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1 **Dietary live yeast alters metabolic profiles, protein biosynthesis**  
2 **and thermal stress tolerance of *Drosophila melanogaster***

3

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23 ***Abstract***

24

25 The impact of nutritional factors on insect's life-history traits such as reproduction and  
26 lifespan has been excessively examined; however, nutritional determinant of insect's thermal  
27 tolerance has not received a lot of attention. Dietary live yeast represents a prominent source  
28 of proteins and amino acids for laboratory-reared drosophilids. In this study, *Drosophila*  
29 *melanogaster* adults were fed on diets supplemented or not with live yeast. We hypothesized  
30 that manipulating nutritional conditions through live yeast supplementation would translate  
31 into altered physiology and stress tolerance. We verified how live yeast supplementation  
32 affected body mass characteristics, total lipids and proteins, metabolic profiles and cold  
33 tolerance (acute and chronic stress). Females fed with live yeast had increased body mass and  
34 contained more lipids and proteins. Using GC/MS profiling, we found distinct metabolic  
35 fingerprints according to nutritional conditions. Metabolite pathway enrichment analysis  
36 corroborated that live yeast supplementation was associated with amino acid and protein  
37 biosyntheses. The cold assays revealed that the presence of dietary live yeast greatly  
38 promoted cold tolerance. Hence, this study conclusively demonstrates a significant interaction  
39 between nutritional conditions and thermal tolerance.

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## 53 1. Introduction

54 A number of studies have examined how nutrition affects various traits in insects, with  
55 special emphasis on the effects of dietary intake on reproduction and longevity (Le Bourg and  
56 Medioni, 1991; Chippindale et al., 1993; Leroi et al., 1994; Anagnostou et al., 2010). More  
57 specifically, the trade-off between reproduction and lifespan resulting from the qualitative and  
58 quantitative manipulations of diet has been studied extensively (Carey et al., 2008; Ellers et  
59 al., 2011; Moore and Attisano, 2011). *Drosophila melanogaster* is a very popular model used  
60 in the dietary restriction (DR) literature of gerontology because of its relatively short  
61 generation time and ease of handling for demographic analysis (Partridge et al., 2005). The  
62 composition of *Drosophila* sp. food recipes often varies among laboratories and medium  
63 types, but the standard ingredients usually include water, agar, sugar, killed yeast, and  
64 fungicides. In addition, the medium can be supplemented with live yeast. Often adding live  
65 yeast on the surface of the diet strongly stimulates females to lay eggs (Markow and O'Grady,  
66 2006; Stocker and Gallant, 2008). Dietary yeast is a major source of nutrition for the adults  
67 and larvae of most saprophagous *Drosophila* (Diptera: Drosophilidae) (Begon, 1982). It  
68 provides essential nutrients for the developmental and reproductive processes such as amino  
69 acids, sterols, vitamins, and fatty acids (Davis, 1975; Anagnostou et al. 2010). As a result, the  
70 concentration of yeast in the artificial diet is the primary determinant of egg production in *D.*  
71 *melanogaster* (Sang and King, 1961; Skorupa et al., 2008), and the formation of yolk proteins  
72 can thus be strongly curtailed by depriving flies of nutritional proteins or essential amino acid  
73 present in yeasts (Sang and King 1961; Bownes et al., 1988; Chippindale et al., 1993). Hence,  
74 the incorporation of live yeast in mediums highly stimulates vitellogenesis because it provides  
75 essential nutrients that are not necessarily present in large amounts in the usual adult food  
76 (Sang and King, 1961; Simmons and Bradley, 1997).

77 Owing to the major importance of the nutritional status on physiological and  
78 biochemical processes of insects, any alteration of nutritional regime is likely to affect all  
79 aspects of their life, including not only reproduction but also stress tolerance (such as thermal  
80 tolerance) (Hallman and Denlinger, 1998; Chown and Nicolson, 2004; Nyamukondiwa and  
81 Terblanche, 2009; Andersen et al., 2010; Colinet and Boivin, 2011; Sisodia and Singh, 2012).  
82 Yet, a limited number of studies have considered the impact of nutritional resources on  
83 environmental stress tolerance, and more particularly on thermal tolerance (Andersen et al.,  
84 2010). In this particular respect, no clear-cut response has been observed as nutritional effects  
85 on thermal tolerance seem to be rather complex and involve many interacting factors.

86 Carbohydrate-rich diets tend to increase drosophilids' cold tolerance compared to protein-rich  
87 diets, and the opposite effect is observed on measures of heat resistance (Andersen et al.,  
88 2010; Sisodia and Singh, 2012). However, when supplemented at high levels, dietary sugars  
89 induce a severe nutritional imbalance and a pathological state in *D. melanogaster* (Wang and  
90 Clark, 1995; Skorupa et al., 2008; Musselman et al., 2011; Colinet et al., 2013a) and these  
91 high sugar doses negatively affect cold tolerance (Colinet et al., 2013a). Quantitative  
92 manipulation of food supply *via* dietary restriction (*i.e.* dilution.) has no detectable effect on  
93 cold tolerance (chill-coma recovery, CCR) of young flies and only marginally reduces cold  
94 tolerance later in adult life (Burger et al., 2007). Removing (or adding) live yeast from *D.*  
95 *melanogaster* food also impacts on thermal traits in a rather complex manner. Le Rohellec  
96 and Le Bourg (2009) found that removing live yeast only weakly decreased cold survival of  
97 females subjected to a 16 h coldshock (0 °C), but only when these were mated. In another  
98 study, absence of live yeast in food killed nearly 100% of flies (males and females) subjected  
99 to the same cold treatment, whereas access to live yeast resulted in medium to high survival  
100 rate depending on age (Le Bourg, 2010). Tolerance to heat (37 °C) was either unaffected (Le  
101 Bourg, 2010) or improved by removal of live yeast (but in young females only) (Le Rohellec  
102 and Le Bourg, 2009). From the above examples, it seems clear that nutritional status can be a  
103 significant component of thermal tolerance of insects, affecting both heat- and cold-related  
104 traits. It also appears that nutritional effects on thermal tolerance depend on several  
105 interacting factors including gender, mating status, and age. Although the physiological and  
106 biochemical basis of thermal responses is becoming clearer through metabolic and  
107 physiological studies (Overgaard et al., 2007; Doucet et al., 2009; Colinet et al., 2012a; Kostál  
108 et al., 2012; Storey and Storey, 2012; Teets and Denlinger 2013), there remains limited  
109 information on the physiology of nutrition-mediated variation in thermal tolerance. A way in  
110 which insects deal with nutrient variations is through altered physiology, namely by affecting  
111 developmental and metabolic processes (Markow et al., 1999). Therefore, it can be assumed  
112 that manipulating the source of essential nutrients found in live yeast, such as amino acids and  
113 proteins, could alter the physiology and also the general stress tolerance.

114 In the present study, we completed a comprehensive assessment of the impact of  
115 dietary live yeast supplementation on body mass characteristics, proteins, metabolic profiles  
116 and basal cold tolerance (to acute and chronic exposures) in *D. melanogaster* females. We  
117 hypothesized that the absence of the source of proteins (*i.e.* live yeast) from adult food would  
118 be associated with deep physiological alterations; therefore, we expected contrasted metabolic

119 profiles (*i.e.* metabotype) between yeast-deprived and yeast-fed females. Because live yeast is  
120 a rich source of proteins and amino acids, we hypothesized that pathways related to protein  
121 biosynthesis would be particularly targeted by dietary live yeast supplementation. In addition,  
122 we expected body mass parameters to be strongly curtailed by depriving females of live yeast.  
123 Finally, we hypothesized that the nutritional and the metabolic variations caused by  
124 manipulating dietary live yeast will translate into altered thermal stress tolerance.

125

## 126 **2. Materials and methods**

### 127 **2.1. Fly culture and diets**

128 We conducted the experiments on a mass-bred *D. melanogaster* line derived from the  
129 mix of two wild populations collected in October 2010 and September 2011 at Plancoët  
130 (Brittany, France). Prior to the experiment, flies were maintained in laboratory in 200 mL  
131 bottles at  $25 \pm 1$  °C (16L:8D) on standard fly medium consisting of deactivated brewer yeast  
132 (80 g/L) (MP Biochemicals, Illkirch, France), sucrose (50 g/L), agar (15 g/L), kalmus (9 g/L)  
133 and Nipagin® (8 mL/L) as described previously (Colinet et al., 2013a). To generate flies for  
134 the experiments, groups of 15 mated females were allowed to lay eggs during a restricted  
135 period of 6 h in bottles (200 mL) containing 25 mL of standard fly medium. This controlled  
136 procedure allowed larvae to develop under uncrowded conditions at  $25 \pm 1$  °C (16L:8D). At  
137 emergence, adult flies were allowed to age for six days on different diets and controls. The  
138 diets were changed every day for six consecutive days. Two different experiments were used  
139 to assess the effect of adult dietary live yeast supplementation (see Fig. 1 for experimental  
140 design).

