bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Metabolic adaptations in a range expanding arthropod

Katrien H. P. Van Petegem [*a], David Renault [b], Robby Stoks [c] and Dries Bonte [a]

[a] Department of Biology, Ghent University, Ghent, Belgium

[b] UMR CNRS 6553 Ecobio, Université de Rennes 1, Rennes Cedex, France

[c] Evolution and Conservation, KU Leuven, Leuven, Belgium

[*] Corresponding author: Katrien.VanPetegem@ugent.be

Running headline: Metabolomics of a range expanding arthropod

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Summary

Despite an increasing number of studies documenting life-history evolution during range expansions or shifts, we lack a mechanistic understanding of the underlying physiological processes. In this explorative study, we used a metabolomics approach to study physiological changes associated with the recent range expansion of the two-spotted spider mite (*Tetranychus urticae*). Mite populations were sampled along a latitudinal gradient from range core to edge and reared under benign common garden conditions for two generations. Using Gas Chromatography-Mass Spectrometry (GC-MS), we obtained metabolic population profiles, which showed a gradual differentiation along the latitudinal gradient, indicating (epi)genetic changes in the metabolome in association with range expansion. These changes seemed not related with shifts in the mites' energetic metabolism, but rather with differential use of amino acids. Particularly, more dispersive northern populations showed lowered concentrations of several essential and non-essential amino acids, suggesting a potential downregulation of metabolic pathways associated with protein synthesis.

Keywords: essential amino acids, common garden, life-history evolution, GC-MS metabolomics, global change, *Tetranychus urticae*

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Introduction

During range expansions or range shifts, species' life histories can evolve on ecological timescales (Phillips, Brown & Shine 2010). Changing environmental conditions force species to locally adapt and spatial assortment of dispersive phenotypes leads to increased dispersiveness at the expanding/shifting range edge (Shine, Brown & Phillips 2011). These evolutionary processes of local adaptation and spatial selection affect key life-history traits like fecundity, development and dispersal (reviewed in Chuang & Peterson 2015). We therefore expect range edge populations to exhibit physiological adaptations that underlie these observed trait evolutions. Such adaptations should be especially significant in energy-producing pathways, and more particularly in glycolysis (Eanes 2011). Indeed, any elevation of the performance of one life-history trait augments its energetic and metabolite demands at the expense of other traits (*cfr.* the "Y" model of resource allocation, Van Noordwijk & de Jong 1986; Zera & Harshman 2001), thus modifying the global metabolic network operation. For instance, variations in lipid biosynthesis in association with dispersal strategy highly impact metabolite fluxes through lipid pathways (see Zera 2011 for a review). As a result, life-history differentiation is expected to be associated with changes in the metabolome (*i.e.* the set of circulating metabolites within an organism, Oliver *et al.* 1998), as was for example found for ageing in *Caenorhabditis elegans* (Fuchs *et al.* 2010) and reproduction in the Malaria Mosquito *Anopheles gambiae* (Fuchs *et al.* 2014).

Metabolomics is a convenient technique which can be used as a candidate approach to explore an organism's response to environmental variations and forthcoming environmental changes (Hines *et al.* 2007; Miller 2007; Viant 2008; Bundy, Davey & Viant

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

2009; Lankadurai, Nagato & Simpson 2013; Hidalgo *et al.* 2014). It provides information on the interaction between an organism's physiology and its natural environment by identifying metabolites of low to moderate molecular mass within the whole body, cells, tissues or biofluids. Compared to other –omics technologies like genomics and transcriptomics, metabolomics has the significant advantage to focus on 'downstream' cellular functions (Snart, Hardy & Barrett 2015), providing a more direct picture of the functional links between causes and consequences of environmental variation (Foucreau *et al.* 2012). Essentially, metabolomics can potentially provide a link between genotypes and phenotypes (Fiehn 2002). When applied on individuals originating from different localities from range core to edge, but reared for several generations under common garden conditions, it should provide insights on the physiological adaptations that underlie life-history evolution during range expansion.

Though a consideration of the whole-organism physiology allows a better understanding of how life-history evolution in natural populations might occur and why this evolution is sometimes constrained (Zera *et al.* 2001; 2011; Ricklefs & Wikelski 2002), few studies documented metabolic variation in wild populations along natural gradients (Sardans, Penuelas & Rivas-Ubach 2011). Instead, most studies assess plastic or evolutionary responses to environmental stressors by manipulating abiotic variables in controlled environments (Sardans *et al.* 2011; Colinet *et al.* 2012; Padfield *et al.* 2016). Notable exceptions are the studies on *Arabidopsis lyrata* that demonstrated distinct metabolic phenotypes along the species' latitudinal distribution, with a typical cold-induced metabolome in the north, indicating adaptation to the local climate (Davey *et al.* 2008; Davey, Woodward & Quick 2009), but no difference in metabolic fingerprint between large

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

connected *versus* marginal fragmented populations (Kunin *et al.* 2009). These studies, however, used plants that were grown from seeds collected directly from the field. Environmental maternal effects can therefore not be excluded.

The two-spotted spider mite, *Tetranychus urticae* Koch (Acari, Tetranychidae; Fig. 1), a generalist pest species in greenhouses and orchards, expanded its European range from the Mediterranean to at least southern Scandinavia (K. H. P. Van Petegem, personal observation in 2011) during the last decades (for more information, see Carbonnelle *et al.* 2007). Previous research with *T. urticae* showed quantitative genetic life-history differentiation along this latitudinal gradient, with daily fecundity, lifetime fecundity and longevity decreasing from range core to edge, and egg survival, dispersal propensity and sex ratio increasing from range core to edge (Van Petegem *et al.* 2016). We expected this life-history differentiation to be associated with an evolution of the species' intermediary metabolism, which would manifest into distinct metabolic phenotypes among populations sampled along its expansion gradient.

Using a metabolomics approach, the current study aimed to test (i) whether the metabolome of *T. urticae* evolved during its recent range expansion; *i.e.* whether a gradual change in the mite's intermediary metabolism is present from range core to range edge, showing in the appearance of progressively distinct metabolic phenotypes (metabotypes) (ii) whether this metabolic differentiation could be associated with the up- or downregulation of certain metabolic pathways, for instance enhanced glycolytic activities or lipid metabolism and (iii) whether this evolutionary change in the species' metabotype is associated with the life-history differentiation that has occurred during its range expansion.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Materials and methods

Field sampling and common garden

In August 2012, we hand-sampled mites from nine localities (one population per locality) along an 800 km latitudinal gradient from northwestern Belgium to northern Denmark (Fig. 2). Mites were found on infested leaves of *Lonicera periclymenum* (European honeysuckle, five populations) at high latitudes and on *Euonymus europaeus* (European spindle, one population), *Humulus lupulus* (common hop, one population),-*Sambucus nigra* (European black elderberry, one population) or *Lonicera periclymenum* (European honeysuckle, one population) at lower latitudes. (More information is provided in appendix A.1.) In the laboratory, fifty to several hundreds of mites per population were put on separate whole bean plants (*Phaseolus vulgaris*, variety Prélude –a highly suitable host for *T. urticae*, see Agrawal et al. 2002; Gotoh et al. 2004) and kept under controlled conditions at room temperature with a light-regime of 16:8 LD. After one generation, ten adult female mites per population were taken from their bean plant and put on a piece of bean leaf (±30cm^2) on wet cotton in a Petri dish. Two such Petri dishes were prepared for each population. The Petri dishes were then used to create a pool of synchronised two-day adult female mites for each population (two-day adult females were preferred, since these are significantly bigger than fresh adults). For this purpose, all females were allowed to lay eggs during 24 hours in a climate room at 27 °C (an optimal temperature for our study species, see Sabelis 1981), with a light-regime of 16:8 LD. The resulting same-aged eggs were subsequently left to develop until they were two-day adult mites, of which only females (which are easily visually recognised) were selected. As mites were kept in common garden for two generations, all direct environmental effects were excluded. Furthermore, since the

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

common garden conditions were optimal for *T. urticae* (bean as host plant, 27°C, 16:8 LD and relatively low mite densities), we could reasonably assume that potential differences among metabotypes of mites from different origins (populations) did not result from differential responses to restrictive/stressful rearing.

Metabolomic profiling using Gas Chromatography-Mass Spectrometry (GC-MS)

As we wanted to scan metabolites from different metabolite families (because of their various but connected roles in general organismal physiology), we used GC-MS metabolomics (Koek *et al.* 2011; Khodayari *et al.* 2013). For each population, we constructed the metabolomic profile of five replicated pooled sets of fifty two-day-adult female mites. Each set was placed in a microtube and directly transferred to -80 °C. To be able to measure true quantities of metabolites, it is important to standardise the initial masses of each extract. However, even when pooling fifty individuals, the masses of the replicates were too low to be accurately measured (the measurement error for the mass of the microtube was greater than the summed mass of the fifty mites). Yet, previous research showed that female adult size does not differ among the nine sampled populations (Van Petegem *et al.* 2016). We could thus confidently use and interpret metabolite concentrations in nmol/sample. The samples were first homogenised in ice-cold (-20 °C) methanol-chloroform (2:1), using a tungsten-bead beating equipment (RetschTM MM301, Retsch GmbH, Haan, Germany) at 25 Hz for 1.5 min. After addition of ice-cold ultrapure water, the samples were centrifuged at 4,000 g for 5 min at 4 °C. The upper aqueous phase was then transferred to new chromatographic glass vials, dried-out and resuspended in 30 µl of 20 mg L-1 methoxyamine hydrochloride (Sigma-Aldrich, St. Louis, MO, USA) in pyridine and incubated under automatic orbital shaking at 40 °C for 60 min. Subsequently, 30 µl of N-methyl-N-

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

(trimethylsilyl) trifluoroacetamide (MSTFA; Sigma, #394866) was added and the derivatisation was conducted at 40 °C for 60 min under agitation. The samples were then analysed in a GC-MS system (Thermo Fischer Scientific Inc., Waltham, MA, USA), using the same settings as in Khodayari *et al.* (2013). For this purpose, one microliter of each sample was injected in the GC-MS system using the split mode (split ratio: 25:1). After that, the selective ion monitoring (SIM) mode (electron energy: -70 eV) was used to search for the sixty primary metabolites that are most often found in arthropod samples and that were included in our spectral database (see appendix A.2 for a complete overview of these sixty metabolites). The SIM mode ensured a precise annotation of the detected peaks. The calibration curves were set using samples consisting of sixty pure reference compounds at concentrations of 1, 2, 5, 10, 20, 50, 100, 200, 500, 750, 1000, 1500 and 2000 µM. Chromatograms were deconvoluted using XCalibur v2.0.7 software (Thermo Fischer Scientific Inc., Waltham, MA, USA). Finally, metabolite concentrations were quantified according to their calibration curves.

Statistics

A total of forty-three metabolites were identified.

In a first step, we examined whether distinct metabotypes existed among the sampled populations of *T. urticae* by running a MANOVA. Nine metabolites were first removed from the dataset because they showed a more than 85% correlation with (an)other metabolite(s). Then, all remaining metabolites were log-transformed to obtain a normal distribution, which allowed to proceed to the MANOVA.

In a second step, we tested whether the metabolic profile was gradually changing as a function of latitude (from range core to edge), or as a function of one of the six life-history

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

176 traits that were previously shown to covary with latitude (daily and lifetime fecundity, egg
177 survival, longevity, dispersal propensity and sex ratio; see Van Petegem *et al.* 2016, see also
178 appendix A.3). The concentrations of all forty-three metabolites were first auto-scaled and
179 transformed (the transformation that best fitted and normalised the data was retained: cube
180 root when looking for covariation with daily fecundity and egg survival; log for latitude; no
181 transformation for lifetime fecundity, longevity, dispersal propensity and sex ratio). Then,
182 metabolic differences among the nine populations were visualised using Partial Least
183 Squares – Discriminant Analysis (PLS-DA). This multivariate analysis was performed using
184 MetaboAnalyst 3.0 (Xia *et al.* 2009; Xia *et al.* 2012; Xia *et al.* 2015). By ordering the
185 populations according to their latitude or according to one of the six life-history traits
186 covarying with latitude, it was possible to check for trends in the metabolite concentrations.
187 To validate the significance of this interpopulation variation, permutation tests (2000
188 permutations) were run for replicates (with 5 replicates per population) using separation
189 distance (B/W) test statistics. The PLS-DA provided Variable Importance in Projection (VIP)
190 scores, which gave a first overview of the possible existence of a general pattern in the
191 concentrations of quantified metabolites along our invasion gradient: low VIP-scores depict
192 a weak and high scores a strong global pattern. Using a step-wise procedure, only those
193 metabolites with a VIP score of at least 1.2 (1.0 for egg survival because removing the
194 metabolites with a score between 1.0 and 1.2 resulted in a decreased percentage of
195 variation explained) for the first and/or second component were retained for further
196 analysis (compared to 0.8 in Tenenhaus 1998).

