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Metabolism, personality and pace of life in the Trinidadian guppy, *Poecilia reticulata*

S.J. White^{1,2}, T.J. Kells¹, A.J. Wilson¹

1. Centre for Ecology and Conservation, University of Exeter (Penryn Campus),
Cornwall, TR10 9FE, UK.
2. Corresponding author, s.j.white@exeter.ac.uk

1 **Summary**

2 While among-individual variation in behaviour, or personality, is common across
3 taxa, its mechanistic underpinnings are poorly understood. The Pace of Life syndrome
4 (POLS) provides one possible explanation for maintenance of personality differences.
5 POLS predicts that metabolic differences will covary with behavioural variation, with
6 high metabolism associated with risk prone behaviour and ‘faster’ life histories (e.g.,
7 high growth, early maturation). We used a repeated measures approach, assaying
8 metabolic traits (rate and scope), behaviour and growth to test these predictions in the
9 Trinidadian guppy, *Poecilia reticulata*. We found that while individuals varied
10 significantly in their behaviour and growth rate, more risk prone individuals did not
11 grow significantly faster. Furthermore, after accounting for body size there was no
12 support for among-individual variation in metabolic traits. Thus, while personality
13 differences are clearly present in this population, they do not covary with metabolism
14 and the POLS framework is not supported.

15

16 **Introduction**

17 Among individual variation in behaviour, or personality, is widespread across taxa, yet
18 our knowledge of the mechanisms driving and maintaining this variation is limited. The
19 Pace of Life Syndrome (POLS) predicts that behaviour and life history covary with
20 physiology along a slow-fast axis (Réale et al., 2010; Ricklefs & Wikelski, 2002).
21 Individuals with higher metabolic rates are predicted to grow more quickly on average,
22 mature earlier, invest in less responsive immune machinery, have more offspring per
23 reproductive bout, and have a reduced longevity. POLS also predicts that a fast pace-
24 of life will be associated with more ‘risk prone’ behavioural types (Briffa et al., 2015)

1 typically defined by greater boldness, exploratory tendency, and/or aggressiveness
2 (Réale et al., 2010).

3 These patterns are relatively well supported by studies comparing suites of traits
4 at among-species and among-population levels. For instance, tropical bird species that
5 live longer have, on average, lower metabolic rates than temperate species (Wiersma et
6 al., 2007; Williams et al., 2010). In addition, species of wild rodent with a faster pace
7 of life rely more on innate immune responses than more expensive adaptive machinery
8 (Previtali et al., 2012), a pattern also seen among populations of house sparrows (*Passer*
9 *domesticus*) (Martin et al., 2006). Empirical studies of behavioural traits have also
10 found correlations as predicted by POLS. For instance Careau et al. (2010) found that
11 domesticated dog breeds that were more trainable and obedient lived longer than more
12 aggressive breeds that had higher metabolisable energy intakes. Bird species exhibiting
13 riskier flight behaviour have higher metabolic rates (Moller, 2009). Populations of
14 Trinidadian guppies, *Poecilia reticulata*, exposed to higher levels of predation tend to
15 exhibit fast growth, early maturation and more risk-prone behaviours (e.g., emerging
16 more rapidly from shelter in personality trials) (Bronikowski et al., 2002; Harris et al.,
17 2010; Reznick et al., 1996).

18 With behaviour, life history and physiology seemingly well integrated at the
19 among species/population level, it is intuitive to ask whether the POLS framework
20 might also explain among-individual variation within populations, including the
21 widespread presence of animal personality (Careau et al., 2008; Réale et al., 2010). If
22 different combinations of metabolic rate, growth and behaviour confer similar lifetime
23 fitness, among-individual variation in these traits may be maintained and significant
24 correlations between traits should persist (Biro & Stamps, 2010; Réale et al., 2010).
25 Individuals exhibiting more risk-prone tendencies (e.g. being bolder, more exploratory

1 or more aggressive) are likely to encounter or acquire more resources at the expense of
2 increased mortality risk from predation, whereas risk-averse individuals may acquire
3 fewer resources but experience less mortality risk. Thus, if optimal growth rate varies
4 among-individuals, perhaps because of underlying metabolic variation, risky
5 behaviours should correlate positively with growth (Mas-Muñoz et al., 2011; Stamps,
6 2007; Ward et al., 2004). This can be expanded further by considering trade-offs
7 between current and future reproductive success: if future reproduction is unlikely, then
8 it pays to employ risky behaviours to gain the resources to fuel a high growth rate. All
9 else being equal, in juveniles, rapid growth facilitates earlier reproduction, while in
10 organisms with indeterminate growth, fast adult growth typically delivers increased
11 fecundity. Conversely, future reproductive prospects may be enhanced by being risk-
12 averse, thus decreasing mortality risk (e.g. from predation), but also resulting in delayed
13 maturation and slower growth (Biro & Stamps, 2008; Wolf et al., 2007).

14 Applied within populations, the POLS framework predicts a positive
15 relationship between metabolic rate and risky personalities, although causality is
16 potentially bidirectional. For instance, if risk-prone individuals have higher food intake
17 they may develop larger food processing organs (liver, intestines etc) that have high
18 mass specific metabolic rate (Biro & Stamps, 2010; Careau & Garland, 2012; Wiersma
19 et al., 2012) (but see Russell & Chappell, 2007, who found no relationship between
20 organ mass and basal metabolic rate). Alternatively, individuals with high metabolism
21 and therefore high base energetic requirements may be compelled to take risks (e.g. by
22 needing to feed sooner after a disturbance than those with lower metabolic costs),
23 resulting in a risk-prone behavioural phenotype (Careau et al., 2008; Finstad et al.,
24 2007). Despite this uncertainty over causation, positive relationships between
25 behaviour and metabolic rate consistent with the POLS framework have been found

1 among-individuals in a range of species, including several fishes (Cutts et al., 2002;
2 Huntingford et al., 2010; McCarthy, 2001; Robertsen et al., 2013). The evidence,
3 however, is far from conclusive since Bouwhuis et al. (2014) actually found a weak
4 negative correlation between exploratory behaviour and basal metabolic rate in female
5 (but not male) great tits (*Parus major*). In the same species, Mathot et al. (2014) found
6 that the sign of the correlation between basal metabolic rate and post-disturbance time
7 to resume feeding depended on the type of disturbance. Context dependent correlations
8 between metabolic traits and risk related behaviours have been reported in juvenile sea
9 bass (*Dicentrarchus labrax*) (Killen et al., 2012, 2011), while several have reported no
10 relationship at all in salamanders (*Desmognathus brimleyorum*), root voles (*Microtus*
11 *oeconomus*) and common lizards (*Zootocai vipara*) (Gifford et al., 2014; Lantová et
12 al., 2011; Le Galliard et al., 2013).

13 A possible reason for the mixed support for the predictions of POLS is that,
14 while most studies to date have focused on basal, resting or standard metabolic rate,
15 metabolic scope may be a more important determinant of the link between individual
16 physiology and behaviour (Careau & Garland, 2012; Mathot & Dingemanse, 2015;
17 Metcalfe et al., 2015). Metabolic scope (MS) can be viewed as the energetic capacity,
18 after base metabolic demands are met, available for processes such as exhibiting
19 behaviours. If individuals vary in MS this could potentially drive and maintain among-
20 individual variation in behaviour. Importantly, relationships between resting metabolic
21 rate and MS vary across species (Careau et al., 2015, 2013; Cutts et al., 2002; Hansen
22 & Hunt Von Herbing, 2009; Speakman et al., 2003), potentially limiting the generality
23 of resting metabolic rate-based investigations of POLS (Mathot & Dingemanse, 2015).
24 In addition, assessing among-individual (co)variation requires repeated measures of all
25 traits concerned (Nakagawa & Schielzeth, 2010). While recent years have seen an

1 increase in the use of repeated measures approaches to the study of behaviour and
2 physiology, more studies taking an integrated approach with multiple measures of each
3 individual are required to fully understand POLS within populations.

