# GENETIC VARIABILITY IN POPULATIONS OF *GLOMERELLA CINGULATA* F. SP. *PHASEOLI*

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## INTRODUCTION

The causal agent of common bean anthracnose, *Colletotrichum lindemuthianum* (Sacc. & Magn.) Scribner, asexual phase, presents a wide genetic variability that has complicated the development of resistant cultivars (Silva et al., 2007). The mechanisms responsible for this variability are very little understood. Probably, the sexual reproduction is one of those processes that contribute to increase it. In Brazil, the sexual phase *Glomerella cingulata* f. sp. *phaseoli*, has been isolated in laboratory, without the use of inducers, from stems, leaves and pods lesions collected in experimental and yield common bean fields (Camargo Junior et al. 2007). The objective of this study was to make genetic variability available in populations of *G. cingulata* f. sp. *phaseoli*, collected in Brazil, using RAPD analysis.

## MATERIALS AND METHODS

Five populations of *G. cingulata* f. sp. *phaseoli* were collected in experimental and yield common bean fields in the states of Minas Gerais (Lavras e Lambari) and Paraná (Guarapuava e Turvo), Brazil, during the year 2006. 40 random ascospores were obtained from each population. A total of 200 isolates were grown in liquid medium $M_3$ for 5 days in a rotary shaker (110 rpm at 22°C). For RAPD reactions, genomic DNA was performed according to Raeder & Broda (1985). 300 oligonucleotide primers were carried out and only those with highly intensity and reproducible bands were selected for analysis. Amplification products were separated by electrophoresis and visualized under Ultraviolet light. The genetic similarities and clustering analysis were performed using the program GDA (Genetic Data Analysis) for Nei & Li coefficient (1979) and UPGMA, respectively. The diversity inside five populations was measured with Shannon index for each population (Shannon, 1948).

## RESULTS AND DISCUSSION

Twenty eight oligonucleotide primers (OP M-1, OP M-2, OP M-3, OP M-4, OP M-5, OP M-6, OP M-7, OP M-8, OP M-9, OP M-10, OP M-11, OP M-12, OP M-13, OP M-14, OP M-15, OP M-16, OP M-17, OP M-18, OP M-19, OP M-20, OP L-1, OP L-2, OP L-3, OP L-4, OP L-5, OP L-6, OP L-7, OP L-8) of Operon kit, among the 300 carried out were employed in the molecular analysis. These primers amplified 128 polymorphic bands. An average of 4.57 bands was generated per primer.

The genetic similarity among the isolates ranged from 0.43 a 1.0. The UPGMA cluster analysis allowed the identification of 73 different groups (Figure 1). Five main groups were found, which showed the five populations. Shannon index's estimates of genetic diversity ranged from 0.0827 (TUR), the least diverse population, to 0.3171 for the most diverse population (VAL). These values found based on populations originated from few plants are compared to studies performed by Silva et al. (2007) with asexual populations originated from a great number of isolates from several locations. Theses results indicate the great potential of the sexual reproduction to generate variability in this pathogen.

**Table 1.** Genetic variability of isolates of *Glomerella cingulata* f. sp. *phaseoli* for the five populations, Brazil.

| Population | Similarity coefficient | Shannon index (*I*) |
|---|---|---|
| GUA | 0.59-0.97 (0.38) | 0.2010 |
| MAJ | 0.60-1.00 (0.40) | 0.1348 |
| TUR | 0.80-1.00 (0.20) | 0.0827 |
| VAL | 0.77-0.99 (0.22) | 0.3171 |
| VCU | 0.54-0.97 (0.43) | 0.1452 |

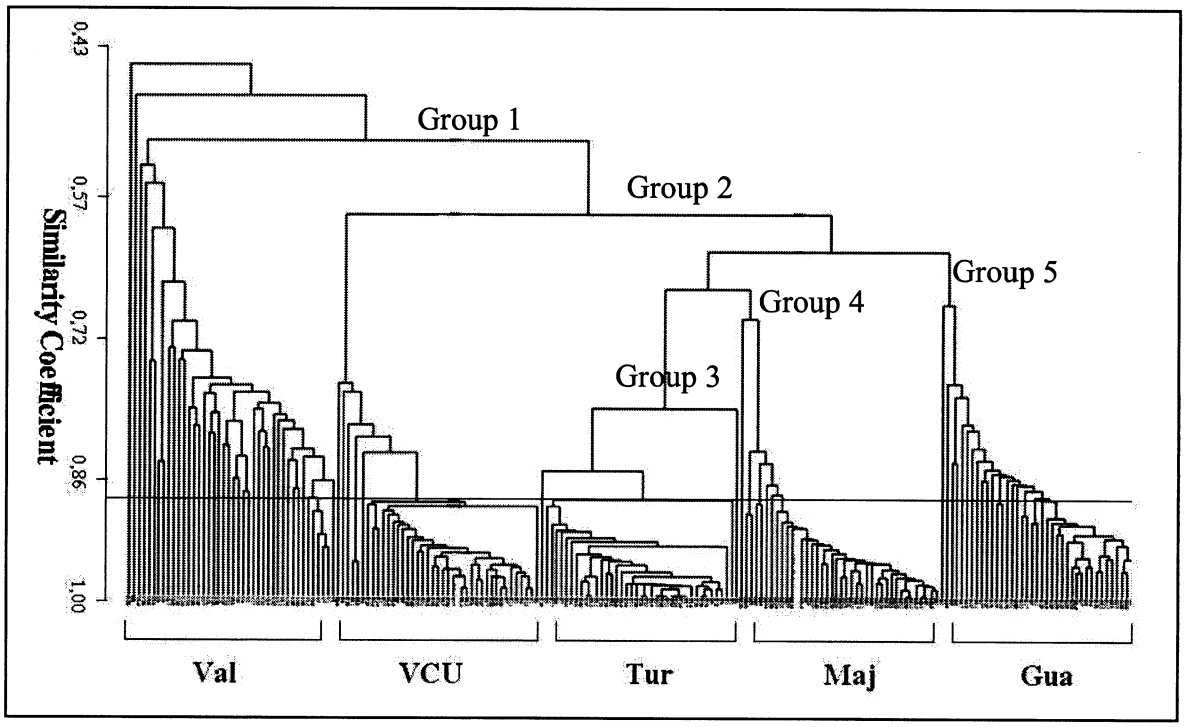


**Figure 1.** Cluster analysis showing the relationship between all 200 isolates of *G. cingulata* f. sp. *phaseoli*, Brazil.

## LITERATURE CITED


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