197 In a third step, univariate analyses were performed to test, metabolite by metabolite,
198 whether the global patterns obtained in the previous step could be confirmed. As we aimed
199 at determining if the metabolite levels showed latitudinal patterns along the expansion, we

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

did not run an ANOVA on individual metabolites, but rather processed regressions. Using SAS 9.4 (SAS Institute Inc. 2013), the linear regressions were run for all influential metabolites (VIP scores >1.2, except for egg survival, as mentioned above). Because all five collected replicates per population originated from only one field sample, we ran the regressions using population averages. As our study is explorative, we wanted to avoid false negatives (with the chance of making a Type II error). We therefore did not correct for multiple comparisons (*e.g.* Bonferroni correction). Given the large number of statistical tests, the limited number of populations, and the fact that we highly smoothed differences among populations by rearing the specimens under common garden conditions for two generations (which is atypical for metabolomics studies, where organisms are usually subject to a stressor to elicit a strong response), such a correction would have greatly diminished the statistical power.

A final step linked the selected individual metabolites with one or more metabolic pathways, thus identifying those pathways that were potentially up- or downregulated during the range expansion of *T. urticae*. Pathway enrichment analyses were performed in Metaboanalyst 3.0 (Xia *et al.* 2009; Xia *et al.* 2012; Xia *et al.* 2015) with those metabolites that showed significant effects in the univariate analyses of step three. These pathway analyses were performed with a Fisher's exact test algorithm, which we ran using the metabolic pathways of *Drosophila melanogaster* (no closer relative of *T. urticae* was available in the program, but primary metabolites are anyway highly conserved, especially among non-blood feeding arthropods). The algorithm calculates the match (number of hits) between the metabolites in a dataset and the totality of metabolites present in a specific pathway. Furthermore, it uses a pathway topology analysis to compute a value for the

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

223 impact of these metabolites on the pathway. As multiple comparisons are made, corrected

224 Holm p-values are provided.

225

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Results

MANOVA

The metabotypes of the female mites significantly differed among the nine sampled populations ($F_{184,160}$=2.2, p<0.001). In further analyses, the potential covariation of metabolite levels with latitude or one of the life-history traits covarying with latitude was then assessed.

Latitudinal covariation

The PLS-DA showed a separation among the nine populations, which was visible on 3-D score plots (see appendix A.4). Of the forty-three identified metabolites, seventeen had VIP scores of at least 1.2 and were thus retained for further analysis (Fig. 3A). They showed a clear general trend from high values in southern to low values in northern populations (Fig. 3A).

In the subsequent linear regressions, eleven of these seventeen metabolite concentrations varied significantly: ten decreased and one increased with increasing latitude (Fig. 3A and appendix A.6). Among these eleven metabolites, five essential amino acids, three non-essential amino acids (see Rodriguez & Hampton (1966) for an overview of all essential amino acids in *T. urticae* –we defined tryptophan, which is not included in this overview, as essential) and one intermediate of the citric acid cycle can be mentioned.

Pathway analysis indicated that of these eleven metabolites, eight play a significant role in the aminoacyl-tRNA biosynthesis (total: 67, hits: 8, impact=0, Holm p=2.7062E-6) and

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

248 four in the valine, leucine and isoleucine biosynthesis (total: 13, hits: 4, impact=0.9999, Holm
249 p=4.0129E-4) (both pathway maps are provided in appendix A.7).

250

251 ***Life history covariation***

252 The PLS-DA showed a separation between the nine (eight for egg survival, for which
253 no data were available for population SVI) populations, which was visible on 3-D score plots
254 (see appendix A.4). Of the forty-three identified metabolites, only those which explained
255 most of the interpopulation variation for a certain life-history trait (high VIP score) were
256 retained for further analysis. Fourteen were retained for daily and sixteen for lifetime
257 fecundity, twenty were retained for egg survival, eleven for longevity, thirteen for dispersal
258 propensity and ten for sex ratio (Fig. 3B-G). Figure 3 (B-G) shows clear indications of a
259 positive correlation between lifetime fecundity and its sixteen selected metabolites. In
260 contrast, figure 3 (B-G) suggests a negative correlation between the twenty and thirteen
261 metabolites selected for, respectively, egg survival and dispersal propensity. For daily
262 fecundity, longevity and sex ratio, no clear trends were visible.

263 In the subsequent linear regressions, one significant correlation was found for egg
264 survival (a sugar alcohol) and seven for dispersal propensity (including four essential amino
265 acids and one sugar). No significant results were found for lifetime fecundity, daily fecundity,
266 longevity and sex ratio (Fig. 3B-G and appendix A.6).

267 Pathway analysis indicated that four of the seven metabolites which negatively
268 correlated with dispersal propensity play a significant role in the aminoacyl-tRNA

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

biosynthesis (total: 67, hits: 4, impact=0, Holm p=0.0417) (the pathway map is provided in appendix A.7). No associated pathways were found for egg survival.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Discussion

Of the forty-three metabolites identified in the GC-MS analysis, eighteen correlated with latitude and/or one or more life-history traits. More specifically, eleven covaried positively or negatively with latitude, seven showed a negative correlation with dispersal propensity and one showed a negative correlation with egg survival. Of the eighteen different metabolites, eleven amino acids could be shown to play an important role in the aminoacyl-tRNA biosynthesis and four in the valine, leucine and isoleucine biosynthesis (see pathway maps provided in appendix A.7).

Contrary to our hypothesis, our results indicate that the life-history evolution which occurred during the recent range expansion of *T. urticae* (Van Petegem *et al.* 2016) was not associated with shifts in the mites' energetic metabolism, but rather with shifts in its anabolism. While our spectral database contained eleven sugars, only one sugar (fructose) accounted for the separation among populations. This suggests that the genes involved in encoding the mite's energetic metabolism (*i.e.* glycolysis, citric acid cycle, which typically involve sugars) have not been significantly affected during the range expansion of *T. urticae*. Instead, the observed differentiation in the mites' metabolome probably involved evolutionary changes in the mites' anabolism, where amino acids play a central role in the metabolic turnover of proteins. In more northern and more dispersive populations, the aminoacyl-tRNA biosynthesis was downregulated. In this pathway, aminoacyl-tRNA is formed by charging tRNA with an amino acid. The aminoacyl-tRNA then serves as a substrate in protein synthesis or plays one of its many other roles in, for example, cell wall formation or antibiotic biosynthesis (Raina & Ibba 2014). In accordance, the valine, leucine and

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

296 isoleucine biosynthesis, important for protein synthesis as well (Ahmed & Khan 2006;
297 Tamanna & Mahmood 2014), was downregulated in more northern populations.
298
299 The affected amino acids showed decreased concentrations toward higher latitudes
300 and showed a negative correlation with the dispersal propensity of *T. urticae*, which
301 increases towards the north. While, in general, amino acids are considered fundamental for
302 egg production and thus fecundity (Tulisalo 1971; O'Brien, Fogel & Boggs 2002; Mevi-Schutz
303 & Erhardt 2005; Fuchs *et al.* 2014, but see Heagle *et al.* 2002), not a single correlation was
304 found for fecundity, despite a clear positive trend in the PLS-DA. Of the eleven affected
305 amino acids, eight were essential and three non-essential. While the non-essential amino
306 acids could have been synthesised *de novo* from glucose, the essential amino acids could
307 only have been supplied through the mite's diet (Rodriguez *et al.* 1966). Though all mites
308 were kept in common garden, mites from northern, more dispersive populations were found
309 to contain lower essential amino acid concentrations. In line with the recent finding of
310 Fronhofer & Altermatt (2015) that a dispersal-foraging trade-off leads to a reduced
311 exploitation of resources at range margins, our results could indicate that northern, more
312 dispersive mites evolved lower essential amino acid concentrations because they consume
313 less of their food source. We should, however, keep in mind that metabolites were
314 measured only at one point in time and from whole organism samples. We are therefore
315 missing the temporal fluctuations of the metabolome over a day, and our data therefore
316 represent only a snapshot of the existing balance in terms of metabolite demand among
317 metabolic pathways.
318

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

319 An important challenge for metabolomics is understanding the relative contribution
320 of environmental and genetic factors in shaping an organism's metabolic phenotype (Bundy
321 *et al.* 2009). In the current study, mites were kept in common garden for two generations,
322 during which they were reared under optimal, non-stressful conditions. In contrast with
323 most metabolomic studies, mites were thus not subjected to a stressor to elicit a strong
324 environmentally-induced plastic stress-response. Therefore, any metabolomic
325 differentiation was expected to be far less pronounced compared to stress-exposure studies.
326 As plastic, environmentally driven field-differences among populations were largely levelled
327 out through the two generations in common garden, only genetic factors were retained.
328 Long-lasting transgenerational plasticity can, however, not be fully excluded and we
329 therefore refer further to (epi)genetic factors (Verhoeven et al. 2016). Though (epi)genetic
330 factors are generally considered less determining than environmental factors (Robinson *et*
331 *al.* 2007; Frank, Noerenberg & Engel 2009; Matsuda *et al.* 2012), our results demonstrate a
332 clear (epi)genetic signal of metabolic differentiation along *T. urticae*'s invasion gradient. We
333 acknowledge, however, that we cannot exclude neutral processes, like for example serial
334 bottlenecks –including surfing mutations (Travis *et al.* 2007; Klopfstein *et al.* 2016) as
335 potential (co)sources of the found latitudinal metabolomic patterns. Furthermore, as the
336 host plant species on which the mites were sampled in the field covaried with latitude (with
337 *L. periclymenum* typically in the north), this could also have influenced our results. Yet,
338 regression slopes barely differed between models including all populations (hence all host
339 plant species) or models run for the subset of six populations collected on *L. periclymenum*
340 only (see appendix A.8). This indicates that the latitudinal signal was independent of host
341 plant identity.
342

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

343 This explorative study specifically examined whether range expansion might result in
344 evolutionary changes in an organism's metabolism. Despite non-stressful common garden
345 conditions, approximately forty per cent of the identified metabolites showed (epi)genetic
346 differentiation among populations. The more dispersive northern mites exhibited lower
347 concentrations of several essential and non-essential amino acids, suggesting a
348 downregulation of certain pathways linked to protein synthesis. Though effects were subtle
349 (but see earlier), our results clearly indicate that the metabolome of *T. urticae* underwent
350 (epi)genetic changes during the species' recent range expansion.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Acknowledgements

This project was funded by the Fund for Scientific Research – Flanders (FWO) (project G.0610.11). DB and RS were supported by BelSpo IAP Project "Speedy". We furthermore thank the INEE-CNRS (ENVIROMICS call, project 'ALIENS') for funding DR.

Data accessibility

- Sample locations and life-history trait values: included in appendix

- Results of GC-MS analysis: will be deposited in the Dryad repository (and added to the reference list)

- Outcomes of statistical analyses: included in appendix

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Figure legends

Figure 1

Picture showing two females and one egg of the two-spotted spider mites (*Tetranychus urticae* Koch; Acari, Tetranychidae).

Figure 2

The map shows the nine field collection sites, which are situated in Belgium, The Netherlands and Denmark. The graph shows the yearly number of frost days and the average yearly temperature for each collection site along the latitudinal gradient. These climatic data were obtained from FetchClimate (Microsoft Research, Cambridge) and were averaged over a period of 35 years (1980 to 2015). Below the graph, arrows for each of six life-history traits depict their trend along the latitudinal gradient (increase, decrease). (For more detailed information, see appendix A.1 and Van Petegem *et al.* 2015.)

