

BACTERIAL DISEASES OF BEANS. PRESENCE OF COMMON
BLIGHT IN FRANCE AND INCIDENCES ON BREEDING LINES^{1/}

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Xanthomonas phaseoli var. fuscans, bacteria responsible of the common blight has been isolated in the south west of France on the cultivar "Coco nain blanc précocoe". We name it "Toulouse strain".

Some inoculations have been done and allowed to study a collection of differential hosts.

A good tolerance to this Xanthomonas phaseoli strain has been observed on the following lines: 334.M.1.1 (Mexico), SG 44 (Zafre), PI 207 262 (Colombia, PI 165 078 (Turkey), 355 BL (Costa Rica), HW 5 (C.N.R.A. - France) and LUMAREP (Vilmorin - France). The line 355 BL shows symptoms of hypersensitivity. The highest level of tolerance (or resistance) has been observed in the lines HW 5 and LUMAREP; these lines more particularly proceed from crosses in which PI 150 414, Maxidor and Lumanel are involved.

Inoculations have been parallely done with X. ph. "Toulouse" and Pseudomonas phaseolicola race n° 2. In the studied lines, the reaction is similar for the two bacterias. Particularly the lines HW 5 and LUMAREP, bred for their resistance to Pseudomonas phaseolicola race n° 2, are both also resistant to Xanthomonas phaseoli strain "Toulouse".

INHERITANCE OF DISEASE RESISTANCE OF DRY BEANS, PHASEOLUS VULGARIS,
IN THE TROPICS. I. Rust, common bean mosaic virus
and common bacterial blight.

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Three main diseases affect significantly dry beans production in the tropical areas of Latin America. These diseases are rust,

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Uromyces phaseoli; common bean mosaic virus and common bacterial blight, Xanthomonas phaseoli; which are being studied intensively by the Bean program of Centro Internacional de Agricultura Tropical (CIAT).

A series of studies have been started to have a better understanding on the genetics of resistance to these diseases. Local strains of the three pathogens were utilized in the inheritance studies, as well as different bean varieties.

Bean Rust. Two different segregating F₂ populations were screened for the disease under field conditions. The resistant varieties Cacahuete 72 from Mexico and PR-5 from Puerto Rico, were crossed independently with the susceptible variety Jamapa-Venezuela (CIAT-G.03645).

As a spreader variety in the field, the Colombian black seeded bean ICA-Tui was used due to its high susceptibility. Two readings for the disease were taken 30 and 40 days after planting.

The results in both crosses indicated a significant goodness of fit to the 3:1 ratio of resistant and susceptible plants; with the probability 0.50 - 0.30, when Cacahuete 72 was used as source of resistance, and 0.10 - 0.05 when PR-5 was utilized. The resistant reaction was dominant in both crosses.

Common Bean Mosaic Virus. In this study, we also analyzed two independent F₂ populations. The screening was done in the greenhouse, by using the strain C5. The plants were inoculated eight days after planting and two separate readings of the disease were taken.

The selected resistant varieties, Porrillo Sintetico from El Salvador (CIAT - G.04495) and Jamapa-Venezuela, were crossed with the highly susceptible bean accession (P.I. 310-878).

The analysis of the two populations showed that the resistance was caused by a single recessive gene. The inheritance data indicated a significant goodness of fit, with a probability in both cases of 0.90-0.30.

Common Bean Bacterial Blight. The well-known tolerant variety GN Tara was used in this study of inheritance, and was crossed with Jamapa-Venezuela as the susceptible variety. The inoculation (2×10^8 cells/ml) was done in the screenhouse with the Colombian strain C6, and by using plants 20 days old. Later on, the plants were incubated in a high temperature and relative humidity growth chamber.

Two readings of the reaction of the foliage to the disease, were taken at 8 and 13 days after inoculation. An arbitrary scale 1-4 was considered to measure the disease reactions; the average reaction of the F₂ population being 2.4. These results showed that the inheritance of the tolerant reaction of Tara's foliage to the strain C6, is on a quantitative basis and with additive gene effects.
