**Hypothesis**:

Plant disease resistance genes may have divergent evolution patterns regarding their roles in innate immune responses.

**Introduction**:

Plants have developed complicated innate immune networks to fight against attacks from plant pathogens. The first layer of active plant defense employs the recognition of pathogen-associated molecular patterns (PAMPs: highly conserved components or molecules from microorganisms, such as bacterial flagellin) by plant pattern recognition receptors (PRRs). PRRs activate the immune response upon recognition of PAMPs, called PAMP-triggered immunity (PTI). The successful pathogens could overcome PTI by injecting effectors into the host plant cytoplasm to suppress PTI responses. During co-evolution, host plants in turn manage to be able to detect the existence of certain effectors from pathogens and trigger effector-triggered response (ETI), the second layer of immune response. Plant disease resistance genes (R-genes) play an essential role in recognizing both the conserved PAMPs and the relatively divergent effectors from various bacteria and fungi. The phylogenetic origin of plant R-genes seems ancient given that certain R-genes motifs are conserved in both animals and plants (indicating common ancestor before speciation???). Computer-based analysis and prediction among different plant species reveal that putative R-genes are abundant in plant genomes and they usually appear in clusters near one another, which also supports a phylogenetically ancient origin (arising through multiple rounds of duplication events: both whole genome duplication and local duplication contribute to the outcome). Despite the common origin and some similar features, R-genes could have undergone divergence considering their roles in disease defense and the distinct evolution pressure they are facing. So, **I am** **extremely happy** to use what I have learned and will learn from the “Molecular Phylogenetics” to examine the evolution patterns among different groups of plant R-genes.

**Data**

Protein sequences of 73 R-genes from 22 plant species with reference of involvement in defense against pathogens from literatures will be downloaded from the website of plant resistance gene database (PRGdb: <http://www.prgdb.org>). The protein sequence of mammalian apoptosis-related protein Apaf1 will be downloaded from NCBI and used as an outgroup.

**Method**:

Phylogenetic Inference

Neighbor joining trees will be obtained using PHYLIP (models for computing distance matrix to be determined, 200?? Bootstrap replicates). RAxML will be used to build ML trees (models to be determined, 200?? Bootstrap replicates). Tree topology will be compared between the two inference methods. The gene clusters from the inferred NJ and ML trees will be validated using the current classifications based on protein structures and motifs of R-genes.

Estimate and Comparison of Evolution Rate Among Different Groups

Use RAxML and obtain trees by using mammalian Apaf1 sequence as an outgroup with different groups of R-genes, respectively. Use the median of clade branch length divided by Apaf1 branch length to compare the relative evolution rate among distinct groups of R-genes.