- 141 - **Experiment 1** (conducted in 2012): minimal control diet *versus* live yeast-  
142 supplemented diet. Sugar and agar [SA] *versus* sugar, agar, live yeast [SAY(+)].
- 143 - **Experiment 2** (conducted in 2013): standard control diet *versus* live yeast-  
144 supplemented diet. Sugar, agar, killed yeast [SAY(-)] *versus* sugar, agar, killed yeast  
145 and live yeast [SAY(±)].

146

147 In the first experiment, emerging flies did not have any nutrient supply except from sugar. It  
148 is thus conceivable that these flies could suffer from malnutrition. Therefore, a second

149 experiment was designed with a standard diet as control that contains protein supply [SAY(-)]  
150 rather than a minimal diet [SA], in order to assess the effect of dietary live yeast  
151 supplementation without any putative malnutrition. In both experiments, the amounts of  
152 sugar, agar and killed yeast when supplied were 50 g/L, 15 g/L and 80 g/L respectively. When  
153 supplemented, the live yeast was provided with *ad libitum* paste placed on the surface of the  
154 food [*i.e.* for SAY(+) and SAY( $\pm$ )]. We used synchronized six day-old adults for all assays to  
155 avoid the uncontrolled variation of stress tolerance during the first days of age (Colinet et al.,  
156 2013b). Adults were sexed visually (with an aspirator) without CO<sub>2</sub> to avoid any confusing  
157 metabolic effects due to anaesthesia (Colinet and Renault, 2012), and only females were kept.  
158 Six day-old females from each nutritional group were either directly used for the cold assays  
159 or snap-frozen in liquid nitrogen and stored at -80 °C for the other assays.

160

## 161 2.2. Body mass and protein levels

162 We assessed total protein content using the Bradford procedure (Bradford, 1976).  
163 Twelve biological replicates, each consisting of a pool of three females, were used for each  
164 experimental condition. Each sample was *vacuum*-dried (GENEVAC, model DNA-23050-  
165 B00) set at 30 °C for 24 h and then weighed (dry mass, Mettler Toledo UMX2, accurate to 1  
166  $\mu$ g) before proteins were extracted in a phosphate buffer (100 mM KH<sub>2</sub>PO<sub>4</sub>, 1 mM DTT and 1  
167 mM EDTA, pH 7.4, Foray et al., 2012) and homogenized using bead-beating at 25 Hz for 1.5  
168 min. The concentration of total proteins was then measured in the whole body extracts using  
169 Bio-Rad Protein Assay (catalog number 500-0006) following manufacturer's instructions.

170 For each nutritional treatment, 15 females were subjected to individual fresh mass  
171 (FM) measurements (Mettler Toledo UMX2, accurate to 1  $\mu$ g). Then, individual females were  
172 dried at 60 °C for two days, and reweighed to measure dry mass (DM). Water mass (WM)  
173 was determined by subtracting DM from FM. Water content (WC) represents the ratio  
174 WM/FM. Lean dry mass (LDM) was measured by extracting total lipids in a  
175 chloroform/methanol solution (Folch reagent 2:1, v:v) for one week under continuous  
176 agitation. The samples were then dried at 60 °C to eliminate residues of the extracting  
177 solution before measurement of LDM. Body lipid mass (LM), corresponding to DM-LDM,  
178 was calculated (see Colinet et al., 2006). Folch reagent may extract a small fraction of other

179 compounds than lipids, but measurements obtained with this method are still considered as a  
180 good index of lipid content for comparative studies ([Williams et al., 2011](#)).

181

### 182 2.3. Cold tolerance assays

183 Different metrics were used to assess cold tolerance. First, recovery time following a  
184 non-lethal chronic cold stress was measured (*i.e.* chill-coma recovery, CCR). Fifty females  
185 were exposed to 0 °C for various durations: 8, 10 and 12 h for the flies of the experiment 1  
186 [*i.e.* SA vs. SAY(+)], and 10 and 12 h for the flies of the experiment 2 [*i.e.* SAY(-) vs.  
187 SAY(±)]. Cold-exposed flies were then allowed to recover at 25 ± 1 °C (16L:8D) and  
188 recovery times were individually recorded; flies were considered recovered when they stood  
189 up. A cold incubator (Model MIR-153, SANYO Electric Co. Ltd, Japan) was used for the  
190 assays. After scoring the recovery times, the same females were returned to 25 ± 1 °C  
191 (16L:8D) on their respective diet and the mortality was scored after 24 h (*i.e.* latent damage  
192 assessment).

193 Second, tolerance to acute cold stress was measured. A total of 100 females (5 replicates, 20  
194 females per replicate) were placed in 42 mL glass vials immersed in a glycol solution cooled  
195 to -3.5 °C for different durations: 90, 120 and 135 min for the flies of the experiment 1 [*i.e.*  
196 SA vs. SAY(+)], and 90 and 120 min for the flies of the experiment 2 [*i.e.* SAY(-) vs.  
197 SAY(±)]. After the acute cold stress, the flies were returned to 25 °C on their respective diet,  
198 and the mortality was scored after 24 h. Most mortality in *D. melanogaster* adults happens  
199 within 24 h after the cold stress ([Rako and Hoffmann, 2006](#)), and we therefore did not  
200 consider a longer period.

201

### 202 2.4. Metabolic fingerprinting

203 The metabolic effect of dietary live yeast supplementation was assessed by comparing the  
204 metabotypes of SA vs. SAY(+) (experiment 1) and SAY(-) vs. SAY(±) (*i.e.* experiment 2). To  
205 ensure that the differences observed were not only related to presence/absence of live yeast in  
206 the gut content, we included an additional treatment where flies were starved before sampling.  
207 In this **experiment 3** (conducted in 2013), the same flies as in the experiment 2 were starved  
208 for 8 h on agar before their metabolic profiles were compared. Hence, we compared the



209 following conditions: sugar, agar, killed yeast, plus 8h starvation (**St-SAY-**) *versus* sugar,  
210 agar, killed yeast and live yeast, plus 8h starvation (**St-SAY±**) (see Fig. 1).

211 For each nutritional group, six biological replicates, each consisting of a pool of 15  
212 females, were used for metabolic fingerprinting. Each sample was weighed (Mettler Toledo  
213 UMX2, accurate to 1 µg) before metabolite extractions. Sample preparation and derivatization  
214 were performed as previously described (Colinet et al., 2012b), with minor modifications.  
215 Briefly, after homogenisation in methanol-chloroform solution (2:1, v:v) and phase separation  
216 with 400 µL of ultrapure water, an 120 µL aliquot of the upper phase, which contained polar  
217 metabolites, was *vacuum*-dried. The dry residue was resuspended in 30 µL of 20 mg mL<sup>-1</sup>  
218 methoxyamine hydrochloride in pyridine before incubation under automatic orbital shaking at  
219 40 °C for 60 min. Then, 30 µL of MSTFA were added and the derivatization was conducted  
220 at 40 °C for 60 min under agitation (see Colinet et al., 2012b). A CTC CombiPal autosampler  
221 (GERSTEL GmbH and Co.KG, Mülheim an der Ruhr, Germany) was used, ensuring  
222 standardized sample preparation and timing. Metabolites were separated, identified and  
223 quantified using a GC/MS platform consisting of a Trace GC Ultra chromatograph and a  
224 Trace DSQII quadrupole mass spectrometer (Thermo Fischer Scientific Inc, Waltham, MA,  
225 USA). The oven temperature ranged from 70 to 170 °C at 5 °C min<sup>-1</sup>, from 170 to 280 °C at 7  
226 °C min<sup>-1</sup>, from 280 to 320 °C at 15 °C min<sup>-1</sup>, and then, the oven remained at 320 °C for 4 min.  
227 We completely randomized the injection order of the samples. All samples were run under the  
228 SIM mode rather than the full-scan mode. We therefore only screened for the 63 pure  
229 reference compounds included in our custom spectral database. Calibration curves for 60 pure  
230 reference compounds at 5, 10, 20, 50, 100, 200, 500, 750, 1000, 1500 and 2000 µM  
231 concentrations were run concurrently. Chromatograms were deconvoluted using XCalibur  
232 2.0.7, and metabolite levels were quantified using the quadratic calibration curve for each  
233 reference compound and concentration. Arabinose was used as the internal standard (see  
234 Colinet et al., 2012b). Among the 63 metabolites included in our spectral library, 37, 34 and  
235 34 compounds were detected in the samples from experiment 1, 2 and 3 respectively (see  
236 Table 1 for compounds' list and abbreviations).

