laboratory
449 selected desiccationresistant and sensitive strains of *D. melanogaster* have shown similar

450 amounts of cuticular lipid mass (Gibbs et al., 1997); and there is also lack of differences in the
451 amount of cuticular lipid mass in northern versus southern population of *D. melanogaster*
452 (Parkash et al., 2008a). However, in two cases (*Melanoplus sanguinipes* and *Z. indianus*), there
453 are significant intrapopulation differences in the amount of cuticular lipid mass per cm² (Rourke,
454 2000; Parkash et al., 2008a; Parkash et al., 2011)

455 The present work provides good evidence that the associations between both desiccation
456 resistance and the rate of water loss with cuticular melanisation in *D. melanogaster* populations
457 from India have a genetic basis, which has been suggested by population comparisons in field
458 and lab populations. This is the first experiment to explore these associations with a long term
459 artificial selection experiment. However, pigmentation clines have been reported in *Drosophila*
460 (Parkash et al., 2008), and desiccation resistance is often proposed as an adaptive benefit of
461 increased melanization. We tested the association between pigmentation and desiccation in *D.*
462 *melanogaster* using selection and found that there was a causative relationship between
463 melanisation and rate of water loss, as selection for both high and low melanin resulted in a
464 correlated response to selection in both desiccation resistance and water balance (however, note
465 that Wittkopp et al., 2011. performed a similar experiment using *D. americana* and *D.*
466 *novamexicana*, and found no effect of pigmentation genotype on desiccation resistance.

467 We observed a substantial increase in both male and female survival to desiccation stress
468 following selection for abdominal melanisation. There was a sexual dimorphism for abdominal
469 melanisation as well as desiccation resistance at the onset of our selection regime, but at the 60th
470 generation of selection these differences vanishes. The presence of similar resistant levels in
471 males and females implies that there is a common genetic basis between the sexes underlying the
472 selection responses. Figure 2 represents a genetic association between traits involved in

473 correlated responses to selection. Selection was associated with an increase in wet weight. This
474 observation is consistent with lines directly selected for desiccation resistance (Gibbs et al.,
475 1997) and in lines selected indirectly in response to very mild desiccation stress (Kennington et
476 al., 2003), but not in other direct selected lines (Bubliy and Loeschcke, 2005; Hoffmann and
477 Parson, 1989). The changes in correlated trait such as desiccation survival with melanisation of
478 selected replicates were independent of body size. The absence of changes in body size suggests
479 that changes in the surface to volume ratio were not involved in increased desiccation tolerance.
480 There were also correlated responses in the weight loss of flies, suggesting that selected strains
481 had a different rate of water loss through the cuticle.

482 Selection experiments are vital tools of evolutionary biology and the results of nearly a
483 century's worth of selection experiments have helped establish the genetic component of
484 evolutionary theory (Provine, 1971; Falconer, 1992). In addition, selection experiments have
485 provided stocks that have been useful for many other topics, from estimating mutation rates to
486 understanding the molecular, biochemical, and physiological foundations of trait variation (Hill
487 and Caballero, 1992; Mackay, 2001; Conner, 2003; Garland, 2003). The association between
488 melanisation and other correlated traits has been well documented in natural populations of *D.*
489 *melanogaster* (Parkash et al., 2008), but such associations have not been analyzed following
490 artificial selection experiment of abdominal melanisation. Selection experiments in other
491 drosophilids and insect have detected patterns of genetic covariance between traits (Pitnick and
492 Miller, 2000, Nunney, 1996, Beldade et al., 2002). The results should be especially informative,
493 since the application of quantitative- genetic theory to the evolution of phenotypic differences
494 between populations assumes the pattern of genetic variances and covariances remains relatively
495 constant across evolving populations (Lande, 1982; Arnold, 1981).

