Melanocyte cells are present in the epidermis and hair follicles and are derived from neural crest cells. They produce melanin which determines hair, skin, and eye colour. When certain oncogenes, such as GNAQ, are mutated in melanocytes, they can cause the cell to proliferate continuously and therefore cause cancer.

In our study, we analyzed data obtained from RNA sequencing of melanocytes of the tail epidermis in a GNAQ mouse model. These melanocyte cells were mutated to express the GNAQ oncogene, however instead of proliferating continuously, the cells that expressed the GNAQ oncogene began to disappear. The goal of our study is to find genes and pathways related to the disappearance of melanocytes that express GNAQ oncogene, and using this information to study how they prevent proliferation and turning into cancer cells. This information can help in preventing cancerous melanocytes from proliferating and further division, and it can also be useful in finding possible treatments for melanoma in humans.

We divided the genes into two groups, up regulated and down regulated, using their z-score. Using David Bioinformatics Resources website, we performed KEGG and Gene Ontology analysis on these two groups. By using the Benjamini value (q-value), we chose 5 significant KEGG and gene ontology pathways related to cancer, cell division, and cell death to further study the genes involved in these pathways and therefore in causing the disappearance of melanocytes expressing GNAQ.

Themes:

Check (highlight) the most applicable theme according to the abstract.

| Innovation and Technology | Health and Wellness | Culture and Society | Sustainability and Conservation |

Comments: The information you provided in your abstract is good. I would recommend rethinking the order of your abstract (i.e. stating your goal before methodology; and ending with the implications instead of your methodology)