|  |  |  |  |
| --- | --- | --- | --- |
| Model: Accumulation | Df | t value | P value |
| Lipid mass (First Day of Final Instar) |  |  |  |
| lean Mass | 79.61 | 2.934 | 0.00437\* |
| Photoperiod | 75.94 | -2.726 | 0.00796\* |
| Model: Accumulation | Df | t value | P value |
| Lipid mass (Wandering Day) |  |  |  |
| Strain | 186.8 | 4.08 | <2e-16 \* |
| Photoperiod | 191.6 | -10.23 | 6.67e-05\* |
| Final model:  lme4::lmer(formula = lipid\_mass ~ photoperiod + strain + (1 | rep/cohort), data = dataLW, REML = TRUE, contrasts = list(photoperiod = "contr.SAS", strain = “contr.SAS”)) | | | |
| Model: Accumulation | Df | t value | P value |
| Lean mass (First Day of Final Instar) |  |  |  |
| Strain | 5.93 | 2.034 | 0.0888 |
| Photoperiod | 77.65 | -1.133 | 0.2609 |
| Model: Accumulation | Df | t value | P value |
| Lean mass (Wandering Day) |  |  |  |
| Strain | 10.87 | 6.845 | 2.95e-05 \* |
| Photoperiod | 133.31 | -9.685 | <2e-16\* |
| Final model:  lme4::lmer(formula = lean\_mass ~ photoperiod + strain + (1 | rep/cohort), data = dataLW,  REML = TRUE, contrasts = list( photoperiod = "contr.SAS", strain = "contr.SAS")) | | | |

Lean D1

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lean\_mass ~ strain + photoperiod + (1 | rep/cohort)

Data: dataL1

REML criterion at convergence: -860.4

Scaled residuals:

Min 1Q Median 3Q Max

-5.6378 -0.3947 -0.0369 0.5377 1.8085

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 1.522e-06 0.001234

rep (Intercept) 1.472e-06 0.001213

Residual 1.736e-06 0.001318

Number of obs: 89, groups: cohort:rep, 13; rep, 6

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0081217 0.0007410 9.0000000 10.961 1.66e-06 \*\*\*

strainUZ 0.0015329 0.0007531 5.9100000 2.036 0.0887 .

photoperiod16 -0.0003314 0.0002866 77.5900000 -1.157 0.2510

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) strnUZ

strainUZ -0.504

photoperd16 -0.223 0.037

Lipid D1

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lipid\_mass ~ photoperiod + lean\_mass + (1 | rep/cohort)

Data: dataL1

REML criterion at convergence: -886.6

Scaled residuals:

Min 1Q Median 3Q Max

-2.4410 -0.6907 -0.1487 0.6502 2.4841

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 0.000e+00 0.0000000

rep (Intercept) 2.579e-07 0.0005078

Residual 6.074e-07 0.0007794

Number of obs: 81, groups: cohort:rep, 13; rep, 6

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0005349 0.0005217 50.5500000 1.025 0.31010

photoperiod16 -0.0004834 0.0001774 75.9400000 -2.726 0.00796 \*\*

lean\_mass 0.1464678 0.0499205 79.6100000 2.934 0.00437 \*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) phtp16

photoperd16 -0.317

lean\_mass -0.885 0.162

Lean DW

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lean\_mass ~ strain + photoperiod + (1 | rep/cohort)

Data: dataLW

REML criterion at convergence: -1162.5

Scaled residuals:

Min 1Q Median 3Q Max

-4.0858 -0.5978 -0.0094 0.5568 3.2045

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 6.640e-07 0.0008149

rep (Intercept) 5.463e-05 0.0073915

Residual 1.148e-05 0.0033879

Number of obs: 146, groups: cohort:rep, 24; rep, 12

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 2.509e-02 2.211e-03 1.190e+01 11.348 9.75e-08 \*\*\*

strainUZ 4.700e-03 6.867e-04 1.087e+01 6.845 2.95e-05 \*\*\*

photoperiod16 -5.811e-03 6.000e-04 1.333e+02 -9.685 < 2e-16 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) strnUZ

strainUZ -0.142

photoperd16 -0.123 -0.050

Lipid DW

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lipid\_mass ~ photoperiod + strain + (1 | rep/cohort)

Data: dataLW

REML criterion at convergence: -1738.7

Scaled residuals:

Min 1Q Median 3Q Max

-4.4963 -0.4314 -0.0320 0.4706 3.2978

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 0.000e+00 0.0000000

rep (Intercept) 7.423e-07 0.0008616

Residual 7.967e-06 0.0028226

Number of obs: 201, groups: cohort:rep, 31; rep, 14

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 1.051e-02 4.109e-04 2.695e+01 25.58 < 2e-16 \*\*\*

photoperiod16 -4.139e-03 4.044e-04 1.916e+02 -10.23 < 2e-16 \*\*\*

strainUZ 1.638e-03 4.014e-04 1.868e+02 4.08 6.67e-05 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) phtp16

photoperd16 -0.457

strainUZ -0.451 -0.057