

Full genome and characterization of a new species of *Chryseobacterium* with phytopathogenic potential on *Vicia faba* (Fabaceae; Papilionoidae)

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Chryseobacterium is a genus of the *Flavobacteriaceae* family whose members are usually chemoorganotrophic and form typical yellow-orange colonies due to flexirubin-type pigment. The genus contains more than 100 species from very diverse ecosystems, including freshwater, soil, marine fish, and human hosts. Other sources include lakes, sediments, water cooling systems, drinking water, lactic acid beverages, beer bottling plants, bioreactor sludge, polluted soil, marine sediment and even permafrost. *Chryseobacterium* strains are associated with a multitude of animal guts and feces - mosquitos, cockroaches, millipedes, penguin guano, freshwater copepods-, but also bird feathers, milk, meat and chicken. In agricultural systems, they were recovered from soils, roots, flowers, or decaying plant material, but none was described as phytopathogen so far. *C. indologenes*, mainly found in soil and water, has been reported as uncommon though deadly human pathogen.

Here, we report the complete genome sequence and the phenotype characterization of a new strain and new species of *Chryseobacterium* with a clear though weak phytopathogenic potential on *Vicia faba*. Initially detected in an aphid-associated *V. faba* seedling growth cabinet, it induced typical soft rot in all aphid-harboring plants. The causal agent was identified as *Chryseobacterium* sp., close to *C. indologenes* by 16S amplicon sequencing, but not identical to any characterized species (databases in early 2019). This prompted us to characterize the F3 strain and determine its genome sequence. The genome of strain F3 consists of a circular chromosome of 5,277 Kb without plasmid. The main phenotypic traits of strain F2 are heavy enzyme secretion, among which pectinases and proteases, no direct transmission by aphids at notable frequency but showing increased symptoms on aphid-infected plants, and potential migration through xylem pathway from crown to apex during in planta artificial infection.

Very recently, this strain was shown to belong to the same species as strain JV274.1, a PGPR strain on maize, which was characterized by French colleagues (Vacheron *et al.* 2017), and soon-to-be published as a novel species (Muller *et al.* in prep).

[1] Rahbé, Y., Guschinskaya, N., Droux, M., Valentovich, L., Briolay, J., & Cotte-Pattat, N. (2019). **Full genome and characterization of *Chryseobacterium* xx, a new phytopathogenic strain with pectinolytic, xylem-association and insect interactions.** *Systematic and Applied Microbiology* 2019, In Prep.