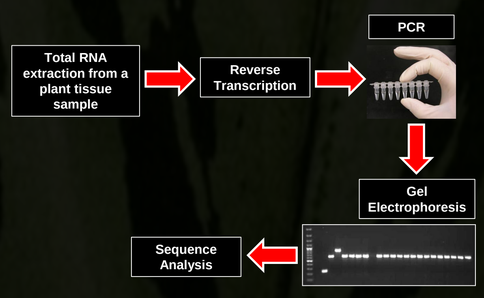
MOLECULAR PLANT PATHOLOGY

Objectives

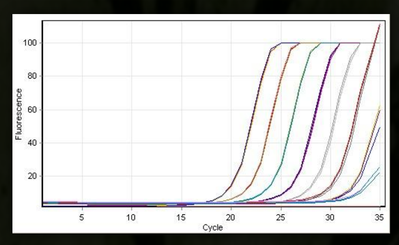
Molecular techniques and technologies are used to accurately and quantitatively detect plant pathogens, to study their interaction with plants on a molecular and/or cellular level, and to investigate plant defense responses against them.

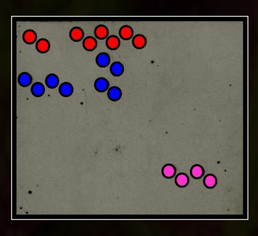
Pathogen identification and quantification

- **PCR**
  The use of species-specific primers, molecular fingerprinting and sequence comparisons to identify important plant pathogens and distinguish between closely-related organisms.



- **Quantitative RT-PCR**
  The quantitative detection of fungal pathogen DNA in plants, water, soil and the air – replacing spore counts. The infection co-efficient (IC) is determined by calculating the ration of pathogen DNA to host DNA.





- **Macro-array analysis**
  Oligonucleotide arrays are developed and used for rapid detection and differentiation of oomycete and fungal species.

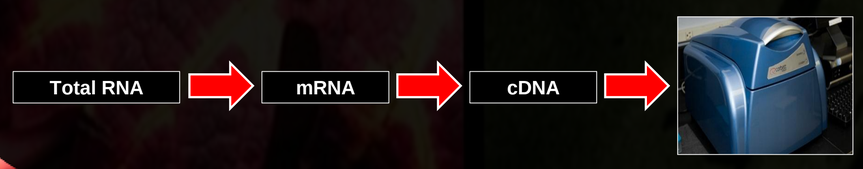
- **Vegetative compatibility groups (VCGs)**
  Fusarium isolates that share common alleles at the same loci are grouped into vegetative compatibility groups following the generation of *nit* mutants that are paired with a known set of VCG testers.

Gene expression analysis

- **Differential gene expression**
  Technologies such as suppression subtractive hybridisation (SSH) are used to compare populations of mRNA in plants and pathogens and isolate differentially expressed genes.

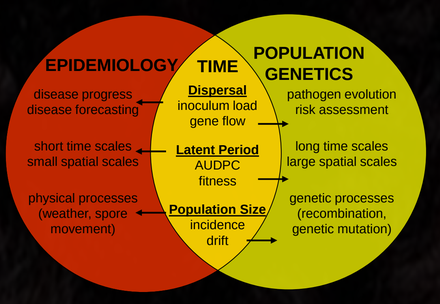
- **Micro-array/Genechip technology**
  The simultaneous expression of large numbers of genes in plants and pathogens are determined by using technologies such as Affimetrix and Agilent.

- **Reverse transcription quantitative PCR (RT-qPCR)**
  RT-qPCR is used to quantify differences in gene expression levels of a specific target (gene) between different samples.

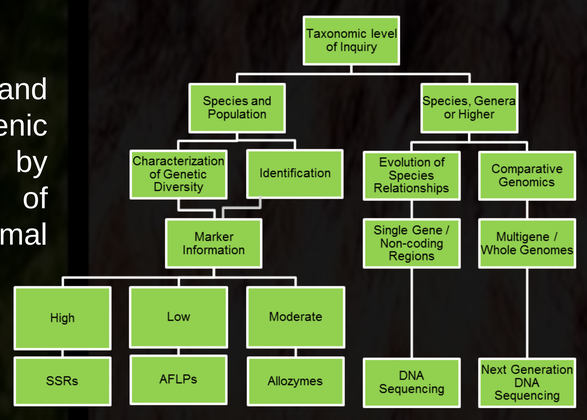


Population genetics and phylogenetics

- **Population genetics**
  Molecular markers, such as short-sequence repeats (SSRs, microsatellites) and AFLPs are used to study variation, migration, gene flow and recombination in fungal populations.



- **Phylogenetics**
  The evolutionary history and taxonomy of plant pathogenic species are determined by phylogenetic analyses of relevant nuclear, ribosomal and mitochondrial genes.



- **Comparative genomics**
  Genes and genomes of plant pathogens are compared by multi-gene and new generation sequencing to study their evolution and diversification.

Genetic modification

- **Recombinant DNA technology**
  Transgenes are inserted in agricultural crops and plant pathogens for studies on host-pathogen interactions and plant resistance.


Red fluorescent *Alternaria* spores


Green fluorescent transgene

- **Mutation breeding**
  Agricultural crops are modified by irradiation for improved resistance to fungal pathogens and their secondary metabolites.

Molecular plant breeding

- **Marker-assisted selection (MAS)**
  Molecular markers are used to identify quantitative trait loci (QTLs) in resistance and susceptible plants that can in future be used for MAS.