4 The aim of this study is to evaluate the POLS framework in Trinidadian guppies
5 (henceforth guppies). We use a captive population of guppies and a multivariate
6 repeated measures approach to assess the (co)variance structure between metabolic rate
7 and scope, risk related personality traits and growth rate. If POLS is present in this
8 population we predict that i) individuals will differ consistently in metabolic traits
9 (metabolic rate and scope), ii) individuals will show personality differences consistent
10 with risk prone–risk averse continuum of behavioural variation and iii) metabolic and
11 behavioural traits will be correlated at the individual level, with fast paced individuals
12 (high metabolic rate, risk-prone) also showing faster growth rates than slower paced
13 conspecifics.

14

15 **Materials and methods**

16 *Study Species*

17 Guppies used in this experiment were from a captive population housed at the
18 University of Exeter’s Penryn campus fish facility. The population is descended from
19 wild individuals caught in 2008 from a high predation site in the lower Aripo River,
20 Trinidad (c. 18-20 generations ago) and has been maintained at an effective population
21 size of several thousand (with no deliberate selection or inbreeding).

22 Thirty-two adult females were sampled from the stock population and tagged using
23 visible implant elastomer tags (VIE). Sampling was haphazard but we tried to limit size
24 variation by selecting fish of similar size. The tagging process consisted of submersion
25 in an 80mg.L⁻¹ MS222 solution buffered with sodium bicarbonate for several minutes,

1 until fish stopped swimming and rested on the tank floor. Sedated fish were then tagged
2 and placed immediately into a large, well-aerated tank and monitored for 5 minutes,
3 during which all fish recovered from anaesthesia. VIE tags have been shown to have
4 no significant effect on growth or behaviour in zebrafish (*Danio rario*) and guppies
5 (Croft et al., 2004; Hohn & Petrie-Hanson, 2013) and there was no tagging related
6 mortality in this experiment.

7

8 As isolation can cause unnecessary stress, each fish was randomly allocated to one of
9 4 groups (8 individuals per group). Groups were housed in separate home tanks (15L,
10 18.5cm x 37cm x 22cm) but shared a common recirculating sump water supply,
11 maintained at 23-24⁰C and on a 12:12 light:dark cycle. The tank stack used was a well
12 aerated closed system subject to a 25% water change once per week with weekly tests
13 for ammonia, nitrite and nitrate levels. All fish were fed to satiation twice daily on
14 commercial flake food and live brine shrimp (*Artemia salina*) nauplii. Female guppies
15 are indeterminate growers, continuing to exhibit significant growth well after maturity,
16 making them ideal to test the predictions of POLS. Males were excluded from this study
17 as growth rate is much lower post maturity.

18

19 The experiment was conducted under the auspices of the Animals (Scientific
20 Procedures Act) under licence from the Home Office (UK) and with local ethical
21 approval from the University of Exeter. All periods of handling and emersion were kept
22 as short as possible. At the end of the experiment, fish were moved to a “retirement”
23 stock tank (containing males and other females) and allowed to reproduce to contribute
24 to the stock population. These fish were not subject to any further licensed procedures.

25

1 *Experimental design*

2 We used a repeated measures approach to test for among-individual (co)variation in
3 metabolic rate, personality and growth. Metabolic rate was assessed from intermittent
4 flow respirometry while personality was assessed using two behavioural testing
5 paradigms (open field trials, OFT and emergence trials, ET). Individuals from all
6 groups experienced a sequence of phenotypic assays comprising: day 1 - OFT, day 2 –
7 routine metabolic rate (RMR), day 4 - ET and day 5 - active metabolic rate (AMR). We
8 repeated this week one sequence for a second week. Fish were then subject to two
9 additional OFT and ET each. These were conducted in weeks 7 and 9 for groups 1 and
10 2 (with one trial per type per week per fish). However, due to space and equipment
11 constraints, we conducted these additional trials in weeks 4 and 6 for groups 3 and 4.
12 This difference is controlled for statistically in the analysis. *Standard length* (measured
13 from tip of snout to end of caudal peduncle, in mm) and mass were measured at every
14 behavioural and metabolic trial and 1 month after the
15 final behavioural trial experienced by each fish to allow calculation of growth rate.
16 Emersion time to conduct these measures (which were not conducted under anaesthetic)
17 was typically less than 10 seconds and fish were fully recovered several minutes after
18 being returned to the tank.

19

20 In total, each fish had 4 metabolic measures, 4 OFT, 4 ET and 13 size measures with
21 total data collection spanning 13 (groups 1 and 2) or 10 (groups 3 and 4) weeks. At
22 each sampling, the order (i.e. 1-8) in which each fish was haphazardly captured from
23 its group tank was also recorded.

24 Our experimental design should have led to 128 metabolic trials (64 *RMR*, 64
25 *AMR*) and 256 behavioural trials (128 OFT, 128 ET). However, we experienced some

1 mortality late in the data collection period and incomplete data were thus obtained for
2 9 individuals (with 120 metabolic and 215 behavioural trials completed). Based on the
3 absence of adverse effects attributable to the protocols a general water quality problem
4 in the facility was the suspected cause, although age may also be a factor (fish were
5 sampled from a stock tank containing larger and, since female guppies exhibit
6 indeterminate growth, putatively older than average fish). In the following analyses we
7 used all available data, however, including individuals with incomplete data collection
8 since the mixed model analyses used are robust to unbalanced data sets. We also
9 account for cumulative trial number and group size in all statistical models (see
10 statistical methods below) to avoid any potential for bias.

11

12 *Metabolic measures*

13 An automated intermittent flow respirometer from Qubit biological systems
14 (<http://qubitsystems.com>) was used to measure metabolic rate. The respiration chamber
15 (1.6cm x 4.5cm, 9ml) was submerged in a 2.5L water bath with water temperature
16 maintained at 24°C (23.9 – 24.1) using a submersible heater (Visi-therm 25W,
17 www.aquariumsolutions.eu) and a UV steriliser to minimise bacterial growth. *RMR* is
18 here defined as the metabolic rate of a post-absorptive non-reproductive fish at rest
19 while including random movement required to maintain position in the water column
20 (Killen et al., 2011). Guppies, even at rest, still exhibit some tail and fin movement to
21 maintain position in the water; we were unable to account for this movement and
22 therefore we define our measures as *RMR* rather than standard metabolic rate (*SMR*).
23 One could argue that such random movements are a necessary part of the metabolic
24 expenditure when an aquatic organism is at rest and should not be removed at all.

1 To measure *RMR*, the focal fish was placed in the respiration chamber
2 following 24 hours of fasting. Oxygen consumption was then measured over four 10
3 minute ‘closed’ periods (i.e. chamber and pump closed off from the water bath)
4 separated by 4 minute ‘flush’ periods. *Standard length* and *mass* were measured
5 immediately after every metabolic trial to be used to calculate mass-specific metabolic
6 traits (see below). *RMR* was estimated as the average of the last three oxygen
7 consumption rates (each determined as the slope over the most stable part of the
8 corresponding 10 minute period in $\text{mg O}_2 \text{ L}^{-1} \text{ s}^{-1}$). The first metabolic rate measure of
9 each trial was excluded as pilot trials suggested it was significantly higher, likely
10 reflecting a response to the physical stressor of being moved into the respirometer. *AMR*
11 was measured similarly, but immediately following 2 minutes of being chased by a
12 hand net. The aim of the net chasing was to provoke a ‘burst and glide’ swimming
13 technique that has been found to be aerobically demanding (Cutts et al., 2002; Norin
14 and Malte, 2011). Due to ethical considerations we did not measure true maximal
15 metabolic rate (*MMR*) as this requires exercising the fish to complete exhaustion,
16 which in guppies may have resulted in mortality. *AMR* was estimated as the rate of
17 oxygen consumption from the first 2 minutes of being in the respiration following the
18 chasing. See supplementary methods for further details on respirometer use and setup.