Figure 3

Variable importance plots resulting from the multivariate analyses (PLS-DA) on the metabolomic data. These plots list those metabolites that, based on their VIP score, contribute the most to explaining the variation among the nine populations in our dataset (ODK, KVS, CAS, LAU, HED, BLA, TVE; SVI, SKA). The metabolites are ordered from high to low VIP scores for component 1 (an overview off all scores for component 1 and 2 is provided in appendix A.5). The colour codes indicate the relative concentration of a given metabolic compound for each population (green=low concentration, to red= high concentration). The populations themselves are ordered according to their latitude (A), or from low values at the

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

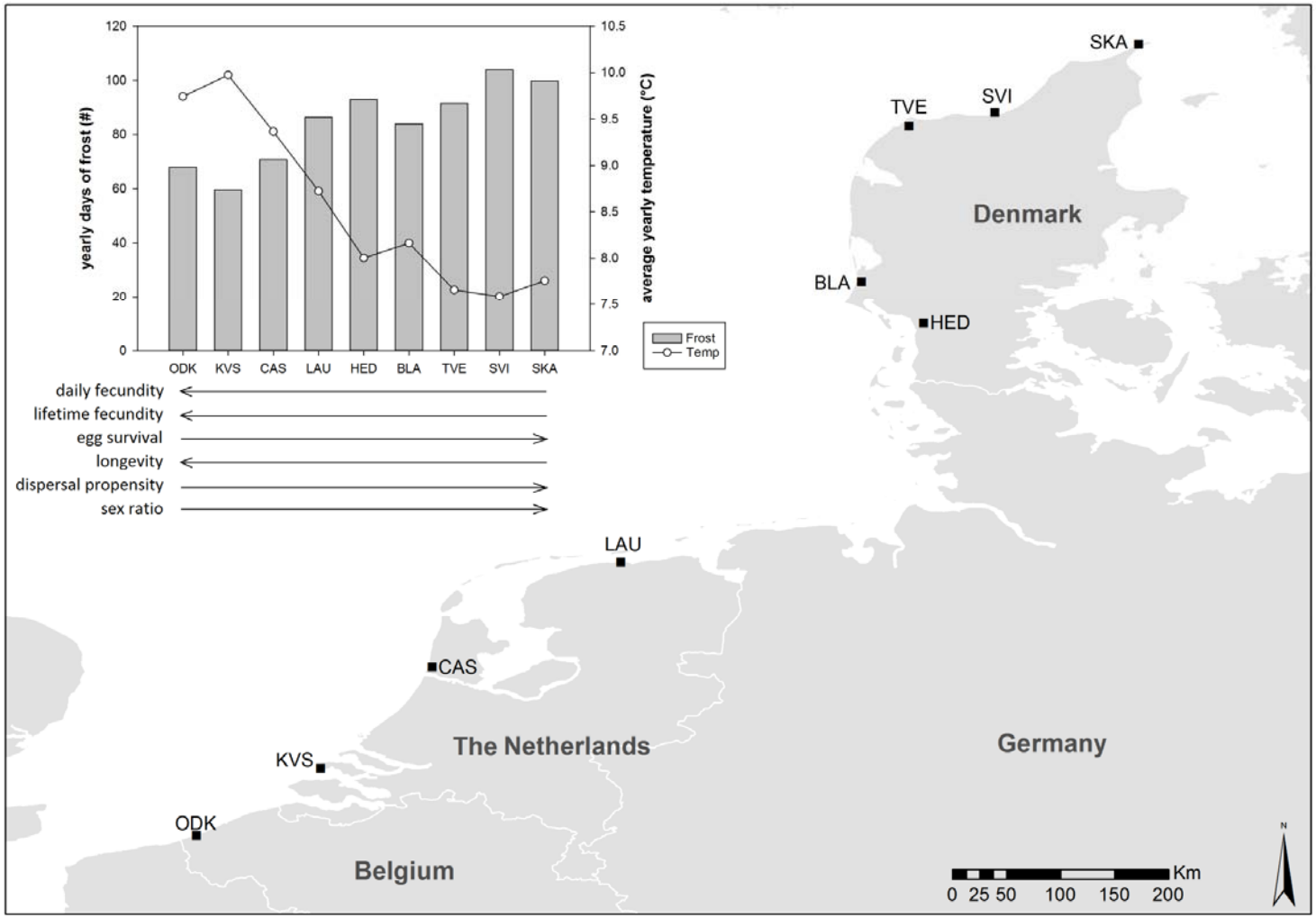
386 left to high values at the right for a given life-history trait (daily (B) or lifetime (C) fecundity,
387 egg survival (D), longevity (E), dispersal propensity (F) or sex ratio (G)). For example, in Fig.
388 3A, LAU is the population with the highest concentration of proline and ODK is the
389 southernmost population (lowest latitude). Below each column (population), a letter
390 signifies the host plant species from which mites were sampled in this population (*H.*= *H.*
391 *lupulus*, *S.*= *S. nigra*, *L.*= *L. periclymenum*, *E.*= *E. europaeus*). At the bottom of each plot, the
392 p-value resulting from the permutation test is given. At the left side of each plot, an asterisk
393 next to a metabolite name indicates a significant correlation between this metabolite and
394 latitude or the denoted life-history trait. For example, in Fig. 3A, proline shows a significant
395 negative correlation with latitude. (A detailed overview, including p- and F-values, of all
396 linear regressions is found in appendix A.6.)
397

Figures

Figure 1

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

403 **Figure 2**

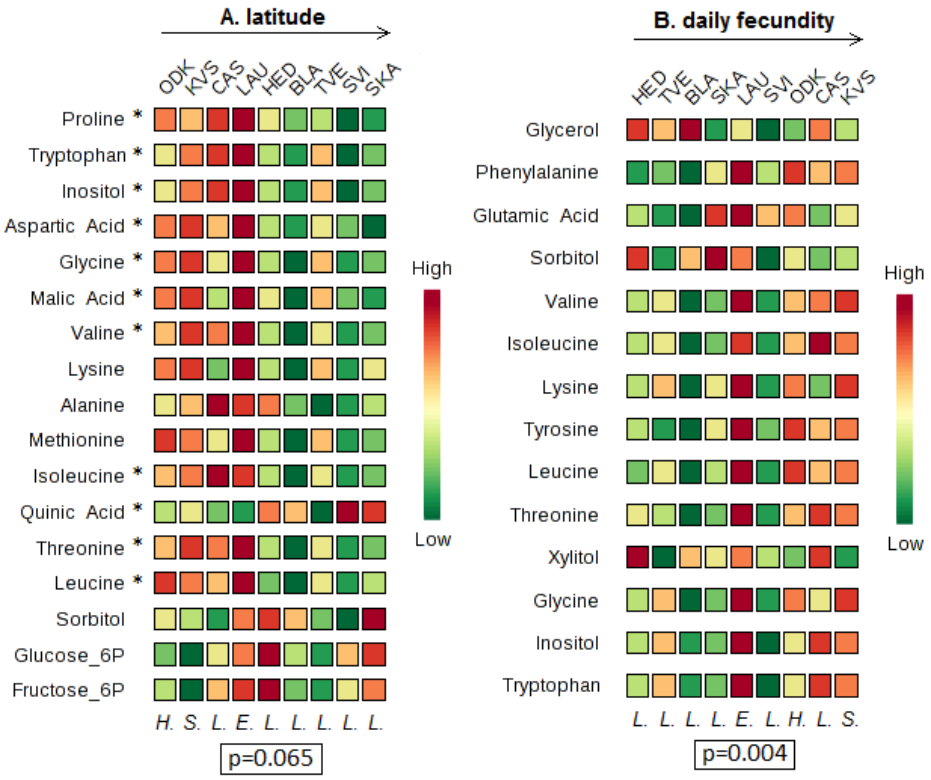


404

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

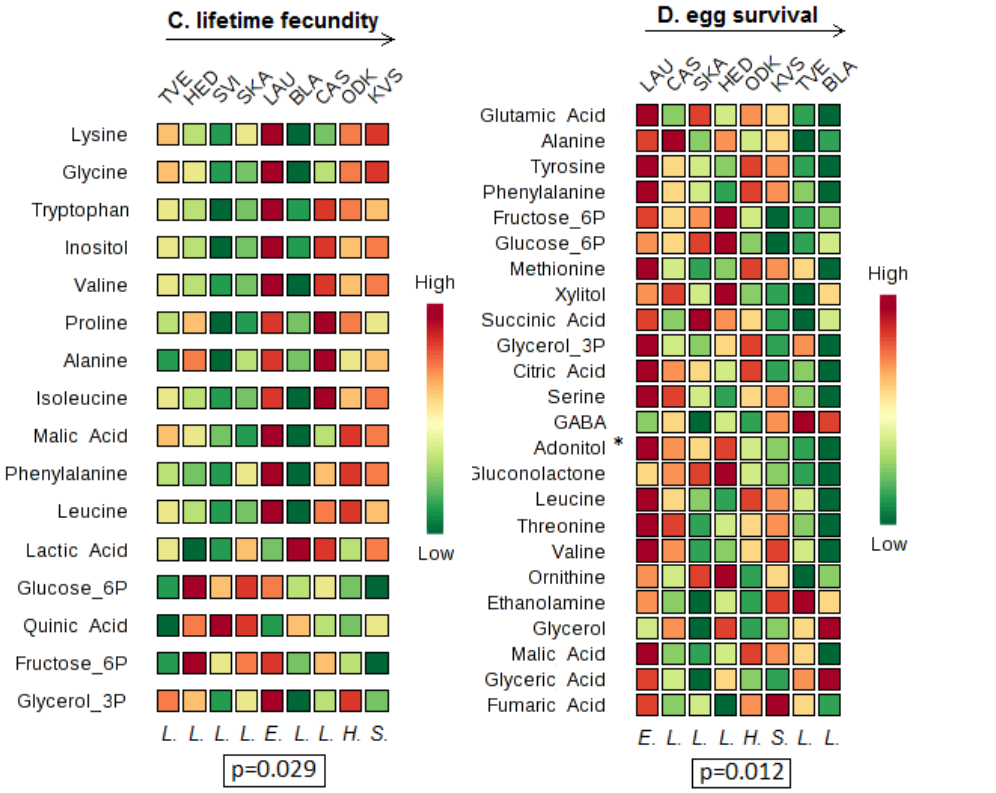
bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

405 **Figure 3**

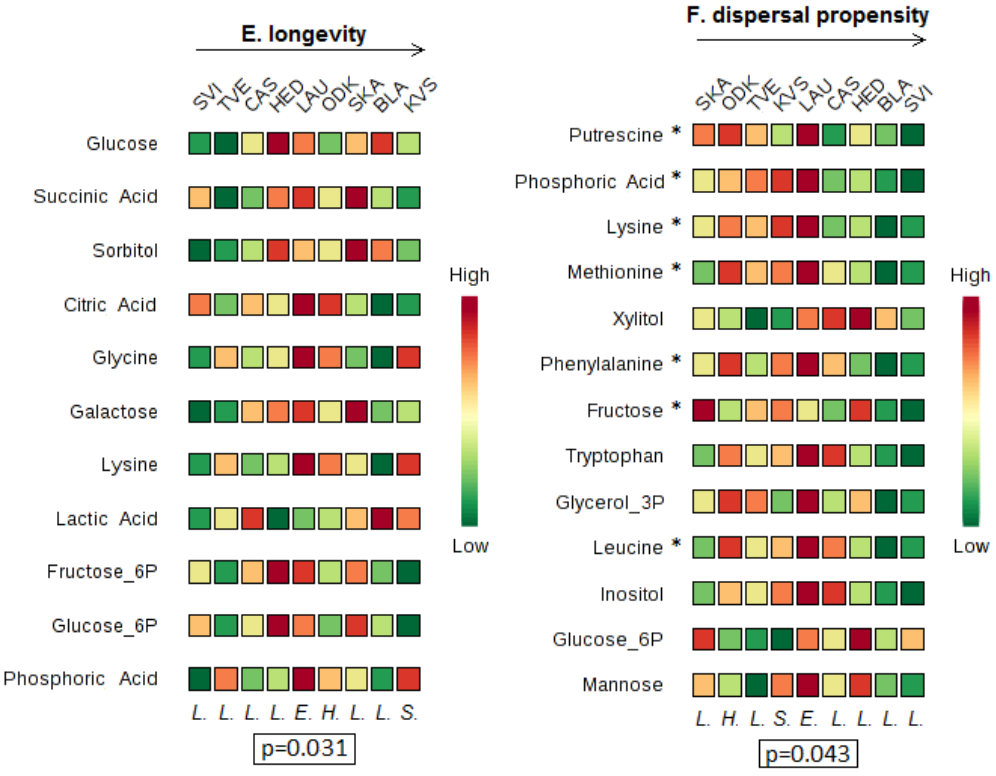


406

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

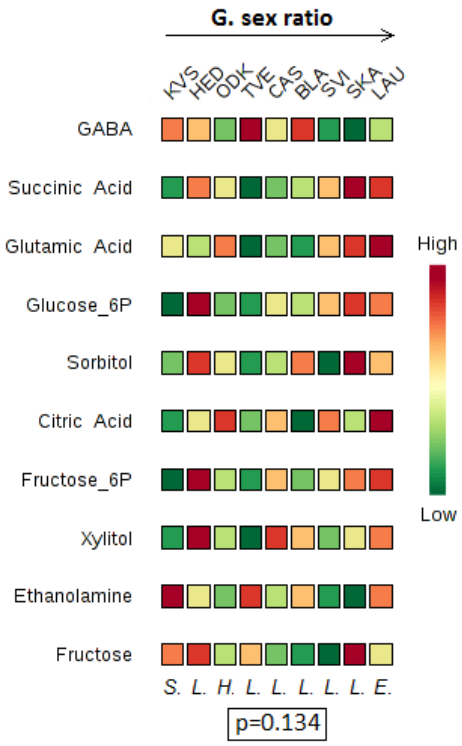


407



408

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



409

410

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

411 ## References

412

413 Agrawal, A.A., Vala, F. & Sabelis, M.W. (2002). Induction of preference and performance
414 after acclimation to novel hosts in a phytophagous spider mite: Adaptive plasticity?
415 *American Naturalist,* **159 (5)**, 553-565.
416 Ahmed, I. & Khan, M.A. (2006) Dietary branched-chain amino acid valine, isoleucine and
417 leucine requirements of fingerling Indian major carp, *Cirrhinus mrigala* (Hamilton).
418 *British Journal of Nutrition,* **96 (3),** 450-460.
419 Bundy, J.G., Davey, M.P. & Viant, M.R. (2009) Environmental metabolomics: a critical review
420 and future perspectives. *Metabolomics,* **5 (1),** 3-21.
421 Carbonnelle, S., Hance, T., Migeon, A., Baret, P., Cros-Arteil, S. & Navajas, M. (2007)
422 Microsatellite markers reveal spatial genetic structure of *Tetranychus urticae* (Acari :
423 Tetranychidae) populations along a latitudinal gradient in Europe. *Experimental and*
424 *Applied Acarology,* **41 (4),** 225-241.
425 Chuang, A. & Peterson, C.R. (2016) Expanding population edges: theories, traits, and trade-
426 offs. *Global Change Biology*, **22 (2)**, 494-512.
427 Colinet, H., Larvor, V., Laparie, M. & Renault, D. (2012) Exploring the plastic response to cold
428 acclimation through metabolomics. *Functional Ecology,* **26 (3),** 711-722.
429 Davey, M.P., Burrell, M.M., Woodward, F.I. & Quick, W.P. (2008) Population-specific
430 metabolic phenotypes of *Arabidopsis lyrata* ssp. *petraea*. *New Phytologist,* **177 (2),**
431 380-388.
432 Davey, M.P., Woodward, F.I. & Quick, W.P. (2009) Intraspecfic variation in cold-temperature
433 metabolic phenotypes of *Arabidopsis lyrata* ssp. *petraea*. *Metabolomics,* **5 (1),** 138-
434 149.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

