

HOMOLOGY SEARCHES

Probes derived from known effectors (e.g. cinnamomin, capsicein, cryptogein) used to hybridise to cDNA libraries

cinnamomin
capsicein
cryptogein

PARA1

1988

1989

1993

1998

Avr1-3069

MAP-BASED CLONING

Classical genetics used to isolate genes required for virulence through a series of backcrosses followed by chromosome walks

MOTIFS

Conserved motifs from known effectors used to search for new candidates from genome and transcriptome sequencing data

CRN1/2

Avr3a +
ATR1

2004

2007

BIOINFORMATIC PIPELINES

In silico hierarchical clustering approaches which combine differential *in planta* expression and multiple known features of effectors to predict and rank candidates

CTP1

2013

GWAS/TWAS

Screen one or multiple populations for phenotypic variation in virulence and analysis of multiple genomes/transcriptomes for the source of this variation. Often paired with map-based cloning.

AvrStb6

2019

NO OR PARTIAL GENOME SEQUENCING ERA

GENOMICS AND POST-GENOMICS ERA

PAN-GENOMES

Avr9

Proteins isolated using polyacrylamide gel electrophoresis (PAGE), reverse-phase HPLC and N-terminal EDMAN sequencing. Later mass spectrometry was used.

PROTEOMICS

2003

Six1

2005

AvrBlb2

2012

Vd2LysM

The genomes of virulent and avirulent phytopathogens compared to identify regions of difference between strains conferring different phenotypes. Subsequently, effector mining was done to identify candidates

LINEAGE SPECIFICITY

2017

Avr_{a9}