



Detection of Curtobacterium flaccumfaciens pv. flaccumfaciens in latently infected mungbean plants

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Introduction

- Work as a Bacteriologist
- Netherlands Institute for Vectors, Invasive plants and Plant health (NIVIP) - Bacteriology
- Part of the Netherlands Food and Consumer product Safety Authority
- Diagnostics, research and quality assurance
- Prevention and control of quarantine bacteria in the Netherlands and the EU
- Test (import) plant samples and perform surveys



Fellowship in Australia on *Cff*

- EPPO fellowship for 3 months (call 2025)
- Research bacterium *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (*Cff*) in mungbean (*Vigna radiata*) - Tan spot
- Hosted at Gatton University of Queensland, Australia
- **Why this organism?**
- Quarantine (A2) status in the European Union and small-scale introductions occur (import seeds)
- Bean species are highly susceptible
- Lots of expertise in Australia, pathogen present for >50 years
- *Cff* is a very versatile vascular pathogen that causes wilt and yield loss
- Seed transmitted and easily established
- Many alternative hosts/niches
- Easily introduced, hard eradicate. Prevention is the best solution!



Current situation

- Use of clean seeds (tested) and (visual) surveys, symptoms
- *Cff* can easily escape detection
- Protocols do not focus on asymptomatic field testing for early detection and rapid measures

Research goals

- Research for protocol development for the sampling of latent plants to prevent early spread
- Research factors that increase detection success



Research focus

- Gain experience on the Australian situation and increase knowledge
- Take photos of symptomatic plants
- Sample fields and test several pooled mungbean tissue types (stem, petiole and leaf) with real-time PCR to determine the best strategy for successful pathogen detection
- Test detection levels in natural negative samples with a positive spike representing survey samples, to determine to what level *Cff* can still be detected
- Test potential alternative hosts (*Fabaceae*) growing in mungbean fields
- **Outcome:** better understanding of disease, better sampling protocol for latent testing, clear confirmed symptom images and possible understanding of alternative hosts

Results

- Sampled 27 mungbean fields – stem, petioles, leaves
- 38 weeds (mainly *Fabaceae*)
- Multiplex real-time PCR works well
- Within first tested samples, many samples positive with a high infection rate
- Fast analysis: stem and petiole are yielding the lowest Ct values
- Many weed samples are positive

- Last experiment dilution series infected material
- Further data analysis



Vigna lanceolata weeds among young mungbean (*Vigna radiata*) plants

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Thanks for listening!

- Questions?

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