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# IMPROVING DISEASE RESISTANCE IN MUNGBEAN- A COMBINED GENETIC AND BIOTECHNOLOGICAL APPROACH

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## INTRODUCTION

Mungbean is an important pulse crop in India mostly grown as a fallow crop in rotation with rice. Mungbean, similar to other pulses, is grown primarily for its protein rich seeds and contains around 20-25% protein. More than 70% of world's mungbean production comes from India. However, demand currently outweighs the production in India. Actual yields are approximately half the yield potential. Most important causes for yield loss are fungal diseases mainly: Cercospora leaf spot (CLS) caused by *Cercospora canescens* and Powdery mildew (PM) caused by *Erysiphe polygoni*. Up to 40% yield losses can be seen because of lack of disease-resistant varieties. Seed treatments and fungicides are cost-prohibitive for small-hold farmers.

## AIM OF THE PROJECT

- Develop a map of CLS and PM diseases across main mungbean growing regions in India as symptoms vary in different geo-ecological regions
- Develop genetic and genomic resources in mungbean to identify and characterize key markers and genes to assist disease resistance breeding
- Identify key pathogenicity related genes in *C. canescens*
- Evaluate HIGS and CRISPR/Cas genome editing to deploy broad-spectrum resistance against CLS and PM, respectively
- Identify best disease management practices by assessing genetic structure and pathogenicity of natural population of *C. canescens*



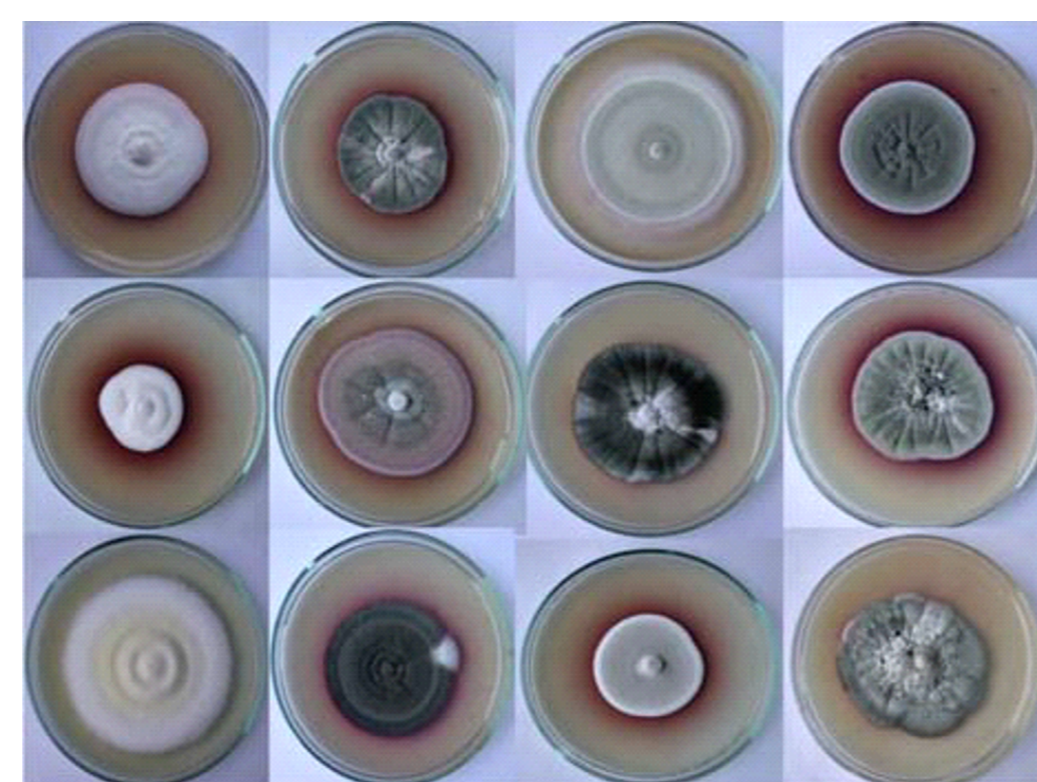
Cercospora leaf spot



Powdery mildew

## UNDERSTANDING CERCOSPORA LEAF SPOT

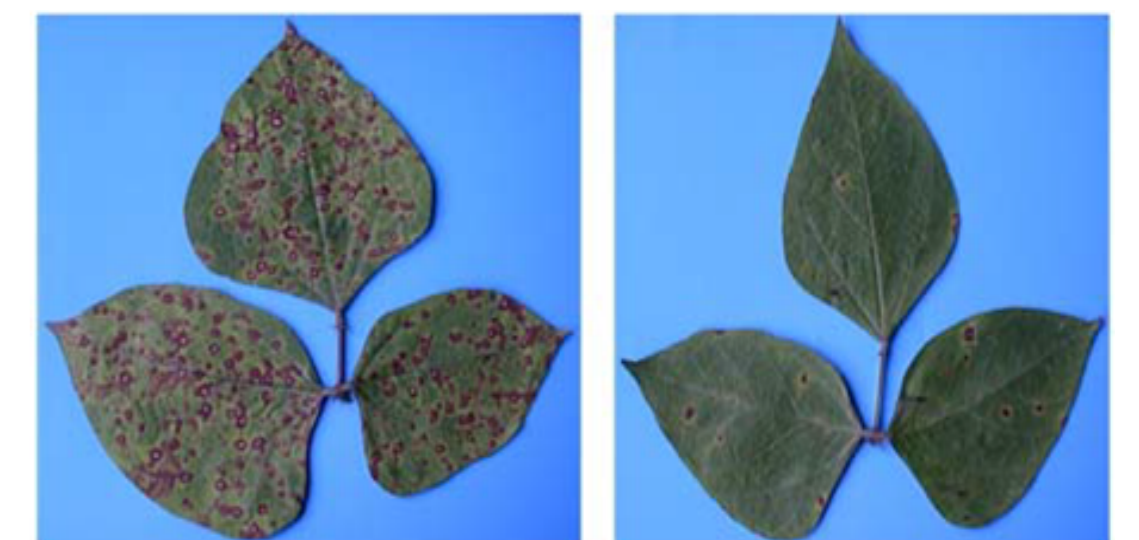
- Huge phenotypic variation between different isolates including growth rate and pigment production
- Isolation of *C. canescens* isolates from major mungbean growing regions in India, which is followed by both *in vitro* and *in planta* characterization for their aggressiveness, pathotype and fungicide sensitivity
- Population structure analysis is being carried out by sequencing to identify genetic variation
- Develop a reference genome sequence to allow identification and future characterization of key pathogenicity related genes



