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Metabolomics analysis of annual killifish (*Austrofundulus limnaeus*) embryos during aerial dehydration stress

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Abstract

The annual killifish, *Austrofundulus limnaeus*, survives in ephemeral ponds in the coastal deserts of Venezuela. Persistence through the dry season is dependent on drought-resistant eggs embedded in the pond sediments during the rainy season. The ability of these embryos to enter drastic metabolic dormancy (diapause) during normal development enables *A. limnaeus* to survive conditions lethal to most other aquatic vertebrates; critical to the survival of the species is the ability of embryos to survive months and perhaps years without access to liquid water. Little is known about the molecular mechanisms that aid in survival of the dry season. This study aims to gain insight into the mechanisms facilitating survival of dehydration stress due to aerial exposure by examining metabolite profiles of dormant and developing embryos. There is strong evidence for unique metabolic profiles based on developmental stage and length of aerial exposure. Actively developing embryos exhibit more robust changes, however, dormant embryos respond in an active manner and significantly alter their metabolic profile. A number of metabolites accumulate in aerial-exposed embryos that may play an important role in survival, including the identification of known antioxidants and neuroprotectants. In addition, a number of unique metabolites not yet discussed in the dehydration literature are identified, such as lanthionine and 2-hydroxyglutarate. Despite high oxygen availability, embryos accumulate the anaerobic end-product lactate. This paper offers an overview of the metabolic changes occurring that may support embryonic survival during dehydration stress due to aerial incubation, which can be functionally tested using genetic and pharmacological approaches.

Introduction

The annual killifish, *Austrofundulus limnaeus*, inhabits temporary pools in the Maracaibo basin of Venezuela. Their habitat is defined by highly unpredictable episodic rain events, which leads to uncertainty in the length of time that a pool will experience inundation. Thus, individual pools may remain dry for months or perhaps years (44, 50, 52). During the rainy season, adult *A. limnaeus* deposit their embryos into the often oxygen-limited pool substrate. As the rainy season ends, the adult fish die and embryos must survive severely dehydrating conditions in the mud, often faced with a variety of other stresses such as extremes in temperature and oxygen until the wet season returns and they can complete development (44). As a result, *A. limnaeus* has evolved extremely stress-resistant embryos with the ability to enter a profound state of metabolic depression termed diapause (48, 49). There are three unique stages of diapause (I, II, and III) which an embryo can enter during development (43, 70, 71). The most stress-tolerant stage, diapause II (DII), occurs midway through development and mostly consists of cardiac and neural tissue (48, 51). The developmental ecology of *A. limnaeus* embryos has not been characterized in the field. However, embryos of other species of annual killifish are primarily found in DII during the peak of the dry season, and in a variety of post-DII stages during the late dry season (53). Thus, DII is likely primarily responsible for dry season survival in *A. limnaeus,* but tolerance of dehydrating conditions is required during the entire duration of post-DII development.

For aquatic organisms, aerial exposure imposes oxygen stress due to an increase in availability compared to most aquatic habitats, but also imposes a severe dehydration stress. A main reason for dehydration injury is attributed to the increased formation of ROS and subsequent oxidative damage due to water stress (14). Free radical formation can lead to lipid peroxidation, denaturation of proteins, and DNA damage which ultimately can affect overall metabolism (18). However, protection against such damage can partially be mitigated by accumulation of antioxidant metabolites, such as glutathione (GSH) (30). Embryos of *A. limnaeus* have a notable tolerance of oxidative stress (65), but the role of antioxidants has not been investigated through the lens of dehydration stress.

Embryos of *A. limnaeus* experience unique resistance to dehydration stress that is not seen in other aquatic vertebrates and can survive for over 500 days at 85% relative humidity (RH) (46, 74); however, this ability has received far less attention than other aspects of their biology. When embryos of *A. limnaeus* are aerially incubated, thus exposed to dehydration stress, they initially lose water from the extraembryonic perivitelline space but embryonic compartments remain fully hydrated (46). After a week, water loss approaches zero. Paradoxically, DII embryos respond to aerial dehydration stress by increasing oxygen consumption, while post-diapause II (post-DII) embryos are either unaffected or severely reduce oxygen consumption. The mechanisms that aid survival during dehydration stress and contribute to these metabolic phenotypes are unknown.

Austrofundulus limnaeus is a promising model organism for developmental physiology and ecology because of their tolerance of a plethora of stresses, annotated genome, and ability to alter developmental trajectories in the lab (43, 47, 54, 64). The current study was performed to expand our knowledge of stress tolerance in *A. limnaeus* by exploring the metabolic pathways that may be providing this species with its remarkable abilities to survive extreme dehydration stress. We examine the metabolite profiles of dormant (DII) and actively developing (post-DII) embryos in response to short and long-term aerial dehydration stress (85% RH). We show that actively developing and dormant embryos share metabolic pathways and accumulation of similar metabolites in response to dehydration stress. However, we also see developmentally distinct differences that suggest stage-specific responses. We identify critical roles for amino acid and lipid metabolism, show accumulation of known antioxidant and neuroprotective compounds, and identify novel metabolites produced in response to aerial dehydration stress.

Materials and Methods

Animal husbandry and embryo collection

Adult annual killifish were housed and embryos collected as previously described (45). All work was performed under established protocols that were reviewed and sanctioned by the Portland State University Institutional Animal Care and Use Committee (PSU IACUC protocols #33 and 64). Briefly, adult fish were kept in male-female pairs and spawned semiweekly. Embryos were collected and stored at 25°C with no light in 15 x 100 mm plastic Petri dishes in media that resembles the environmental conditions from which adults were collected in 1995 (10 mmol l^{-1} NaCl, 2.15 mmol l^{-1} $MgCl_2$, 0.8 mmol l^{-1} $CaCl_2$, 0.14 mmol l^{-1} KCl, 1.3 mmol l^{-1} $MgSO_4$) (45, 50). For the first 4 days post-fertilization (dpf), embryo medium contained methylene blue (0.0001%) to prevent fungal infection. Embryos were then treated with two 5 min washes of a 0.01% sodium hypochlorite solution (separated by a 5 min rest in embryo medium) to prevent bacterial and fungal growth, as previously described (45). Following sodium hypochlorite treatment, embryos were transferred to embryo medium containing 10 mg l^{-1} gentamicin sulfate and allowed to develop to DII (32–64 d). To break DII, embryos were subjected to a temperature of 30°C and full spectrum light for 48 h (31). Following this treatment, embryos were sorted into synchronized cohorts of embryos by developmental stage (Wourms' stage [WS]) as described in Podrabsky et al. (43).

Embryonic stages investigated

Experiments were performed on dormant (DII) and actively developing post-DII embryos (43, 70, 71) to identify stage-specific responses to dehydration stress and to capture different levels of dehydration tolerance. DII embryos are metabolically dormant, have halted development, and have a lethal time to 50% mortality (LT_{50}) in aerial incubation (85% relative humidity [RH]) of 325 d (74). DII embryos tend to stay in diapause during aerial exposure. Post-DII embryos are metabolically active, continue developing during aerial exposure when oxygen is not limiting, and have reduced tolerance of dehydrating conditions. When exposed to aerial conditions during early post-DII development (WS 36, 4 days post-diapause II), dehydration tolerance is reduced to an LT_{50} of 84 d. Late

post-DII embryos (WS 40–42) have a further reduced ability to survive aerial incubation and exhibit LT_{50} values around 28–29 d (74).

Metabolomics analysis

Aerial incubation

Embryos were exposed to 85% relative humidity (RH) air at 25°C with no light in a sealed glass desiccator with a porcelain plate shelf (250 mm diameter, 08615B, Fisher Scientific, Hampton, NH, USA). Relative humidity was controlled by using a saturated solution of potassium chloride (750 ml) placed below the shelf and continually mixed with a stir bar to ensure uniform RH within the aerial portion of the chamber (46, 68). Prior to exposure, embryos were treated with sodium hypochlorite (see above) and incubated in embryo medium containing 10 mg l^{-1} gentamicin sulfate for 3 h prior to aerial exposure. Embryos were placed on filter pads containing 2.5 ml embryo medium containing gentamicin. Care was taken to make certain that single embryos were isolated and not touching other embryos. Embryos were then exposed to 85% RH at 25°C without light. DII embryos were sampled after 7 and 28 d while post-DII embryos were sampled at 7 (WS 40) and 18 d (WS 42/43). Control embryos (DII and WS 36) were collected at t = 0 by quickly blotting away embryo medium prior to sampling. Six biological replicates (N = 6), comprised of 25 embryos each, were flash frozen with liquid N_2 and stored at –80°C until shipped to Metabolon for metabolite profiling. To better visualize the sampling regimen, see **Figure 1.**

Metabolon metabolomics analysis

Sample preparation and metabolomics analysis occurred at Metabolon, but is briefly detailed here. Samples were prepared using an automated MicroLab STAR system (Hamilton Company, Reno, NV, USA). Proteins were precipitated with methanol under vigorous shaking for 2 min (Glen Mills GenoGrinder 2000) followed by centrifugation. This method ensured dissociation of small molecules bound to protein, trapped in the precipitated protein matrix, and recovery of chemically diverse metabolites. The resulting extract was divided into four fractions: two for analysis by two separate reverse phase (RP)/UPLC-MS/MS methods with positive ion mode electrospray ionization (ESI),

one for analysis by RP/UPLC-MS/MS with negative ion mode ESI, and one for analysis by HILIC/UPLC-MS/MS with negative ion mode ESI. To remove methanol, samples were placed briefly on a TurboVap (Zymark, Hopkinton, MA, USA). The sample extracts were stored overnight under nitrogen before preparation for analysis. Prior to analysis, sample extracts were reconstituted in solvents compatible to each of the four methods described above. Raw data was extracted, peak-identified, and quality control processed using Metabolon's proprietary hardware and software. At the time of analysis, identification of known biochemicals was based on comparison to metabolomic libraries of more than 3300 commercially available purified standard compounds. Several curation procedures were carried out to ensure high quality data and removal of those data representing system artifacts, mis-assignments, and background noise. The present dataset comprises a total of 673 compounds of known identity (metabolites). Data for each metabolite is presented relative to control samples (t = 0) and expressed as non-normalized, protein-normalized (Bradford assay), and DNA-normalized (Table 1). Due to the changing amount of water in the samples over the course of aerial incubation, and continued development in post-DII embryos, we have chosen to use the DNA-normalized data to most accurately reflect the relative amounts of metabolites per cell. Bradford protein concentration increases in a linear manner during dehydration while at the same time embryo mass decreases in a similar manner (Supplemental Fig S1; for all supplementary material see https://doi.org/10.6084/m9.figshare.12502085). We interpret this pattern as an artifact of water loss (especially in the DII embryos which are dormant) and so normalization per protein would exaggerate fold changes.