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CONCLUSIONS

498 We detected through the analysis of correlated responses to direct selection on abdominal
499 melanisation, a pattern of genetic co-variation among desiccation related traits. A direct selection
500 for cuticular melanisation has selected correlated traits (water balance related traits) in *D.*
501 *melanogaster*. The evidence for correlated traits is based on trait correlation analysis i.e. darker
502 flies have lower rate of water loss which confers greater desiccation resistance. In contrast,
503 higher rate of water loss in lighter flies sustains lower desiccation tolerance. Results of this study
504 therefore indicate the potential for abdominal melanisation evolution to facilitate or constrain the
505 evolution of desiccation resistance in *Drosophila melanogaster*. Still, the generality of these
506 results deserves further investigations.

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508

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758 **Legend to figures**

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760 Fig. 1 (A) Variation ($m \pm s.d.$) of abdominal melanisation in a sample of flies ($n= 1236$) after
761 mass breeding for seven generations in the laboratory at 21 °C and before onset of laboratory
762 selection. (B) data on regression of R (response to selection) on ΣS (cumulative selection
763 differential) are shown for estimation of realized heritability of laboratory selected dark and light
764 lines of *D. melanogaster*.

765

766 Fig 2 .(A) Results of laboratory selection upto 60th generation for changes in total body
767 melanisation per fly in control and selected dark and lighter lines of *D. melanogaster*. (B - D)
768 correlated changes in desiccation resistance, cuticular water loss and dehydration tolerance are
769 shown after every five generations of laboratory selection in darker and lighter lines alongwith
770 their respective control lines. For each trait, data are shown as means of five replicate lines.
771 Selection was made on the melanisation of female flies but corresponding changes in males are
772 also shown.

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774 Figure 3. (A) Changes ($\text{mean} \pm s.d.$) in cuticular melanisation; (B) desiccation resistance hours
775 (C) cuticular water loss; and (D) cutitcular lipid content in dark and light selected lines of *D.*
776 *melanogaster* as compared with control lines. Trait values represent data on 60th generation of
777 selection. Each value is based on analysis of ten replicates of ten individual flies each of five
778 replicate lines of control as well as selected dark and light lines of *D. melanogaster*.

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780 Fig. 4 (A) Desiccation survival curves of control and laboratory selected darker and lighter body
781 color lines of *D. melanogaster* (n = 5 each; values are shown as average percentage survival per
782 hour) when stressed in groups of ten female flies of 60th generation. Correlated changes in
783 desiccation resistance, cuticular water loss and dehydration tolerance in control and five selected
784 (dark and light) lines. Between line variability (mean \pm s.d.) are shown for desiccation related
785 traits as a function of changes in body melanisation of control and selected lines of dark and light
786 body color.

