**Project Proposal**

(i) Six keywords (these will help us to allocate appropriate Examiners/Markers to your project)

1. Gene Flow

2. Gene Regulatory Network

3. Robustness

4. Local adaptation

5. Epistasis

6. Alleles

(ii) Introduction to the project idea and proposed questions

In just a few centuries, societal development has caused many anthropogenic changes, many of which will have harmful long-term effects to many species. This coupled with geological changes, will lead to future shifts in the distribution of land as well as alteration of habitat states. One effect of this change can be migration. Whether it is forced migration or new route opportunities, the distribution and movement of species will also change in generations to come. These migrations can cause the introduction of novel genes into local habitats, implicating future evolutionary effects in these local habitats. Evolution of both the local species and migratory species. The presence of these novel suboptimal genes, along with the interaction of species in the environment will lead to evolutionary change. After many generations, this change will be seen in a phenotypic level as well as genotypic.

Genes interaction within and across loci can result in robustness. This stems from the effects of epistasis, additivity and dominance, all of which are connected (Omholt et al. 2000). The concern is on how a network responds to the effect of gene flow and seeing the evolving genetic interactions. Previous research looked at the effects of gene flow, selection and mutation at generating local adaptation at the phenotypic level, showing how maintenance of alleles and linkage is important in adaptation (Yeaman and Whitlock 2011). It was shown that with random perturbations and aid of genetic modifiers, there are bounds for which selection for canalization can act on, leading to evolution of robustness. They also showed that under migration selection balance, selection for robustness increases with the migration rates (Proulx et al. 2004). The purpose of the research will be looking at the change in genetic architecture dynamics and structure with the interactions of the systems that maintains this robustness. Furthermore, ﻿as the network evolves, it has been shown that there exists a threshold which is actively regulating these homeostatic genes (Gjusvland et al. 2007). As selection of robustness occurs within the local population, it can give insight into the change in architecture and statistically significant interaction (Gjusvland et al. 2006). Using computer models, we can simulate the effects over many generations and see how the output of the network changes, specifically looking at allelic interaction and possibility of epistasis and dominance.

(iii) Proposed methods

Using software packages including RStudio, SLiMgui, I will write ann algorithm to run simulations to see the effects of gene flow on a population, looking at the changes at the genetic level. Using a well understood gene network as a model system to represent one population, another model population will be introduced to run simulations of migrations and see the evolution of the model network. This model system can either be of small scale, containing one or two genes, intermediate scale of around 10 genes or a whole genome. The populations are not representative of any specific species but rather just to see the effects over many simulated generations. The well understood network will be the model system in which gene flow is introduced. The focus is solely on the effects of migration and genetic adaptions, thus environmental influence will not be considered in these simulations. However, stochasticity such as mutation will included in the model.

(iv) Anticipated outputs and outcomes (including stakeholders involved if applicable)

With the introduction of gene flow in the gene network, the anticipated output would be an evolved network with different dynamics and interactions from the start. The expectation is that with gene flow, genetic interaction will cause a change in genetic polymorphisms, and allelic and loci interaction. Selection for canalization will lead to a more robust network with the possibility of different alleles, allelic frequency and gene interactions. With the effects of epistasis, it is possible that the locus selecting for robustness is influenced by another locus in the network, and the latter locus is the one evolving.

(v) Project feasibility supported by a timeline of tasks (including a Gantt chart)

April May June July August September

Migration simulation x x x x

* Choose Model networks x
* Design Genetic Network x
* Be able to run simulations x x x

Write thesis x

* Introduction and Method x
* Results, Discussion and Conclusion x
* Formatting, citation and appendices x

Gather literature x x x x x

Preparation for FREE Symposium and Vivas x x

(vi) An itemized budget

$500 for the travel

(vii) Cited references.

1.Gjuvsland, A. B. *et al.* (2007) ‘Statistical epistasis is a generic feature of gene regulatory networks’, *Genetics*, 175(1), pp. 411–420. doi: 10.1534/genetics.106.058859.

2. Gjuvsland, A. B., Plahte, E. and Omholt, S. W. (2007) ‘Threshold-dominated regulation hides genetic variation in gene expression networks’, *BMC Systems Biology*, 1. doi: 10.1186/1752-0509-1-57.

3. Omholt, S. W. *et al.* (2000) ‘Gene regulatory networks generating the phenomena of additivity, dominance and epistasis’, *Genetics*, 155(2), pp. 969–980.

4. Proulx, S. R. and Phillips, P. C. (2005) ‘The opportunity for canalization and the evolution of genetic networks’, *American Naturalist*, 165(2), pp. 147–162. doi: 10.1086/426873.

5. Yeaman, S. and Whitlock, M. C. (2011) ‘The genetic architecture of adaptation under migration-selection balance’, *Evolution*, 65(7), pp. 1897–1911. doi: 10.1111/j.1558-5646.2011.01269.x.

**“I have seen and approved the proposal and the budget”**

Thomas Bell 16/3/2020

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Name and date