237

## 238 **2.5. Statistics**

239 Since allometric relationship may exist between the body mass parameters and size, we  
240 first determined if the variables were linearly related to LDM (with least-squares regressions)

241 (Packard and Boardman, 1999). Analysis of covariance (ANCOVA) was then used if linear  
242 relationships was established, using LDM as co-variable, whereas analysis of variance  
243 (ANOVA1) was used with nutritional treatment as factor when the allometric relationship was  
244 not found. The same approach was used for analysing the protein content but with DM as co-  
245 variable. Comprehensive details on regression statistics and individual plots are shown in  
246 [supplementary file S1](#). For cold tolerance, Chi-square contingency tests were used to compare  
247 mortality rates between nutritional groups (with Yates' correction to prevent overestimation of  
248 statistical significance). For CCR, the data were used to generate temporal recovery curves  
249 which were compared with Mantel-Cox (Log rank) test. This non parametric method tests the  
250 null hypothesis that there is no difference between the populations in the probability of an  
251 event at any time point (i.e. a curve comparison test). Analyses were performed using Prism v.  
252 5.01 (GraphPad Software, Inc., San Diego, CA, USA, 2007) or the statistical software 'R  
253 2.13.0' (R Development Core Team, 2008). For metabolic data, a principal component  
254 analysis (PCA) was performed on the whole dataset to detect the compounds contributing the  
255 most to the separation between the nutritional groups. The inertia calculated in the PCA  
256 represents the part of the total variance that is due to the difference between modalities.  
257 Scaled data (i.e. mean-centered and divided by  $\sqrt{SD}$ ) were used in the multivariate analyses to  
258 prevent the effects of the metabolite concentration means and ranges of variability on the  
259 correlations with the principal components (PCs). This analysis was performed using the  
260 'ade4' library in the statistical software 'R 2.13.0'. In addition, to look for evidence of enriched  
261 metabolic pathways in response to dietary live yeast supplementation, metabolite pathway  
262 enrichment analysis (MPEA) was conducted using MetPA online package, with *D.*  
263 *melanogaster* specific library (Xia and Wishart, 2010), as previously described (Colinet et al.,  
264 2013a).

265

### 266 **3. Results**

#### 267 **3.1. Body mass and protein levels**

268 The [Figure 2](#) summarizes the variations in mass parameters according to nutritional  
269 treatments. The DM corresponds to the sum of LM and LDM, and FM corresponds to the sum  
270 of LM, LDM and WM ([Fig. 2](#)). Females fed with live yeast [SAY(+) and SAY( $\pm$ )] were  
271 heavier in terms of FM and DM than their counterparts fed without live yeast. Since FM and

272 DM were linearly related to LDM ( $P < 0.05$ ; see [supplementary file S1](#)), we used ANCOVA  
273 to assess the effect of nutritional treatment with LDM as co-variable. The effect of the  
274 treatment remained significant even when the allometric effect of size was removed (FM:  $F =$   
275  $30.69$ ,  $df = 3$ ,  $P < 0.001$ ; DM:  $F = 8.27$ ,  $df = 3$ ,  $P < 0.001$ ;  $n = 15$ ). Multiple comparisons  
276 revealed that  $SA < SAY(-) < SAY(+) = SAY(\pm)$  for FM, and  $SA < SAY(-) = SAY(+) =$   
277  $SAY(\pm)$  for DM. The WM was also correlated to LDM ( $P < 0.05$ ; see [supplementary file S1](#)).  
278 The ANCOVA revealed a significant effect of the treatment ( $F = 29.94$ ,  $df = 3$ ,  $P < 0.001$ ;  $n =$   
279  $15$ ). Multiple comparisons revealed that  $SA < SAY(-) < SAY(+) = SAY(\pm)$  for WM. Contrary  
280 to WM, the WC was unrelated to LDM ( $P > 0.05$ ; see [supplementary file S1](#)) and the  
281 ANOVA did not detect variation according to the diet treatment ( $F = 0.197$ ,  $df = 3$ ,  $P = 1.61$ ;  
282  $n = 15$ ). The LM was unrelated to LDM ( $P > 0.05$ ; see [supplementary file S1](#)), and ANOVA  
283 detected a significant effect of nutritional treatment, with a lower total lipid content for the  
284 treatment SA ( $F = 10.4$ ,  $df = 3$ ,  $P < 0.001$ ;  $n = 15$ ). The LDM varied according to nutritional  
285 treatment ( $F = 76.14$ ,  $df = 3$ ,  $P < 0.001$ ;  $n = 15$ ), with the following rank order:  $SA < SAY(-)$   
286  $< SAY(+) < SAY(\pm)$ . Finally, the total protein content was not related to DM ( $P > 0.05$ ; see  
287 [supplementary file S1](#)), and ANOVA revealed a significant effect of nutritional treatment ( $F =$   
288  $155.3$ ,  $df = 3$ ,  $P < 0.001$ ;  $n = 12$ ), with higher protein contents in females fed with live yeast  
289 [*i.e.*  $SA < SAY(-) < SAY(+) < SAY(\pm)$ ].

290

### 291 **3.2. Cold tolerance**

292 Concerning cold tolerance, we found that CCR significantly varied between the two  
293 nutritional groups of the experiment 1, with females fed on SAY(+) diet recovering faster  
294 than females fed on SA diet ([Fig. 3](#)). This difference manifested for all the durations of cold  
295 stress that were tested in the experiment 1 (8h:  $Chi^2 = 19.17$ ,  $df = 1$ ,  $P < 0.001$ ; 10 h:  $Chi^2 =$   
296  $16.29$ ,  $df = 1$ ,  $P < 0.001$ ; 12 h:  $Chi^2 = 14.65$ ,  $df = 1$ ,  $P < 0.001$ ;  $n = 50$ ). Survival after chronic  
297 cold stress was also affected by nutritional regime. For all the durations of cold stress at 0 °C  
298 (8, 10 and 12 h), the post-stress mortality was significantly lower when females fed on  
299 SAY(+) diet compared to SA diet (8 h:  $Chi^2 = 21.23$ ,  $df = 1$ ,  $P < 0.001$ ; 10 h:  $Chi^2 = 19.10$ ,  $df$   
300  $= 1$ ,  $P < 0.001$ ; 12 h:  $Chi^2 = 21.23$ ,  $df = 1$ ,  $P < 0.001$ ;  $n = 50$ ) ([Fig. 3](#)). Finally, the acute cold  
301 tolerance also varied with the nutritional regimes of the experiment 1 ([Fig. 3](#)). For all the  
302 durations of cold stress at -3.5 °C (90, 120 and 135 h), the post-stress mortality was  
303 significantly lower when females fed on SAY(+) diet compared to SA diet (90 min:  $Chi^2$

304 =39.61,  $df = 1$ ,  $P < 0.001$ ; 120 min:  $Chi^2 = 35.57$ ,  $df = 1$ ,  $P < 0.001$ ; 135 min:  $Chi^2 = 17.56$ ,  $df =$   
305 1,  $P < 0.001$ ;  $n = 100$ ).

306 The cold tolerance of the flies from the experiment 2 was also affected by the  
307 nutritional treatments; however, this was not manifested on CCR. Females feeding on SAY(-)  
308 and SAY( $\pm$ ) recovered from chronic cold stress with similar temporal dynamics (10 h:  $Chi^2 =$   
309 2.55,  $df = 1$ ,  $P = 0.10$ ; 12 h:  $Chi^2 = 1.01$ ,  $df = 1$ ,  $P = 0.31$ ;  $n = 50$ ) (Fig. 4). On the other hand,  
310 the survival after the chronic cold stress was affected by the nutritional regimes. For both  
311 durations of chronic cold stress (10 and 12 h), the post-stress mortality was significantly lower  
312 when females fed on SAY( $\pm$ ) diet compared to SAY(-) diet (10 h:  $Chi^2 = 5.02$ ,  $df = 1$ ,  $P =$   
313 0.025; 12 h:  $Chi^2 = 16.94$ ,  $df = 1$ ,  $P < 0.001$ ;  $n = 50$ ) (Fig. 4). Finally, the acute cold tolerance  
314 also varied with the nutritional regimes of the experiment 2. For both durations of acute cold  
315 stress at -3.5 °C (90 and 120 h), the post-stress mortality was significantly lower when  
316 females fed on SAY( $\pm$ ) diet compared to SAY(-) diet (90 min:  $Chi^2 = 69.01$ ,  $df = 1$ ,  $P < 0.001$ ;  
317 120 min:  $Chi^2 = 66.66$ ,  $df = 1$ ,  $P < 0.001$ ;  $n = 100$ ) (Fig. 4).

