Sage Sularz

Comparative Physiology

Fall 2024

Effect of Genotype, Life-Stage and Temperature on Oxidative Stress

*Discussion*

Figures



*Figure 1: Box plots showing catalase activity (I.U./mg) in different experimental groups based on life stage, genotype, and temperature treatments. In the first plot, a significant effect of life stage on catalase activity was observed (p = 0.020), with higher activity in one stage over the other, as indicated by the ANOVA. Genotype and the interaction between life stage and genotype were not significant (p > 0.05). In the second plot, neither temperature treatment nor genotype showed significant effects on catalase activity.*

Life Stage Analysis

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| Life S. | 1 | 1.38 | 1.3752 | 5.54 | 0.02 |
| Genotype | 1 | 0.23 | 0.2274 | 0.916 | 0.34 |
| Life S. ~ Genotype | 1 | 0.42 | 0.4228 | 1.703 | 0.194 |
| Residuals | 140 | 34.75 | 0.2482 |  |  |

*Table 1: Analysis of Variance (ANOVA) summary for the effects of life stage, genotype, and their interaction on the response variable. Degrees of freedom (Df), sum of squares (Sum Sq), mean squares (Mean Sq), F-values, and p-values (Pr(>F)) are shown for each factor and interaction term. A statistically significant effect of life stage was observed at the 0.05 significance level, with a p-value of 0.020. No significant effects were found for genotype or the life stage and genotype interaction.*

Heat Shock Analysis

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
| Temp | 1 | 0.08 | 0.07977 | 0.307 | 0.581 |
| Genotype | 1 | 0.23 | 0.22745 | 0.874 | 0.351 |
| Temp ~ Genotype | 1 | 0.05 | 0.05366 | 0.206 | 0.65 |
| Residuals | 140 | 36.42 | 0.26013 |  |  |

*Table 2: Analysis of Variance (ANOVA) summary for the effects of temperature (temp), genotype, and their interaction on the response variable. Degrees of freedom (Df), sum of squares (Sum Sq), mean squares (Mean Sq), F-values, and p-values (Pr(>F)) are presented for each factor and interaction term. No statistically significant effects were observed at a 0.05 significance level.*

Literature Cited

Weber, A. L., Khan, G. F., Magwire, M. M., Tabor, C. L., Mackay, T. F. C., & Anholt, R. R. H. (2012). Genome-wide association analysis of oxidative stress resistance in *Drosophila melanogaster*. *PLOS ONE, 7*(4), e34745. <https://doi.org/10.1371/journal.pone.0034745>

Guio, L. (2018). Stress affects the epigenetic marks added by Bari-Jheh: A natural insertion associated with two adaptive phenotypes in *Drosophila*. *bioRxiv*. <https://doi.org/10.1101/037598>

Habib, S., Lwin, Y. Y., & Li, N. (2021). Down-regulation of *SlGRAS10* in tomato confers abiotic stress tolerance. *Genes, 12*(5), 623. <https://doi.org/10.3390/genes12050623>

Zhang, B., Peng, Y., Zheng, J., Liang, L., Hoffmann, A. A., & Ma, C.-S. (2016). Response of heat shock protein genes of the oriental fruit moth under diapause and thermal stress reveals multiple patterns dependent on the nature of stress exposure. *Cell Stress and Chaperones, 21*(4), 653–663. <https://doi.org/10.1007/s12192-016-0690-8>

Hadwan, M. H. (2018). Simple spectrophotometric assay for measuring catalase activity in biological tissues. *BMC Biochemistry, 19*(1), 7. <https://doi.org/10.1186/s12858-018-0097-5>

Annotations

**Guio, L., Vieira, C., & González, J. (2018).** Stress affects the epigenetic marks added by natural transposable element insertions in Drosophila melanogaster. Scientific Reports, 8(1), 12197. DOI:10.1038/s41598-018-30491-w  
This study explores the role of transposable elements, specifically Bari-Jheh, in modulating gene expression and stress responses through epigenetic modifications in Drosophila melanogaster. Under oxidative stress, specific histone modifications spread from transposon sites to nearby genes, influencing stress response. This research is valuable for understanding the epigenetic regulation of genes related to oxidative stress resilience, highlighting potential mechanisms for adaptive responses in genomic studies​(Guio et al 2018).

**Habib, S., Lwin, Y.Y., & Li, N. (2021).** Down-Regulation of SlGRAS10 in Tomato Confers Abiotic Stress Tolerance. Genes, 12(5), 623. DOI:10.3390/genes12050623  
This paper discusses the down-regulation of the SlGRAS10 gene in tomatoes and its effects on stress tolerance. The study found that reduced expression of SlGRAS10 increased the activity of key antioxidant enzymes, such as catalase and peroxidase, helping the plant cope with salt and drought stress. This research is relevant to your work as it highlights the role of transcription factors in regulating oxidative stress tolerance through ROS-scavenging mechanisms, providing insights into potential genetic targets for enhancing stress resilience​(Habib et al 2021).

**Hadwan, M.H. (2018).** Simple spectrophotometric assay for measuring catalase activity in biological tissues. BMC Biochemistry, 19(1), 7. DOI:10.1186/s12858-018-0097-5  
Hadwan's paper introduces a precise method for measuring catalase activity, a critical enzyme in oxidative stress responses. This method is highly sensitive and can be used in a variety of biological samples, including plant tissues, making it ideal for evaluating antioxidant responses. This work supports the methodological foundation for measuring catalase activity in studies focused on oxidative stress, adding a reliable tool for assessing enzymatic activity relevant to your research​(Hadwan et al 1018).

**Weber, A.L., Khan, G.F., Magwire, M.M., Tabor, C.L., Mackay, T.F.C., & Anholt, R.R.H. (2012).** Genome-Wide Association Analysis of Oxidative Stress Resistance in Drosophila melanogaster. PLoS ONE, 7(4), e34745. DOI:10.1371/journal.pone.0034745  
This study performs a genome-wide association analysis to identify genetic variants associated with oxidative stress resistance in Drosophila. The study found that resistance to oxidative stress is highly heritable and identified candidate genes involved in DNA metabolism and neuronal development. This resource is useful for your research as it provides a comprehensive approach to understanding genetic variations in oxidative stress response, emphasizing the importance of specific genes that may also be conserved in other species​(Weber et al 2012).

**Zhang, B., Peng, Y., Zheng, J., Liang, L., Hoffmann, A.A., & Ma, C.S. (2016).** Response of heat shock protein genes of the oriental fruit moth under diapause and thermal stress reveals multiple patterns dependent on the nature of stress exposure. Cell Stress and Chaperones, 21(4), 653-663. DOI:10.1007/s12192-016-0690-8  
This paper investigates the expression of heat shock proteins (HSPs) in the oriental fruit moth under diapause and various thermal stresses. The study shows that HSPs exhibit distinct expression patterns depending on the stress type, which may serve as bioindicators of thermal stress resilience. This research is pertinent to understanding how organisms regulate protein stability and protection under stress, which aligns with your focus on stress responses and adaptive molecular mechanisms​(Zhang et al 2016).