435 Eanes, W.F. (2011) Molecular population genetics and selection in the glycolytic pathway.
436 *Journal of Experimental Biology,* **214 (2)**, 165-171.
437 Fiehn, O. (2002) Metabolomics - the link between genotypes and phenotypes. *Plant*
438 *Molecular Biology,* **48 (1-2),** 155-171.
439 Foucreau, N., Renault, D., Hidalgo, K., Lugan, R. & Petillon, J. (2012) Effects of diet and
440 salinity on the survival, egg laying and metabolic fingerprints of the ground-dwelling
441 spider *Arctosa fulvolineata* (Araneae, Lycosidae). *Comparative Biochemistry and*
442 *Physiology a-Molecular & Integrative Physiology,* **163 (3-4),** 388-395.
443 Frank, T., Noerenberg, S. & Engel, K.-H. (2009) Metabolite Profiling of Two Novel Low Phytic
444 Acid (lpa) Soybean Mutants. *Journal of Agricultural and Food Chemistry,* **57 (14),**
445 6408-6416.
446 Fronhofer, E.A. & Altermatt, F. (2015) Eco-evolutionary feedbacks during experimental range
447 expansions. *Nature Communications,* **6**.
448 Fuchs, S., Behrends, V., Bundy, J.G., Crisanti, A. & Nolan, T. (2014) Phenylalanine Metabolism
449 Regulates Reproduction and Parasite Melanization in the Malaria Mosquito. *Plos*
450 *One,* **9 (1)**.
451 Fuchs, S., Bundy, J.G., Davies, S.K., Viney, J.M., Swire, J.S. & Leroi, A.M. (2010) A metabolic
452 signature of long life in *Caenorhabditis elegans*. *Bmc Biology,* **8**.
453 Gotoh, T., Suwa, A., Kitashima, Y. & Rezk, H.A. (2004) Developmental and reproductive
454 performance of *Tetranychus puerariсola* Ehara and Gotoh (Acari : Tetranychidae) at
455 four constant temperatures. *Applied Entomology and Zoology,* **39 (4)**, 675-682.
456 Heagle, A.S., Burns, J.C., Fisher, D.S. & Miller, J.E. (2002) Effects of carbon dioxide
457 enrichment on leaf chemistry and reproduction by twospotted spider mites (Acari :
458 Tetranychidae) on white clover. *Environmental Entomology,* **31 (4),** 594-601.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

459 Hidalgo, K., Mouline, K., Mamai, W., Foucreau, N., Dabire, K., Bouchereau, A., Simard, F. &
460 Renault, D. (2014) Novel insights into the metabolic and biochemical underpinnings
461 assisting dry-season survival in female malaria mosquitoes of the *Anopheles gambiae*
462 complex. *Journal of Insect Physiology,* **70,** 102-116.
463 Hines, A., Oladiran, G.S., Bignell, J.P., Stentiford, G.D. & Viant, M.R. (2007) Direct sampling of
464 organisms from the field and knowledge of their phenotype: Key recommendations
465 for environmental metabolomics. *Environmental Science & Technology,* **41 (9),** 3375-
466 3381.
467 Khodayari, S., Moharramipour, S., Larvor, V., Hidalgo, K. & Renault, D. (2013) Deciphering the
468 Metabolic Changes Associated with Diapause Syndrome and Cold Acclimation in the
469 Two-Spotted Spider Mite *Tetranychus urticae*. *Plos One,* **8 (1)**.
470 Klopfstein, S., Currat, M., Excoffier, L. (2006) The fate of mutations surfing on the wave of a
471 range expansion. *Molecular Biology and Evolution,* **23 (3)**, 482-490.
472 Koek, M.M., Jellema, R.H., van der Greef, J., Tas, A.C. & Hankemeier, T. (2011) Quantitative
473 metabolomics based on gas chromatography mass spectrometry: status and
474 perspectives. *Metabolomics,* **7 (3),** 307-328.
475 Kunin, W.E., Vergeer, P., Kenta, T., Davey, M.P., Burke, T., Woodward, F.I., Quick, P.,
476 Mannarelli, M.-E., Watson-Haigh, N.S. & Butlin, R. (2009) Variation at range margins
477 across multiple spatial scales: environmental temperature, population genetics and
478 metabolomic phenotype. *Proceedings of the Royal Society B-Biological Sciences,* **276**
479 **(1661),** 1495-1506.
480 Lankadurai, B.P., Nagato, E.G. & Simpson, M.J. (2013) Environmental metabolomics: an
481 emerging approach to study organism responses to environmental stressors.
482 *Environmental Reviews,* **21 (3),** 180-205.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

483 Matsuda, F., Okazaki, Y., Oikawa, A., Kusano, M., Nakabayashi, R., Kikuchi, J., Yonemaru, J.-I.,
484 Ebana, K., Yano, M. & Saito, K. (2012) Dissection of genotype-phenotype associations
485 in rice grains using metabolome quantitative trait loci analysis. *Plant Journal,* **70 (4),**
486 624-636.
487 Mevi-Schutz, J. & Erhardt, A. (2005) Amino acids in nectar enhance butterfly fecundity: A
488 long-awaited link. *American Naturalist,* **165 (4),** 411-419.
489 Miller, M.G. (2007) Environmental metabolomics: A SWOT analysis (strengths, weaknesses,
490 opportunities, and threats). *Journal of Proteome Research,* **6 (2),** 540-545.
491 O'Brien, D.M., Fogel, M.L. & Boggs, C.L. (2002) Renewable and nonrenewable resources:
492 Amino acid turnover and allocation to reproduction in Lepidoptera. *Proceedings of*
493 *the National Academy of Sciences of the United States of America,* **99 (7),** 4413-4418.
494 Oliver, S.G., Winson, M.K., Kell, D.B. & Baganz, F. (1998) Systematic functional analysis of the
495 yeast genome. *Trends in Biotechnology,* **16 (9),** 373-378.
496 Padfield, D., Yvon-Durocher, G., Buckling, A., Jennings, S. & Yvon-Durocher, G. (2016) Rapid
497 evolution of metabolic traits explains thermal adaptation in phytoplankton. *Ecology*
498 *Letters,* **19 (2),** 133-142.
499 Phillips, B.L., Brown, G.P. & Shine, R. (2010) Life-history evolution in range-shifting
500 populations. *Ecology,* **91 (6),** 1617-1627.
501 Raina, M. & Ibba, M. (2014) tRNAs as regulators of biological processes. *Frontiers in Genetics,*
502 **5,** 171.
503 Ricklefs, R.E. & Wikelski, M. (2002) The physiology/life-history nexus. *Trends in Ecology &*
504 *Evolution,* **17 (10),** 462-468.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

505 Robinson, A.R., Ukrainetz, N.K., Kang, K.-Y. & Mansfield, S.D. (2007) Metabolite profiling of
506 Douglas-fir (*Pseudotsuga menziesii*) field trials reveals strong environmental and
507 weak genetic variation. *New Phytologist,* **174 (4),** 762-773.
508 Rodriguez, J.G. & Hampton, R.E. (1966) Essential amino acids determined in 2-spotted spider
509 mite *Tetranychus urticae* KOCH (Acarina, Tetranychidae) with glucose-U-C^{14}. *Journal*
510 *of Insect Physiology,* **12 (10),** 1209-1216.
511 Sabelis, M.W. (1981) Biological control of two-spotted spider mites using phytoseiid
512 predators. Part I. Modelling the predator-prey interaction at the individual level.
513 Department of Theoretical Production Ecology, Department of Entomology.
514 Wageningen, Agricultural University. Doctor in Agricultural Sciences: 242.
515 Sardans, J., Penuelas, J. & Rivas-Ubach, A. (2011) Ecological metabolomics: overview of
516 current developments and future challenges. *Chemoecology,* **21 (4),** 191-225.
517 Shine, R., Brown, G.P. & Phillips, B.L. (2011) An evolutionary process that assembles
518 phenotypes through space rather than through time. *Proceedings of the National*
519 *Academy of Sciences of the United States of America,* **108 (14),** 5708-5711.
520 Snart, C.J.P., Hardy, I.C.W. & Barrett, D.A. (2015) Entometabolomics: applications of modern
521 analytical techniques to insect studies. *Entomologia Experimentalis Et Applicata,* **155**
522 **(1),** 1-17.
523 Tamanna, N. & Mahmood, N. (2014) Emerging roles of branched-chain amino acid
524 supplementation in human diseases. *International Scholarly Research Notices,* **2014**.
525 Tenenhaus, M. (1998) *La régression PLS*. Editions Technip, Paris.
526 Travis, M.J., Muenkemueller, T., Burton, O.J., Best, A., Dytham, C., Johst, K. (2007)
527 Deleterious mutations can surf to high densities on the wave front af an expanding
528 population. *Molecular Biology and Evolution,* **24 (10)**, 2334-2343.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

529 Tulisalo, U. (1971) Free and bound amino acids of three host plant species and various
530 fertilizer treatments affecting the fecundity of the two-spotted spider mite,
531 *Tetranychus urticae* Koch (Acarina, Tetranychidae). *Annales Entomologicae Fennicae,*
532 **37,** 155-163.
533 Van Noordwijk, A.J. & de Jong, G. (1986) Acquisition and allocation of resources - Their
534 influence on variation in life-history tactics. *American Naturalist,* **128 (1),** 137-142.
535 Van Petegem, K.H.P., Boeye, J., Stoks, R. & Bonte, D. (2016) Spatial selection and local
536 adaptation jointly shape life-history evolution during range expansion. bioRxiv
537 031922; doi: http://dx.doi.org/10.1101/031922.
538 Verhoeven, K.J.F., vonHoldt, B.M. & Sork, V.L. (2016) Epigenetics in ecology and evolution:
539 what we know and what we need to know. *Molecular Ecology*, **25 (8)**, 1631-1638.
540 Viant, M.R. (2008) Recent developments in environmental metabolomics. *Molecular*
541 *Biosystems,* **4 (10),** 980-986.
542 Xia, J., Mandal, R., Sinelnikov, I.V., Broadhurst, D. & Wishart, D.S. (2012) MetaboAnalyst
543 2.0—a comprehensive server for metabolomic data analysis. *Nucleic Acids Research*.
544 **40 (W1)**, W127-W133.
545 Xia, J., Psychogios, N., Young, N. & Wishart, D.S. (2009) MetaboAnalyst: a web server for
546 metabolomic data analysis and interpretation. *Nucleic Acids Research,* **37 (suppl2),**
547 W652-W660.
548 Xia, J., Sinelnikov, I.V., Han, B. & Wishart, D.S. (2015) MetaboAnalyst 3.0—making
549 metabolomics more meaningful. *Nucleic Acids Research*. **43 (W1)**, W251-W257.
550 Zera, A.J. (2011) Microevolution of intermediary metabolism: evolutionary genetics meets
551 metabolic biochemistry. *Journal of Experimental Biology,* **214 (2)**, 179-190.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

552 Zera, A.J. & Harshman, L.G. (2001) The physiology of life history trade-offs in animals. *Annual*

553 *Review of Ecology and Systematics,* **32,** 95-126.