Statistical analysis

Graphical and statistical analyses were performed using Prism 8.0 software (GraphPad, La Jolla, CA, USA) or through Metabolon's user interface. Statistical significance was set to $P < 0.05$ for all comparisons. For metabolomics data analysis, missing values due to being under the limit of detection of the instruments were imputed with the minimum value on a per metabolite basis. For each metabolite, raw counts were scaled to set the median across all samples for that metabolite to 1 and the data log transformed.

198 Following normalization to Bradford protein or DNA concentration, Welch's two-sample
199 *t*-test was used to identify metabolites that differed significantly between treatments,
200 with a threshold for statistical significance set to $P < 0.05$. Additionally, an estimate of
201 the false discovery rate (q-value) was calculated to take into account the multiple
202 comparisons that normally occur in metabolomic-based studies. A low q-value ($q <$
203 0.10) is an indication of high confidence in a result. Thus, only metabolites with $P < 0.05$
204 and $q < 0.10$ are considered significant in this study. Pathway enrichment analysis was
205 performed using MetaboLync (Metabolon Inc.) with all metabolites and their pre-
206 assigned pathways as background and reference pathways, respectively. Enriched
207 pathways were calculated based on the following formula, where significance was
208 defined as $P < 0.05$:

209 $$\text{Enrichment value} = (k/m)/((n-k)/(N-m))$$

210 Where: k, total number of significant metabolites in pathway; m, total number of
211 detected metabolites in pathway; n, total number of significant metabolites; N, total
212 number of detected metabolites in the study. A pathway enrichment value greater than
213 one indicates that the pathway contains more significantly changed compounds relative
214 to the study overall. Fisher's exact test ($P < 0.05$) was used to determine if pathway
215 enrichment was significant.
216

Results and Discussion

This is the first metabolomics study to explore the profound ability of *A. limnaeus* embryos to survive prolonged aerial dehydration stress. The metabolic profiles of DII and post-DII embryos vary greatly, but due to continued development of post-DII embryos during dehydration stress, we cannot confirm if the metabolites accumulated in post-DII embryos are dehydration-specific or developmentally regulated. It is also important to note that the levels of metabolites reported in this paper are from whole embryos. The location of the metabolites, whether they be in the developing embryo, yolk, or perivitelline fluid, is not known. Recognizing the limitations of this study, we introduce new insights into survival of embryos of *A. limnaeus* to aerial dehydration stress by focusing on pathways and metabolites that change in a similar manner in both dormant (DII) and actively developing (post-DII) embryos. Below we outline metabolic pathways and metabolites of interest that may be supporting survival of *A. limnaeus* during dehydration stress induced by aerial exposure.

Metabolomics profiles overview

We measured a total of 673 metabolites of known identity (Supplemental Table S1). A summary of metabolites that achieved statistical significance ($P < 0.05$) using various methods of normalization are presented in Table 1. We provide lists of the top significantly downregulated and upregulated metabolites in response to short-term or long-term aerial incubation in DII and post-DII embryos (Supplemental Tables S2–S9). Although the method of normalization is important, it does not affect the statistical significance of the vast majority of compounds that experience large fold-changes during aerial dehydration stress (see boldface metabolites in Supplemental Tables S2–S9). Here we focus on data normalized to total DNA content to take into account the developmental changes that occur in post-DII embryos. Overall metabolite abundance was found to generally increase following aerial exposures, with the exception of short-term incubation of post-DII embryos (Table 1). These changes in metabolites, especially in DII embryos, indicate a large-scale active response to aerial dehydration stress. The

increase in some metabolites is consistent with the observed rise in oxygen consumption seen in DII embryos when exposed to aerial conditions (74).

Superpathways

Metabolites were categorized as belonging to 1 of 8 superpathways (Fig 2). Of the metabolites measured, 70% belonged to lipid (*N* = 306) and amino acid (*N* = 164) metabolism. The remaining 30% belonged to nucleotide (*N* = 70), carbohydrate (*N* = 42), cofactors and vitamins (*N* = 30), xenobiotics (*N* = 30), peptide (*N* = 20), and energy metabolism (*N* = 11). Within each superpathway, metabolites were clustered based on 81 subpathways (Fig 2).

Enriched subpathways

Diapause II.

Seven subpathways were enriched in DII embryos following short-term aerial dehydration stress and 4 were enriched during long-term exposures (Table 2). The most enriched pathways were associated with fatty acid and amino acid metabolism. Additionally, nicotinate and nicotinamide metabolism was enriched. The amino acid subpathways enriched are shared between long-term and short-term exposures.

Post-DII embryos.

In general, there was more variation in pathway enrichment in post-DII embryos compared to DII embryos (Table 2). There were 10 enriched subpathways in response to short-term (*N* = 5) and long-term (*N* = 5) aerial incubation. Most enriched pathways belonged to lipid and amino acid metabolism. There were three pathways that were consistently enriched during short and long-term exposures: phosphatidylcholine (PC), gamma-glutamyl amino acid, and monoacylglycerol metabolism.

Shared metabolites (long-term dehydration)

Due to continued development of post-DII embryos during dehydration exposure, we chose to focus on metabolites that showed shared responses (upregulation or downregulation) in DII and post-DII embryos in response to aerial dehydration stress.

Since DII embryos remained in diapause, we can more easily attribute metabolic change as primarily a direct response to dehydration stress and not an effect of active development. DII embryos have a suppressed metabolism, thus changes in metabolic profiles may not be apparent after short-term incubation. We therefore chose to focus on metabolites shared following long-term exposures.

When compared to controls, there were a total of 71 shared metabolites that significantly increased during long-term exposures (Fig 3); whereas there were only 18 metabolites that decreased (Fig 3). Of the metabolites that increased, 48 belonged to lipid (*N* = 24) and amino acid (*N* = 24) metabolism. The remainder belonged to carbohydrate (*N* = 8), nucleotide (*N* = 7), xenobiotics (*N* = 6), cofactors and vitamins (*N* = 1), and peptide metabolism (*N* = 1). Of the metabolites that decreased, a majority belonged to monoacylglycerol metabolism (*N* = 11). The remaining downregulated metabolites belonged to nucleotide (*N* = 2), cofactors and vitamins (*N* = 2), amino acid (*N* = 1), carbohydrate (*N* = 1), and xenobiotics (*N* = 1) metabolism.

Many of these metabolites are in pathways found to be enriched in response to short or long-term aerial incubation (Table 2). In addition to those enriched pathways, there are several metabolites that belong to shared pathways that will be explored further below.

Pathways of interest

Amino acids and dipeptides

Methionine, Cysteine, and Gamma-Glutamyl Amino Acids. There are indications of altered transsulfuration activity and antioxidant demand and utilization in embryos exposed to aerial dehydration stress (Fig 4). Transsulfuration is a highly conserved pathway involved in metabolizing sulfur-containing amino acids such as methionine and cysteine. Methionine, via the transsulfuration pathway, can be converted to cysteine and several other compounds that play roles in redox balance and antioxidant defense (e.g., glutathione, taurine, etc.). Notably, an increase in cystathionine is observed in both DII and post-DII embryos (Figs 3,4).

The metabolite with the largest fold-change in this study is lanthionine (Fig 3; greater than 800-fold increase in post-DII embryos). Lanthionine is formed when

309 cysteine is metabolized in lieu of homocysteine or cystathionine by the transsulfuration
310 pathway enzymes cystathionine β-synthase (CBS) and cystathionine γ-lyase (CSE) (Fig
311 4). A common product of lanthionine biosynthesis is hydrogen sulfide (H_2S), which has
312 been recognized as an important biological signaling molecule (11, 38). H_2S has been
313 shown to protect heart mitochondrial function during ischemic events and induce a state
314 of suspended animation associated with a lower metabolism and body temperature in
315 mice (4, 11). In addition, lanthionine can also be further metabolized in mammalian
316 brain tissue to form the cyclic thioether, lanthionine ketimine, which is known to be
317 associated with high affinity (58 nmol) to neuronal membranes (13) and has been
318 demonstrated to have neuroprotective, neurotrophic and anti-inflammatory activities in
319 mice during cerebral ischemia (19, 35). Embryos of *A. limnaeus* may experience
320 dehydrating conditions for months and perhaps years before water returns (44, 52) and
321 very likely depend on suppression of metabolism and induction of cellular protective
322 mechanisms for survival (74). Thus, it is possible that lanthionine accumulation may
323 support long-term survival of dehydration stress through suppression of metabolism
324 mediated by H_2S production, and through the cytoprotective actions of lanthionine
325 ketimine in cardiac and neural tissues.
326 The large observed increase in lanthionine suggests a potential role as a
327 compatible osmolyte. However, in the relatively few studies that exist, elevated
328 lanthionine (0.3–2 μmol l^{-1}) appears to have generally negative effects on fish embryo
329 physiology and development, though some of these effects were counteracted with
330 addition of glutathione (42). Lanthionine may also interfere with angiogenic signaling,
331 increasing intracellular calcium, and impairing H_2S production (42, 63). Thus, the ability
332 of *A. limnaeus* embryos to tolerate such large increases in lanthionine without apparent
333 negative effects is interesting. Although we do not know the concentrations of
334 lanthionine in embryos of *A. limnaeus*, an 800-fold change from even the picomolar
335 level would reach biologically relevant concentrations (42). The biology of lanthionine,
336 and its association with survival of long-term dehydration stress warrants further
337 investigation.
338 Both the oxidized and reduced forms of glutathione (GSSG and GSH,
339 respectively) were found to be accumulated in post-DII embryos, whereas only GSSG