318

### 319 3.3. Metabolic fingerprinting

320 The metabolic profiles of flies from experiment 1 showed that a number of metabolites  
321 had their concentrations affected by dietary live yeast, which resulted in contrasted  
322 metabolotypes between the two nutritional groups (Fig. 5). A clear-cut separation was observed  
323 along the first principal component (PC1) of the PCA, which accounted for 43.9% of the total  
324 inertia (Fig. 5). GDL, Fru, Glc, Tre and sorbitol were the molecules the most positively  
325 correlated to PC1 (*i.e.* accumulated in SA flies), whereas on the opposite side, the amino acids  
326 Val, Ile, Leu, Thr, Gly, Phe and Glu were the molecules the most negatively correlated to PC1  
327 (*i.e.* accumulated in SAY(+) flies) (Fig. 5). The other principal components accounted for  
328 28.4% (PC2) and 11.3% (PC3) of the total inertia and mainly represented within-treatment  
329 variations. MPEA based on the metabolites that were positively correlated to PC1 revealed  
330 three enriched metabolic pathways (Holm adjust  $P < 0.05$ ), and all were directly involved in  
331 carbohydrate metabolism. MPEA based on all the metabolites that were negatively correlated  
332 to PC1 revealed three enriched metabolic pathways; all were directly involved in amino acids  
333 and protein biosynthesis (see Dataset S1 for detailed concentrations and fold changes).

334 Similar results were obtained with the flies from experiment 2. A clear-cut separation  
335 was observed along the PC1 of the PCA, which accounted for 47.1% of the total inertia (Fig.  
336 6). Fru, Tre, xylitol, Glc and GDL were the most positively correlated to PC1 (*i.e.*  
337 accumulated in SAY(-) flies), whereas on the opposite side, Glu, inositol, Leu, Phe and Val  
338 were the most negatively correlated metabolites to PC1 (*i.e.* accumulated in SAY( $\pm$ ) flies)  
339 (Fig. 6). The other principal components accounted for 31.6% (PC2) and 6.4% (PC3) of the  
340 total inertia and mainly represented within-treatment variations. MPEA also revealed that that  
341 carbohydrate metabolism was enriched in the SAY(-) flies, while amino acids and protein  
342 biosynthesis were enriched in the SAY( $\pm$ ) flies (see [Dataset S2](#) for detailed concentrations and  
343 fold changes).

344

345 Finally, the addition of a starvation period to empty the gut content of the flies before  
346 assessing the flies (*i.e.* experiment 3) resulted in a similar metabolic response. Again, a clear-  
347 cut separation was observed along the PC1, which accounted for 57.3% of the total inertia  
348 (Fig. 7). Xylitol, Man, Ala, Fru, Tre and Glc were the most positively correlated metabolites  
349 to PC1 (*i.e.* accumulated in St-SAY(-) flies), whereas Glu, Thr, Ile, Phe, inositol and Leu  
350 were the most negatively correlated to PC1 (*i.e.* accumulated in SAY( $\pm$ ) flies) (Fig. 7). The  
351 other principal components accounted for 21.2% (PC2) and 7.15% (PC3) of the total inertia.  
352 MPEA also revealed that that carbohydrate metabolism was enriched in the St-SAY(-) flies,  
353 while amino acids and protein biosynthesis were enriched in the St-SAY( $\pm$ ) flies (see [Dataset](#)  
354 [S3](#) for detailed concentrations and fold changes).

355

## 356 4. Discussion

357 Dietary yeast is a major source of nutrition for the adults and larvae of most  
358 saprophagous *Drosophila* sp. (Diptera: Drosophilidae) ([Begon, 1982](#)), and as a consequence,  
359 yeast is typically incorporated into artificial diets ([Markow and O'Grady, 2006](#); [Stocker and](#)  
360 [Gallant, 2008](#)). Dietary yeast provides essential nutrients such as amino acids, sterols,  
361 vitamins, and fatty acids ([Davis, 1975](#); [Anagnostou et al., 2010](#)). We assumed that removing  
362 or adding live yeast from adult food at eclosion would be associated with physiological  
363 remodelling that would subsequently affect fitness-related traits such as body size and stress  
364 tolerance. In the present study, we completed a comprehensive assessment of the impact of

365 dietary live yeast supplementation on body mass characteristics, stored proteins, metabolic  
366 profiles and basal cold tolerance (to acute and chronic exposures) in *D. melanogaster* females.

367 We expected body mass parameters to be affected by dietary live yeast  
368 supplementation. Indeed, the body mass of the flies is known to reflect protein level in food,  
369 with high levels of dietary yeast leading to heavier flies (Skorupa et al., 2008). We have  
370 conclusively shown that body mass parameters (FM, DM, WM, LM and LDM) increased  
371 when females were fed with live yeast, which is consistent with previous studies (Simmons  
372 and Bradley, 1997; Le Rohellec and Le Bourg, 2009). For all the considered mass parameters,  
373 the SA flies had significantly smaller values than the SAY(-) flies which shows that SA flies  
374 disproportionally suffered from the complete lack of dietary protein and suggests a  
375 malnutrition in this group. Concerning the fat (*i.e.* LM), we found that the SA flies had lower  
376 stored fat than the live yeast-fed flies [*i.e.* SAY(+), SAY( $\pm$ )], but this reduction was not  
377 observed in SAY(-) flies. Hence, the reduction of fat was not related to the suppression of live  
378 yeast *per se*, but to the complete suppression of proteins supply from the diet (*i.e.* SA). It was  
379 previously reported that the increase in body mass with dietary live yeast is almost  
380 exclusively due to increased ovary size (Simmons and Bradley, 1997), and ovaries comprise  
381 approximately 15% of the body lipids of insects (Lease and Wolf, 2011). The lower LM of  
382 the flies on SA diet is not surprising as these flies had small ovaries and hardly produced eggs  
383 (data not shown). The LDM was different among all treatments and a corresponding pattern  
384 was observed for the protein content. This suggests that feeding on a diet that contains killed  
385 yeast [SAY(-)] provides proteins to the flies, but feeding on a diet that also contains live yeast  
386 provides additional amounts of proteins. Storage of proteins is largely independent of dietary  
387 carbohydrates but is almost exclusively determined by the presence and concentration of yeast  
388 in the medium (Skorupa et al., 2008). Our data corroborate this idea.

389 A way in which insects deal with nutrient variations is through altered physiology,  
390 namely by affecting developmental and metabolic processes (Markow et al., 1999). Therefore,  
391 we assumed that manipulating the adult food (*via* live yeast supplementation) would be  
392 associated with physiological changes that would translate into contrasted metabolic profiles  
393 between nutritional groups. We have conclusively shown that a number of metabolites had  
394 their concentrations affected by the nutritional treatments, which resulted in contrasted  
395 metabotypes between live yeast-supplemented flies [SAY(+) and SAY( $\pm$ )] and the control  
396 flies. Whatever the control used [SA or SAY(-) or St-SAY(-)], a similar response was  
397 repeatedly observed : sugars (Fru, Glc, and Tre) exhibited elevated amounts in the control