19

20 *Behavioural trials*

21 Open Field Trial

22 Our OFT followed a protocol very similar to that described by Boulton et al. (2014).
23 The focal fish was placed into an empty tank (30cm x 20cm x 20cm) with 5cm water
24 depth, and lit from below using a light box. A video camera fixed above the tank
25 allowed the movement of the fish to be tracked using Viewer software

1 (www.biobserve.com), removing observer bias and minimising measurement error.
2 Placing a cardboard screen around the tank during the trials prevented disturbance by
3 researcher activity. Following 30 seconds of acclimation, a 4 min 30 sec tracking period
4 was used to determine total *tracklength* swum (cm), *activity* (percent time swimming
5 above 4cm s⁻¹) and percent of tank *area covered*. We also recorded the amount of time
6 spent in an outer ‘safe’ zone near to the side of the tank and an inner ‘risky’ zone
7 (Henceforth, *Time in middle*), the zones being defined as equal in size following
8 Boulton et al. (2014). These behaviours have been shown to predict risky or ‘bold’
9 personality effectively in other poeciliid fishes (Boulton et al., 2014; Burns, 2008), with
10 bolder individuals expected to have a longer track length, be more active, cover more
11 tank area, and spend more time in the ‘risky’ middle tank zone. The water in the OFT
12 tank was changed between each group of fish. We controlled for any effects of order of
13 testing (within group) that might arise due to, for instance, release of hormones or other
14 chemicals into the tank by including *order caught* as a fixed effect in models for all
15 traits in our statistical analysis (see below).

16

17 Emergence trial

18 The focal fish was placed in a shelter area within a larger tank (40cm x 20cm x 20 cm)
19 filled to 8cm depth and screened as described above with a video camera placed
20 overhead. It was allowed to acclimate for 30 seconds before a sliding door in the shelter
21 wall was opened, allowing access to the rest of the tank. Time to emergence (henceforth
22 *emergence time*) was then recorded and trials were ended at emergence or at 15 minutes
23 if the fish had not emerged by this time (6 out of 106 trials).

24

25 *Statistical methods*

1 We used a series of univariate and multivariate linear mixed effect models to test
2 among-individual (co)variation in metabolic traits, personality and growth as predicted
3 by POLS. Random regression methods were used to characterise variation in *MS* and
4 growth as described fully below. We applied a log transformation to metabolic rate data
5 to help control for size effects (since the relationship between metabolic rate and *weight*
6 appeared linear on a log-log scale) and to *emergence time* to reduce slight positive
7 skew. We also mean-centred all (transformed) traits and scaled them to standard
8 deviation units. This was to facilitate multivariate model convergence and prevent
9 different trait scales from driving conclusions. Linear mixed effects models were then
10 fitted with restricted maximum likelihood (REML) using ASReml 4.0
11 (www.vsni.com). Conditional F statistics were used to determine significance of all
12 fixed effects while inference on random effects used likelihood ratio tests (LRT). Twice
13 the difference in log-likelihood between full and reduced models was assumed to be
14 distributed as χ^2 with degrees of freedom (df) equal to the number of additional
15 parameters in the full model. For testing a single variance component only, we assumed
16 a 50:50 mix of χ^2_0 and χ^2_1 (subsequently denoted $\chi^2_{0,1}$) following the recommendations
17 of Visscher (2006).

18

19 Metabolic traits

20 Univariate models containing individual as a random effect were fitted to the metabolic
21 rate data. Repeatability (conditional on fixed effects) was then calculated as the
22 intraclass correlation, $R = V_I / (V_I + V_R)$, where V_I is the among-individual variance and
23 V_R is the residual variance (Nakagawa & Schielzeth, 2010). We included fixed effects
24 of *group*, *trial* number (the cumulative number of trials of any type previously
25 experienced), *order caught* (1-8 within each group) and measure type (*RMR* or *AMR*).

1 The *group* effect controls for differences in physical and social environments among
2 tanks. *Order caught* refers to the order in which each fish in a group was assayed on a
3 trial day and is intended to account for any cumulative disturbance effect of removing
4 fish sequentially from the home tank. The *measure type* fixed effect accounts for any
5 differences between mean *RMR* and mean *AMR* measures, allowing all 4 measures per
6 individual to be included in the calculation of repeatability.

7 This model tests for among-individual variance in metabolic rate (across routine
8 and active contexts) as well as for the expected increase in average oxygen consumption
9 with activity. We then characterised variation in *MS* by adding a random interaction of
10 *fish identity* with measure type to the above model. Measure type was treated as a
11 continuous variable indicative of activity level and arbitrarily scaled (such that at *RMR*
12 activity = -0.5, and at *AMR* activity = 0.5). Note that conventionally *MS* is measured as
13 the difference between standard (*SMR*) and maximal metabolic rates (*MMR*), neither
14 of which were formally assayed in our experiment. However, *MS* can equally be
15 represented as the slope of an individual's reaction norm between two activity states on
16 an arbitrarily scaled axis (i.e., 'standard' and 'maximal'; Figure 1). Since a slope is
17 defined by any two points on the reaction norm, we are able to characterise rank order
18 variation in *MS* using assays of metabolic rate at intermediate 'routine' and 'active'
19 levels instead (Figure 1). Although complete correspondence is strictly contingent upon
20 a linear reaction norm through all four activity states (Figure 1), in practice the *RMR*-
21 *AMR* reaction norm slope will be strongly correlated to, and thus a suitable proxy for,
22 *MS* as standardly defined over a much wider range of scenarios. The reaction norm
23 framework, using random regression, allows the value of a random effect to vary with
24 an additional covariate. This technique has been used extensively to model among-
25 individual variation in morphological and life history traits as well as genotype-by-

1 environment interactions (Dingemanse et al., 2010; Nussey et al., 2007; Roff & Wilson,
2 2014). Both models were first fitted using log metabolic rate data uncorrected for mass.
3 We then refitted with log body mass as an additional fixed covariate such that V_1 is
4 interpretable as variance in mass-specific metabolic rate while (in the reaction norm
5 formulation) among-individual variance in slope (V_S) is interpretable as variance in
6 mass-specific MS.

7

8 Fig. 1 here

9

10 Behavioural traits

11 Behavioural traits were similarly modelled with a random effect of individual and fixed
12 effects of *temperature*, *group*, *order caught*, *trial number* and *weight*. Interestingly pilot
13 analysis indicated that the *order caught* was itself repeatable, and so this was modelled
14 as an additional behaviour potentially indicative of risk-taking (note *order caught* was
15 necessarily not fitted as a fixed effect in this case). Following Boulton et al. (2014), we
16 then fitted a multivariate mixed model with all 6 behavioural traits (i.e., *tracklength*,
17 *activity*, *area covered*, *time in middle* from OFT; *emergence time* from ET; and, *order*
18 *caught* from both OFT and ET). This allowed us to test the prediction that all OFT
19 behaviours would be positively correlated with each other at the individual level and
20 negatively correlated with *emergence time* and *order caught*, consistent with an
21 underlying axis of shyness-boldness. The resulting variance/covariance matrix was
22 subject to eigenvector decomposition, allowing us to identify the major axes of
23 variation and see how the behavioural traits load on to these axes. Eigenvector
24 decomposition is analogous to principle component analysis, but used here to describe

1 only the among-individual component of phenotypic (co)variance, after partitioning the
2 component (Wilson et. al., 2011; Boulton et. al., 2014).