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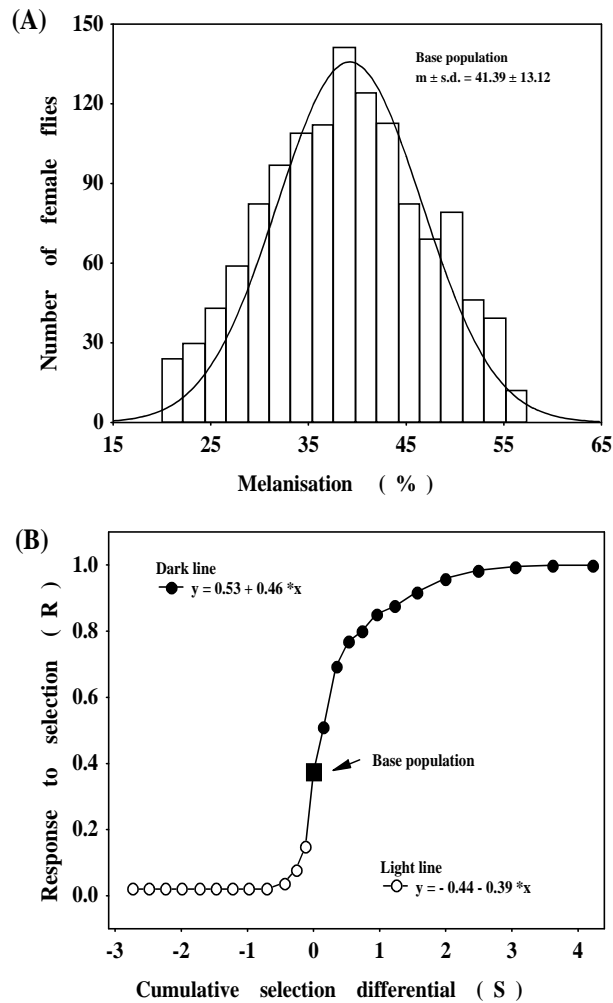
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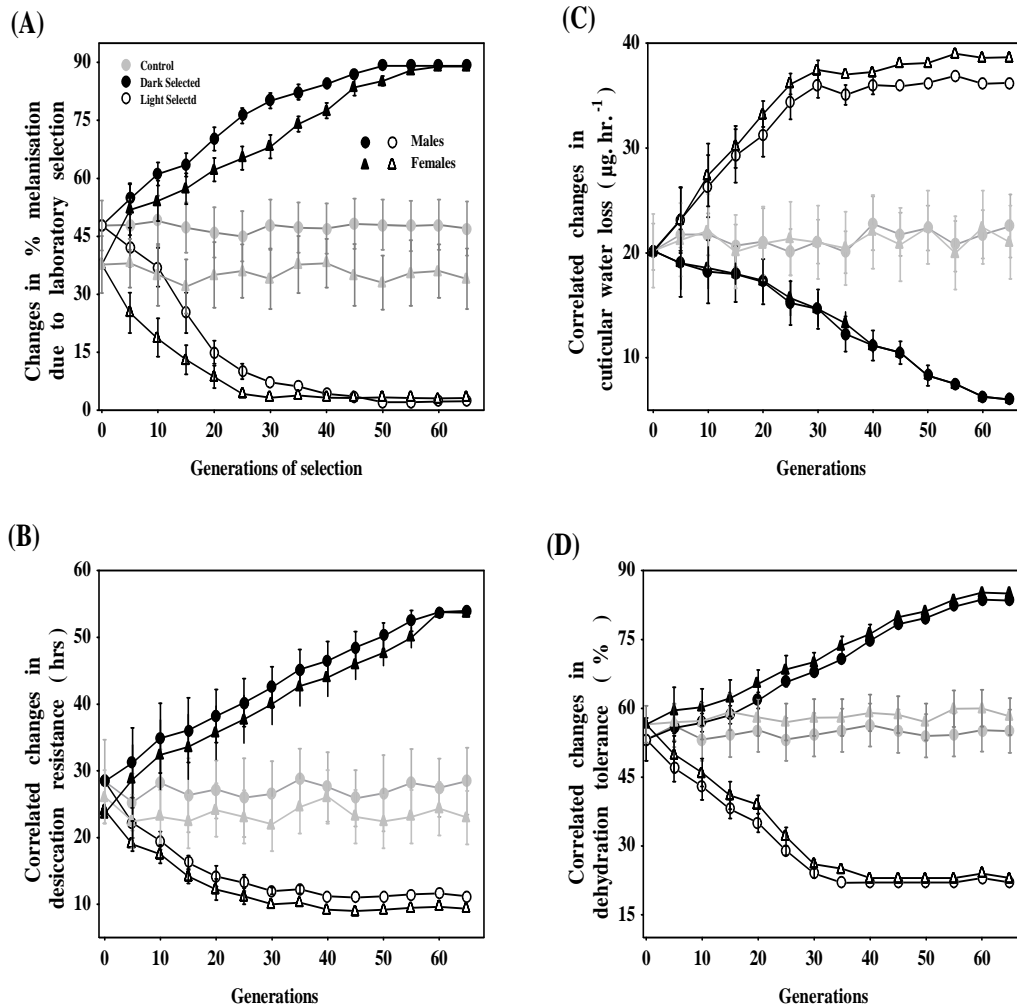
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Fig. 1 (A) Variation ($m \pm s.d.$) of abdominal melanisation in a sample of flies ($n= 1236$) after mass breeding for seven generations in the laboratory at 21 °C and before onset of laboratory selection. (B) data on regression of R (response to selection) on $\sum S$ (cumulative selection differential) are shown for estimation of realized heritability of laboratory selected dark and light lines of *D. melanogaster*.



