

# *Curtobacterium flaccumfaciens* on bean and soybean: engaging the old enemy



*Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (CORBFL) - <https://gd.eggo.int>



## Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 138 000

## Research consortium

ILVO (BE), ANSES (FR), CREA (IT), NVWA (NL), NIB (SI), UNIFI (IT), Naktuinbouw (NL), NAQS (NG)

## Contact information

Project coordinator: Johan van Vaerenbergh  
[johan.vanvaerenbergh@ilvo.vlaanderen.be](mailto:johan.vanvaerenbergh@ilvo.vlaanderen.be)

## Goals

*Curtobacterium flaccumfaciens* is listed in the EPPO A2 list of pests recommended for regulation since 1975. Over the last two decades, the disease has only sporadically been reported on dry beans in the EPPO region. Although the identity of the bacterium is well established and identification methods are available, its diversity in terms of phenotype (i.e. pigmented variants), genotype (i.e. virulence repertoires) and pathogenicity (differences in aggressiveness on bean cultivars) is remarkable. The project aims to better understand the virulence of the bacterium and to improve its detection/identification

## Objectives

The project objectives are:

- to collect strains and isolates to cover the biological and geographical diversity of legume-associated *Curtobacterium flaccumfaciens*
- to assess the performance of available diagnostic tests: phenotype characterization (e.g. BIOLOG), serological tests, PCR-based tests (e.g. DNA fingerprinting and DNA barcoding), MALDI-TOF mass spectrometry and whole genome sequencing
- to assess the performance of conventional PCR, real-time PCR and LAMP tests in legume plants and seeds
- to identify virulence markers
- to assign strains of *Curtobacterium flaccumfaciens* to phylogenetic clusters and resolve their taxonomic position

## Key outputs and results

The main project results are:

- Inventory of the *Curtobacterium flaccumfaciens* strains available in certified public collections and in laboratory collections of the project partners with metadata (e.g. biological and geographical origin, year of isolation)
- DNA sequences
- Validated methods for detection/identification
- Map of the main virulence factors