554

555

Appendix

A.1: Overview of the field collection sites and their respective life-history trait values

An overview of the localities where *T. urticae* was sampled in the field, together with population-level life-history trait values (daily fecundity (#eggs/day), lifetime fecundity (total #eggs), egg survival (%), longevity (#days), dispersal propensity (%) and sex ratio (#male/total)). These values, originating from a previous study (Van Petegem *et al.* 2016), were used as the independent values in our linear regressions. Field collection sites were located along a latitudinal gradient, spanning the coasts of Belgium (BEL), The Netherlands (NTL), Germany and Denmark (DEN). The denoted plant species (*Lonicera periclymenum*, *Euonymus europaeus*, *Sambucus nigra* and *Humulus lupulus*) are the species on which the mites were found and sampled.

code	collection site	city, country	Coordinates (WGS 84)	plant species	daily fecundity	lifetime fecundity	egg survival	longevity	dispersal propensity	sex ratio
SKA	Flagbakkevej	Skagen, DEN	57.72, 10.53	*L. periclymenum*	3.85	33.42	96.72	10.80	9.47	0.33
SVI	Sletteåvej	Fjerritslev, DEN	57.15, 9.33	*L. periclymenum*	5.19	29.33	.	6.33	41.41	0.32
TVE	Hindingvej	Thisted, DEN	57.04, 8.62	*L. periclymenum*	3.65	23.42	100.00	7.42	14.53	0.26
BLA	V. Hennebysvej	Henne, DEN	55.74, 8.22	*L. periclymenum*	3.72	40.92	100.00	11.00	39.47	0.29
HED	picnic-place along 11/24	Gredstedbro, DEN	55.39, 8.74	*L. periclymenum*	3.48	29.17	96.88	9.60	31.45	0.22
LAU	Schildhoek	Lauwersoog, NTL	53.41, 6.22	*E. europaeus*	4.25	37.00	87.30	9.75	16.75	0.34
CAS	Hoofdweg	Heemskerk, NTL	52.53, 4.65	*L. periclymenum*	5.54	41.75	96.15	9.40	19.21	0.28
KVS	Bosweg	Burgh-Haamstede, NTL	51.68, 3.72	*S. nigra*	6.34	98.67	99.02	17.55	15.03	0.19
ODK	Duinparklaan	Koksijde, BEL	51.12, 2.68	*H. lupulus*	5.22	50.42	98.99	10.08	9.81	0.25

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.2: Overview of the 60 metabolites included in our spectral database

A list of all 60 metabolites screened for in our single quadrupole GC-MS. Each of these metabolites can be characterised by several ions of different masses. We used the selective ion monitoring mode (SIM, see Waller *et al.* 2007) instead of the full scan mode. In this SIM mode, the MS instrument is set to only look for specific previously-known ion masses of interest rather than to screen for all masses over a wide range. The instrument can therefore be very specific for a particular compound of interest. Our original database contained spectral information for 85 primary metabolites from a range of plant and invertebrate models. After removing all metabolites specific to plant models and those (polyamines for instance) having concentrations lower than the detection limit of our equipment, only the 60 specific metabolites listed in the table below remained in our spectral database. Metabolites are classified according to six categories: amino acid, polyol, sugar, intermediate of the citric acid cycle, 'other' metabolite and metabolite not found in any of our samples.

category	metabolite
amino acid	Alanine
amino acid	Aspartic acid
amino acid	Glutamic acid
amino acid	Glycine
amino acid	Isoleucine
amino acid	Leucine
amino acid	Lysine
amino acid	Methionine
amino acid	Phenylalanine
amino acid	Proline
amino acid	Serine
amino acid	Threonine
amino acid	Tryptophan
amino acid	Tyrosine
amino acid	Valine
intermediate citric acid cycle	Citric acid
intermediate citric acid cycle	Fumaric acid
intermediate citric acid cycle	Malic acid
intermediate citric acid cycle	Succinic acid
polyol	Adonitol
polyol	Arabitol
polyol	Glycerol
polyol	Glycerol-3-phosphate
polyol	Inositol
polyol	Sorbitol
polyol	Xylitol
sugar	Fructose
sugar	Fructose-6-phosphate
sugar	Galactose
sugar	Glucose

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

sugar	Glucose-6-phosphate
sugar	Mannose
sugar	Ribose
other	Ethanolamine
other	GABA
other	Gluconolactone
other	Glyceric acid
other	Lactic acid
other	Ornithine
other	Phosphoric acid
other	Putrescine
other	Quinic acid
other	Spermidine
not found	Arabinose
not found	Asparagine
not found	Cadaverine
not found	Citrulline
not found	Cytosine
not found	Erythritol
not found	Galactitol
not found	Galacturonic acid
not found	Maltose
not found	Mannitol
not found	Octopamine
not found	Pipecolic acid
not found	Saccharose
not found	Spermine
not found	Trehalose
not found	Tyramine
not found	Xylose

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.3: correlation matrix

LAT (latitude), LIFE (lifetime fecundity), DAFE (daily fecundity), DISP (dispersal propensity), EGSU (egg survival), LONG (longevity), DIAP (diapause incidence) and SERA (sex ratio). All significant correlations (Bonferroni correction not implemented) are in bold. As only a selection of populations was included in the current study, the strength of the correlations between latitude and the shown life-history traits decreased relative to the correlations found in Van Petegem *et al.* (2016).

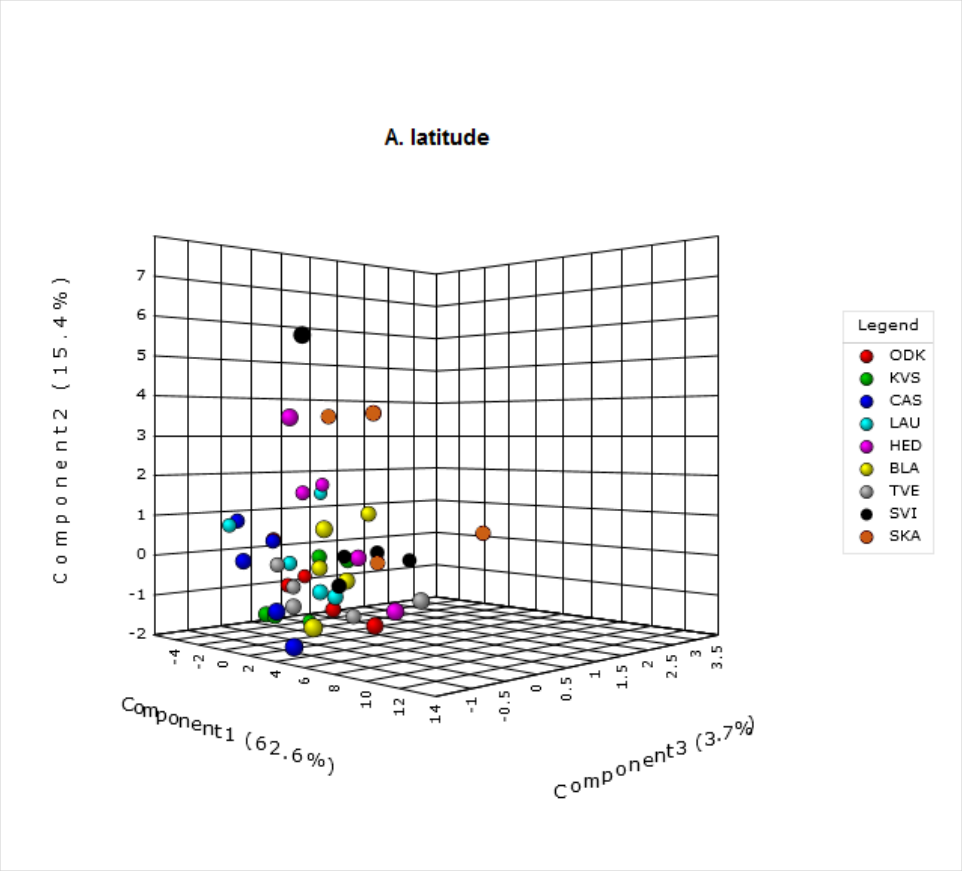
Pearson Correlation Coefficients
Prob > |r| under H0: Rho=0
Number of Observations

	LAT	LIFE	DAFE	DISP	EGSU	LONG	DIAP	SERA
LAT	1	-0.67384	-0.67452	0.38101	0.13882	-0.52688	0.47464	0.43955
		0.0466	**0.0463**	0.3117	0.743	0.145	0.1967	0.2365
	9	9	9	9	8	9	9	9
LIFE	-0.67384	1	0.75065	-0.27469	0.18641	0.9203	-0.337	-0.5922
	0.0466		**0.0198**	0.4744	0.6585	**0.0004**	0.3752	0.0929
	9	9	9	9	8	9	9	9
DAFE	-0.67452	0,75065	1	-0.18302	0.06919	0.46919	0.13277	-0.33554
	0.0463	**0.0198**		0.6374	0.8707	0.2026	0.7335	0.3774
	9	9	9	9	8	9	9	9
DISP	0.38101	-0.27469	-0.18302	1	0.14537	-0.31841	0.66023	0.11912
	0.3117	0.4744	0.6374		0.7313	0.4037	0.0529	0.7602
	9	9	9	9	8	9	9	9
EGSU	0.13882	0.18641	0.06919	0.14537	1	0.16269	0.19129	-0.59346
	0.743	0.6585	0.8707	0.7313		0.7003	0.65	0.1209
	8	8	8	8	8	8	8	8
LONG	-0.52688	0.9203	0.46919	-0.31841	0.16269	1	-0.52876	-0.54739
	0.145	**0.0004**	0.2026	0.4037	0.7003		0.1433	0.1271
	9	9	9	9	8	9	9	9
DIAP	0.47464	-0.337	0.13277	0.66023	0.19129	-0.52876	1	0.29697
	0.1967	0.3752	0.7335	0.0529	0.65	0.1433		0.4377
	9	9	9	9	8	9	9	9
SERA	0.43955	-0.5922	-0.33554	0.11912	-0.59346	-0.54739	0.29697	1
	0.2365	0.0929	0.3774	0.7602	0.1209	0.1271	0.4377	
	9	9	9	9	8	9	9	9

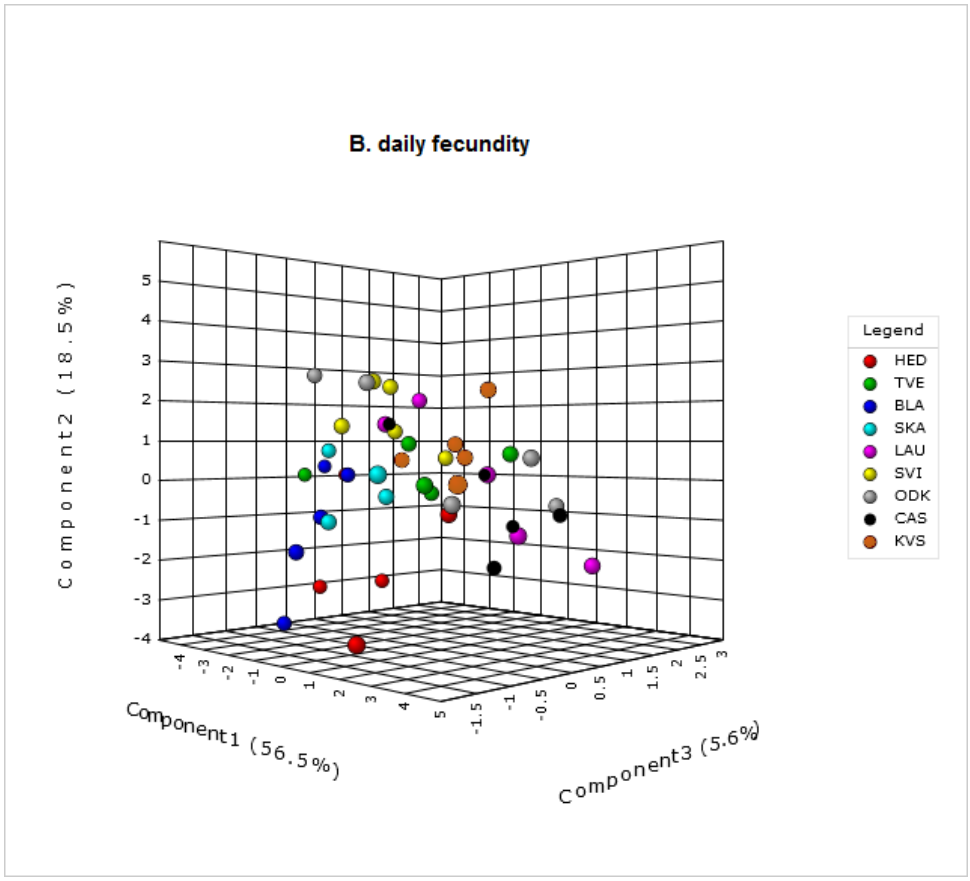
bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.4: 3-D score plots

3-D score plots resulting from the multivariate analyses (PLS-DA) performed on our metabolomic data are given for latitude (A) and each of six life-history traits (daily fecundity (B), lifetime fecundity (C), egg survival (D), longevity (E), dispersal propensity (F) and sex ratio (G)). The mean metabolic phenotypes for each replicate (five in total) of all nine populations (eight for egg survival) are represented by a dot and arranged in space according to their projections on three component axes. Each of these axes explains a certain amount (%) of the metabolic variation that is present in the dataset. More similar points (populations with a similar metabolome) are placed closer together.