398 whereas amino acid amounts (Val, Ile, Leu, Thr, Gly, Phe and Glu) were more abundant in  
399 the live yeast-supplemented groups. The fact that the relative abundance of sugars was higher  
400 in SA metabotype is not surprising, as these flies were fed on a minimal diet with no access to  
401 any source of proteins from adult eclosion. For the flies fed on SAY(-) and St-SAY(-) diets,  
402 the increased levels of sugars likely translates that these diets were proportionally richer in  
403 sugar than the corresponding live yeast-supplemented diets. We also found that GDL, sorbitol  
404 and xylitol contributed to the control metabotypes. GDL is a metabolite (a lactone) resulting  
405 from the degradation of Glc through the pentose phosphate pathway (Garrett and Grisham,  
406 1999). Polyols such as sorbitol are derived from hexose monophosphates and can be produced  
407 from both Glc and Fru (Storey, 1983; Wolfe et al., 1998). The higher relative abundance of  
408 these sugar-related compounds is thus congruent with the nutritional regime of the flies.  
409 Moreover, MPEA revealed several enriched metabolic pathways associated with the control  
410 metabotypes [SA or SAY(-) or St-SAY(-)], and all of them were directly involved in the  
411 carbohydrate metabolism. This further confirmed the relative higher impact of sugars in  
412 shaping the metabotype of these nutritional groups. Concerning the live yeast-fed flies, we  
413 found a higher relative abundance of amino acids (*e.g.* Val, Ile, Leu, Thr, Gly, Phe and Glu)  
414 associated with these nutritional groups. This response was observed whatever the treatment  
415 used [SAY(+) or SAY( $\pm$ ), or St-SAY( $\pm$ )]. This is congruent with the nutritional regime of  
416 these flies. Live yeast is known to provide essential nutrients such as proteins and amino acids  
417 (Davis 1975; Anagnostou et al. 2010). This most likely explains why MPEA revealed several  
418 enriched metabolic pathways related to amino acids and protein biosynthesis in these  
419 nutritional groups. This biological interpretation also coincides with the larger body protein  
420 content detected in these nutritional groups. The differences observed in the metabolic  
421 profiles between the live yeast-supplemented and the control groups may also be partly due to  
422 different food intake and thus incorporation of nutrients. Indeed, food intake increases with  
423 concentration of dietary yeast in *D. melanogaster* (Min and Tara, 2006). The fact that  
424 metabolic patterns were consistent among experiments suggest that (i) live yeast promotes  
425 amino acids biosynthesis even when the flies are already fed with killed yeast, and (ii) that  
426 differences observed were not related to presence/absence of live yeast in the gut content.

427 Many insect species feed on yeasts and the effects of this nutritional resource on the  
428 growth, fecundity and survival has been demonstrated in a wide range of species (*e.g.*  
429 Starmer and Fogleman, 1986; Ganter 2006; Anagnostou et al. 2010). In spite of this, there is  
430 limited information on nutrition-mediated variations in stress tolerance in insects, and more

431 particularly regarding thermal tolerance (Andersen et al., 2010). Here, we report convincing  
432 evidence that supplementing adult flies with sources of dietary proteins and amino acids  
433 (live yeast) promoted their subsequent cold tolerance. This positive effect of live yeast was  
434 repeatedly found in almost all of the metrics used to assess their cold tolerance (acute and  
435 chronic tolerance), and for all the stress intensities applied in the first experiment. In the  
436 second experiment, CCR was not affected by live yeast supplementation, but all the other  
437 assays (post-stress survival) supported a positive effect of live yeast on cold tolerance.  
438 Previous works reported an effect of dietary yeast on *Drosophila* cold tolerance, but the  
439 effects ranged from weak to very intense, and were thus difficult to interpret. For instance,  
440 Le Rohellec and Le Bourg (2009) found that removing live yeast weakly decreased cold  
441 survival of females subjected to a 16h cold-shock (0 °C), but only when these were mated.  
442 In another study, the absence of live yeast in food killed nearly all flies (males and females)  
443 subjected to the same cold treatment, whereas access to dietary yeast resulted in medium to  
444 high survival rates, depending on the age of the specimens (Le Bourg, 2010). These  
445 incongruities likely arise from the fact that nutrition-related variation in thermal tolerance  
446 involves interacting factors such as age, mating and gender. It remains unclear why in our  
447 study the CCR was affected by the nutritional treatment in the experiment 1 but not in the  
448 experiment 2. Longer temporal recovery dynamics of the SA flies (experiment 1) could  
449 result from the lack of essential nutrients necessary for an optimal functioning of the whole-  
450 system physiology, or from an excessive amount of consumed sugars (as sugar was the sole  
451 source of food in this specific group). With regard to sugars, it appears that carbohydrate-  
452 enriched diets tend to increase *Drosophila* cold tolerance (Andersen et al., 2010; Sisoda and  
453 Singh, 2012). However, when provided at too high levels, dietary sugars induce a severe  
454 nutritional imbalance and a pathological state in *D. melanogaster* (Wang and Clark, 1995;  
455 Skorupa et al., 2008; Musselman et al., 2011; Colinet et al., 2013a), which in turn negatively  
456 affects cold tolerance including CCR (Colinet et al., 2013a). In spite of this, our data and  
457 earlier observations (Le Rohellec and Le Bourg, 2009; Le Bourg, 2010) all converge  
458 towards the same conclusion that cold tolerance of the females of *D. melanogaster* is  
459 generally promoted by dietary live yeast. Females fed with live yeast had increased body  
460 mass and contained more lipids and proteins, and MPEA corroborated that live yeast  
461 supplementation was associated with amino acids and protein biosyntheses. Interestingly, it  
462 was previously found in *D. melanogaster* that the level of glycogen, triglycerides, and total  
463 proteins was higher in cold-selected than in control lines (Chen and Walker, 1994). The  
464 same authors also noted that these levels quickly decreased 24 h after a cold stress and



465 suggested that higher storage of energy reserves entails increased cold tolerance of cold-  
466 selected lines. Thus, the higher energy reserves of the live yeast-supplemented flies may  
467 explain why cold survival (assessed after 24 h) was higher in this nutritional group.

468         Stressful conditions are known to critically increase energy expenditure because the  
469 repairing mechanisms require excess of energy (Parsons, 1991). We suggest that in nutrient-  
470 unbalanced conditions (*e.g.* SA), individuals might disproportionately suffer from stressful  
471 conditions because the metabolically available energy is already constrained. The ability to  
472 synthesize essential stress-related proteins, due to dietary depletion of amino acids and  
473 protein building blocks could be an alternate explanation for the reduced cold tolerance.  
474 Hence, dietary balance is likely to be a key point of environmental stress physiology. Stress  
475 tolerance is probably compromised under conditions of excessive nutritional imbalance, as  
476 for life-history traits (Skorupa et al., 2008). In the natural environment, larvae may  
477 occasionally face nutritional stress and this might further affect the stress tolerance of the  
478 adults (carry-over effect), however, this question has not been examined. This study  
479 conclusively demonstrates an interaction between dietary live yeast and thermal stress  
480 tolerance of *D. melanogaster* females. Whether dietary live yeast positively affects the  
481 tolerance to other stressors remains to be further examined. Moreover, the mechanistic link  
482 between thermal tolerance and dietary live yeast remains an open question. Understanding  
483 the link between thermal stress tolerance and nutrient quality represents an important step in  
484 physiological ecology that may further add to our understanding of thermal biology of  
485 ectotherms.

486

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495 **Reference**

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**Table 1: List of metabolites detected in females of *Drosophila melanogaster***

Compounds abbreviations in brackets

***Free amino acids***

Alanine (Ala)  
Valine (Val)  
Serine (Ser)  
Leucine (Leu)  
Threonine (Thr)  
Proline (Pro)  
Methionine (Met)  
Ornithine (Orn)  
Glycine (Gly)  
Isoleucine (Ile)  
Glutamate (Glu)  
Lysine (Lys)  
Phenylalanine (Phe)  
Tyrosine (Tyr)

***Sugars***

Sucrose (Suc)  
Fructose (Fru)  
Glucose (Glc)  
Trehalose (Tre)  
Mannose (Man)  
Galactose (Gal)  
Ribose (Rib)  
Maltose (Mal)  
Glucose-6-phosphate (G6P)

***Polyols***

Sorbitol  
Glycerol  
Glycerol-3-Phosphate  
Inositol  
Xylitol

***Intermediate metabolites***

Succinate  
Malate  
Citrate  
Fumarate

***Other metabolites***

Lactate  
Ethanolamine (ETA)  
Free phosphate (PO4)  
Gamma-aminobutyric acid (GABA)  
Glucono delta-lactone (GDL)  
Spermine