340 was increased in abundance in DII embryos. Cells use glutathione to scavenge reactive
341 oxygen species (ROS) in order to reduce oxidative damage. A previous study showed a
342 significant increase in total glutathione content in *A. limnaeus* embryos during post-DII
343 development (65). However, close to 100% of the glutathione measured was in its
344 reduced form, thus the increases in GSSG observed in this study appear to be the
345 result of aerial incubation. In their natural habitat, *A. limnaeus* embryos are exposed to a
346 variety of conditions (e.g. hypoxia, high temperatures) as they endure the dehydrating
347 conditions of the dry season, which could lead to increases in ROS production. A rise in
348 GSSG is usually indicative of some form of oxidative stress. One explanation for the
349 observed rise in GSSG in DII embryos may be due to increased oxidative stress as a
350 consequence of increased oxygen availability and increased oxygen consumption
351 observed in response to aerial dehydration stress (74). Another possibility is that GSSG
352 is assisting in reducing protein synthesis during dehydration, as GSSG is a known
353 potent inhibitor of protein synthesis (12).
354 Post-DII embryos also display significant decreases in 5-oxoproline, an
355 intermediate of gamma-glutamyl amino acid metabolism, which could be reflective of
356 changes in glutathione recycling. Fourteen gamma-glutamyl metabolites decreased in
357 aerially incubated post-DII embryos and not surprisingly this pathway is enriched in
358 post-DII embryos (Table 2; Fig 5). The function of the gamma-glutamyl pathway is
359 somewhat controversial. The original theory suggested the main function was amino
360 acid transport into the cell via their conversion to gamma-glutamyl amino acids, a
361 glutathione-dependent process (39). The release of amino acids from gamma-glutamyl
362 amino acids by gamma-glutamyl cyclotransferase generates 5-oxoproline as an
363 intermediate (Fig 4). However, recent findings suggest a role for the gamma-glutamyl
364 cycle as a regulator of redox metabolism of free radicals and xenobiotics (22). A recent
365 review by Bachhawat and Yadav proposes a “glutathione cycle” to replace the
366 established gamma-glutamyl cycle (2). The discrepancies in these cycles is beyond the
367 scope of this article, but there is a clear role for both glutathione and gamma-glutamyl
368 metabolism in *A. limnaeus* embryos worth further exploration.
369

Tryptophan Metabolism. There were 2 metabolites that increased in the pathway for metabolism of tryptophan: C-glycosyltryptophan and picolinate. Of note is picolinate, which exhibited a 65-fold change in DII embryos (Fig 3; Supplemental Tables S2–5). The large increase observed in metabolically suppressed embryos suggests an important role for picolinate, a small molecule with known neuroprotective, immunological, and anti-proliferative effects (5, 17) in survival of aerial dehydration stress.

Creatine Metabolism. DII and post-DII embryos exhibited different creatine metabolite profiles (Fig 6). Creatine phosphate (PCr) serves as a diffusible high-energy phosphate reserve in vertebrate cells. The accumulation of PCr in DII embryos indicates a positive energy balance and is consistent with previous reports of high ATP/ADP ratios during diapause (48). The decline in PCr and subsequent rise in creatine in post-DII embryos suggests that ATP demand is outpacing ATP production. This may suggest that aerial exposure is a metabolic stress for post-DII embryos and not for DII embryos. In addition to its role in buffering cellular ATP levels, creatine and PCr have been shown to exhibit a number of cytoprotective effects associated with membranes including: stabilization, alteration of phase transition temperature, and reduction of leak (62). Additionally, PCr can have protective effects against ischemic injury (26, 56). Thus, the accumulation of PCr in DII embryos may offer protective effects that contribute to their much higher tolerance of aerial dehydration stress compared to post-DII embryos.

Glutamate Metabolism. Gamma-aminobutyrate (GABA) is accumulated in both DII (1.6-fold) and post-DII embryos (20-fold) during long-term exposures (Fig 3; Supplemental Table S5). GABA is known to accumulate during anoxia in embryos of *A. limnaeus* and blocking GABA production reduces anoxic survival (51, 75). When GABA is measured spectrophotometrically, it is often undetectable during normal *A. limnaeus* development (75). Thus, the amount of GABA accumulating during dehydration stress probably represents micromolar quantities, and not millimolar levels as seen during anoxia (75). GABA is known to have neuroprotective roles in organisms (21, 36), and is also important in reducing ROS production and protecting against oxidative stress in yeast

(7). Although the levels are likely lower than during anoxia, GABA may still have an important role as a neuroprotective and antioxidant agent during exposures to dehydration.

Carbohydrate

Glycolysis, Gluconeogenesis, and Pyruvate Metabolism and the Pentose Phosphate Pathways. There were 4 metabolites from these pathways that increased in both DII and post-DII embryos: Glucose-6-phosphate, pyruvate, lactate, and sedoheptulose-7-phosphate (Figs 3,7). There were also two stage-specific metabolites that accumulated: glycerate in DII, and phosphoenolpyruvate (PEP) in post-DII embryos (Fig 7; Supplemental Tables S2–4). We previously hypothesized that aerial dehydration stress would limit gas exchange with the environment in concert with the observed decrease in evaporative water loss (46) and lead to self-imposed hypoxia or anoxia. The large increase in GABA and lactate in post-DII embryos supports this hypothesis. Further, the relatively small fold-change in lactate and GABA for DII embryos is consistent with their increase in oxygen consumption in response to aerial dehydration stress (74). Thus, these metabolomics data are consistent with hypoxic metabolism in post-DII but not DII embryos during long-term dehydration stress. Interestingly, the increase in lactate resembles that of the Warburg effect, which is commonly observed in many cancer cells, where enhanced glycolysis and lactate fermentation occur even in the presence of sufficient oxygen. Relying partially on anaerobic mechanisms may offset the reliance on aerobic metabolism which can ultimately lead to increases in ROS. Additionally, lactate in appropriate amounts has been shown to help regulate gene expression through inhibition of histone deacetylase activity and post-translational modifications of histones, act in a neuroprotective role by preventing excitotoxic cell death, and promote oxidative stress resistance (3, 27, 61, 77). Thus, aerobic accumulation of lactate may help fuel a response to dehydration stress through a variety of mechanisms outside of its role in the maintenance of cytoplasmic redox balance.

The accumulation of glucose-6-phosphate and sedoheptulose-7-phosphate (S7P) is consistent with activation of the pentose phosphate pathway (PPP; Fig 7) (41). Shunting of carbon into the PPP results in the production of NADPH used to support

anabolic processes, and also critical for the regeneration of reduced glutathione (33, 41). Accumulation of S7P, but not glyceraldehyde-3-phosphate (G3P) suggests that the oxidative portion of the PPP is used to produce NADPH, but not all of the carbon is shuttled back into glycolysis and instead is allowed to accumulate as S7P. In addition, the accumulation of several ribose metabolism intermediates (Fig 3) is also consistent with increased flux through the PPP. This hypothesis provides a mechanism to support antioxidant capacity (see above discussion of glutathione) while allowing limited immediate carbon flow through glycolysis in the form of G3P, and accumulating a source of carbon (S7P) that could be readily utilized by glycolysis at a later time. These data suggest a critical role for the PPP in supporting aerial dehydration stress in *A. limnaeus* embryos.

Lipids

Fatty Acid, Dicarboxylate. Seven metabolites increased following long-term dehydration: Glutarate (C5-DC), 3-methylglutarate/2-methylglutarate, 2-hydroxyglutarate, adipate (C6-DC), 3-hydroxyadipate, maleate, and sebacate (C10-DC) (Fig 3). Of interest is the accumulation of 2-hydroxyglutarate (2-HG), a molecule known to be produced during hypoxia and a known oncometabolite (23, 37, 66) that can inhibit alpha-ketoglutarate-dependent enzymes involved in many biological processes (73). TET enzymes (DNA demethylases) and histone demethylases are inhibited by 2-HG which can lead to changes in the epigenetic landscape of cells and large-scale changes in gene expression (10, 24, 73). There are several routes for production of 2-HG, including through ‘promiscuous’ reduction of alpha-ketoglutarate by lactate dehydrogenase and malate dehydrogenase (23, 24). Further, 2-HG has been shown to inhibit ATP synthase activity and extend lifespan of *Caenorhabditis elegans* (15) suggesting this molecule could have a number of beneficial effects on *A. limnaeus* embryos during dehydration stress due to aerial incubation.

Fatty Acid, Acyl carnitine. Several acyl carnitine metabolites (*N* = 5) were upregulated: arachidoylcarnitine (C20), arachidonoylcarnitine (C20:4), docosapentaenoylcarnitine (C22:5n6), stearoylcarnitine (C18), palmitoleoylcarnitine (C16:1) (Fig 3). Acyl carnitines

play an essential role in regulating the balance of intracellular sugar and lipid metabolism (28) primarily as carriers for long-chain fatty acids into mitochondria to support β-oxidation (28, 60). Accumulation of these metabolites may suggest reduced mitochondrial fatty acid metabolism during aerial incubation.

*Phospholipid*s. The only metabolite in the phospholipid subpathway to be accumulated in both DII and post-DII embryos was cytidine 5'-diphosphocholine (Fig 3). Cytidine 5'-diphosphocholine is an intermediate product of phosphatidylcholine synthesis. The compound has been used extensively in clinical settings to treat patients with neurological disorders, including cerebral ischemia. The main protective role of cytidine 5'-diphosphocholine is through membrane stabilization (78). Further research has shown cytidine 5'-diphosphocholine protects rat livers from ischemia and reperfusion injury, thus preserving mitochondrial function and reducing oxidative stress (76). Stabilization of cell membranes and reduction of free radical generation may be beneficial to survival of *A. limnaeus* embryos during aerial dehydration stress.

Bile Acid Metabolism. Both taurolithocholate and taurochenodeoxycholate accumulate during long-term exposures (Fig 3). Taurolithocholate accumulates to higher levels in DII embryos (almost 10-fold), while taurochenodeoxycholate exhibits an over 100-fold increase in post-DII embryos. In general, bile acids are toxic due to their ability to act as detergents, but the tauro-derivatives of bile acids tend to be less toxic (55). It is interesting that DII embryos accumulate bile acids despite the absence of liver tissue. In addition to their role in digestion, bile acids can act as signaling molecules via a variety of pathways, including the regulation of a number of nuclear receptors (20). It is possible that these potentially toxic compounds are produced to activate signaling pathways that help support survival. This possibility is intriguing and warrants further investigation.