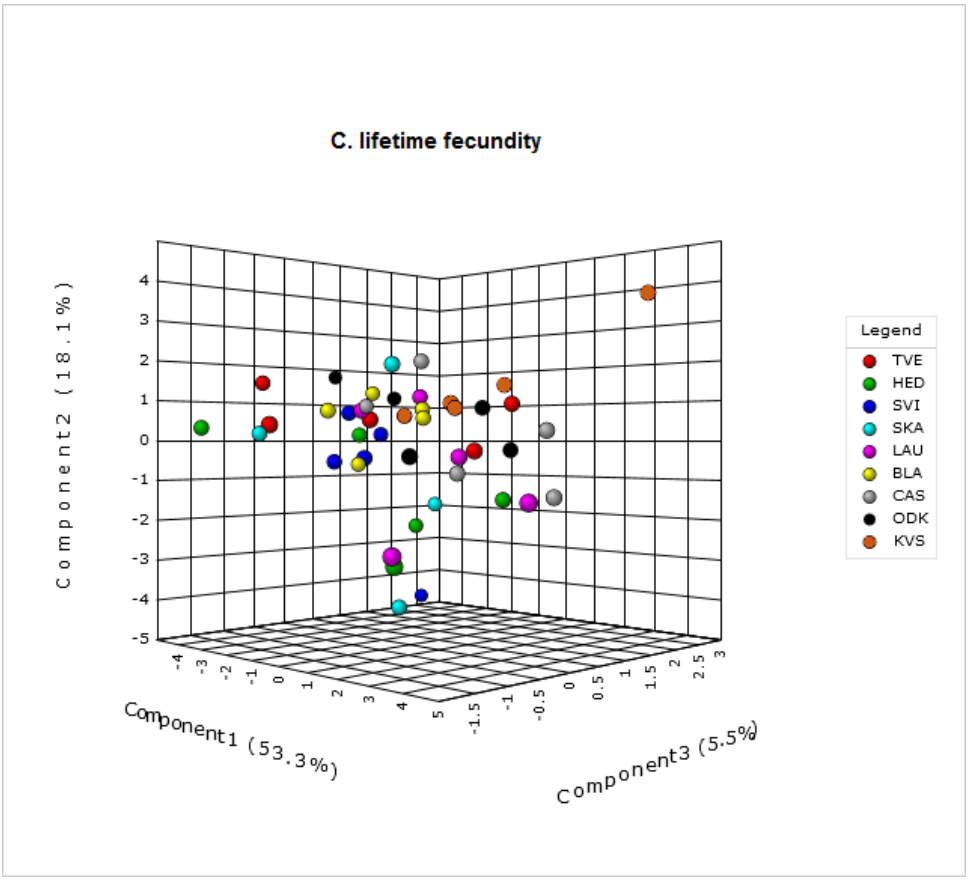


bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



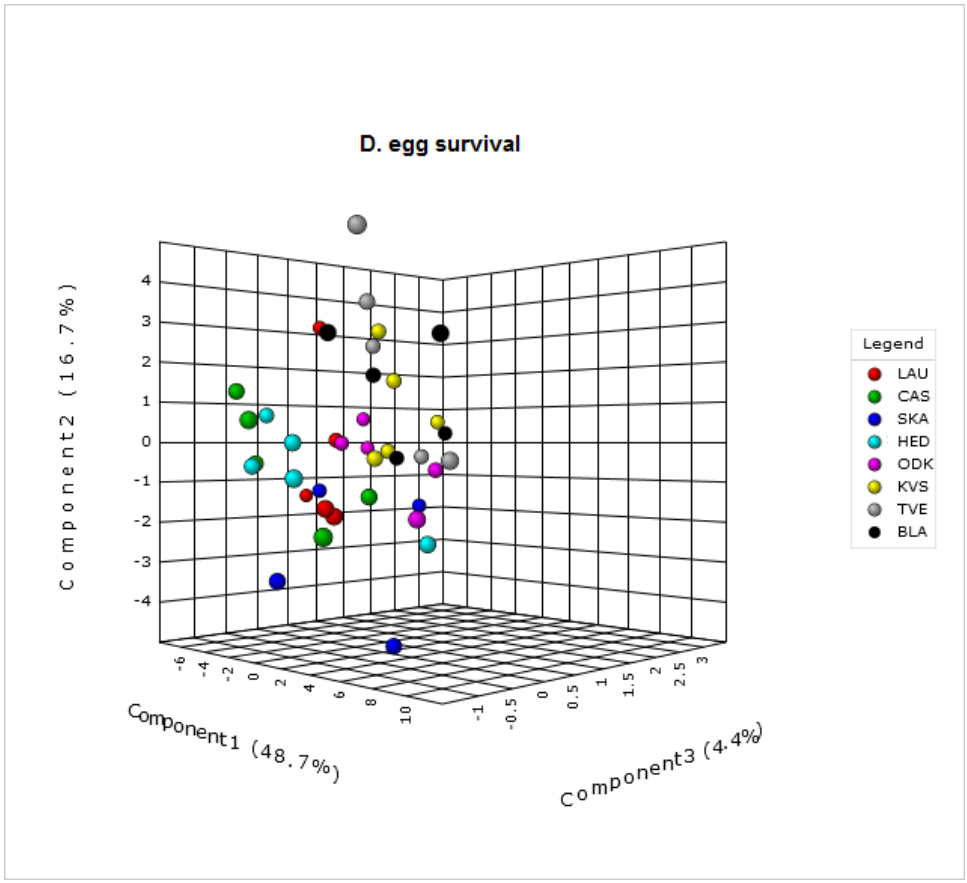
591

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



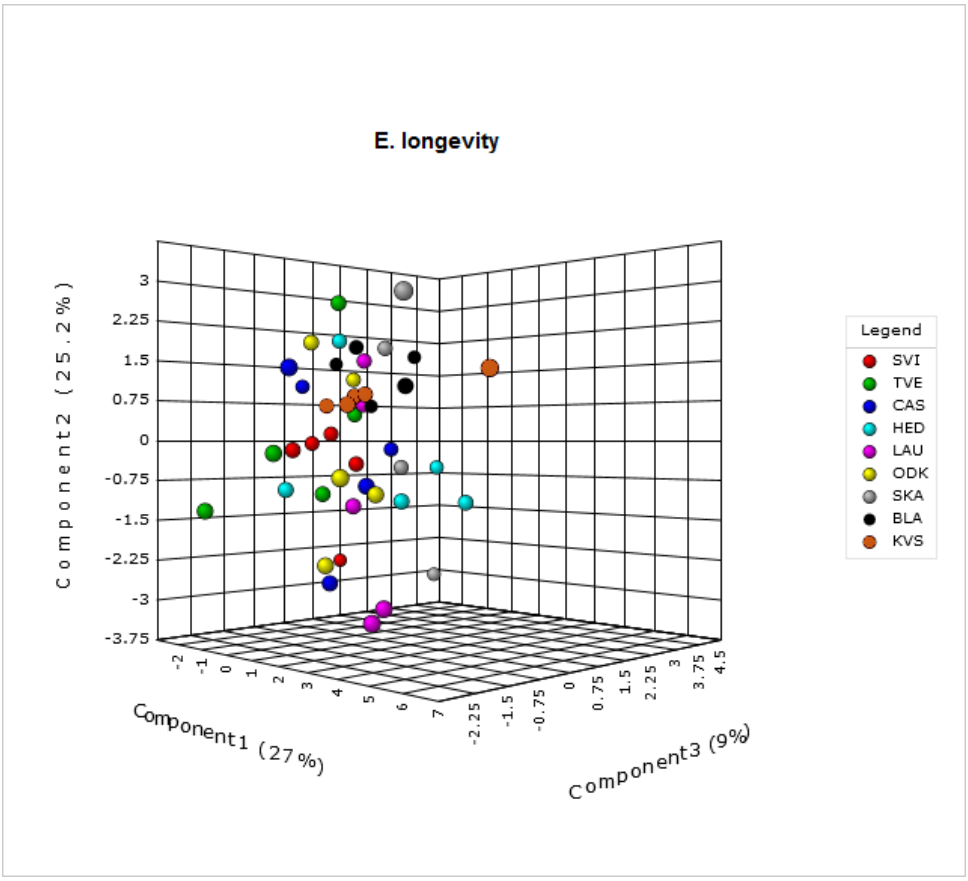
592

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



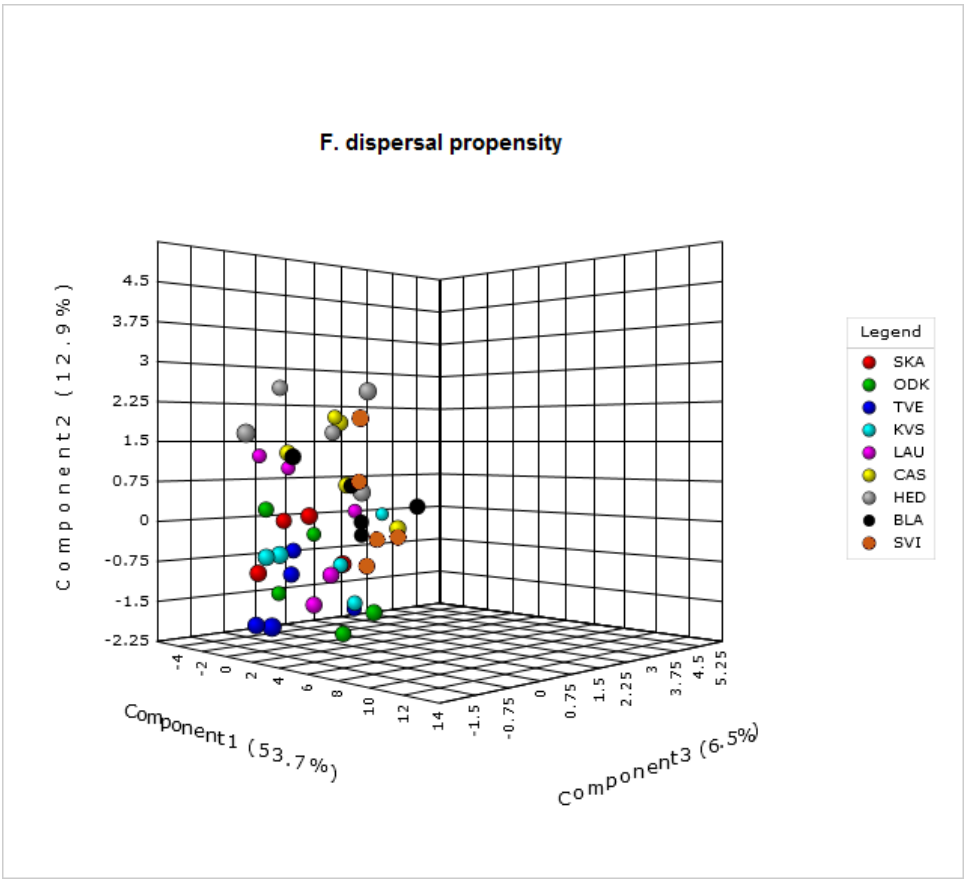
593

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



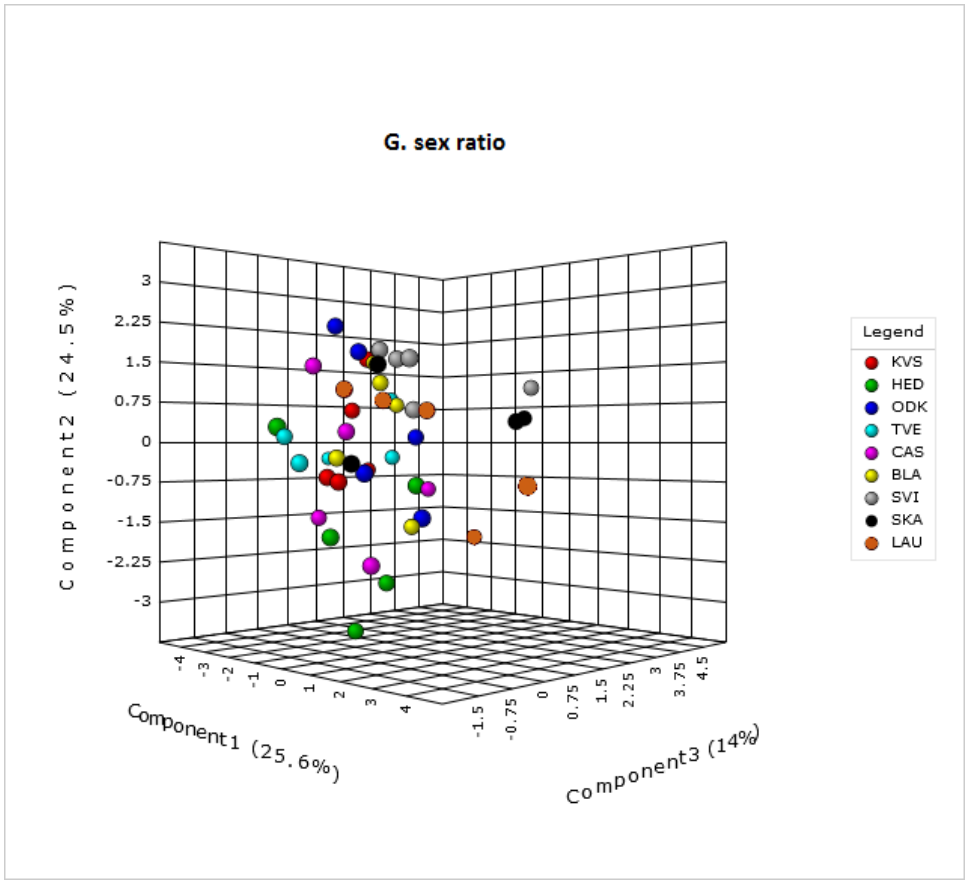
594

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



595

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



596

597

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.5 overview of the VIP scores resulting from the PLS-DA

An overview off all metabolites with a VIP score of at least 1.2 (1.0 for egg survival because removing the metabolites with a score between 1.0 and 1.2 resulted in a decreased percentage of variation explained) for component 1 and/ or 2 in the PLS-DA performed for latitude (A) and each of six life-history traits (daily fecundity (B), lifetime fecundity (C), egg survival (D), longevity (E), dispersal propensity (F) and sex ratio(G)). Note that in the tables below, the VIP scores for the original dataset (containing all forty-three identified metabolites) are given. The order of the metabolites (from high to low VIP scores) in these tables can therefore deviate from the order in Fig. 3 (main text), as Fig. 3 is based on VIP scores of the final dataset (after removal of all non-explanatory metabolites).