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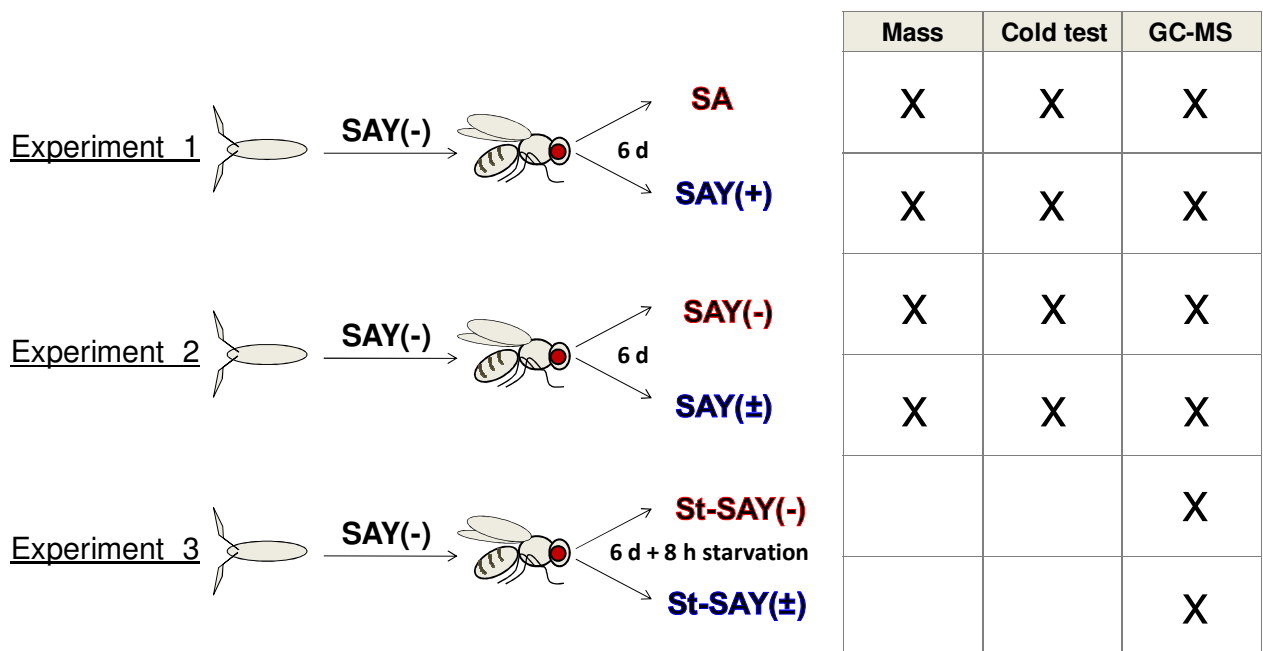
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652 **Figure 1:** Schematic diagram of the experimental design used to investigate the effect of  
 653 dietary live yeast supplementation on mass parameters, cold tolerance and GC-MS metabolic  
 654 profiles of *D. melanogaster*. In all experiments, the flies developed from egg to adult on a  
 655 standard diet [SAY(-)]. Emerging females were then fed on different diets for 6 days: SA vs.  
 656 SAY(+) for experiment 1 and SAY(-) vs. SAY( $\pm$ ) for experiment 2. In the experiment 3,  
 657 females were fed on the same experimental conditions as in experiment 2, but they were  
 658 starved for 8 h before sampling, St-SAY(-) vs. St-SAY( $\pm$ ). Symbols S, A and Y for sugar,  
 659 agar and yeast, respectively. Sign (+), (-) and ( $\pm$ ) for live yeast only, killed yeast only, and  
 660 both live and killed yeast, respectively.

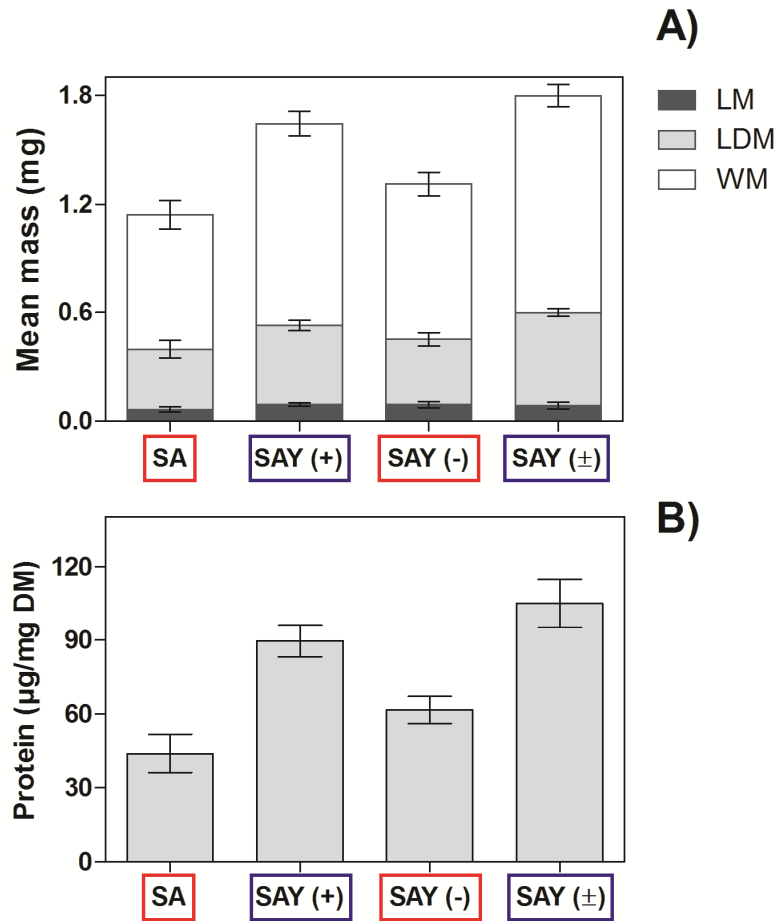
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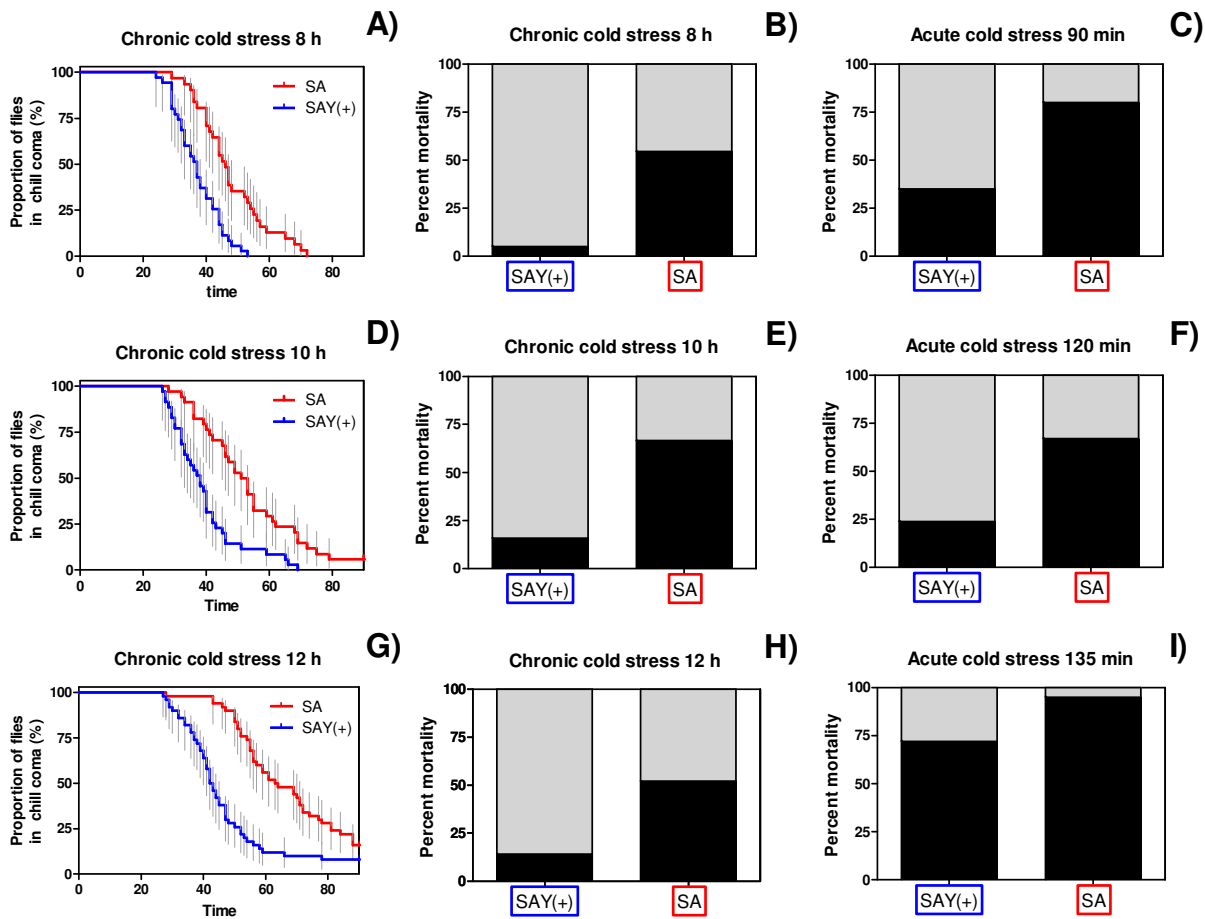


674 **Figure 2:** (A) Body mass parameters showing changes in lipid mass (LM), lean dry mass  
675 (LDM), and water mass (WM) according to nutritional treatment [SA, SAY(+), SAY(-),  
676 SAY( $\pm$ )] ( $n = 15$ ). (B) Total protein content of female *D. melanogaster* ( $n = 12$ ).



