Table S2. Relationship between the length of a subjective year (phase difference between subjective and environmental annual cycles, in days) species-specific annual survival probability (model 1) and species-specific BMR (model 2), accounting and not accounting for the phylogenetic effect. In model 1 both variables were adjusted to log(BMR) and in model 2 to log(Survival). In both models, an explanatory variable Cycle was included to account for the possible effect of the cycles being fully (Cyclefull ) or partly (Cycletransitory) undergone in unvarying photoregime. The posterior estimates (means) of the effect sizes with the highest posterior density intervals (95% credible interval, limited by lower and upper CI) for the models accounting for phylogenetic effects are calculated from the joint posterior distribution of 100 separate runs each with one of 100 separate phylogenetic trees from http://birdtree.org. pMCMC is the two times the smaller of the two quantities: MCMC estimates of i) the probability that a<0 or ii) the probability that a>0, where a is the parameter value. The output parameters of the models of the same structure, with shorebirds excluded from the sample, are presented in brackets. The MCMC chains ran for 1 300 000 iterations with a burn-in of 30 000 and a thinning interval of 50. Each model generated ~1,100 independent samples of model parameters. Tests for autocorrelation were applied to assess for independence of samples in the Markov chain.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **no phylogeny** |  |  |  | **with phylogeny (on 100 phylogenetic trees in mulTree)** | | |  |  |
| **model 1** |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
| **fixed terms** | **Estimate** | **lower CI** | **upper CI** | **pMCMC** | **posterior mean** | **lower CI** | **upper CI** | **pMCMC, mean** | **pMCMC, range** |
| intercept | -6.4 (-11.2) | -40.8 (-54.0) | 26.6 (30.6) | 0.699 (0.584) | -8.9 (-12.7) | -63.0 (-64.0) | 44.3 (37.8) |  |  |
| Cyclefull | 10.4 (8.3) | 1.5 (-6.2) | 19.2 (22.9) | 0.021 (0.263) | 10.2 (7.4) | 1.3 (-7.3) | 19.1 (22.0) | 0.025(0.322) | 0.006 - 0.053(0.255 - 0.394) |
| Survival : Cycletransitory | 196.1 (222.4) | 71.4 (68.2) | 325.5 (380.5) | 0.003 (0.005) | 211.3 (245.1) | 61.6 (59.8) | 363.6 (435.9) | 0.008(0.012) | 0.001 - 0.024(0.001- 0.027) |
| Survival : Cyclefull | 119.0 (110.3) | -1.8 (-35.3) | 239.4 (263.6) | 0.052 (0.130) | 132.5 (128.5) | -13.7 (-51.4) | 279.2 (309.7) | 0.074(0.150) | 0.035 - 0.122(0.1 - 0.206) |
| **random terms** | **posterior mean** | **lower CI** | **upper CI** |  | **posterior mean** | **lower CI** | **upper CI** |  |  |
| bird ID | 558.7 (762.9) | 262.2 (337.5) | 880.8 (1196.0) |  | 560.9 (764.5) | 284.4 (380.9 ) | 923.8 (1258.1) |  |  |
| life-cycle stage | 1077.0 (1175.0) | 263.0 (211.7) | 2375.0 (2478.0) |  | 1099.0 (1184.0) | 376.9 (329.8) | 2870.6 (3101.4) |  |  |
| study | 1379.0 (2144.0) | 199.4 (204.4) | 3129.0 (5182.0) |  | 1297.0 (1781.0 ) | 309.1 (349.3 ) | 3705.1 (5544.8) |  |  |
| species | 670.9 (922.3) | 112.9 (113.5) | 1566 (2382.0) |  | 716.9 (944.1) | 190.5 (211.5) | 2107.8 (3071.7) |  |  |
| phylogenetic variance |  |  |  |  | 1175.0 (1296.0) | 233.6 (246.5 ) | 4065.7 (4522.4) |  |  |
| residual variance | 1282.0 (1344.0) | 1059.0 (1028.0) | 1520.0 (1681.0) |  | 1281.0 (1342.0) | 1066.4 (1047.3 ) | 1534.5 (1710.1) |  |  |
|  |  |  |  |  |  |  |  |  |  |
| **model 2** |  |  |  |  | **with phylogeny (on 100 phylogenetic trees in mulTree)** | | | |  |
|  |  |  |  |  |  |  |  |  |  |
| **fixed terms** | **Estimate** | **lower CI** | **upper CI** | **pMCMC** | **posterior mean** | **lower CI** | **upper CI** | **pMCMC, mean** | **pMCMC, range** |
| intercept | -3.7 (-13.4) | -36.5 (-55.7) | 29.9 (26.6) |  | -7.4 (-16.7) | -61.2(-66.7) | 44.9 (32.6) |  |  |
| Cyclefull | 9.3 (15.2) | 0.27 (2.3) | 18.1 (28.4) | 0.042 (0.021) | 9.1(14.8) | 0.04 (1.5) | 18.1 (28.0) | 0.049 (0.03) | 0.022 - 0.082 (0.006 - 0.055) |
| BMR : Cycletransitory | -91.8 (-105.0) | -161.0 (-187.6) | -23.3 (-23.4) | 0.010 (0.011) | -98.4 (-117.9) | -176.6 (-212.2) | -20.9 (-24.8) | 0.015 (0.015) | 0.002 – 0.043 (0.002 - 0.039) |
| BMR : Cyclefull | -63.3 (-50.8) | -127.8 (-129.5) | 1.7 (26.8) | 0.054 (0.188) | -68.54 (-61.6) | -141.7 (-150.8) | 5.2 (28.0) | 0.07 (0.165) | 0.035 – 0.10 (0.108 – 0.216) |
| **random terms** | **posterior mean** | **lower CI** | **upper CI** |  | **posterior mean** | **lower CI** | **upper CI** |  |  |
| bird ID | 544.2 (761.4) | 249.8 (333.6) | 826.5 (1194.0) |  | 544.0 (764.8) | 271.8 (381.4) | 902.8 (1257.2) |  |  |
| life-cycle stage | 1079.0 (1069.0) | 251.6 (196.9) | 2292.0 (2444.0) |  | 1084.0 (1094.0) | 368.5 (327.9) | 2827.2 (3083.0) |  |  |
| study | 1317.0 (2077.0) | 185.4 (213.4) | 3023.0 (5054.0) |  | 1239.0 (1723.0) | 295.9 (338.4 ) | 3550.8 (5388.0) |  |  |
| Species | 675.3 (887.4) | 115.3 (120.7) | 1571 (2263.0) |  | 702.9 (920.8) | 187.5 (208.6) | 2062.8 (2988.9) |  |  |
| phylogenetic variance |  |  |  |  | 1154.0 (1258.0) | 230.7 (241.7) | 3969.0 (4377.2) |  |  |
| residual variance | 1304.0 (1339.0) | 1079.0 (1027.0) | 1543.0 (1683.0) |  | 1304.0 (1337.0) | 1086.5 (1044.2) | 1561.6 (1705.2) |  |  |
|  |  |  |  |  |  |  |  |  |  |