Cofactors and Vitamins

Nicotinate and Nicotinamide metabolism. Metabolites linked to *de novo* and salvage (nicotinamide, nicotinamide riboside, nicotinamide ribonucleotide, and nicotinate)

494 pathways of NAD+ synthesis were found to be significantly altered in response to aerial
495 exposure in both DII and post-DII embryos (Fig 8). One difference between DII and
496 post-DII embryos was the significant accumulation of nicotinamide adenine dinucleotide
497 (NAD+) in DII embryos (Fig 8; 17-fold increase). NAD+ is a coenzyme that plays a vital
498 role in redox reactions associated with glycolysis, the TCA cycle, and oxidative
499 phosphorylation. Increasing NAD+ levels in mammals has been linked to improved
500 mitochondrial function under stress (6, 8). Enhancing NAD+ availability in *C. elegans*
501 has been shown to increase lifespan and protect against ROS (34). Conversely,
502 reduction in NAD+ levels is an indication of senescence, as seen in various animal cell
503 lines (16, 34). There is an initial rise in quinolinate in DII embryos followed by a
504 decrease after long-term exposure. It is likely that the decrease in quinolinate
505 contributed to the increase in NAD+ via *de novo* synthesis (Fig 8). The overall rise in
506 NAD+ in DII embryos and maintained levels in post-DII embryos following long-term
507 dehydration stress suggest changes in both demand and synthesis. The accumulation
508 of NAD+ in DII suggests an available pool of NAD+ to contribute to metabolism, while
509 the static levels of NAD+ in post-DII embryos suggests supply and demand are in
510 synergy. The rise in the associated metabolites in the pathway provide a molecular
511 supply for further synthesis of NAD+ via the salvage pathway.
512
513 *Xenobiotics*
514 Xenobiotics refer to compounds not expected to be present within an organism. There
515 were several metabolites that accumulated which are traditionally thought to be
516 produced by animal microbiomes including: 3 tyrosine metabolites (phenol sulfate, 4-
517 hydroxyphenylpyruvate, and 3-methoxytyrosine) and 3 benzoate metabolites (hippurate,
518 guaiacol sulfate, p-cresol sulfate). Both DII and post-DII embryos exhibited an over 50-
519 fold increase in phenol-sulfate following long-term exposures and hippurate increased
520 over 100-fold in DII embryos (Fig 3). Of these metabolites, hippurate and p-cresol
521 sulfate are known markers for microbiome diversity (40). Hippurate, along with other
522 benzoates, has been shown to inhibit the growth of tumors in mouse cell lines (58). The
523 accumulation of these metabolites in *A. limnaeus* is interesting and may suggest a
524 maternally packaged microbiome in these embryos. While it is possible that these

compounds accumulate due to microbial growth on the surface of the embryos, this is unlikely given the use of antibiotics in the medium, the detection of these metabolites at t = 0, and the lack of other more general microbially-derived compounds that would be expected to accumulate. Interestingly, there is evidence of specific enzymes in the yolk sacs of chicken and tortoise embryos that are capable of producing metabolites that otherwise only exist in microorganisms and plants (9). For example, chicken embryos synthesize lanthionine via enzymes exclusively found in yolk sac endodermal cells. These enzymes disappear upon hatching, which may help explain the lack of lanthionine references in the literature. Alternatively, it is possible that these metabolites are produced by a yolk sac specific microbiome that aids in survival of dehydration stress. Further research needs to be done to elucidate the location, origin, and role of these metabolites in *A. limnaeus* embryos.

Conclusions and Future Directions

The goal of this metabolic profiling study was to gain insight into the biochemical pathways facilitating survival of aerial dehydration stress in *A. limnaeus* embryos. There is evidence of a robust metabolic response to aerial dehydration stress even in metabolically dormant embryos. Evidence exists for a progressive imposition of hypoxia in long-term responses to aerial dehydration stress in post-DII embryos but not during diapause. However, further studies need to be done to delineate whether the responses seen in the post-DII embryos are developmental differences or dehydration-specific responses. In general, amino acid and lipid metabolism appear to play central roles in metabolic adjustments during aerial dehydration stress, and it is clear that embryos are not solely relying on carbohydrate reserves to fuel metabolism. Increased capacity for detoxification of ROS and maintenance of redox balance appear to be of major importance to supporting development and surviving under aerial dehydration stress. It is also interesting that several accumulated metabolites have previously been identified as neuroprotectants. This work offers a first glimpse into the metabolic programs that may support survival of long-term aerial dehydration stress in embryos of *A. limnaeus* that can be functionally tested using genetic and pharmacological approaches.

Perspectives

Embryos of *A. limnaeus* likely spend many months, the preponderance of their life span, aerially incubated in the wild. During aerial exposure, there are a number of metabolites accumulated that are usually associated with waste or have the potential to be toxic (e.g., bile acids, hippurate, lanthionine). Many of these compounds contain nitrogen or other typical waste products of metabolism that are excreted in the urine and feces. When exposed to aerial conditions, embryos of annual killifish must presumably rely on detoxification or compartmentalization of waste product metabolites to ensure the developing embryo remains unharmed. One possible compartment for storage of waste products is the yolk. It is possible that metabolites are being shuttled into the yolk to protect the developing tissues, as seen with sequestration of ammonia in the yolk sac of rainbow trout (59). In amniotic eggs, the eggs of terrestrial vertebrates, waste is transported from the developing embryo into extraembryonic compartments, notably the amnionic, and the allantoic fluid (1, 32, 67). In the anamniotic eggs of fish, waste products such as ammonia or bile acids can be relatively easily lost due to diffusion into the perivitelline fluid during early development, and excretion during late development as the chorion is not a substantial barrier for diffusion of relatively small metabolites (72). However, in *A. limnaeus* the perivitelline fluid is quickly lost during aerial exposures and can no longer function as a mechanism for diffusive loss of metabolic waste products. Indeed, the embryos of annual killifish embryos exposed to aerial incubation have several unique features that approximate the functions of the shell and extraembryonic components of the amniotic eggs of terrestrial species. First, the egg envelope of annual killifish lacks pores, is substantially thicker than in most species of fish, and may serve a physical role in protection of embryos encased in dry mud (57). Second, the enveloping cell layer of annual killifish embryos does not contribute to the skin of the developing embryos as it does in most fishes, instead it forms a syncytial membrane that surrounds the embryo and is shed upon hatching (69). This membrane constitutes the major permeability barrier between the embryo and its environment and has a unique structure with few embedded proteins (25) and an extremely low permeability to water and salts (29). The enveloping layer in annual killifishes effectively creates an extra-embryonic membrane-bound compartment that surrounds and protects

587 the embryo in a manner similar to an amniotic chamber in terrestrial eggs. Thus, it is
588 possible that a number of the compounds that are typically excreted as waste may be
589 stored in either the yolk sac, or in extraembryonic fluid bound by the enveloping cell
590 layer. In fact, many of the accumulated compounds identified in this study are known
591 components of amniotic and allantoic fluid in other species (1, 32, 67) and may suggest
592 a unique extraembryonic compartment in annual killifish embryos. Further exploration
593 into the localization of these metabolites will help elucidate their possible function during
594 survival of dehydration stress due to aerial incubation.
595
596
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605 The authors declare no competing interests.
606
607

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857 **Figure Captions**

858

859 **Figure 1. Schematic of the experimental design and sampling regimen used for**
860 **metabolomics analysis.** Embryos were exposed to 85% relative humidity (RH) at the
861 developmental stage listed (DII or WS 36) for up to 28 d (*N* = 6, each replicate
862 contained 25 embryos). Developmental stage at time of sampling is included below
863 each timepoint. WS, Wourms' stage; DII, diapause II.

864

865 **Figure 2. Heat maps of fold change from t = 0 of 673 metabolites detected in**
866 **embryos.**
867 Heat maps (organized by superpathway) represent the $\log_2$ fold change of each
868 metabolite in response to short-term (S) and long-term (L) aerial dehydration stress in
869 diapause II (DII) and post-DII embryos when compared to control embryos at t = 0.
870 Metabolites are clustered by subpathways. Major subpathways are indicated on the left
871 of each heat map. Within each heatmap, fold changes are displayed for all
872 comparisons, even though fold changes may not be statistically significant for all
873 columns. For details on sampling, see Figure 1.

874

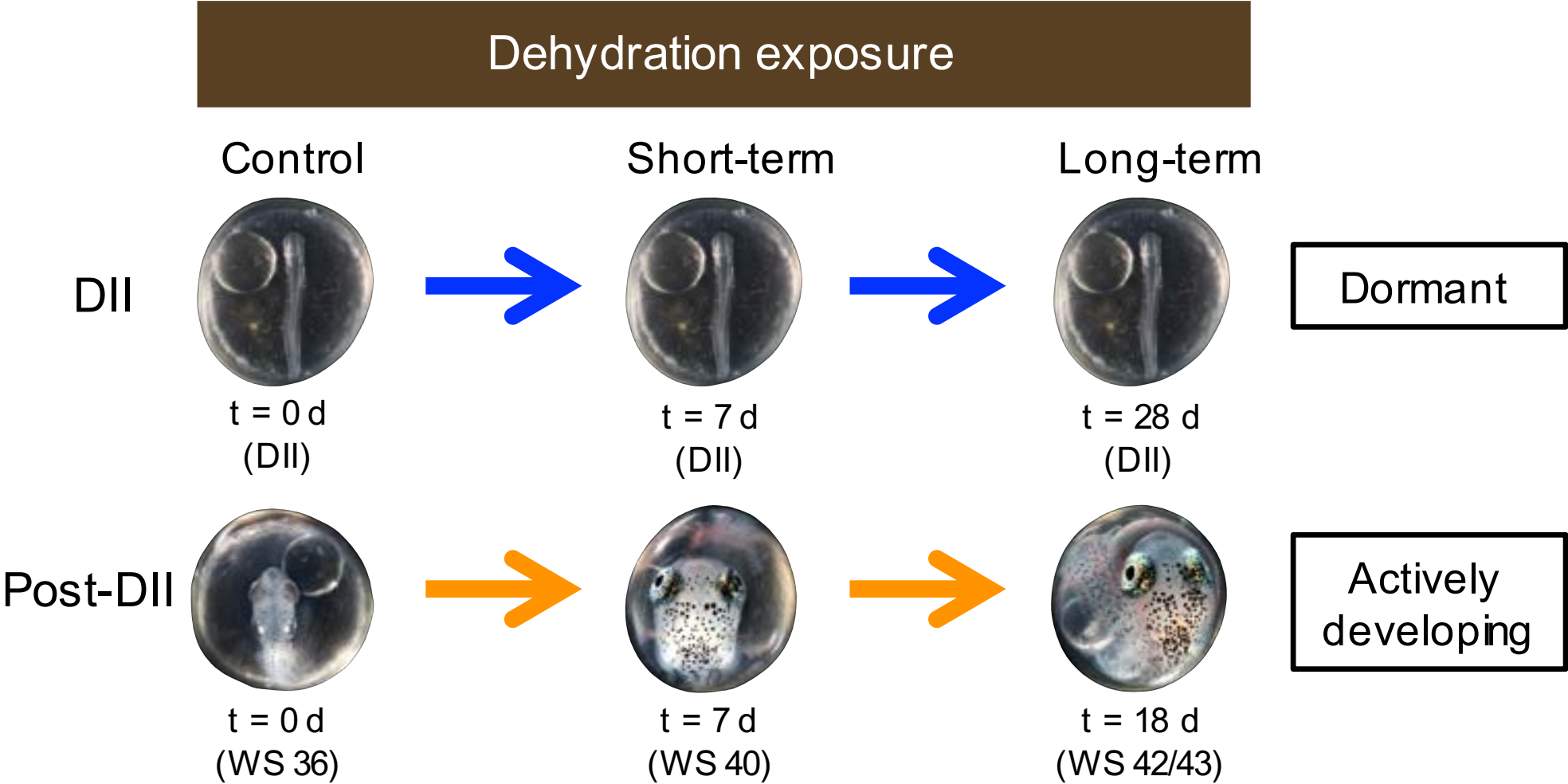
875 **Figure 3. Shared metabolites that significantly change during long-term aerial**
876 **dehydration stress in DII and post-DII embryos.** A total of 18 metabolites decreased
877 and 71 metabolites increased in both stages. Values are $\log_2$ fold changes relative to t =
878 0. The vertical dotted line separates the downregulated (left) and upregulated (right)
879 metabolites. The color of each metabolite denotes superpathway. Metabolites with
880 asterisks indicate compounds that have not been confirmed based on standards, but
881 Metabolon is confident in their identity.