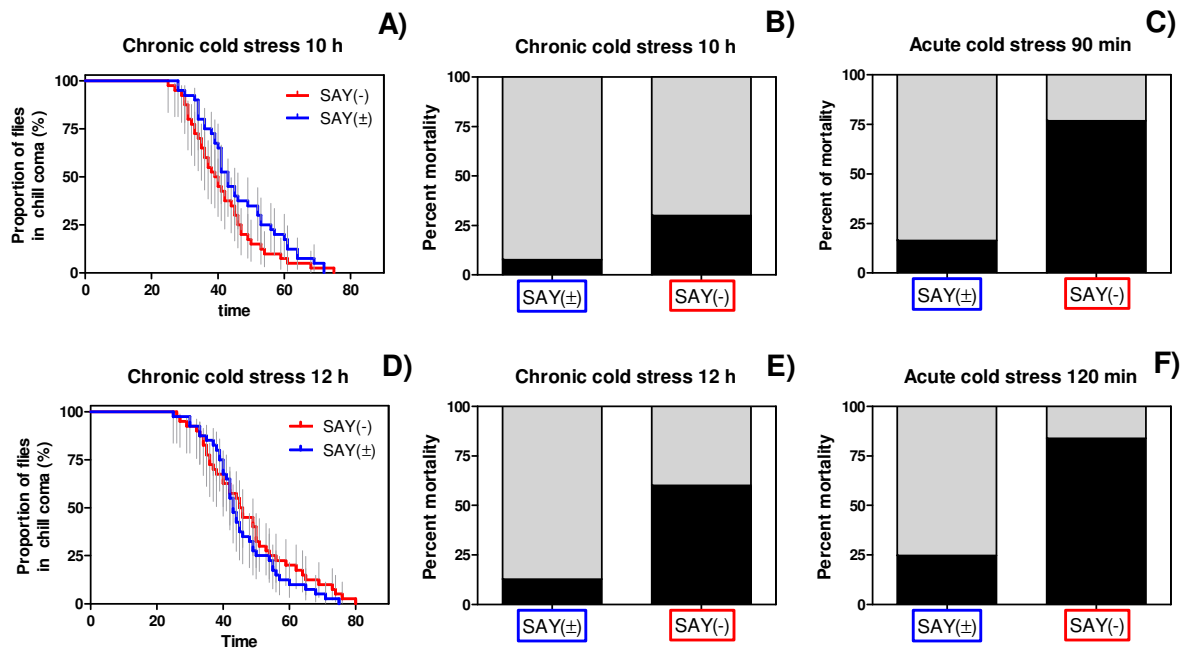
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690 **Figure 3:** Composite panel summarizing all the cold tolerance assays of the experiment 1.  
 691 Temporal recovery curves of live yeast-fed females [blue line, SAY(+)] and yeast-deprived  
 692 females [red line, SA] exposed to chronic cold stress (0 °C) for various durations: 8, 10 and  
 693 12 h in figures A, D, and G, respectively. Each line represents the mean proportion ( $\pm$  95%  
 694 confidence interval) of recovering flies in relation to time after cold stress ( $n = 50$ ). Mortality  
 695 rates, assessed 24 h after the chronic cold stresses, are shown in figures B, E and H for each  
 696 nutritional treatment [SA vs. SAY(+)] ( $n = 50$ ). Mortality rates assessed 24 h after an acute  
 697 cold stress (-3.5 °C) for various durations: 90, 120, 135 min are shown in figures C, F and I,  
 698 respectively ( $n = 100$ ). The black part of the bars represents the percent mortality and grey  
 699 part is percent survival.



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706 **Figure 4:** Composite panel summarizing the cold tolerance assays of the experiment 2.  
 707 Temporal recovery curves of live yeast-fed females [blue line, SAY( $\pm$ )] and live yeast-  
 708 deprived females [red line, SAY(-)] exposed to chronic cold stress (0 °C) for various  
 709 durations: 10 and 12 h in figures A and D, respectively. Each line represents the mean  
 710 proportion ( $\pm$  95% confidence interval) of recovering flies in relation to time after cold stress  
 711 ( $n = 50$ ). Mortality rates, assessed 24 h after the chronic cold stresses, are shown in figures B,  
 712 and E for each nutritional treatment [SAY(-) vs. SAY( $\pm$ )] ( $n = 50$ ). Mortality rates assessed 24  
 713 h after an acute cold stress (-3.5 °C) for various durations: 90 and 120 min are shown in  
 714 figures C and F, respectively ( $n = 100$ ). The black part of the bars represents the percent  
 715 mortality and the grey part is percent survival.



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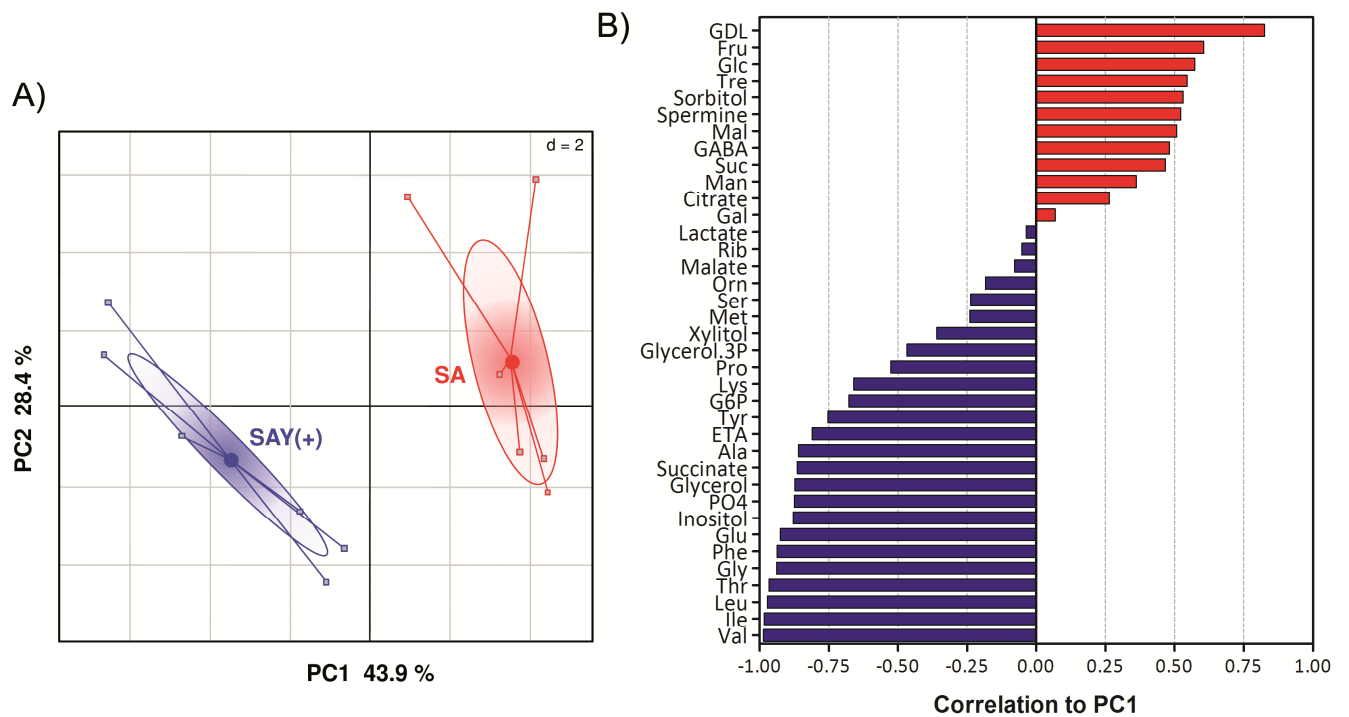
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723 **Figure 5:** (A) Multivariate analysis (PCA) based on the GC/MS metabolomic data of the  
 724 experiment 1 illustrating the plotting of PC1 against PC2. The unit "d" (top right of the plot)  
 725 represents the side-length of a square in the grid. A clear separation was observed between  
 726 live yeast-fed [blue ellipse, SAY(+)] and yeast-deprived metabolotypes [red ellipse, SA]. Lines  
 727 link replicates to their respective centroids ( $n = 6$ ). (B) Correlation values of the different  
 728 metabolite concentrations to the principal components PC1 in the principal component  
 729 analysis. Correlations are ranked on Y-axis according to their values. Blue bars for negative  
 730 correlations (*i.e.* accumulated in SAY(+) flies) and red bars for positive correlations (*i.e.*  
 731 accumulated in SA flies). See [Dataset S1](#) for detailed concentrations and fold changes.

