

The model organism *Drosophila melanogaster* to investigate the role in metabolism and behavior of obesity-linked genes

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Human obesity has been found to have a non-negligible genetic component in certain affected individuals, and despite the common understanding of the problem, a well-balanced diet and life style not always ensures a proper body weight. The reasons leading to obesity are multiple, entrenched in both the metabolic and neurological sphere. The current progress and knowledge in genetics characterizing metabolism and food intake, laid the foundation for development of new selective strategies capable of curing or at least mitigating the effects of this condition. Recently, several genes have been found to be in some way related to the onset of this condition in *Homo sapiens*. Surprisingly these have been found in other species like *Gallus gallus* (chicken) or *Drosophila melanogaster* (fruit fly), suggesting that they have an important function in the metabolism of an organism. By employing the fruit fly as model, it is possible to investigate how these genes affect the activity and the sleeping time, how their expression is affected by different diets and by other environmental conditions such as starvation. The approach used in this work is to artificially reduce the expression of these genes (silencing also known as Knocking Down) to produce flies that are partially lacking the products of their transcription and translation (from DNA to RNA and finally to proteins). The newborn flies should show specific phenotypes that can make us understand the role that a certain gene has on the organism. As a first step of this work, it was required to verify that the activity of these obesity-linked genes is properly reduced. To do so their expression level has been quantified and compared to flies that don't present this modification in gene expression. By the use of a Quantitative Polymerase Chain reaction (qPCR) it was possible to compare the expression of experimental flies (reduced gene expression) with normal flies (presenting normal expression level). This technology allows to amplify a certain gene and to determine its amount in comparison to a control gene. After showing that the gene expression was reduced, a behavioral assay was performed. The *Drosophila* Activity Monitoring System (DAMS) was employed to monitor the sleeping time and the activity of Knocked-down flies and normal flies over 48 hours, and I have seen that indeed the flies which have a reduced gene expression behave differently compared to normal flies (gene expression not reduced). Therefore, since these genes are involved in obesity, it was tested whether or not they are up or down-regulated if the flies are fed with different types or diet, or if they undergo a 24 hours period of starvation. For doing this I have been using normal flies (gene expression not reduced) and again the qPCR for determining the amount of a specific gene and compare it to a control group. By doing so I have proven that starved flies do not have a different gene expression compared to non-starved flies, and also that flies which are fed with different diets (low nutrients, protein enriched and carbohydrates enriched) have the same expression profile of flies fed normally.

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