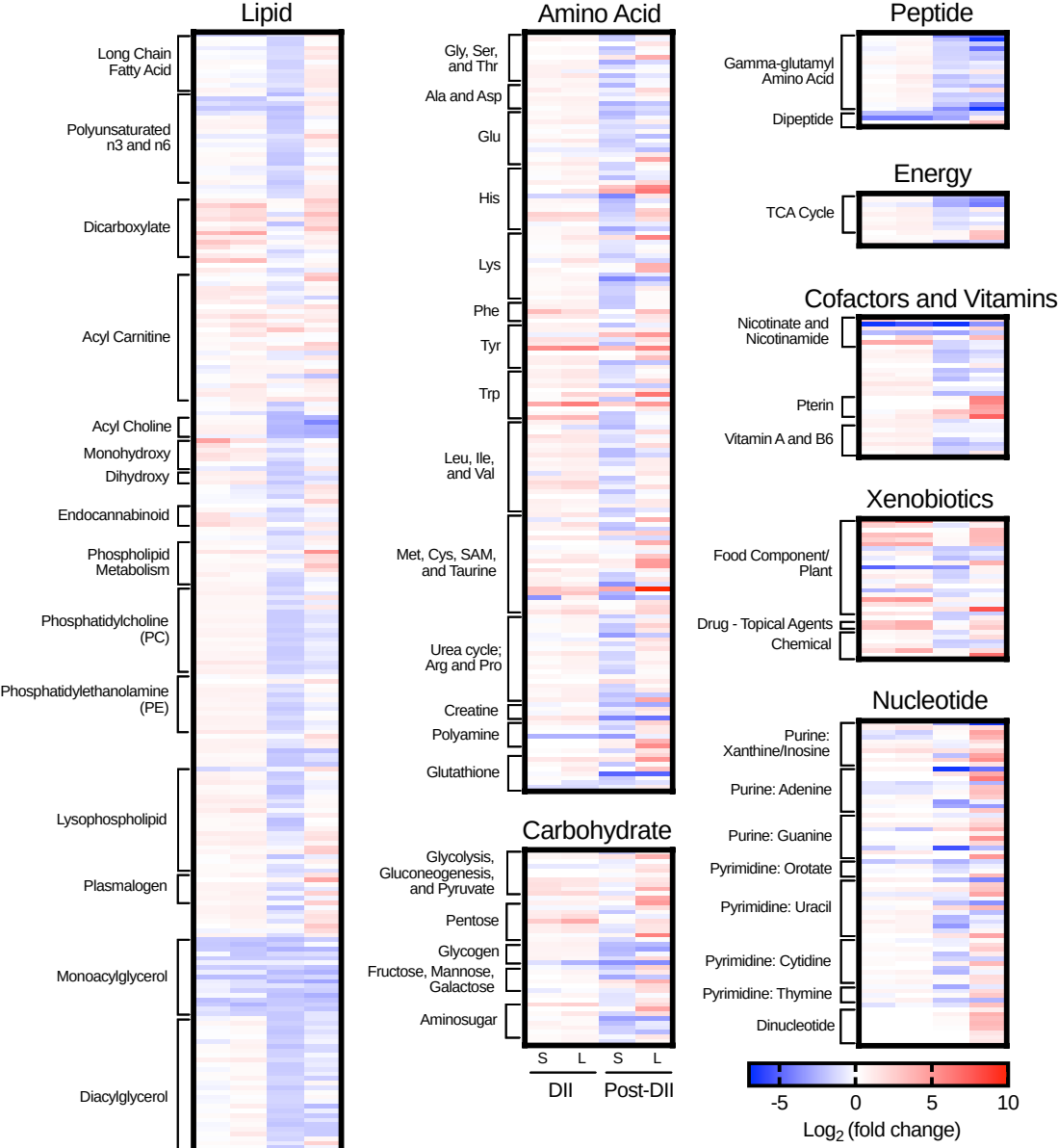
882

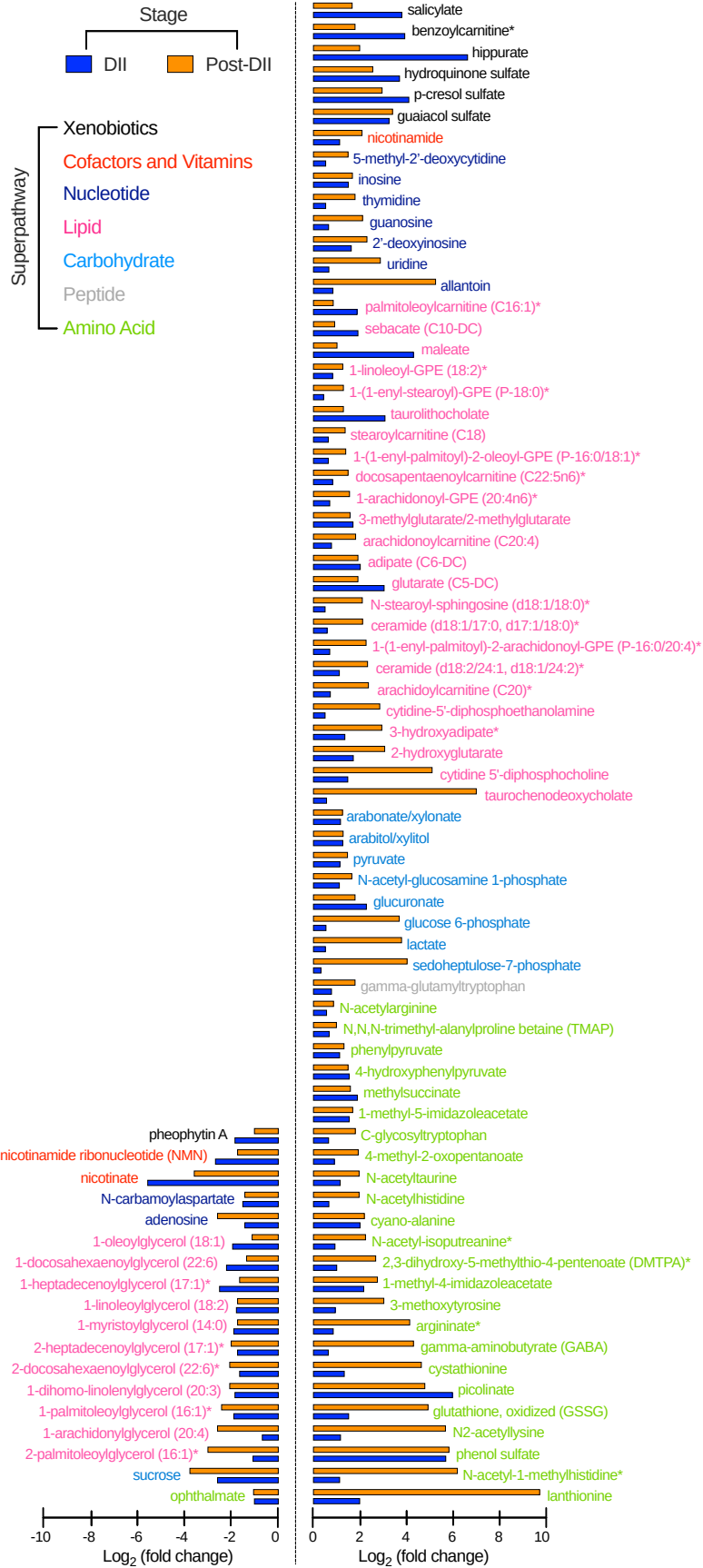
883 **Figure 4. Indications of altered transsulfuration activity and antioxidant utilization**
884 **in DII and post-DII embryos.** Box plot data illustrating metabolites contributing to
885 methionine, cysteine, and glutathione metabolism. Data (scaled intensity) are presented
886 as box plots with a line drawn at the median (mean indicated by a plus symbol) and the
887 box indicating upper and lower quartiles. Error bars are distribution minimums and

