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Identifying genetic background effects for cancer susceptibility

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The study of cancer susceptibility is incredibly important due to the harmful effects of cancer and the difficulty in predicting and preventing it. Individuals can vary in their degree of cancer susceptibility due to different genetic backgrounds (4). A major goal in biomedicine is to identify genomic regions that influence cancer severity. Here, we used the *Drosophila melanogaster* model system to identify genetic background effects on the severity of a cJUN NH2-terminal kinase (JNK) mutation. Under normal circumstances, JNK serves as a tumor-suppressor and regulator of cell proliferation (1). When mutated, the JNK gene loses control its regulatory capabilities, causing cells to enter premature death cycles. Similarly, the loss of regulation can also lead to increased prevalence of oncogenes. One of the noticeable effects of the JNK mutation is that yields a phenotypic variation of decreased eye pigment due to increased cell death (2). We crossed a set of 7 different inbred lines with a line that mutates the Eiger (EGR) gene, an upstream regulator of JNK, to create a F1 offspring that are heterozygous. To identify the effect of genetic background (founder line) on the severity of this mutation, we photographed the eyes of these offspring with standard parameters and used imageJ to measure total pigment area of the eye to analyze the difference in coloration. Once all images were acquired, I analyzed the differences between the different founder genotypes to identify any significant genetic background effects. This project is significant because it would be an important finding and steppingstone for further research into genetic relaying of cancer genes. It would also give us insight into cancer susceptibility and metastatic factors. Much of the biological organization of *D. melanogaster* is conserved in humans so results found in this species could possibly be similar in our own.