

HrpN-responsive accession



HrpN-unresponsive accession



X



Phenotype F₁



Phenotype and group F₂

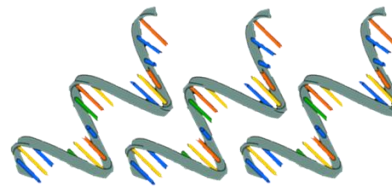
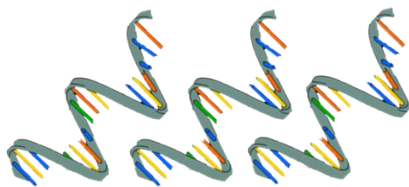
HrpN-responsive



HrpN-unresponsive



Pool DNA samples and sequence



Identify SNPs and other polymorphisms

Reference

A T T G C C G G T T A A T

Read 1

G T T A A T

Read 2

A T T G C C G G T

Read 3

C C G G T T A A

A T T G C C G G T T A A T

G G T A A T

A T T G C C G G G

C C G G G T A A

Overview of Objectives 1 & 2. Tobacco accessions with contrasting responses to HrpN will be crossed to generate F₁ populations. The F₁ will be selfed to generate F₂ populations that display segregation for the HrpN phenotype. Individuals will be grouped into two phenotypic pools, and bulked DNA samples will be generated for each pool. After DNA sequencing, reads from each sample will be aligned to the tobacco reference genome. Genetic polymorphisms present in the HrpN-unresponsive sample (e.g. the red 'G') but not the HrpN-responsive sample will be used to identify candidate genes mediating the phenotype.