A. latitude

metabolite	Comp. 1	Comp. 2
Proline	1.6583	1.0501
Tryptophan	1.5937	1.0289
Inositol	1.5831	1.0274
Malic acid	1.4947	0.9356
Lysine	1.4669	0.9290
Valine	1.4577	0.9261
Isoleucine	1.4219	0.9054
Methionine	1.4115	0.8879
Glycine	1.4090	0.8936
Aspartic acid	1.3881	0.8733
Threonine	1.3705	0.9118
Alanine	1.3572	0.8500
Leucine	1.3414	0.9084
Quinic acid	1.3313	1.6940
Glucose-6-phosphate	0.6854	2.0669
Sorbitol	1.0691	1.9186
Fructose-6-phosphate	0.4123	1.7967
Ribose	0.8471	1.2669

B. daily fecundity

metabolite	Comp. 1	Comp. 2
Glycerol	1.7613	1.8109

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Phenylalanine	1.6599	1.2292
Sorbitol	1.6526	1.4537
Valine	1.5163	1.1636
Xylitol	1.4767	1.2651
Lysine	1.4179	1.0710
Isoleucine	1.4127	1.1010
Glutamic acid	1.3973	0.9667
Tyrosine	1.3441	1.0950
Leucine	1.3261	1.1045
Threonine	1.2862	1.0977
Inositol	1.2444	0.9216
Glycine	1.2215	0.9496
Tryptophan	1.2095	0.9172

608

609 **C. lifetime fecundity**

metabolite	Comp. 1	Comp. 2
Lysine	1.5753	0.8880
Glycine	1.5660	0.8728
Tryptophan	1.5312	0.8706
Inositol	1.5101	0.8566
Valine	1.4669	0.9187
Proline	1.4248	0.8628
Alanine	1.4119	0.7920
Isoleucine	1.3774	0.8873
Malic acid	1.3485	0.8655
Phenylalanine	1.3188	0.9131
Leucine	1.3161	0.9319
Lactic acid	1.2638	1.3055
Glucose-6-phosphate	1.2298	1.7909
Quinic acid	1.2139	0.9298
Fructose-6-phosphate	0.9630	1.6380

610

611 **D. egg survival**

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

metabolite	Comp. 1	Comp. 2
Glutamic acid	1.7874	1.3641
Alanine	1.6795	1.1028
Tyrosine	1.4029	0.9337
Phenylalanine	1.3828	0.9234
Fructose-6-phosphate	1.3581	0.8561
Glucose-6-phosphate	1.3492	0.8500
Methionine	1.2596	0.8576
Xylitol	1.2585	1.0527
Glycerol-3-phosphate	1.2193	0.7804
Citric acid	1.2164	0.8394
Serine	1.1977	0.9293
GABA	1.1951	2.2339
Gluconolactone	1.1857	0.8810
Adonitol	1.1823	0.8112
Succinic acid	1.1628	1.0936
Leucine	1.1035	0.9157
Threonine	1.0640	0.9255
Valine	1.0216	0.8728
Ornithine	1.0141	0.6404
Ethanolamine	0.8772	1.9297
Glycerol	0.5981	1.7154
Fumaric acid	0.0152	1.5159
Glutamic acid	1.7874	1.3641
Glyceric acid	2.1181	1.3224

612

613 **E. longevity**

metabolite	Comp. 1	Comp. 2
Glucose	2.1463	1.4658
Succinic acid	1.9802	1.3826
Sorbitol	1.9329	1.3478
Citric acid	1.6265	1.5863
Glycine	1.4818	1.1018

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Galactose	1.4447	1.1659
Lysine	1.4091	1.0542
Lactic acid	1.3965	1.0108
Fructose-6-phosphate	1.3276	1.4043
Glucose-6-phosphate	1.3168	1.3696
Phosphoric acid	1.2220	1.0486

614

615 **F. dispersal propensity**

metabolite	Comp. 1	Comp. 2
Putrescine	1.9187	1.2144
Phosphoric acid	1.7678	1.0416
Lysine	1.7503	1.0280
Methionine	1.7343	1.0303
Xylitol	1.7230	1.9394
Phenylalanine	1.5574	0.9821
Fructose	1.4964	0.9235
Tryptophan	1.2684	0.7950
Glycerol-3-phosphate	1.2602	0.7514
Leucine	1.2553	0.9363
Inositol	1.2549	0.7824
Glucose-6-phosphate	0.6820	1.4379
Mannose	0.2110	1.3947

616

617 **G. sex ratio**

metabolite	Comp. 1	Comp. 2
GABA	2.7316	2.5800
Succinic acid	2.5829	2.4256
Glutamic acid	2.0087	1.8893
Glucose-6-phosphate	1.7334	1.6527
Sorbitol	1.5872	1.4965
Citric acid	1.4820	1.4001

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Fructose-6-phosphate	1.4541	1.3954
Xylitol	1.2478	1.3554
Ethanolamine	1.2072	1.3270
Fructose	0.9418	0.9842*

618 **** After removal of the least explanatory metabolites in the dataset, the VIP score of fructose changed to >1.2. Fructose was therefore***

619 ***retained for further analysis.***

620

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.6 overview of all linear regressions

An overview of all linear regressions according to latitude (A) and each of the six life-history traits (daily fecundity (B), lifetime fecundity (C), egg survival (D), longevity (E), dispersal propensity (F) and sex ratio(G)) known to covary with latitude in the study species (see Van Petegem *et al.* 2016). The direction of change (correlation) is each time given, together with the F- and *p*-value of the linear regression. The degrees of freedom used in determining the F-value (Num DF and Den DF) are also shown.

A. latitude

metabolite	correlation	Num DF	Den DF	F	p
Proline	negative	1	7	9.85	**0.0164**
Tryptophan	negative	1	7	6.48	**0.0383**
Inositol	negative	1	7	6.43	**0.0389**
Aspartic acid	negative	1	7	6.62	**0.0369**
Glycine	negative	1	7	7.19	**0.0315**
Malic acid	negative	1	7	6.59	**0.0372**
Valine	negative	1	7	8.15	**0.0245**
Lysine	negative	1	7	3.77	0.0932
Alanine	negative	1	7	4.16	0.0808
Methionine	negative	1	7	3.06	0.1238
Isoleucine	negative	1	7	8.81	**0.0209**
Quinic acid	positive	1	7	5.59	**0.0500**
Threonine	negative	1	7	7.35	**0.0301**
Leucine	negative	1	7	6.71	**0.0359**
Sorbitol	positive	1	7	1.13	0.3221
Glucose-6-phosphate	positive	1	7	1.00	0.3511
Fructose-6-phosphate	positive	1	7	0.34	0.5789

B. daily fecundity

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

metabolite	correlation	Num DF	Den DF	F	p
Glycerol	negative	1	7	1.91	0.2096
Phenylalanine	positive	1	7	1.87	0.2135
Glutamic acid	positive	1	7	0.47	0.5193
Sorbitol	negative	1	7	3.37	0.0947
Valine	positive	1	7	2.41	0.1648
Isoleucine	positive	1	7	2.46	0.1606
Lysine	positive	1	7	1.34	0.2588
Tyrosine	positive	1	7	1.31	0.2897
Leucine	positive	1	7	1.54	0.2553
Threonine	positive	1	7	1.83	0.2182
Xylitol	negative	1	7	0.46	0.5193
Glycine	positive	1	7	1.51	0.2587
Inositol	positive	1	7	0.71	0.4284
Tryptophan	positive	1	7	0.62	0.4584

630

631 **C. lifetime fecundity**

metabolite	correlation	Num DF	Den DF	F	p
Lysine	positive	1	7	2.57	0.1531
Glycine	positive	1	7	3.86	0.0903
Tryptophan	positive	1	7	0.60	0.4629
Inositol	positive	1	7	0.61	0.4592
Valine	positive	1	7	1.61	0.2455
Proline	positive	1	7	0.36	0.5665
Alanine	positive	1	7	0.15	0.7089

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Isoleucine	positive	1	7	1.47	0.2653
Malic acid	positive	1	7	1.24	0.3026
Phenylalanine	positive	1	7	0.70	0.4317
Leucine	positive	1	7	0.91	0.3717
Lactatic acid	positive	1	7	0.22	0.6503
Glucose-6-phosphate	negative	1	7	2.38	0.1671
Quinic acid	negative	1	7	0.58	0.4716
Fructose-6-phosphate	negative	1	7	2.15	0.1862
Glycerol-3-phosphate	negative	1	7	1.07	0.3363

632

633 **D. egg survival**

metabolite	correlation	Num DF	Den DF	F	p
Glutamic acid	negative	1	6	3.79	0.0994
Alanine	negative	1	6	4.40	0.0808
Tyrosine	negative	1	6	5.24	0.0621
Phenylalanine	negative	1	6	2.70	0.1516
Fructose-6-phosphate	negative	1	6	4.55	0.0770
Glucose-6-phosphate	negative	1	6	4.66	0.0742
Methionine	negative	1	6	1.84	0.2238
Xylitol	negative	1	6	0.37	0.5649
Succinic acid	negative	1	6	3.02	0.1327
Glycerol-3-phosphate	negative	1	6	4.70	0.0733
Citric acid	negative	1	6	4.61	0.0754
Serine	negative	1	6	5.03	0.0661
GABA	positive	1	6	0.38	0.5580

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Adonitol	negative	1	6	9.07	**0.0237**
Gluconolactone	negative	1	6	0.60	0.4697
Leucine	negative	1	6	3.16	0.1260
Threonine	negative	1	6	2.85	0.1425
Valine	negative	1	6	2.23	0.1860
Ornithine	negative	1	6	2.68	0.1525
Ethanolamine	negative	1	6	0.00	0.9891
Glycerol	positive	1	6	0.03	0.8651
Malic acid	negative	1	6	2.22	0.1871
Glyceric acid	negative	1	6	0.94	0.3698
Fumaric acid	negative	1	6	0.44	0.5305

E. longevity

metabolite	correlation	Num DF	Den DF	F	p
Glucose	positive	1	7	0.52	0.4955
Succinic acid	negative	1	7	0.00	0.9482
Sorbitol	positive	1	7	0.05	0.8306
Citric acid	negative	1	7	2.14	0.1870
Glycine	positive	1	7	2.83	0.1365
Galactose	positive	1	7	1.13	0.3236
Lysine	positive	1	7	1.65	0.2404
Lactic acid	positive	1	7	0.89	0.3777
Fructose-6-phosphate	negative	1	7	1.16	0.3174
Glucose-6-phosphate	negative	1	7	1.16	0.3172
Phosphoric acid	positive	1	7	0.97	0.3573

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Ornithine	positive	1	7	0.79	0.4023
Ribose	positive	1	7	0.23	0.6430
Xylitol	negative	1	7	0.07	0.7935
Ethanolamine	positive	1	7	1.09	0.3310
Glycerol	positive	1	7	0.06	0.8184
Glutamic acid	positive	1	7	0.18	0.6826
Mannose	positive	1	7	0.88	0.3804
Glycerol-3-phosphate	negative	1	7	0.61	0.4607
Methionine	positive	1	7	0.05	0.8332
Arabitol	positive	1	7	0.15	0.7066
Serine	positive	1	7	0.15	0.7117
Adonitol	positive	1	7	0.00	0.9879