3

4 Growth

5 Among-individual variation in growth was also characterised using random regression
6 mixed models of *standard length* that included random effects of *fish identity* and a fish
7 by *time since start of experiment interaction* (zero centred from an actual mean across
8 all size measurements of 25 days). Fixed effects included were *group*, *last day seen* (to
9 account for mortality effects on average growth) and *time since start of experiment*
10 (days) as a linear covariate to account for average growth. We chose a simple linear
11 function because actual age of fish was unknown (though all females were mature) and
12 growth was observed over a short period only. In this model V_I is interpretable as the
13 among-fish variation in *standard length* at the intercept (i.e. 25 days from the start of
14 the experiment) while the variance in individual regression slopes (V_S) is among-fish
15 variance in growth rate. Finally, *standard length* was added to the above multivariate
16 model to assess the among-individual (co)variance structure of size and growth with
17 behaviour.

18

19 **Results**

20 While whole animal metabolic rate shows significant among-individual variation
21 ($R=0.27$ (0.11), $\chi^2_{0,1}=8.031$, $P=0.002$), inclusion of *log weight* as a fixed effect results
22 in the estimate of V_I being bound to zero to stay in allowable parameter space. We thus
23 estimate a repeatability of zero for mass-specific metabolic rate (across the two activity
24 levels). Furthermore, comparison of the random regression model to this simple
25 formulation provide no evidence that individuals vary significantly in either whole

1 animal MS ($\chi^2_2 = 0.277$, $P=0.871$) or mass-specific MS ($\chi^2_2 = 0.702$, $P=0.704$; note 2DF
2 for the model comparisons as the random regression formulation includes intercept-
3 slope covariance as well as the two variance terms). A significant positive effect of
4 measure type (*AMR* relative to *RMR*) was found confirming the expectation that *AMR*
5 should be significantly higher on average (coefficient = 0.758 (0.062), $F_{1,106}=150.66$,
6 $P<0.001$). Other fixed effect results are not directly relevant to current hypotheses but
7 can be found in supplemental table 1 for completeness.

8 Thus we conclude that while whole animal metabolic rate varies significantly
9 among-individuals, this can be explained by body size alone, and there is no evidence
10 of among-individual variation in mass-specific metabolic rate (reaction norm height)
11 or slope (reaction norm slope; figure 2a). This study applies the POLS framework at
12 the among-individual level, and among-individual variance in metabolic traits is a
13 prerequisite for among-individual covariance between metabolism and other traits.
14 Consequently, metabolic traits are not included in subsequent multivariate models (We
15 note of course that while within-individual covariance between metabolism and
16 behaviour is still expected our data are not informative for this as metabolic rate and
17 behaviour were not measured simultaneously).

18 In contrast to metabolic traits, univariate models show moderately high
19 repeatabilities (SE in parentheses) for behavioural traits, ranging from 0.31 (0.12) for
20 *tracklength* to 0.46 (0.11) for *area covered*, and statistically significant in all cases
21 (Table 2). Of the OFT traits, only *tracklength* and *area covered* changed significantly
22 over the trials with both increasing with increasing trial number (see supplemental table
23 1). Our univariate model of *standard length* confirm that fish vary significantly in size,
24 as was obvious *a priori* (comparison of models with and without random *fish identity*
25 effect; $\chi^2_{0,1}=387$, $P<0.001$), but also growth rate (comparison of the random regression

1 formulation including *fish identity* by *time* to a model with just *fish identity*; $\chi^2_2=18.5$,
2 $P<0.001$). Thus, while there is a modestly positive average rate of growth (of 0.013
3 (0.003) sdu day⁻¹ (or 0.265 mm day⁻¹)) there is also significant variation around this
4 (Figure 2b).

5

6 Fig. 2 here

7

8 Table 1 here

9

10 Multivariate models of the behavioural traits confirm significant covariance structure
11 between behaviours at the among-individual level (comparison of full model to a
12 reduced multivariate model in which all among-individual covariance terms are fixed
13 to zero; $\chi^2_{15}=34.5$, $P=0.003$). Post hoc testing of pairwise covariances with a series of
14 bivariate mixed models (see supplemental table 2) suggests significant among-
15 individual covariance structure is largely driven by a strong positive relationship
16 between *tracklength* and *activity*, and strong negative relationships between these two
17 traits and *time in middle* (Table 1). We note that not all pairwise correlations among
18 behavioural traits are as expected *a priori* (Table 1; see discussion for full
19 interpretation). Eigenvector decomposition of the variance-covariance matrix (see
20 supplemental table 3) does not clearly support our *a priori* expectation that among-
21 individual (co)variance in behavioural traits would be consistent with a single
22 underlying personality trait. Finally, extending the multivariate model to include
23 *standard length* as an additional response variable shows that, while some moderate
24 among-individual correlations between behaviours and size were estimated, only the

1 correlation between *area covered* and growth is significant ($\chi^2_{2} = 6.05$, $P = 0.048$)
2 (tested using bivariate models; Supplemental table 4).

3

4 Table 2 here

5

6 **Discussion**

7 Using a repeated measures design we tested the prediction of POLS that among-
8 individual differences in metabolic traits (rate and scope) covary with behaviour and
9 growth variation, with the additional prediction that it is among-individual variation in
10 MS that drives behaviour variation. All observed behaviours tested were repeatable,
11 consistent with the presence of underlying personality variation, and growth rate also
12 varied significantly among-fish over the experimental period. However, after
13 accounting for the expected increase of oxygen consumption with body size, we found
14 no support for repeatable variation in mass specific metabolic rate or MS. Furthermore,
15 there was little evidence of the predicted among-individual correlation between risky
16 behaviour and growth rate. Thus our data are not consistent with our assertion that
17 metabolic processes drive personality variation and we also conclude that the POLS is
18 not supported in this population.

19 The lack of among-individual repeatability in metabolic traits in this study
20 contrasts notably with other work on wild caught fish species held under laboratory
21 conditions. For instance, mass-specific SMR has generally been reported to have
22 moderate to high repeatabilities (e.g., R ranging from 0.50-0.74) in most fish species
23 tested under highly controlled conditions (Boldsen et al., 2013; Maciak & Konarzewski,
24 2010; McCarthy, 2000; Seppänen et al., 2010; Svendsen et al., 2014). Mass-specific
25 RMR is sometimes expected to exhibit greater variation within individuals than SMR

1 (due to uncontrolled activity during measurement of the latter), but nonetheless is often
2 characterised by more moderate ($R= 0.3-0.6$) repeatability (Killen et al., 2014, 2011;
3 Marras et al., 2010). Furthermore, variable, but significant, repeatability estimates have
4 also been reported for mass-specific MMR (e.g., R from 0.27-0.76; (Marras et al., 2010;
5 McCarthy, 2000; Norin & Malte, 2011; Norin et al., 2015; Svendsen et al., 2014) and
6 MS (e.g., R from 0.39-0.43 (Norin & Malte, 2011; Norin et al., 2015).

