Accepting EOIs to PhD positions focusing on Eco-Evo-Genomics studies led by Dr. Yang Liu, Research Fellow of the University of Queensland

In contemporary environments with extreme and rapid anthropogenic changes, a pressing question is how quickly organisms can adapt to environments that are available to them. Our team address the overarching question by conducting four pillars of research including (1) revealing the patterns of phenotypic, genetic, and transcriptional coordination, (2) quantifying multivariate selection acting on interacting traits, the genome, and the transcriptome, (3) detecting and validating the genomic signatures of selection and adaptation, and (4) assessing environmental effects of distant-, parental-, and present-generations on responses to the selection of phenotypic traits.

Dimensionality, modularity, and integration. Organisms are functionally integrated systems, where interactions among phenotypic traits make the whole more than the sum of its parts. How is a suite of traits assembled into an adaptive module? How is an intramodule rewired to form a regulatory network? What is the persistence and stability of a module at a perturbation triggered by altered interactions between the response to disparate environmental conditions or between the responses of multiple traits to the same environment? What constrains modules to vary independently, reflecting the integration and canalization of evolutionary trajectories? Our efforts to elucidate the multi-dimensional nature of genetic and transcriptional variation primarily include identifying modularity at the phenotypic, genomic, and transcriptomic levels under manipulative environmental conditions, characterizing the modularity of genes involved in adaptation, and deciphering the function of genes in module nodes. Ultimately, we apply such functional enrichments to multivariate genomic selection, in the hope of enhancing multilayered omics-enabled prediction.

Evolution of genetic architecture and gene expression in relation to adaptation. Natural selection does not operate on phenotypic traits in isolation but acts on combinations of traits. We relate standing genetic variation to phenotypic divergence. We disentangle the effects of additive and non-additive (dominance and epistasis) genetics, environment, and interactions thereof on phenotypic variation. Moreover, we use a set of metrics based on (co)variance matrices of phenotypes and genotypes to estimate additive genetic effects within or among populations. Through this analysis, we aim to address how environmental heterogeneity influences phenotypic/ genetic variance. At the molecular level, a single genome can encode multiple distinct traits by varying expression levels of the underlying loci. Moreover, genetic loci affect phenotypes possibly by changing coding or regulatory sequences and thus transcriptional abundance. We study genome-wide allele-specific expression and modes of gene expression inheritance to explore *cis-* or *trans*-evolution in the divergence of parental and hybrid genomes. Our findings have the potential to shed light on how differential gene expression underpins adaptation.

Functional validation of genomic prediction for adaptive alleles. Selection from standing genetic variation, as opposed to novel mutations, has been expected to hasten evolution. If a population is to persist under strong selection, important is the existence of adaptive standing genetic variation. Global climate change is inducing shifts in the selective pressures that shape locally adaptive genetic variation. Using genomic data, we can predict future disruptions to locally adaptive genotype-environment associations. However, what has long been overlooked is to assess the robustness of such predictions, let alone implement reliable predictive results for elite germplasm selection. This line of research allows for moving towards not only estimating but also validating genomic predictions using molecular biological experiments.

Transgenerational environmental effects. Environmental effects could dissipate over time. However, little is known about how much a genotype is able to change its phenotype in response to prior environments. Our endeavors to understand cascading environmental responsiveness are to reveal the extent to which organisms can transmit effects of ancestral and parental environments to distant descendants, whether an antecedent environment reinforces or antagonizes response to

present environments, and how such carryover effects from preceding generations affect response to selection. We eventually hope to address how the ability of plants to memorize prior diverse environments evolves in response to selection and how the environment affects trait variation and thereby the direction and strength of selection on traits.

Our groups of the ARC Centre of Excellence for Plant Success are performing a large-scale divergent selection experiment to generate multiple segregating populations based on pedigree breeding strategies by making crosses over successive generations using a foundation population from the 1,001 Arabidopsis genome project. By performing genomic sequencing of all parental and hybrid individuals, we study the genetic architecture and variation for focal traits and identify genes that lead to significant genetic improvement of traits. Furthermore, we conduct experimental evolution by manipulating biotic and abiotic environments (e.g., soil properties, droughts, CO_2 concentrations, and herbivores) at the University's Plant Growth Facility[1]. We measure the shoot branching and flowering timing phenotypes, coupled with RNA-seq, of each individual under given growth conditions over multiple generations. We use these data to examine many compelling questions with respect to ecology, evolution, and genetics including the four lines of research outlined above. To attain research goals, we utilize a blend of statistic, mathematical, computational, and experimental approaches such as Bayesian modeling in Stan, forward-time genetic simulation in SLiM, coalescent models, machine learning, analytical investigations in Mathematica, population/ quantitative/ phylo-/ functional/ comparative genomics, CRISPR/Cas9 genome editing, etc.

If you are a highly motivated student and seek to pursue a PhD through our project, please email your CV and cover letter to yang.liu4@uq.edu.au to discuss the possibility of joining the team. Additional documents supporting personal qualifications are highly desirable.

Drafted on 5/04/2023 in Brisbane.

P.S. Relevant publications of the principal supervisor over the last three years 2021-2023:

Liu Y.*[2], Erbilgin N., Cappa E.P., Chen C., Ratcliffe B., Wei X., . . . El-Kassaby Y.A. (2023) Decoupling of height growth and drought or pest resistance tradeoffs is revealed through multiple common-garden experiments of lodgepole pine. *Evolution,* **77**, 893-906. DOI: https://doi.org/10.1093/evolut/qpad004

This paper demonstrated the decoupling of resource-dependent allocational tradeoffs between four competing traits using common-garden experiments along a thermal cline.

Liu Y.*, Erbilgin N., Ratcliffe B., Klutsch J.G., Wei X., Ullah A., . . . El-Kassaby Y.A. (2022) Pest defences under weak selection exert a limited influence on the evolution of height growth and drought avoidance in marginal pine populations. *Proceedings of the Royal Society B: Biological Sciences*, **289**, 20221034. DOI: https://doi.org/10.1098/rspb.2022.1034

This is an evolutionary ecology work investigating the adaptability and evolvability of several phenotypic traits of a long-lived tree species in a multidimensional trait space.

Liu Y.* (2022) Conservation prioritization based on past cascading climatic effects on genetic diversity and population size dynamics: Insights from a temperate tree species. *Diversity and Distributions*, **28**, 2712-2728. DOI: https://doi.org/10.1111/ddi.13490

This paper dealt with paleoclimatic effects on genetic diversity and demography, based on which insight was gained into the use of assisted-migration strategies for conservation practices.

Liu Y.* & El-Kassaby Y.A. (2021) Transcriptome-wide analysis of introgression-resistant regions reveals genetic divergence genes under positive selection in *Populus trichocarpa*. *Heredity*, **126**, 442-462. DOI: https://doi.org/10.1038/s41437-020-00388-4

This paper uncovered patterns of genetic and expression divergence across the genome of introgression-resistant attributes in poplar trees.

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[1] ref. https://coo.uq.edu.au/plant-growth-facility
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