F. dispersal propensity

metabolite	correlation	Num DF	Den DF	F	p
Putrescine	negative	1	7	8.64	**0.0218**
Phosphoric acid	negative	1	7	7.33	**0.0303**
Lysine	negative	1	7	6.38	**0.0394**
Methionine	negative	1	7	8.16	**0.0245**
Xylitol	positive	1	7	0.66	0.4436
Phenylalanine	negative	1	7	9.05	**0.0197**
Fructose	negative	1	7	7.29	**0.0307**
Tryptophan	negative	1	7	5.10	0.0585
Glycerol-3-phosphate	negative	1	7	3.67	0.0969
Leucine	negative	1	7	8.14	**0.0246**

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Inositol	negative	1	7	4.94	0.0615
Glucose-6-phosphate	positive	1	7	0.37	0.5608
Mannose	negative	1	7	0.02	0.9013

638

639 **G. sex ratio**

metabolite	correlation	Num DF	Den DF	F	p
GABA	negative	1	7	3.26	0.1141
Succinic acid	positive	1	7	3.49	0.1038
Glutamic acid	positive	1	7	0.91	0.3716
Glucose-6-phosphate	positive	1	7	2.60	0.1511
Sorbitol	positive	1	7	0.83	0.3932
Citric acid	positive	1	7	1.82	0.2193
Fructose-6-phosphate	positive	1	7	1.91	0.2089
Xylitol	negative	1	7	0.26	0.6281
Ethanolamine	negative	1	7	1.20	0.3091
Fructose	negative	1	7	0.70	0.4294

640

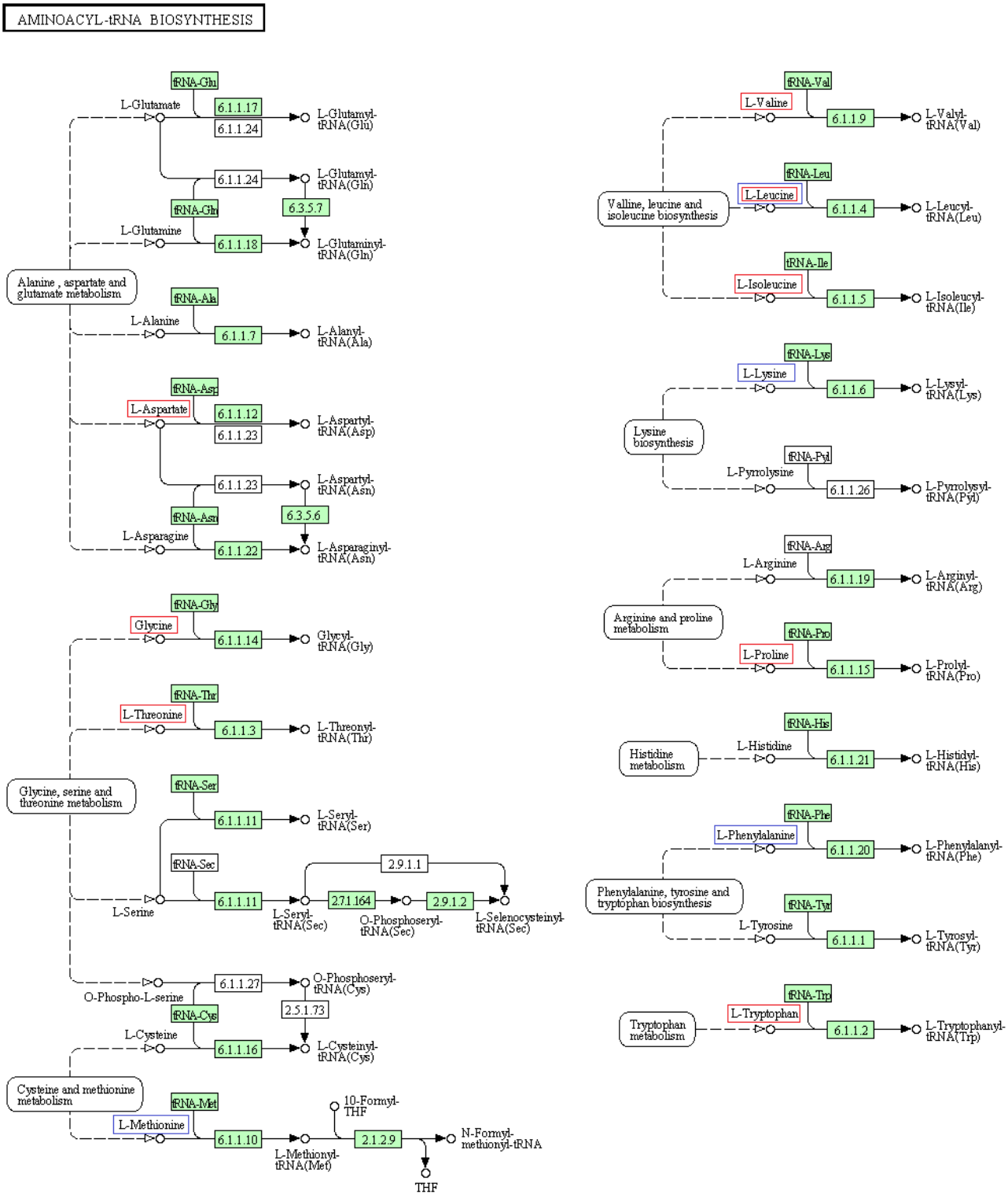
641

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.7 pathway maps

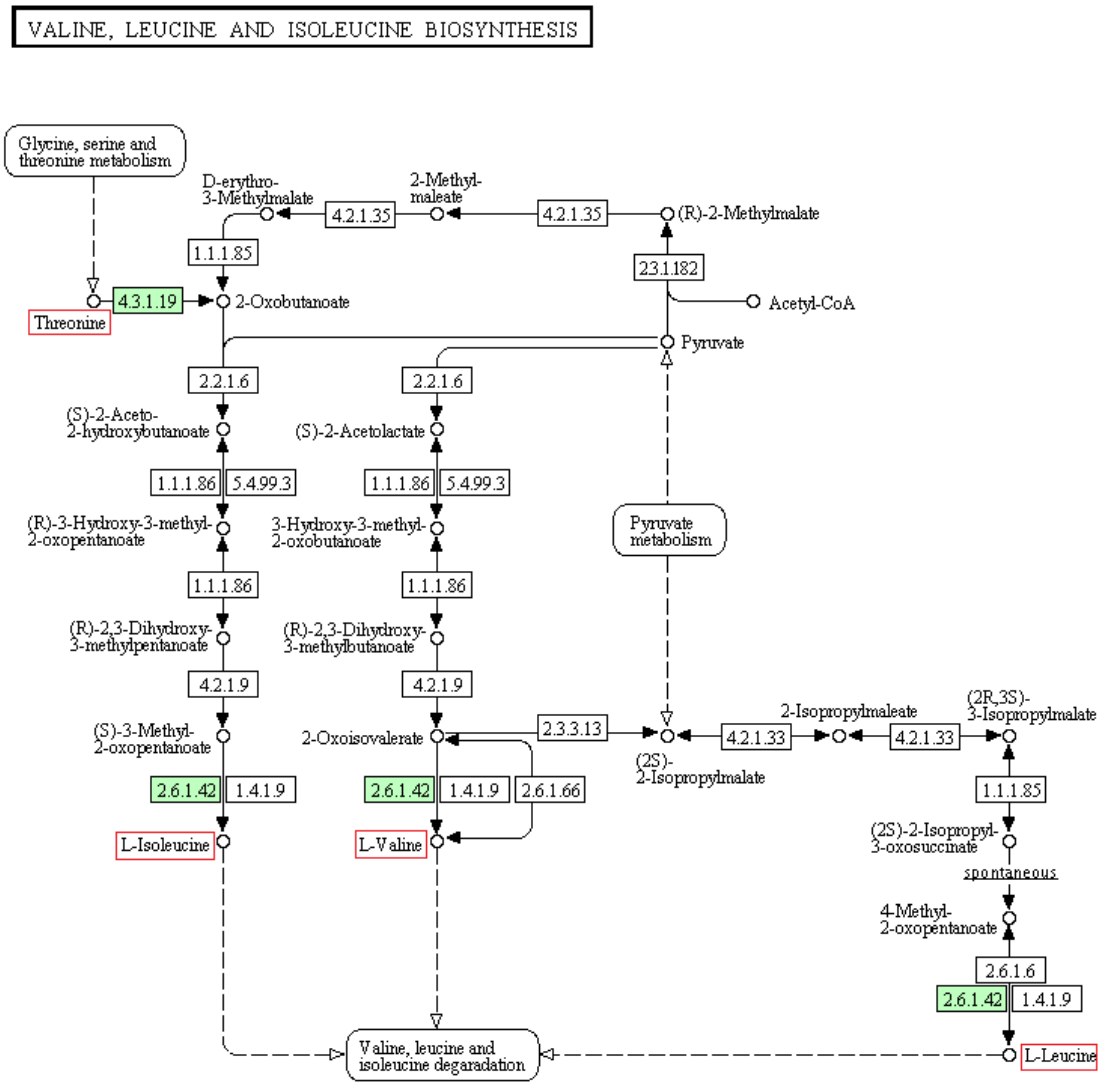
Pathway maps of the two pathways in which some of the metabolites identified in the GC-MS analysis (visualised with either red or blue rectangles) play an important role. In the aminoacyl-tRNA biosynthesis pathway, the metabolites in the red rectangles correlate negatively with latitude and the blue ones correlate negatively with dispersal propensity. In the valine, leucine and isoleucine biosynthesis pathway, the metabolites in the red rectangles correlate negatively with latitude. The maps were used from KEGG (Kyoto Encyclopedia of Genes and Genomes) (Kanehisa *et al.* 2015).

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



00970 4/17/13
(c) Kanehisa Laboratories

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



649

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

A.8 regression for all populations *versus* for *L. periclymenum* only

For those metabolites that gave significant results (see appendix A.6) for latitude or a specific life-history trait (daily fecundity, lifetime fecundity, egg survival, longevity, dispersal propensity or sex ratio) in the regressions run for all nine populations (hence for *L. periclymenum*, *Euonymus europaeus*, *Sambucus nigra* and *Humulus lupulus*), we repeated these regressions but then for *L. periclymenum* only (hence for only six populations –see appendix A.1). The table gives the slopes and p-values of both the regressions run for all populations (slope_all and p_all) and those run for *L. periclymenum* only (slope_*per* and p_*per*).

trait	metabolite	slope_*per*	slope_all	p_*per*	p_all
latitude	Proline	-0.04354	-0.02733	0.0205	0.0164
latitude	Tryptophan	-0.05170	-0.04474	0.1766	0.0383
latitude	Inositol	-0.05628	-0.04890	0.1880	0.0389
latitude	Aspartic acid	-0.01956	-0.02840	0.2757	0.0369
latitude	Glycine	-0.00681	-0.03254	0.6500	0.0315
latitude	Malic acid	-0.00703	-0.03858	0.6992	0.0372
latitude	Valine	-0.02914	-0.02727	0.1726	0.0245
latitude	Isoleucine	-0.03947	-0.02997	0.0947	0.0209
latitude	Quinic acid	0.02094	0.01594	0.2119	0.0500
latitude	Threonine	-0.02807	-0.02700	0.2046	0.0301
latitude	Leucine	-0.01727	-0.02270	0.3466	0.0359
egg survival	Adonitol	-0.00651	-0.00258	0.0751	0.0237
dispersal propensity	Putrescine	-0.00092	-0.00108	0.0854	0.0218
dispersal propensity	Phosphoric acid	-0.10219	-0.13336	0.0492	0.0303
dispersal propensity	Lysine	-0.00277	-0.00553	0.0942	0.0394
dispersal propensity	Methionine	-0.00793	-0.01081	0.1461	0.0245
dispersal propensity	Phenylalanine	-0.01652	-0.02201	0.1208	0.0197
dispersal propensity	Fructose	-0.00266	-0.00221	0.0744	0.0307
dispersal propensity	Leucine	-0.03211	-0.04462	0.1224	0.0246

bioRxiv preprint doi: https://doi.org/10.1101/043208; this version posted July 5, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

658 **References**

659

660 Kanehisa, M., Sato, Y., Kawashima, M., Furumichi, M. & Tanabe, M. (2015) KEGG as a
661 reference resource for gene and protein annotation. *Nucleic Acids Research*.
662 Van Petegem, K., Boeye, J., Stoks, R. & Bonte, D. (2016) Spatial selection and local adaptation
663 jointly shape life-history evolution during range expansion. *bioRxiv*.
664 Waller, M., Whitney, R., Taylor, M., Miyagawa, H., Matsuda, K. & Nakagawa, K. (2007)
665 Multiresidue pesticides analysis using synchronous Scan/SIM mode GC-MS. *Lc Gc*
666 *North America*, 39-39.

667

668