7 We note of course that measurement error could be a non-trivial source of
8 within fish variation, and inadequate precision of respirometers can cause low
9 repeatability of metabolic traits (Careau et al., 2008; Nespolo & Franco, 2007).
10 Nonetheless, we feel this is unlikely to explain the complete absence of detectable V_I
11 here. Firstly, within each RMR sampling assay, we averaged the three oxygen
12 consumption slopes estimated over the 50 minute period to reduce error as described
13 above. However, scrutiny of these measures shows significant repeatability among
14 slopes within-assay, even without being able to control for changing level of fish
15 activity ($R=0.56$, $\chi^2_1=52.47$, $P<0.001$) indicating stable performance of the
16 instrumentation at least over the short term. Secondly, our repeated measures sampling
17 was designed to detect repeatabilities as low as 20% (i.e below published estimates)
18 with high (>75%) power (following Wilson et al. (2011)). Thirdly, we note that the
19 experiment did in fact successfully detect among-individual variation in whole
20 organism metabolic rate ($R=0.27$), but that our results show this can be totally explained
21 by differences in individual weight.

22 Previous studies have shown the potential role of early life conditions, including
23 the maternal nutritional environment, in generating variation in, and correlations
24 between putative components of POLS. For instance food restriction during juvenile
25 stages can increase the repeatability of metabolic rate later in life, with individuals

1 varying in response to nutritional stress experienced as juveniles (Careau et al., 2014a,
2 2014b; O'Connor et al., 2000). The environment experienced by parents, particularly
3 the mother, can also lead to variation between individuals in a range of traits, including
4 adult metabolic rate (Burton et al., 2011; Régnier et al., 2010; Tobler et al., 2007; Van
5 Leeuwen et al., 2015). In our study, the laboratory conditions experienced by fish
6 during these important developmental windows were likely relatively homogeneous by
7 comparison to field environments. This could have resulted in a reduction of among-
8 individual variance in metabolic rate and scope, relative to wild caught fish used in
9 other studies that have experienced greater patchiness of resources (Grether et al., 2001;
10 Magurran, 2005).

11 Since we found no support for among-individual variation in metabolic traits,
12 our data do not support the hypothesis that metabolism is an important determinant of
13 individual differences in behaviour. Nonetheless, such differences are clearly present
14 among the guppies tested, with significant repeatability found for *emergence time* and
15 all OFT traits. In general, repeatabilities were of similar magnitude to those reported in
16 the literature for behaviours generally, and in poeciliid fishes specifically (Bell et al.,
17 2009; Boulton et al., 2014; Cote et al., 2011). We also found that, within each housing
18 group, the order in which fish were caught was repeatable. The tendency for some
19 individuals to be trapped or caught more easily than others has been used as a measure
20 of boldness or risk taking behaviour. In general bolder/risk-prone individuals are more
21 easily caught than the shy/risk-averse (Biro & Sampson, 2015; Le Coeur et al., 2015;
22 Petelle et al., 2015; Réale et al., 2000), consistent with the predicted consequences of
23 this personality trait for predation risk (but see Diaz Pauli et al., 2015). Since fish in
24 this study were actively collected (albeit haphazardly), there is an obvious possibility
25 that some form of researcher bias that would not be exhibited by a natural predator in

1 the field contributes to the repeatability of *order caught*. We note that fish tags are only
2 clearly visible after capture, and researchers were blind to the behavioural profile data
3 of each fish. Regardless, this finding also suggests initial sampling of experimental fish
4 from stock tanks could itself have been selective with respect to behaviours to be
5 studied. The possibility of samples not being fully representative of behavioural
6 variation in a studied population has wider implications for personality studies (Carter
7 et al., 2012).

8 The individual traits observed in OFT and emergence trials have been widely
9 used to assay risky or bold behaviour in fishes, including guppies (Budaev, 1997;
10 Burns, 2008; Diaz Pauli et al., 2015). However our analysis provided somewhat mixed
11 support for our second prediction, that individuals would show (multivariate)
12 personality variation consistent with a simple axis of variation along a risk prone–risk
13 averse continuum. Under this model, we expected that all OFT traits would be
14 positively correlated with each other and negatively correlated with time to emerge and
15 capture order at the individual level. In fact, significant among-individual correlations
16 were found only between *tracklength* and *activity* (positive as predicted) and between
17 these two traits and *time in middle*. Surprisingly, time in the middle was actually
18 negatively correlated among-individuals with the former two traits. Eigenvector
19 decomposition of the among-individual variance-covariance matrix (**I**) estimate
20 identifies two major vectors that, together, explain 74% of the variation. The first
21 vector, accounting for 47% of the variation, is dominated by *tracklength*, *activity* and
22 *time in the middle*. The second vector, accounting for 27% of the variation, is more
23 characterised by *emergence time* and *area covered*.

24 Thus the among-individual covariance structure of behavioural traits suggests
25 that the simple model of a risk-prone risk-averse continuum is not valid in this

1 population, and/or that it is being masked by other aspects of personality being
2 expressed in our trials. This result differs from a study on a different poeciliid,
3 *Xiphophorus birchmanni* by Boulton et al. (2014) in which strong positive correlations
4 between the same OFT traits were found, with the **I** matrix dominated by a single-vector
5 interpretable as a risk averse – risk prone axis (or shy-bold). Thus an important
6 conclusion emerging from the current behavioural data is that a particular assay or
7 observed trait(s) may not be informative for the same personality trait in different
8 species, even if closely related. Indeed this may also be the case for different
9 populations of a single species. For instance, while we know that mean boldness differs
10 among natural populations of guppies according to predation regime (Reznick et al.,
11 1996), among-population comparisons of **I** matrices would add considerable resolution
12 to our understanding of where among-individual variation is maintained and how it is
13 structured by genetic and ecological factors. In this instance, differences in the
14 behavioural ecology between guppies and swordtails could contribute to differences in
15 OFT patterns, with swordtails being more territorial relative to the shoaling, social
16 guppy. Regardless, by measuring multiple behaviours from different tests, measures of
17 personality can be validated rather than relying on *a priori* definitions of personality
18 that may not be appropriate for a given species.

19 More speculatively, we consider it likely that OFT traits in this case are
20 capturing elements of behavioural stress response or coping style (Boulton et al., 2015;
21 Koolhaas et al., 1999), particularly as this was a ‘forced’ rather than voluntary trial
22 (Carter et al., 2013; Huntingford, 1976; Walsh & Cummins, 1976). Behavioural
23 responses to stress in fish have been described as ranging from reactive (often
24 characterised by freezing behaviour) to proactive (e.g., highly active fight or flight
25 behaviour). This axis is sometimes, but not always, viewed as synonymous with

1 variation in risky behaviour (Brelvi et al., 2005; Koolhaas et al., 1999; Øverli et al.,
2 2007; Silva et al., 2010; van Raaij et al., 1996). Here we note that video observations
3 revealed a relatively common behavioural pattern of swimming rapidly back and forth
4 along one side of the tank (generating high *tracklength* and *activity*, but low *time in the*
5 *middle*). This was more consistent with expectations for a proactive coping style (i.e.
6 active attempt to escape) rather than risky or bold behaviour as normally defined (e.g.,
7 reduced thigmotaxis, higher exploration).

8 A final prediction made under the POLS was that individuals with more risk-
9 prone personalities would have higher growth rates. Even in the absence of metabolic
10 variation as a driver, the prediction of a risky personality trait being positively
11 associated with resource acquisition is unchanged (Biro & Stamps, 2008; Stamps,
12 2007). While several studies of fish species to date have found this relationship
13 (Huntingford et al., 2010; Mas-Muñoz et al., 2011; Ward et al., 2004), it is not
14 supported by our data. Individuals did vary significantly in growth rate over the short
15 term study, but only *area covered* showed a significant correlation with growth rate,
16 and it was negative not positive as predicted. Given the lack of a clear risk-prone risk-
17 averse behavioural axis it may be misleading to over-interpret this finding from a single
18 behavioural trait (i.e. we do not conclude that risk-averse fish grow faster).