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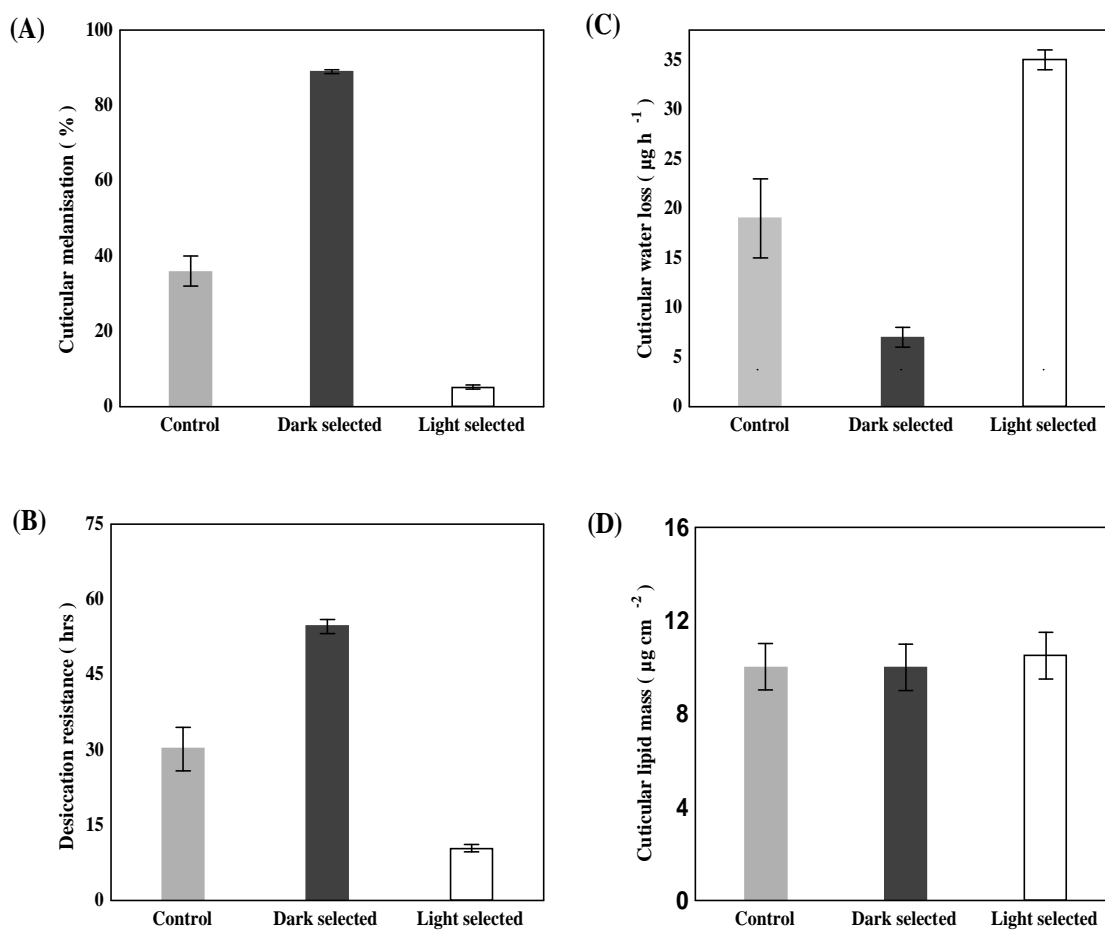
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Fig 2. (A) Results of laboratory selection upto 60th generation for changes in total body melanisation per fly in control and selected dark and lighter lines of *D. melanogaster*. (B - D) correlated changes in desiccation resistance, cuticular water loss and dehydration tolerance are shown after every five generations of laboratory selection in darker and lighter lines alongwith their respective control lines. For each trait, data are shown as means of four replicate lines. Selection was made on the melanisation of female flies but corresponding changes in males are also shown.