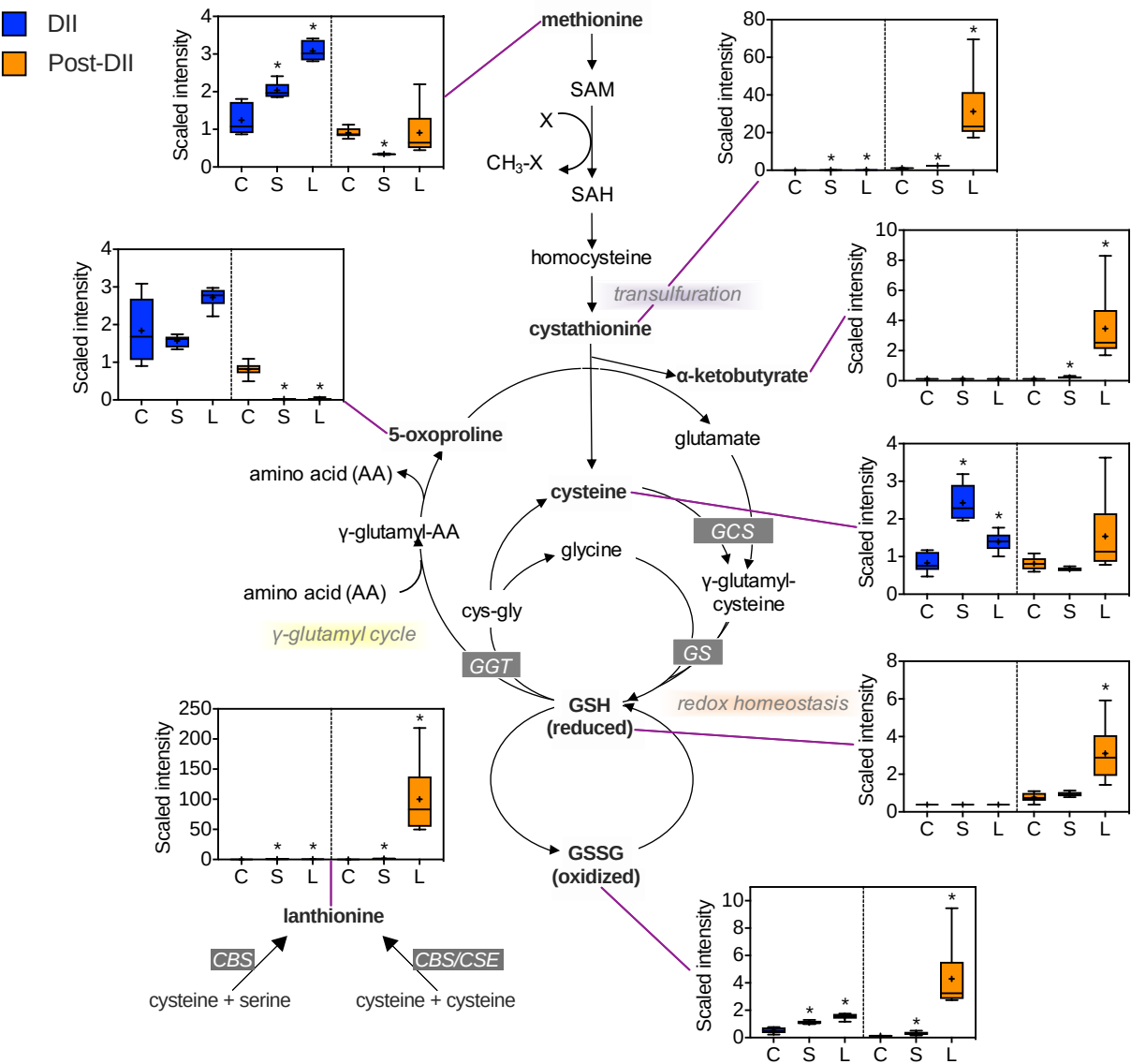
888 maximums. Vertical dotted lines separate data from DII (blue) and post-DII embryos
889 (orange). Data are organized by aerial exposure treatment (C, control; S, short-term; L,
890 long-term). Asterisks represent metabolites that were significantly different from t = 0
891 (Welch's two-sample t-test, $P < 0.05$). Raw values for each metabolite were scaled to
892 set the median across all samples to 1 and were normalized to DNA content. Relevant
893 enzymes are included (grey boxes). CBS, cystathionine β-synthase; CSE, cystathionine
894 γ-lyase; GCS, gamma-glutamylcysteine synthetase; GS, glutathione synthase; GGT,
895 gamma-glutamyl transferase.
896
897 **Figure 5. Changes in gamma-glutamyl amino acid metabolism in DII and post-DII**
898 **embryos.** Box plots illustrating metabolites involved in gamma-glutamyl amino acid
899 metabolism that were significantly altered in at least one stage. For details of box plots
900 and presentation of scaled intensity data, please see the legend of Figure 4. Asterisks
901 represent metabolites that were significantly different from t = 0 (Welch's two-sample t-
902 test, $P < 0.05$). Gamma-glutamylisoleucine (asterisk) had not been confirmed based on
903 a standard, but Metabolon is confident in the identity.
904
905 **Figure 6. Changes in creatine metabolism in DII and post-DII embryos.** Box plots
906 illustrating metabolites involved in creatine metabolism. For details of box plots and
907 presentation of scaled intensity data, please see the legend of Figure 4. Asterisks
908 represent metabolites that were significantly different from t = 0 (Welch's two-sample t-
909 test, $P < 0.05$).
910
911 **Figure 7. Changes in glycolysis and pentose phosphate pathway metabolism in**
912 **DII and post-DII embryos.** Box plots illustrating metabolites involved in glycolysis and
913 pentose phosphate pathway (PPP) metabolism. For details of box plots and
914 presentation of scaled intensity data, please see the legend of Figure 4. Asterisks
915 represent metabolitrs that were significantly different from t = 0 (Welch's two-sample t-
916 test, $P < 0.05$).
917

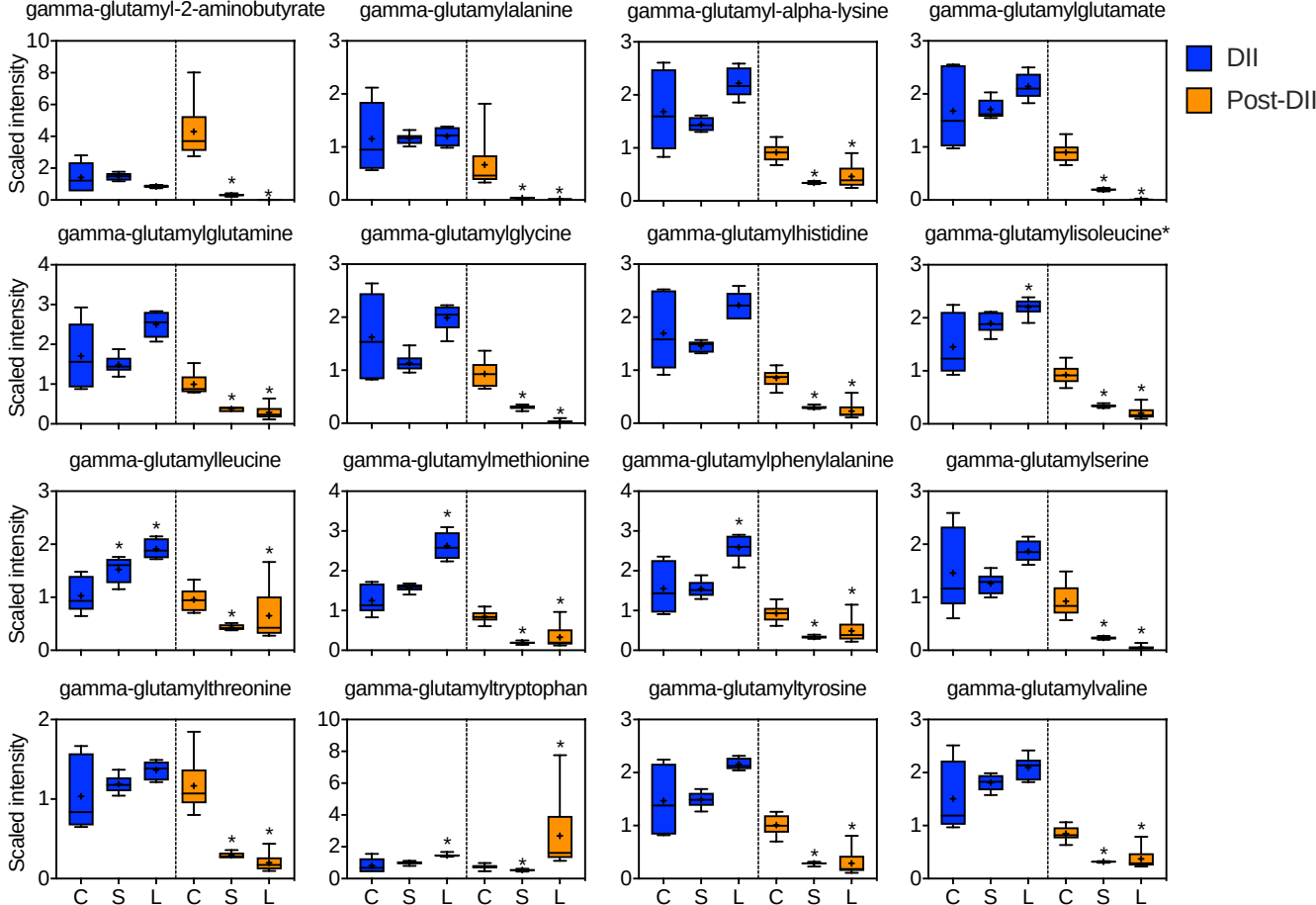
918 **Figure 8. Changes in nicotinate and nicotinamide metabolism in DII and post-DII**
919 **embryos.** Box plots illustrating metabolites contributing to nicotinate and nicotinamide
920 metabolism. For details of box plots and presentation of scaled intensity data, please
921 see the legend of Figure 4. Asterisks represent metabolites that were significantly
922 different from t = 0 (Welch's two-sample t-test, $P < 0.05$).
923