Variation between twelve

## DEVELOPING A BREEDING STRATEGY

- High-density genotyping and QTL analysis to identify genetic markers linked to CLS resistance in mungbean mapping populations and a large diversity panel
- Genotyping by sequencing (GBS) technology on a Ion Torrent PGM system to generate large numbers (>10-20K) of SNPs
- Develop a set of PCR-based diagnostic markers of CLS resistance

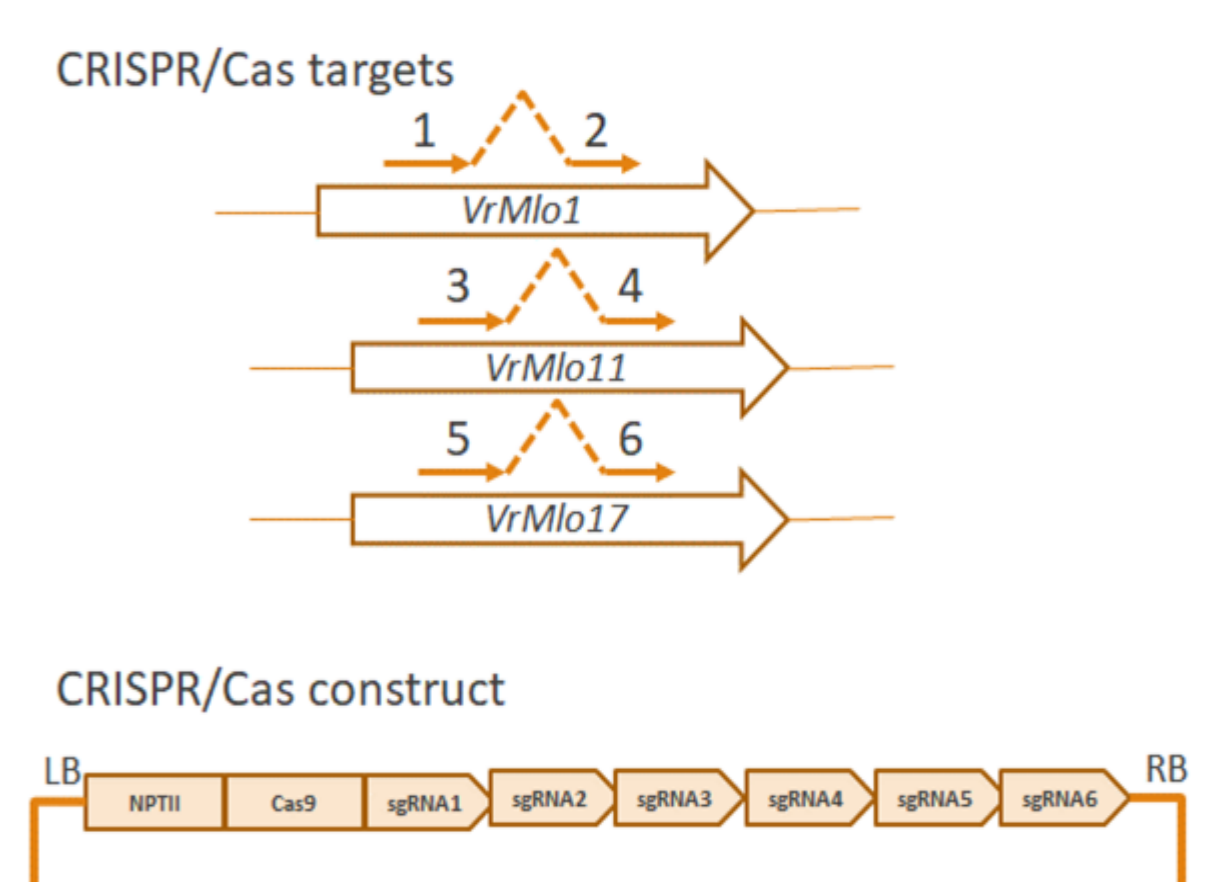


HUM 8 HUM 12  
Mungbean varieties susceptible (HUM8) or resistant (HUM12) to CLS

## HOST-INDUCED GENE SILENCING FOR BROAD SPECTRUM RESISTANCE TO CLS

## CRISPR-CAS9 EDITING FOR PM RESISTANCE

CRISPR/Cas has been used to confer PM resistance in tomato by causing a



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