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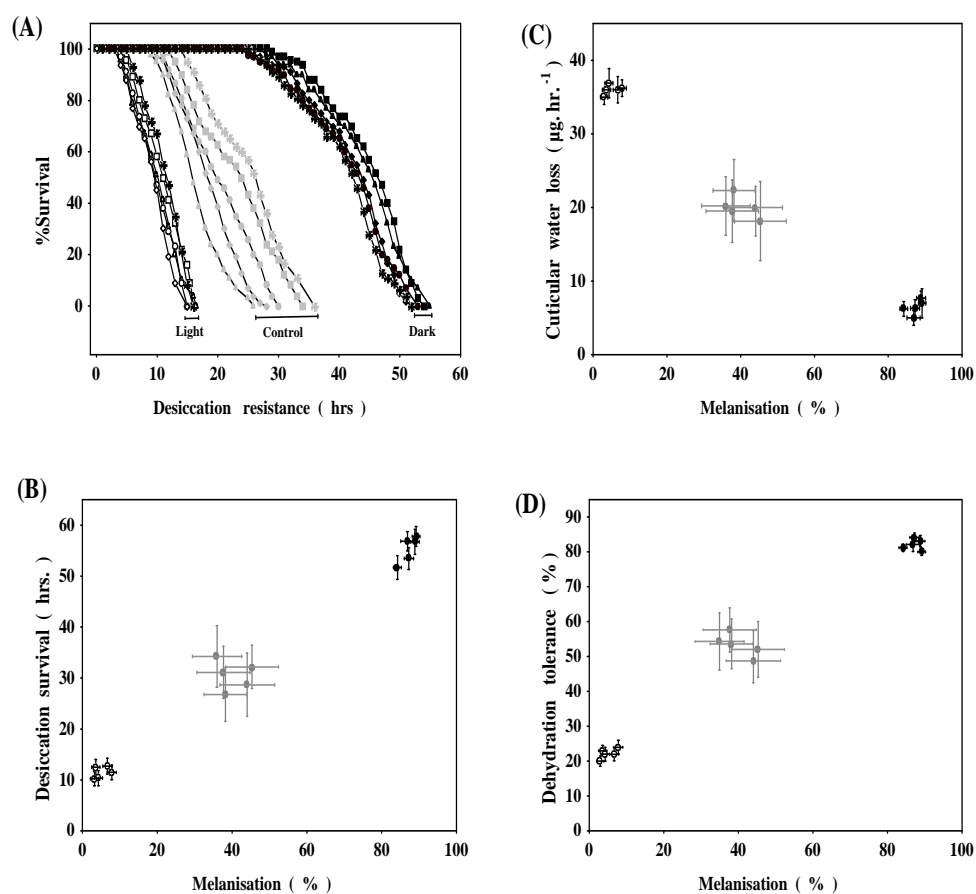
833 Figure 3. (A) Changes (mean \pm s.d.) in cuticular melanisation; (B) desiccation resistance
 834 hours (C) cuticular water loss; and (D) cuticular lipid content in dark and light selected
 835 lines of *D. melanogaster* as compared with control lines. Trait values represent data on
 836 60th generation of selection. Each value is based on analysis of ten replicates of ten
 837 individual flies each of four replicate lines of control as well as selected dark and light
 838 lines of *D. melanogaster*.