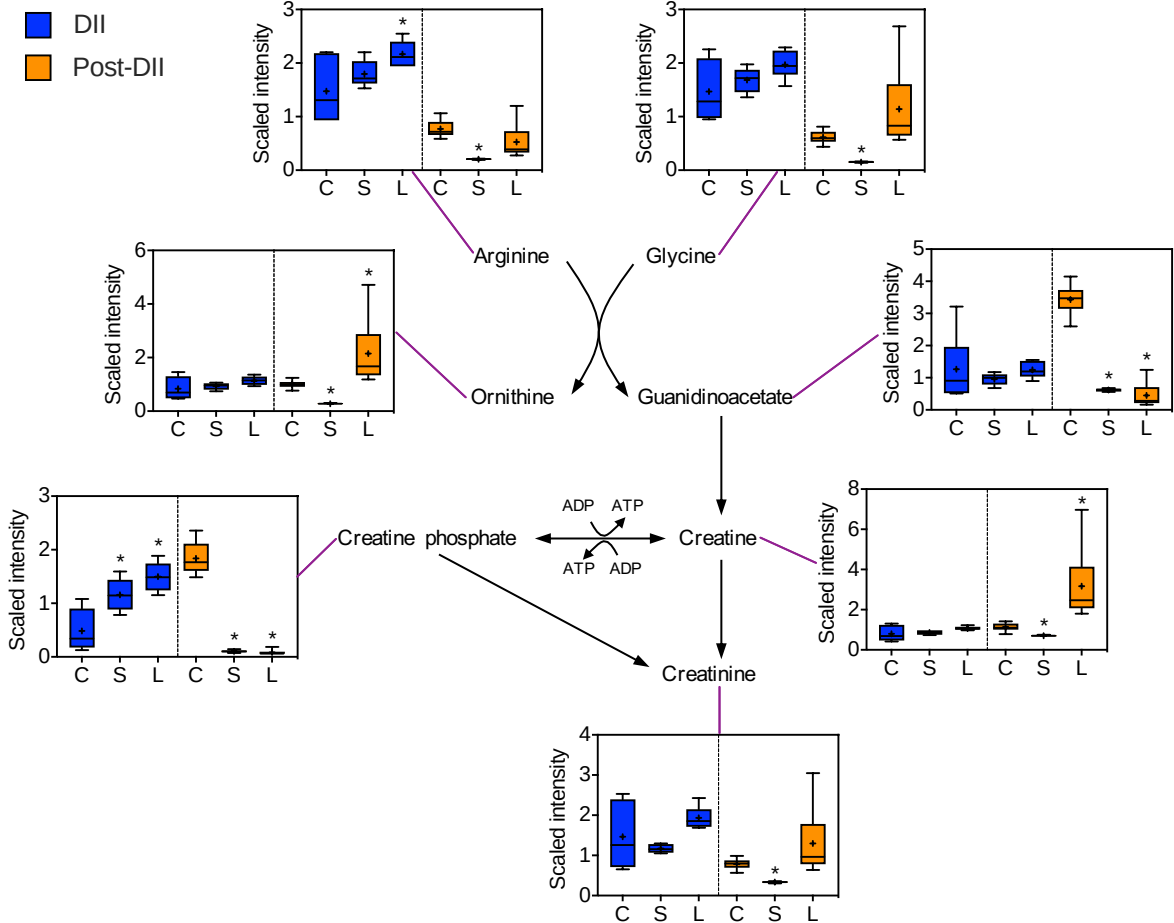

Dehydration exposure
Control
Short-term
Long-term
DII
Dormant
t = 0 d
(DII)
t = 7 d
(DII)
t = 28 d
(DII)
Post-DII
Actively developing
t = 0 d
(WS 36)
t = 7 d
(WS 40)
t = 18 d
(WS 42/43)

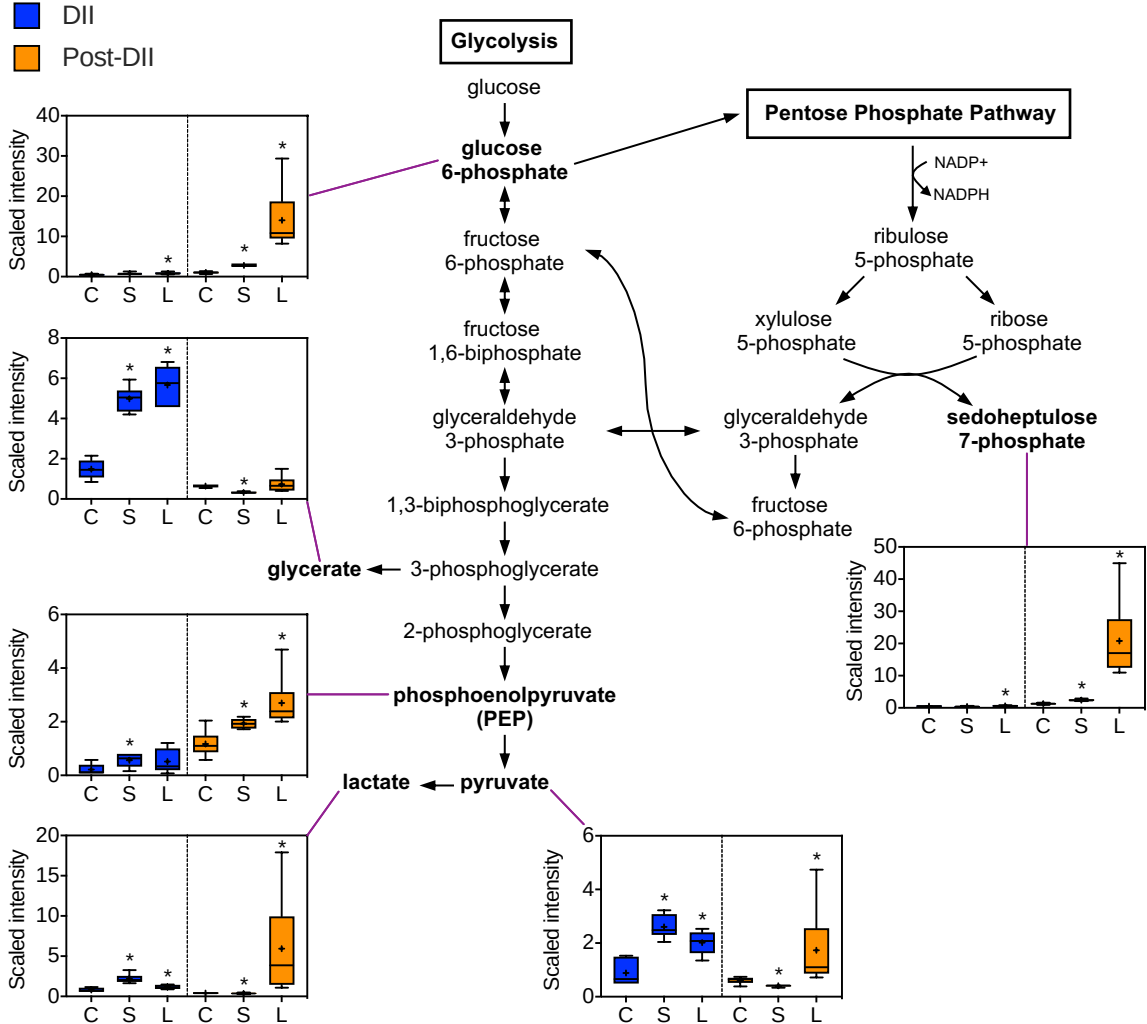

Lipid
Long Chain Fatty Acid
Polyunsaturated n3 and n6
Dicarboxylate
Acyl Carnitine
Acyl Choline
Monohydroxy
Dihydroxy
Endocannabinoid
Phospholipid Metabolism
Phosphatidylcholine (PC)
Phosphatidylethanolamine (PE)
Lysophospholipid
Plasmalogen
Monoacylglycerol
Diacylglycerol
Ceramides
Dihydrosphingomyelins
Sphingomyelins
Sterol
Bile metabolism
Amino Acid
Gly, Ser, and Thr
Ala and Asp
Glu
His
Lys
Phe
Tyr
Trp
Leu, Ile, and Val
Met, Cys, SAM, and Taurine
Urea cycle; Arg and Pro
Creatine
Polyamine
Glutathione
Carbohydrate
Glycolysis, Gluconeogenesis, and Pyruvate
Pentose
Glycogen
Fructose, Mannose, Galactose
Aminosugar
S L S L
DII Post-DII
Peptide
Gamma-glutamyl Amino Acid
Dipeptide
Energy
TCA Cycle
Cofactors and Vitamins
Nicotinate and Nicotinamide
Pterin
Vitamin A and B6
Xenobiotics
Food Component/ Plant
Drug - Topical Agents
Chemical
Nucleotide
Purine: Xanthine/Inosine
Purine: Adenine
Purine: Guanine
Pyrimidine: Orotate
Pyrimidine: Uracil
Pyrimidine: Cytidine
Pyrimidine: Thymine
Dinucleotide
-5 0 5 10
Log2 (fold change)


Stage
DII
Post-DII
Superpathway
Xenobiotics
Cofactors and Vitamins
Nucleotide
Lipid
Carbohydrate
Peptide
Amino Acid
salicylate
benzoylcarnitine*
hippurate
hydroquinone sulfate
p-cresol sulfate
guaiacol sulfate
nicotinamide
5-methyl-2'-deoxycytidine
inosine
thymidine
guanosine
2'-deoxyinosine
uridine
allantoin
palmitoleoylcarnitine (C16:1)*
sebacate (C10-DC)
maleate
1-linoleoyl-GPE (18:2)*
1-(1-enyl-stearoyl)-GPE (P-18:0)*
taurolithocholate
stearoylcarnitine (C18)
1-(1-enyl-palmitoyl)-2-oleoyl-GPE (P-16:0/18:1)*
docosapentaenoylcarnitine (C22:5n6)*
1-arachidonoyl-GPE (20:4n6)*
3-methylglutarate/2-methylglutarate
arachidonoylcarnitine (C20:4)
adipate (C6-DC)
glutarate (C5-DC)
N-stearoyl-sphingosine (d18:1/18:0)*
ceramide (d18:1/17:0, d17:1/18:0)*
1-(1-enyl-palmitoyl)-2-arachidonoyl-GPE (P-16:0/20:4)*
ceramide (d18:2/24:1, d18:1/24:2)*
arachidoylcarnitine (C20)*
cytidine-5'-diphosphoethanolamine
3-hydroxyadipate*
2-hydroxyglutarate
cytidine 5'-diphosphocholine
taurochenodeoxycholate
arabonate/xylonate
arabitol/xylitol
pyruvate
N-acetyl-glucosamine 1-phosphate
glucuronate
glucose 6-phosphate
lactate
sedoheptulose-7-phosphate
gamma-glutamyltryptophan
N-acetylarginine
N,N,N-trimethyl-alanylproline betaine (TMAP)
phenylpyruvate
4-hydroxyphenylpyruvate
methylsuccinate
1-methyl-5-imidazoleacetate
C-glycosyltryptophan
4-methyl-2-oxopentanoate
N-acetyltaurine
N-acetylhistidine
cyano-alanine
N-acetyl-isoputreanine*
2,3-dihydroxy-5-methylthio-4-pentenoate (DMTPA)*
1-methyl-4-imidazoleacetate
3-methoxytyrosine
argininate*
gamma-aminobutyrate (GABA)
cystathionine
picolinate
glutathione, oxidized (GSSG)
N2-acetyllysine
phenol sulfate
N-acetyl-1-methylhistidine*
lanthionine
pheophytin A
nicotinamide ribonucleotide (NMN)
nicotinate
N-carbamoylaspartate
adenosine
1-oleoylglycerol (18:1)
1-docosahexaenoylglycerol (22:6)
1-heptadecenoylglycerol (17:1)*
1-linoleoylglycerol (18:2)
1-myristoylglycerol (14:0)
2-heptadecenoylglycerol (17:1)*
2-docosahexaenoylglycerol (22:6)*
1-dihomo-linolenylglycerol (20:3)
1-palmitoleoylglycerol (16:1)*
1-arachidonylglycerol (20:4)
2-palmitoleoylglycerol (16:1)*
sucrose
ophthalmate
-10
-8
-6
-4
-2
0
Log2 (fold change)
0
2
4
6
8
10
Log2 (fold change)