19 More generally we note that while a degree of social competition is expected,
20 fish were all fed to satiation in the study. Social environments can certainly contribute
21 to development of personality traits (Webster and Ward, 2011) and could also influence
22 wider patterns of trait correlation. Thus if personality-growth correlations found
23 elsewhere are generated by competitive advantage of, for instance, risk-prone over risk-
24 averse individuals (Biro & Stamps, 2010; Niemelä et al., 2012), then these are expected
25 to be stronger under conditions of resource limitation (Wilson, 2014). In contrast,

1 relationships should be weaker under conditions that tend to equalise food intake levels
2 between risk-prone and risk-averse individuals, such as under high resource
3 environments.

4 In conclusion this study found no support for POLS in the guppy population
5 tested. Once the dependence on body size was accounted for, we found no support for
6 variation among-individuals in metabolic rate or scope. Thus we conclude that
7 metabolism is not always a plausible driver of among-individual variation in behaviour.
8 All behavioural traits chosen as putative indicators of a risk-averse – risk-prone
9 behavioural axis were repeatable. However, the among-individual covariance structure
10 was not actually consistent with the presence of a single underlying latent personality
11 trait, and there was no support for the predicted association of risky behaviour with
12 faster growth. Although we note that patterns of among-individual trait (co)variation
13 are certainly expected to show environmental sensitivity, our behavioural results
14 highlight the value of multivariate (i.e., multiple trait and multiple trial type) repeated
15 measures data. In seeking to test mechanistic explanations for the maintenance of
16 animal personality it is important that we have an understanding of how behavioural
17 variation is actually structured among-individuals in the focal population (i.e. to what
18 extent do individual behaviours provide information about personality axes that are
19 generalizable over population or species). This is particularly important in POLS
20 research where the expectation of positive correlations between behaviour, physiology
21 and growth may be dependent on access to resources, territory or mates.

22 Finally, we stress that while among-individual (co)variation provides the raw
23 material upon which selection can act, it is the structure of genetic (co)variation that
24 will determine how traits such as personality evolve, and coevolve, under selection.
25 Others have found abundant evidence for heritable variation underpinning personality

1 (Dingemanse et al., 2012; Oswald et al., 2013; van Oers et al., 2005), though tests
2 of genetic (co)variance structures remain limited. While we found no support here
3 for POLS at the level of the individual phenotype, we suggest that quantitative genetic
4 studies to test for and characterise genetic integration of behaviour, physiology and life
5 history traits would provide a useful route to understanding the evolution of personality.

6

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1 Table 1: Estimated repeatabilities of behavioural traits (conditional on fixed effects)
 2 assayed in open field and emergence trials. Estimates are from univariate models with
 3 standard errors in parentheses.

<i>Trait</i>	<i>Repeatability</i>	$\chi^2_{0.1}$	<i>P</i>
<i>Emergence Time</i>	0.33 (0.12)	9.37	0.001
<i>Track Length</i>	0.31 (0.12)	6.84	0.005
<i>Activity</i>	0.37 (0.12)	9.32	0.001
<i>Order Caught</i>	0.27 (0.07)	66.4	<0.001
<i>Area Covered</i>	0.46 (0.11)	21.8	<0.001
<i>Time in Middle</i>	0.42 (0.12)	14.4	<0.001

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1 Table 2: Among individual variance-covariance-correlation matrix from the final
2 multivariate model incorporating all behavioural traits, size and growth showing
3 variances (V_I , diagonal), covariances (COV_I , lower triangle) and correlations (r_i , upper
4 diagonal) with standard errors in parentheses. Note since (transformed) data were
5 scaled to standard deviation units V_I for behavioural traits (but not Length and Growth)
6 can be interpreted as a repeatability (but not conditioned on fixed effects). * denotes
7 statistical significance at $\alpha = 0.05$ based on likelihood ratio tests of parameter in
8 univariate (for variances) or bivariate (for covariances) mixed models (see
9 supplemental table 3).

	<i>Emergence time</i>	<i>Track Length</i>	<i>Activity</i>	<i>Order Caught</i>	<i>Area Covered</i>	<i>Time in Middle</i>	<i>Length</i>	<i>Growth</i>
<i>Emergence Time</i>	0.328* (0.152)	0.157 (0.320)	0.181 (0.307)	0.197 (0.287)	-0.296 (0.278)	-0.327 (0.297)	0.436 (0.231)	0.205 (0.313)
<i>Track Length</i>	0.052 (0.108)	0.337* (0.161)	0.967* (0.022)	0.070 (0.281)	0.216 (0.280)	-0.756* (0.158)	0.315 (0.238)	0.225 (0.330)
<i>Activity</i>	0.067 (0.116)	0.363* (0.168)	0.418* (0.182)	0.282 (0.250)	0.253 (0.263)	-0.772* (0.143)	0.324 (0.224)	0.145 (0.330)
<i>Order Caught</i>	0.059 (0.090)	0.021 (0.086)	0.096 (0.094)	0.277* (0.091)	0.073 (0.254)	-0.176 (0.262)	0.383 (0.187)	-0.026 (0.289)
<i>Area Covered</i>	-0.107 (0.107)	0.079 (0.115)	0.104 (0.123)	0.024 (0.087)	0.402* (0.151)	0.384 (0.261)	0.200 (0.225)	-0.508* (0.240)
<i>Time in Middle</i>	-0.114 (0.111)	-0.267* (0.133)	-0.303* (0.142)	-0.056 (0.085)	0.148 (0.110)	0.370* (0.153)	-0.091 (0.242)	-0.294 (0.316)
<i>Length</i>	0.208 (0.132)	0.152 (0.127)	0.174 (0.135)	0.168 (0.099)	0.106 (0.124)	-0.046 (0.124)	0.692* (0.197)	0.223 (0.248)
<i>Growth</i>	0.024 (0.039)	0.027 (0.041)	0.019 (0.045)	-0.003 (0.031)	-0.067* (0.039)	-0.037 (0.043)	0.039 (0.045)	0.043* (0.017)

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1 **Figure legends**

2 Figure 1: Metabolic scope (MS) is defined as the difference between standard
3 metabolic rate (SMR) and maximal metabolic rate (MMR) (blue arrow) but can
4 equally be determined as the slope of a reaction norm (black line) between resting and
5 maximal activity states (black circles). Here we use observations of routine metabolic
6 rate (RMR) and active metabolic rate (AMR) made at intermediate activity levels
7 (grey circles) to infer the reaction norm slope.

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9 Figure 2: Metabolic traits (a) and *standard length* as a function days since the start of
10 the experiment (b). Black lines show (a) the predicted mean metabolic reaction norm
11 between activity state specific means (\pm SE) and (b) mean growth trajectory. Grey
12 lines indicate reaction norms and growth lines for each individual as predicted by the
13 mixed model analysis.