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 844 Fig. 4 (A) Desiccation survival curves of control and laboratory selected darker
 845 and lighter body color lines of *D. melanogaster* ($n = 5$ each; values are shown as
 846 average percentage survival per hour) when stressed in groups of ten female flies
 847 of 60th generation. Correlated changes in desiccation resistance, cuticular water
 848 loss and dehydration tolerance in control and four selected (dark and light) lines.
 849 Between line variability (mean \pm s.d.) are shown for desiccation related traits as a
 850 function of changes in body melanisation of control and selected lines of dark and
 851 light body color.
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864 Table 1. Data (mean \pm s.e.) for changes in body melanisation, desiccation resistance and rate of water
 865 loss in four replicate lines of dark and light selected as compared with control lines ($n = 4$). For each
 866 trait, ANOVA values represent statistical differences between selected (dark- D or light- L) and control
 867 lines. Each value is based on analysis of ten replicates of ten individual flies of each sex.
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	Replicate lines	Melanisation (%)		Desiccation resistance (hrs)		RWL ($\mu\text{g fly}^{-1}$)	
		♂	♀	♂	♀	♂	♀
		Control (C)	C 1	47.21 \pm 5.21	43.50 \pm 4.25	26.01 \pm 3.21	29.1 \pm 3.10
	C 2	48.32 \pm 7.02	38.21 \pm 4.98	29.53 \pm 4.29	34.4 \pm 4.02	20.21 \pm 3.98	23.21 \pm 4.22
	C 3	47.25 \pm 3.25	42.57 \pm 5.65	25.55 \pm 4.71	32.8 \pm 4.21	18.14 \pm 5.36	21.50 \pm 3.65
	C 4	46.36 \pm 4.98	39.57 \pm 6.21	21.22 \pm 3.89	26.5 \pm 3.29	20.30 \pm 4.22	22.11 \pm 4.78
Dark selected (D)	D 1	90.00 \pm 0.65	87.25 \pm 0.33	52.21 \pm 1.22	54.4 \pm 1.12	6.30 \pm 1.20	7.21 \pm 1.00
	D 2	86.58 \pm 0.36	88.26 \pm 0.18	53.11 \pm 2.00	56.7 \pm 2.45	7.12 \pm 0.89	7.56 \pm 0.89
	D 3	89.14 \pm 0.12	88.56 \pm 0.14	50.98 \pm 1.89	51.6 \pm 1.30	6.23 \pm 1.01	6.39 \pm 1.77
	D 4	87.98 \pm 0.14	86.00 \pm 0.54	54.22 \pm 1.25	56.8 \pm 1.89	6.89 \pm 1.00	7.14 \pm 0.77
Light selected (L)	L 1	3.60 \pm 0.21	4.22 \pm 0.54	14.00 \pm 1.70	16.5 \pm 0.56	36.21 \pm 1.13	37.54 \pm 1.32
	L 2	1.10 \pm 0.13	3.23 \pm 0.36	13.74 \pm 0.99	16.5 \pm 0.49	35.98 \pm 1.02	36.87 \pm 1.00
	L 3	2.25 \pm 0.19	3.21 \pm 0.25	16.04 \pm 1.74	18.0 \pm 0.51	36.89 \pm 0.98	37.00 \pm 1.89
	L 4	2.32 \pm 0.17	5.00 \pm 0.52	12.36 \pm 1.12	16.0 \pm 0.61	36.11 \pm 1.00	36.98 \pm 1.00
Mean squares for ANOVAs (df)							
C vs. D	Lines (7)	17512.7***	19854.3***	3264.47***	2963.52***	546.61***	547.85***
	Error (72)	4.141	3.012	0.723	0.954	0.519	0.405
C vs. L	Lines (7)	12242.5***	10254.1***	3065.28***	2732.96***	629.46***	759.78***
	Error(72)	5.323	4.901	0.712	0.623	0.730	0.619
df – degree of freedom; MS – means square ***p< 0.001; ns = non-significant. ANOVAs on melanisation were carried out on arcsine- transformed data.							