DII
Post-DII
Scaled intensity
C S L C S L
methionine
SAM
X
CH3-X
SAH
homocysteine
transulfuration
cystathionine
α-ketobutyrate
5-oxoproline
glutamate
amino acid (AA)
γ-glutamyl-AA
amino acid (AA)
γ-glutamyl cycle
cysteine
glycine
cys-gly
GCS
γ-glutamyl-cysteine
GS
GGT
GSH (reduced)
redox homeostasis
GSSG (oxidized)
lanthionine
CBS
CBS/CSE
cysteine + serine
cysteine + cysteine


gamma-glutamyl-2-aminobutyrate
gamma-glutamylalanine
gamma-glutamyl-alpha-lysine
gamma-glutamylglutamate
gamma-glutamylglutamine
gamma-glutamylglycine
gamma-glutamylhistidine
gamma-glutamylisoleucine*
gamma-glutamylleucine
gamma-glutamylmethionine
gamma-glutamylphenylalanine
gamma-glutamylserine
gamma-glutamylthreonine
gamma-glutamyltryptophan
gamma-glutamyltyrosine
gamma-glutamylvaline
Scaled intensity
DII
Post-DII
C S L C S L


DII
Post-DII
Scaled intensity
C S L C S L
Arginine
Glycine
Ornithine
Guanidinoacetate
Creatine phosphate
ADP ATP
ATP ADP
Creatine
Creatinine


DII
Post-DII
Glycolysis
glucose
glucose 6-phosphate
fructose 6-phosphate
fructose 1,6-biphosphate
glyceraldehyde 3-phosphate
1,3-biphosphoglycerate
3-phosphoglycerate
glycerate
2-phosphoglycerate
phosphoenolpyruvate (PEP)
pyruvate
lactate
Pentose Phosphate Pathway
NADP+
NADPH
ribulose 5-phosphate
xylulose 5-phosphate
ribose 5-phosphate
glyceraldehyde 3-phosphate
sedoheptulose 7-phosphate
fructose 6-phosphate
Scaled intensity
C S L C S L

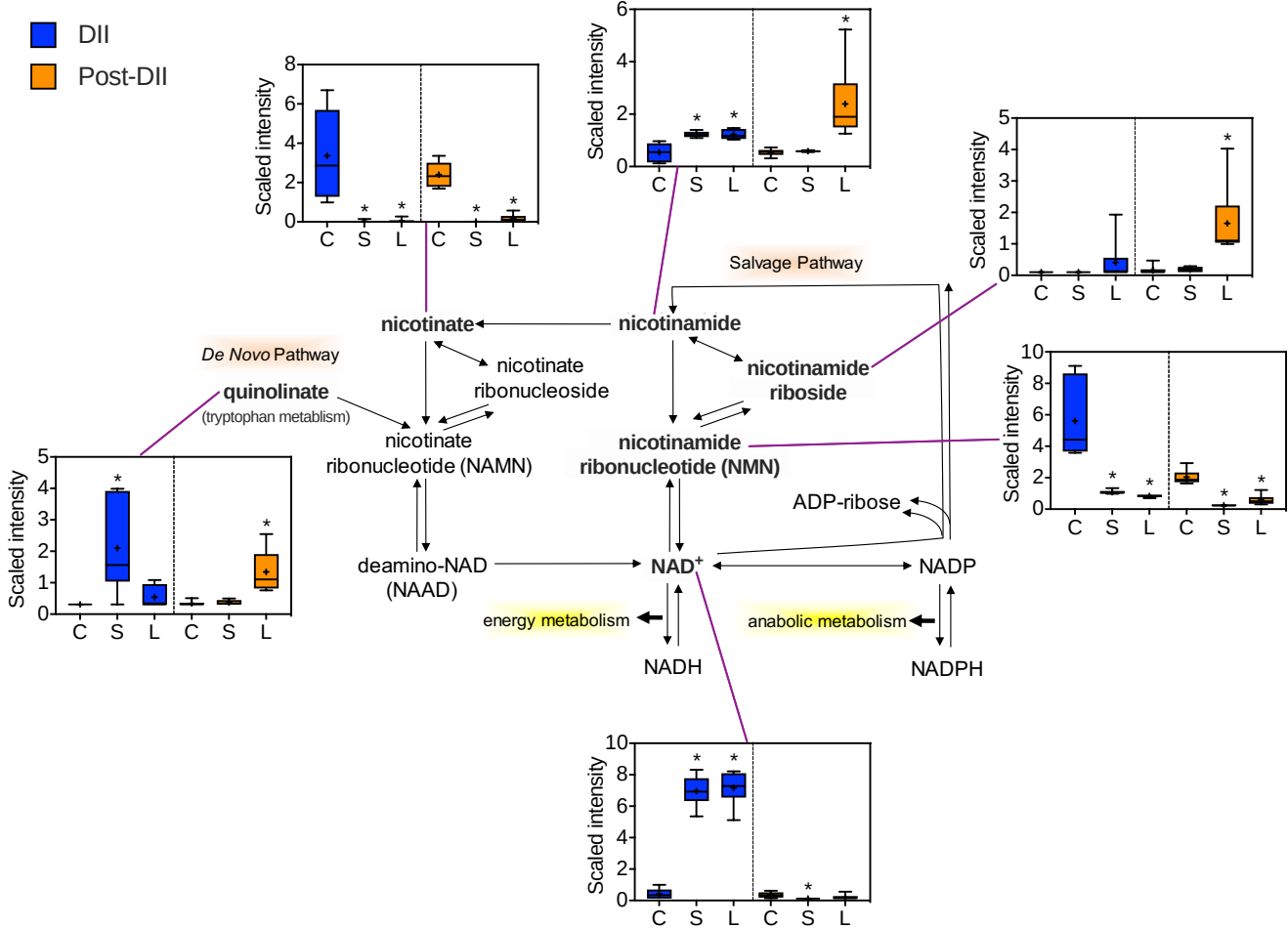

DII
Post-DII
Scaled intensity
C S L C S L
Salvage Pathway
nicotinate
nicotinamide
De Novo Pathway
nicotinate ribonucleoside
nicotinamide riboside
quinolinate
(tryptophan metablism)
nicotinate ribonucleotide (NAMN)
nicotinamide ribonucleotide (NMN)
ADP-ribose
deamino-NAD (NAAD)
NAD+
NADP
energy metabolism
anabolic metabolism
NADH
NADPH

Table 1. Total number of significant metabolites (among 673 total metabolites identified) that were significantly affected by short and long-term aerial dehydration stress in DII and post-DII embryos initially exposed at WS 36.

Stage	Comparison	Non-normalized		Protein-normalized		DNA-normalized	
		Total metabolites $P < 0.05$	Metabolites (up | down)	Total metabolites $P < 0.05$	Metabolites (up | down)	Total metabolites $P < 0.05$	Metabolites (up | down)
DII	7 d / 0 d (short-term)	243	156 | 87	238	85 | 153	204	174 | 30
	28 d / 0 d (long-term)	346	298 | 48	200	77 | 123	267	233 | 34
Post-DII	7 d / 0 d (short-term)	466	383 | 83	438	269 | 169	553	74 | 479
	18 d / 0 d (long-term)	558	430 | 128	544	354 | 190	390	212 | 178

Table 2. Metabolic pathways that were significantly enriched by short and long-term aerial dehydration stress in DII and post-DII embryos normalized to DNA concentration.

Treatment (# significant metabolites)	Subpathway	Enrichment Value	P-value	k	m
DII short-term (n = 204)	Fatty Acid, Dihydroxy	3.3	0.03	3	3
	Fatty Acid, Dicarboxylate	2.6	6.34E-04	10	13
	Fatty Acid, Monohydroxy	2.4	0.03	5	7
	Nicotinate and Nicotinamide Metabolism	2.4	0.03	5	7
	Tyrosine Metabolism	2.4	0.01	7	10
	Methionine, Cysteine, SAM and Taurine Metabolism	2.0	4.17E-03	13	22
	Leucine, Isoleucine and Valine Metabolism	1.9	0.02	11	20
DII long-term (n = 267)	Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	1.9	0.05	6	8
	Tyrosine Metabolism	1.8	0.05	7	10
	Monoacylglycerol	1.7	0.03	11	17
	Methionine, Cysteine, SAM and Taurine Metabolism	1.6	0.02	14	22
Post-DII short-term (n = 553)	Phosphatidylcholine (PC)	1.2	0.02	19	19
	Urea cycle; Arginine and Proline Metabolism	1.2	0.02	19	19
	Gamma-glutamyl Amino Acid	1.2	0.03	17	17
	Monoacylglycerol	1.2	0.03	17	17
	Diacylglycerol	1.2	7.71E-03	34	35
Post-DII long-term (n = 390)	Aminosugar Metabolism	1.7	0.01	8	8
	Purine Metabolism, Adenine containing	1.6	0.03	9	10
	Gamma-glutamyl Amino Acid	1.5	7.36E-03	15	17
	Monoacylglycerol	1.5	7.36E-03	15	17
	Phosphatidylcholine (PC)	1.5	0.01	16	19

Enrichment value was computed as follows: (k/m)/((n-k)/(N-m)), where: k, total number of significant metabolites in pathway; m, total number of detected metabolites in pathway; n, total number of significant metabolites; N, total number of detected metabolites (673). A pathway enrichment value greater than one indicates that the pathway contained more significantly changed metabolites relative to the study overall. Fisher's exact test was used to determine if pathway enrichment was significant ($P < 0.05$*).*