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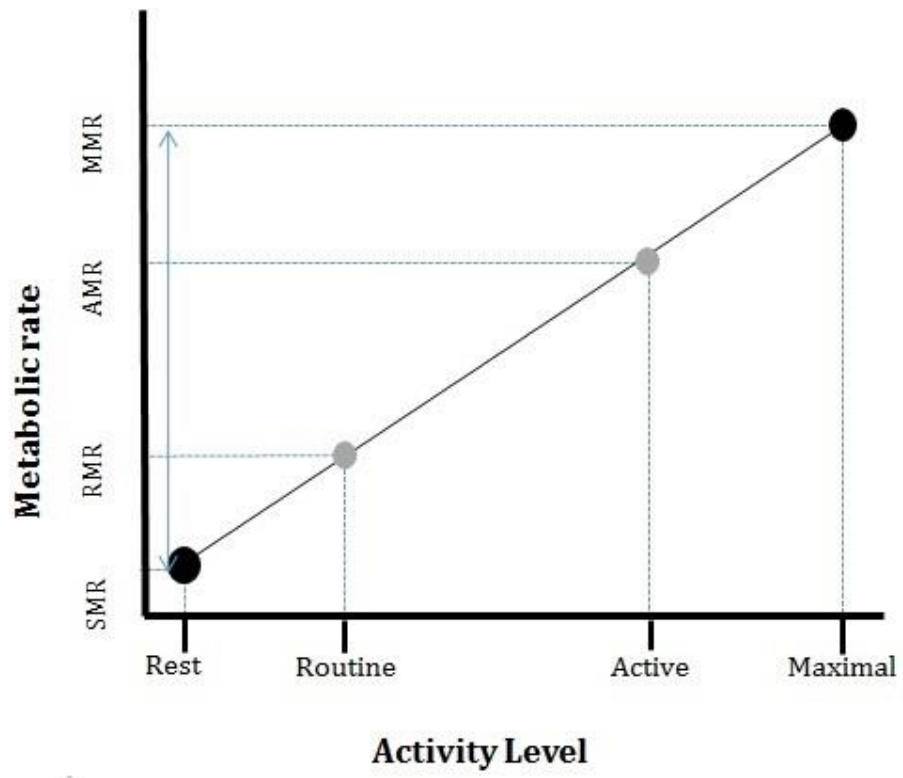
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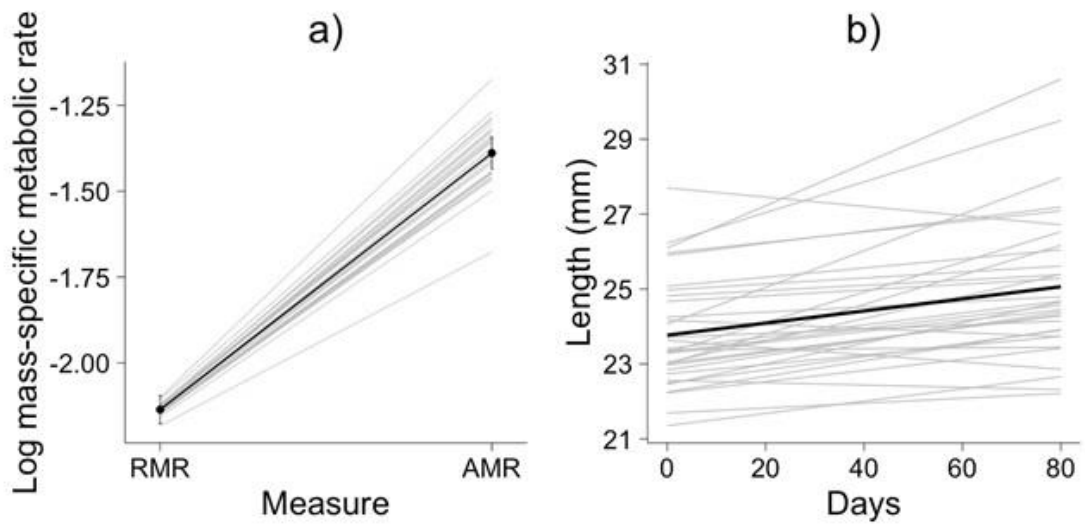
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1 Figure 1
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1 Figure 2
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1 **Supplementary materials for White, Kells & Wilson**

2 Metabolism, personality and pace of life in the Trinidadian guppy, *Poecilia reticulata*

3 **Supplemental methods: Metabolic rate estimation**

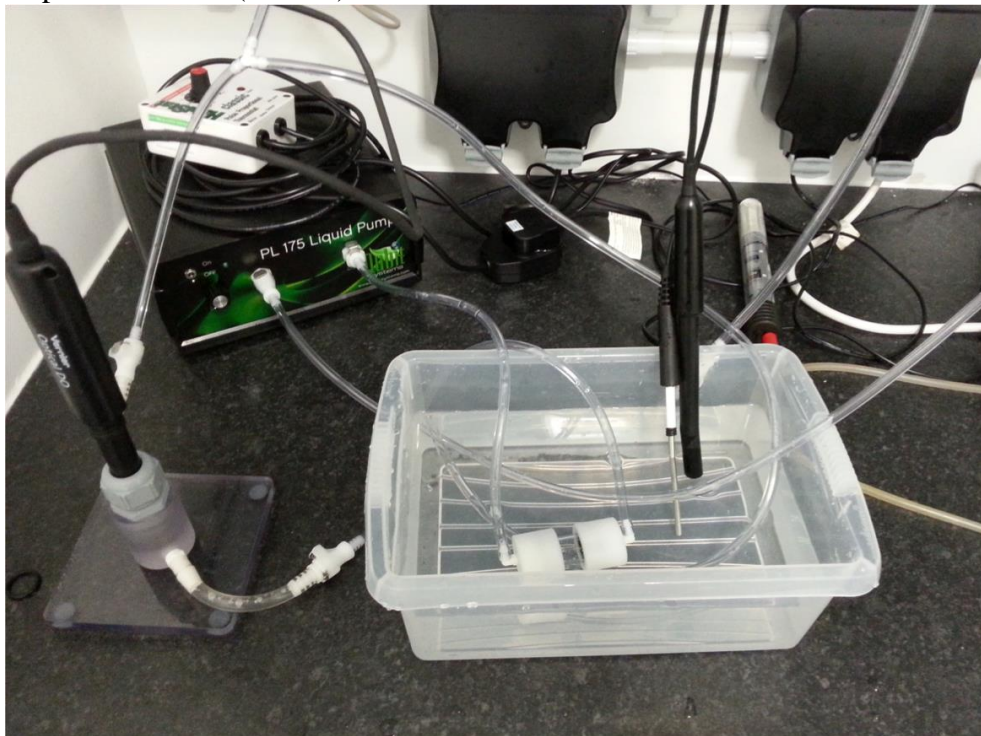
4 A pump was used to deliver water from the water bath through to the respiration
5 chamber past the optical dissolved oxygen (DO) probe and back into the water bath,
6 in what is termed the 'flush' state. For oxygen consumption measures to take place
7 the system was switched to a 'closed' state in which water only flowed between the
8 pump, respiration chamber and DO probe, reverting back to the flush state upon
9 completion of the measurement. This allows precise measurement of oxygen
10 consumption while preventing the build-up of CO₂ and other waste products in the
11 respiration chamber.

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13 To account for bacterial respiration in the system, oxygen consumption of the empty
14 respiration chamber was taken either before or after each fish measure and subtracted
15 from corresponding fish metabolic rate measures. Finally, the fish volume relative to
16 the system volume was corrected to produce whole animal metabolic rate in mg O₂
17 hr⁻¹:

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$$\mathbf{VO_2 = DO\ slope*(Vol_R-Vol_A)*3600}$$

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21 Where **VO₂** is the oxygen consumption rate (mgO₂ hr⁻¹), **DO slope** is the rate of
22 decrease of dissolved oxygen (mg O₂ L⁻¹ s⁻¹), **Vol_R** is the volume of the active
23 respirometer in L (0.069L) and **Vol_A** is the volume of the fish also in L.



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1 **Supplemental table 1:** Fixed effect estimates from univariate models of metabolic
 2 rate, all behaviours assayed, and standard length (see main text for details).

