

Nowadays, coevolution of a plant host–pathogen Gene-for-gene System is an exciting research topic. Natural selection is known to leave signatures on both of the host-pathogen genes and the linked genomic regions. We can detect these signatures on a whole-genome scale due to recent progress of efficient DNA sequencing technology.

‘Arms Race’ model and ‘Red Queen’ model are two popular models, which describe the dynamics of the coevolutionary processes between host and pathogen genes. In the Arms Race model, an effector allele of the pathogen rapidly increases in the pathogen population, and a new host effector allele rapidly increases correspondingly. In contrast, not only one dominant allele exists in the pathogen population from the Red Queen model. The allele with the largest contribution to pathogen fitness allele increases in frequency, and the host allele related to the effector also increase its frequency in the population. These two types of coevolutionary processes may leave contrasting patterns of DNA polymorphisms and divergence in the genomes of the organisms involved.

An organism’s evolutionary history can be revealed by DNA sequence, which is greatly facilitated by the massively parallel sequencing technologies. The whole-genome population genomics is very powerful in detecting natural selection signatures. There are various tools and applications of population genomics, including genome-wide scans for regions with significantly reduced genetic diversity; tests for the divergence of synonymous: nonsynonymous sites; tests for intraspecies polymorphisms; comparison of interspecies divergence and intraspecies polymorphisms; linkage disequilibrium mapping; identification of target region of selection through the combination of association mapping and evolutionary analysis, *etc.* Besides the plant side, population genomics can also be adopted on the pathogen side to detect selection signatures.

On the host plant side, there are many studies addressing DNA polymorphisms of NBS-LRR R genes and plant defence-related genes. Genes for R proteins directly interacting with AVRs appears to be evolving in an Arms Race manner, whereas genes for guarding R proteins seem to be evolving mainly by balancing selection conforming to the Red Queen scenario. Whole-genome analysis shows the genes for receptor-like kinases, F-box and NBS-LRR proteins are highly variable.

Our presentation will focus on the statistical tools used for population genomics and their applications. We will also present a brief background of the host-pathogen gene-for-gene model. Lastly, we will provide an example from *Magnaporthe oryzae*.