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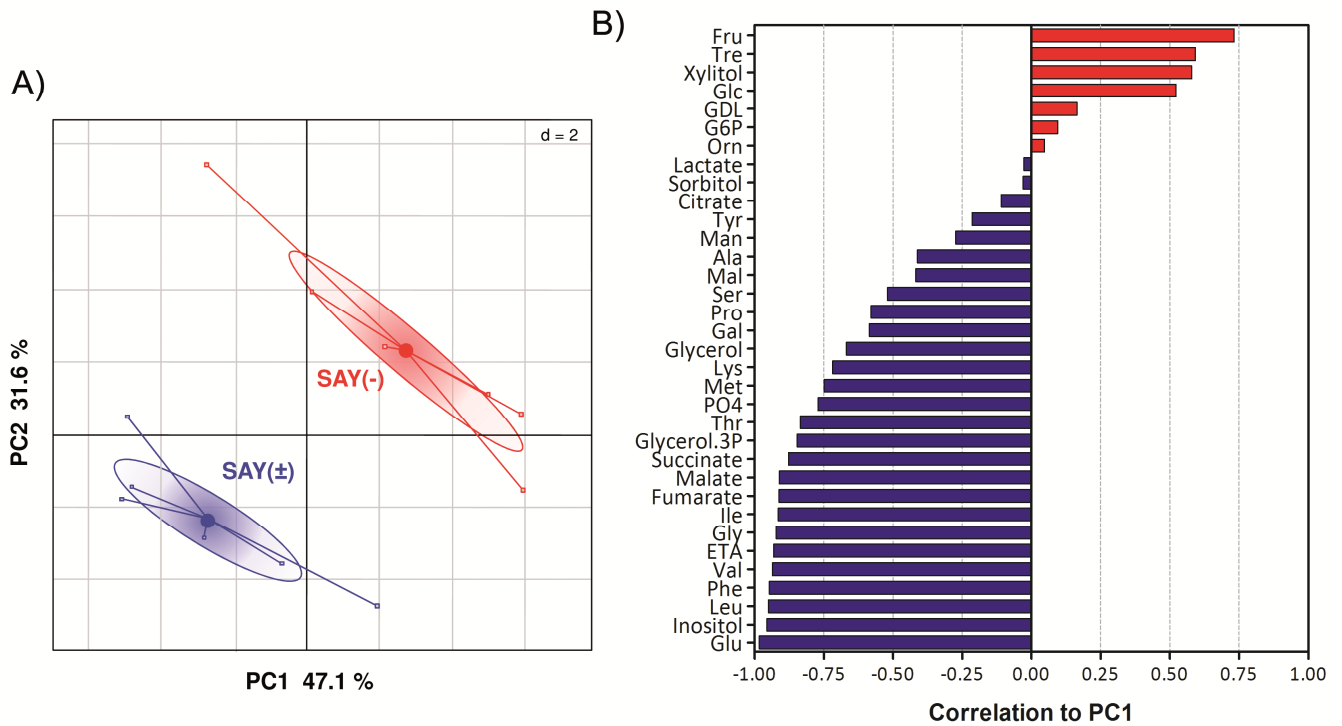
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740 **Figure 6:** (A) Multivariate analysis (PCA) based on the GC/MS metabolomic data of the  
 741 experiment 2 illustrating the plotting of PC1 against PC2. The unit "d" (top right of the plot)  
 742 represents the side-length of a square in the grid. A clear separation was observed between  
 743 live yeast-fed [blue ellipse, SAY( $\pm$ )] and live yeast-deprived metabolotypes [red ellipse,  
 744 SAY(-)]. Lines link replicates to their respective centroids ( $n = 6$ ). (B) Correlation values of  
 745 the different metabolite concentrations to the principal components PC1 in the principal  
 746 component analysis. Correlations are ranked on Y-axis according to their values. Blue bars for  
 747 negative correlations (*i.e.* accumulated in SAY( $\pm$ ) flies) and red bars for positive correlations  
 748 (*i.e.* accumulated in SAY(-) flies). See [Dataset S2](#) for detailed concentrations and fold  
 749 changes.

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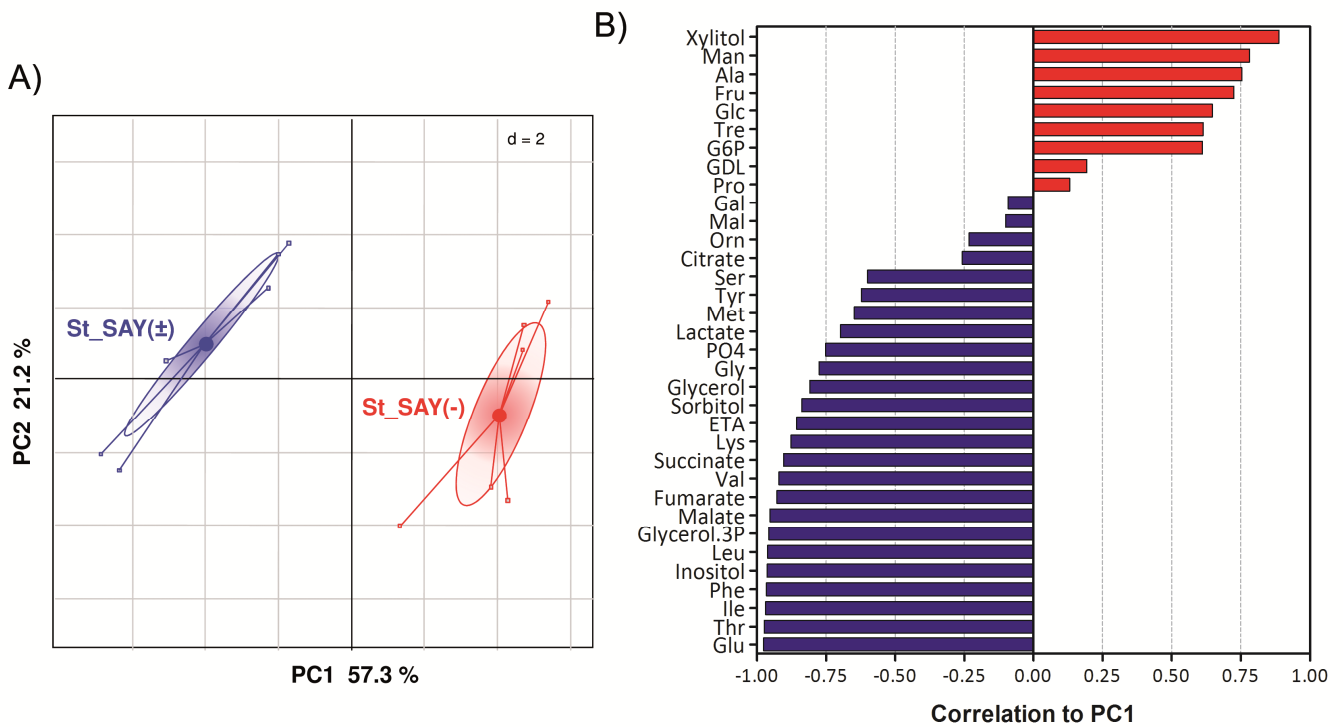
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757 **Figure 7:** (A) Multivariate analysis (PCA) based on the GC/MS metabolomic data of the  
 758 experiment 3 illustrating the plotting of PC1 against PC2. The unit "d" (top right of the plot)  
 759 represents the side-length of a square in the grid. A clear separation was observed between  
 760 live yeast-fed [blue ellipse, St-SAY( $\pm$ )] and live yeast-deprived metabolotypes [red ellipse, St-  
 761 SAY(-)]. Lines link replicates to their respective centroids ( $n = 6$ ). (B) Correlation values of  
 762 the different metabolite concentrations to the principal components PC1 in the principal  
 763 component analysis. Correlations are ranked on Y-axis according to their values. Blue bars for  
 764 negative correlations (*i.e.* accumulated in St-SAY( $\pm$ ) flies) and red bars for positive  
 765 correlations (*i.e.* accumulated in St-SAY(-) flies). See [Dataset S3](#) for detailed concentrations  
 766 and fold changes.



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