Trait	Fixed effect	Level	Effect size (SE)	DF	F	P
Emergence	Mean Temp Group		-0.279 (3.378)	1, 73.9	0.01	0.919
			0.001 (0.142)	1, 74.1	0.00	0.992
	Order caught	Group 2	0.076 (0.387)	3, 25.2	0.72	0.550
		Group 3	0.303 (0.401)			
		Group 4	0.484 (0.366)			
		1	0.588 (0.372)	7, 87.7	1.06	0.397
		2	0.770 (0.369)			
		3	0.566 (0.368)			
		4	0.828 (0.376)			
		5	0.511 (0.381)			
	7	0.502 (0.424)				
8	1.026 (0.497)					
Trial Weight			-0.041 (0.027)	1, 74.6	2.29	0.137
			0.197 (0.449)	1, 61.9	0.19	0.656
Track length	Mean Temp Group		2.205 (6.664)	1, 71.7	1.57	0.218
			-0.042 (0.289)	1, 71.7	0.02	0.880
	Order caught	Group 2	-0.214 (0.352)	3, 23.8	2.18	0.118
		Group 3	-0.214 (0.351)			
		Group 4	0.548 (0.344)			
		1	-0.597 (0.362)	7, 87.2	1.21	0.304
		2	-0.738 (0.351)			
		3	-0.055 (0.340)			
		4	-0.194 (0.339)			
		5	-0.493 (0.333)			
	7	-0.144 (0.368)				
8	-0.111 (0.419)					
Trial Weight			0.050 (0.025)	1, 78.2	3.92	0.053
			1.064 (0.385)	1, 76	7.65	0.008
Activity	Mean Temp Group		1.846 (6.498)	1, 70.8	1.34	0.253
			-0.019 (0.283)	1, 70.8	0.00	0.941
	Order caught	Group 2	-0.288 (0.369)	3, 24.1	1.92	0.154
		Group 3	-0.346 (0.369)			
		Group 4	0.435 (0.363)			
		1	-0.655 (0.354)	7, 85.2	1.59	0.150
		2	-0.865 (0.345)			
		3	-0.066 (0.335)			
		4	-0.272 (0.334)			
		5	-0.573 (0.327)			
	7	-0.302 (0.363)				
8	-0.178 (0.412)					
Trial Weight			0.032 (0.025)	1, 77.3	1.64	0.207
			0.983 (0.388)	1, 81	6.41	0.014
Order caught	Mean Group	Group 2	0.198 (0.349)	1, 26.4	0.13	0.726
		Group 3	-0.096 (0.295)	3, 26.9	0.30	0.822
		Group 4	-0.237 (0.297)			
	Trial		0.017 (0.292)			
			-0.052 (0.013)	1, 425	17.39	<0.001

	Weight		-0.202	(0.263)	1, 201	0.59	0.443	
Area covered	Mean		17.78	(5.822)	1, 72.2	2.53	0.119	
	Temp		-0.747	(0.253)	1, 72.2	8.72	0.004	
	Group	Group 2		0.067	(0.375)	3, 27.1	0.41	0.750
		Group 3		-0.298	(0.375)			
		Group 4		0.053	(0.369)			
		Order caught	1	0.043	(0.319)	7, 83.5	3.64	0.002
		2	-0.069	(0.313)				
		3	-0.098	(0.303)				
		4	-0.594	(0.303)				
		5	-0.628	(0.295)				
	7	-1.188	(0.331)					
	8	-1.186	(0.372)					
	Trial		0.081	(0.022)	1, 77.9	13.19	<0.001	
	Weight		0.280	(0.366)	1, 89.1	0.59	0.445	
Time in middle	Mean		-0.517	(5.91)	1, 71	1.65	0.205	
	Temp		-0.025	(0.257)	1, 71	0.01	0.919	
	Group	Group 2		0.616	(0.362)	3, 25.2	1.99	0.142
		Group 3		0.461	(0.362)			
		Group 4		-0.128	(0.356)			
		Order caught	1	0.142	(0.323)	7, 83.8	1.95	0.072
		2	0.307	(0.317)				
		3	-0.449	(0.306)				
		4	-0.287	(0.306)				
		5	-0.085	(0.298)				
	7	-0.570	(0.334)					
	8	-0.729	(0.377)					
	Trial		0.021	(0.227)	1, 77.2	0.89	0.349	
	Weight		-0.788	(0.364)	1, 86	4.69	0.035	
Length	Mean		-0.722	(0.578)				
	Group	Group 2		-0.112	(0.437)			
		Group 3		0.339	(0.455)			
		Group 4		-0.254	(0.422)			
	Last day		0.012	(0.007)				
Days since start		0.167	(0.502)					
Mass-spec Metabolic rate	Mean		-0.668	(0.175)	1, 106	18.71	<0.001	
	Measuretype		0.748	(0.058)	1, 106	163.85	<0.001	
	Group	Group 2		0.049	(0.840)	3, 106	0.22	0.884
		Group 3		0.035	(0.084)			
		Group 4		0.639	(0.082)			
		Weight		0.929	(0.129)	1, 106	51.17	<0.001
	Order caught	1		-0.077	(0.112)	7, 106	1.35	0.233
		2		-0.025	(0.113)			
		3		-0.106	(0.114)			
		4		0.731	(0.116)			
5			-0.163	(0.115)				
7			0.133	(0.124)				
8		0.052	(0.127)					
	Trial		-0.005	(0.127)	1, 106	0.18	0.664	

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Supplemental table 2: Statistical inference among-individual covariance estimates between behavioural traits.

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Among-individual covariance (COV_I) was tested in each case by likelihood ratio test comparison of a bivariate mixed models with COV_I freely estimated to one in which COV_I was constrained to equal zero. We assume twice the difference in model log-likelihood is distributed as χ^2_1 .

Trait 1	Trait 2	χ^2_1	P
Track length	Order caught	0.028	0.867
Track length	Area covered	0.530	0.467
Track length	Time in middle	-7.34	0.007
Track length	Activity	8.51	0.004
Activity	Order caught	0.070	0.791
Activity	Area covered	0.781	0.377
Activity	Time in middle	-7.86	0.005
Order caught	Time in middle	0.002	0.964
Order caught	Area covered	0.04	0.841
Time in middle	Area covered	2.59	0.108
Emergence	Track length	0.312	0.576
Emergence	Activity	0.224	0.636
Emergence	Order caught	0.504	0.478
Emergence	Area covered	0.946	0.331

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1 **Supplemental table 3:** Eigen vector decomposition of the among-individual
 2 variance-covariance matrix (I) for behavioural traits as estimated from the
 3 multivariate mixed model.
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	Eigen 1	Eigen 2	Eigen 3	Eigen 4	Eigen 5	Eigen 6
Eigen values	0.983	0.554	0.336	0.199	0.009	0.001
Percentage variance explained	47.2	26.6	16.2	9.58	0.409	0.032
Trait loadings:						
Emergence	0.159	-0.410	0.660	0.607	0.045	0.024
Track length	0.546	0.118	-0.139	0.122	-0.688	0.424
Activity	0.624	0.154	-0.062	0.033	0.072	-0.760
Order	0.198	0.051	0.651	-0.725	-0.042	0.084
Area Covered	0.093	0.810	0.198	0.269	0.388	0.272
Time in middle	-0.490	0.367	0.281	0.132	-0.606	-0.401

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1 **Supplemental table 4:** Statistical inference of among-individual covariance terms
2 between standard length (SL) and each behavioural trait. Note SL is modelled as a
3 reaction norm with both intercept (size) and slope (growth) terms
4

Behavioural trait	χ^2_2	P
Emergence	2.49	0.288
Track length	2.26	0.322
Activity	1.95	0.377
Order caught	2.348	0.309
Area covered	6.053	0.048
Time in middle	1.78	0.411

5
6 Among-individual covariance (COV_I) was tested in each case by likelihood ratio test
7 comparison of a bivariate mixed models with COV_I freely estimated between
8 behaviour and both $SL_{intercept}$ and SL_{slope} to one in which both behaviour-SL
9 covariance terms were constrained to equal zero. We assume twice the difference in
10 model log-likelihood is distributed as χ^2_2
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12