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880 Table 2. *Data (mean ± s.e.) for changes in body water content, hemolymph volume and dehydration*
 881 *tolerance in four replicate lines of dark and light selected as compared with control lines. For each*
 882 *trait, ANOVA values represent statistical differences between selected (dark- D or light- L) and*
 883 *control lines. Each value is based on ten replicates of ten individual flies.*

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	Replicate lines	Water content (mg fly ⁻¹)		Hemolymph (%)		Dehydration tolerance (%)	
		♀	♂	♀	♂	♀	♂
Control (C)	C 1	1.25±0.04	1.23±0.04	15.25±2.21	13.43±3.21	56.66±2.32	50.01±3.21
	C 2	1.22±0.05	1.19±0.04	13.54±3.21	12.00±2.21	54.32±3.21	49.53±4.29
	C 3	1.19±0.04	1.18±0.03	14.12±2.36	12.12±2.98	52.01±2.98	50.55±4.71
	C 4	1.21±0.03	1.20±0.04	14.00±2.07	12.56±2.13	53.65±3.14	51.22±3.89
Dark selected (D)	D 1	1.32±0.01	1.29±0.02	20.21±0.89	18.19±1.01	84.20±1.21	82.21±1.22
	D 2	1.34±0.02	1.30±0.01	21.32±1.11	19.30±0.98	83.11±1.58	81.11±2.00
	D 3	1.33±0.02	1.31±0.01	22.32±0.85	20.11±1.00	81.21±1.05	81.98±1.89
	D 4	1.33±0.01	1.28±0.02	21.27±0.99	20.21±0.88	82.11±0.97	82.22±1.25
Light selected (L)	L 1	1.06±0.01	1.03±0.02	11.67±0.21	10.11±0.87	22.23±1.23	21.00±1.70
	L 2	1.09±0.01	1.05±0.02	10.99±0.80	10.00±1.03	23.13±2.51	21.74±0.99
	L 3	1.05±0.02	1.02±0.01	9.78±0.74	11.21±0.56	22.98±1.58	22.04±1.74
	L 4	1.06±0.02	1.03±0.02	10.23±0.81	10.88±0.87	22.19±1.21	21.36±1.12
Mean squares for ANOVAs (df)							
C vs. D	Lines (7)	0.038**	0.406**	0.015***	0.019***	0.3013***	0.2843***
	Error (72)	0.003	0.002	0.00001	0.00004	0.0004	0.0007
C vs. L	Lines (7)	0.291**	0.191**	0.0026***	0.0061	0.7427***	0.6943***
	Error (72)	0.002	0.001	0.0001	0.0002	0.001	0.002
df – degree of freedom; MS – means square ***p< 0.001; ns = non-significant. ANOVAs on percent data were carried out on arcsine- transformed data.							

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897 Table 3. Correlation values ($r \pm s.e.$) for each of different ecophysiological traits with
 898 changes in cuticular melanisation and with cuticular lipid mass in selected lines for dark and
 899 light body color of *D. melanogaster*.

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Traits	Trait correlation ($r \pm s.e.$)			
	% Melanisation		Cuticular lipids	
	Dark	Light	Dark	Light
1. Melanisation (%)	--	--	-0.24±0.28 ns	0.33±0.27 ns
2. Cuticular lipid mass ($\mu\text{g cm}^{-2}$)	-0.24±0.28 ns	0.18±0.31 ns	--	--
3. Body water content	0.89±0.07**	0.85±0.08**	-0.21±0.21 ns	0.28±0.31 ns
4. Hemolymph (%)	0.91±0.03***	0.89±0.07***	-0.35±0.19 ns	0.31±0.27 ns
5. Desiccation (hrs)	0.98±0.04***	0.99±0.03***	-0.25±0.27 ns	0.32±0.27 ns
6. Cuticular water loss ($\mu\text{g h}^{-1}$)	-0.96±0.07***	-0.97±0.05***	0.19±0.23 ns	-0.30±0.27 ns
7. Dehydration tolerance	0.96±0.05***	0.90±0.12***	-0.21±0.23 ns	0.15±0.28 ns

ns = nonsignificant, ** $P < 0.01$; *** $P < 0.001$

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