***Article***

***Bean common mosaic virus* and *Alternaria alternata* epidemiological behavior in 12 *Phaseolus vulgaris* genotypes**

**Agustín Gonzalez-Cruces1**, **Esly Arista-Carmona1**, **Karen Vianey Díaz-Arias1**, **Karina Ramírez-Razo1, Adrián Hernández-Livera1**, **Gustavo Mora-Aguilera1,2\*, Gerardo Acevedo-Sánchez2 and Coral Mendoza-Ramos2**. 1Colegio de Postgraduados, Km 36.5 Carretera México-Texcoco, Montecillo, Texcoco, Estado México, CP 56230, México, Campus Montecillo. 2Laboratorio de Análisis de Riesgo Epidemiológico Fitosanitario (CP-LANREF).

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| ***\*Author correspondence:***Gustavo Mora-Aguilera morag@colpos.mx***Section:***This article was submitted to Special issue “COVID-19 and Plant Health” of this journal.***Received***: 28 Jul. 2020***Accepted***: 05 Aug. 2021***Published***: 01 Sep. 2021 **Citation:**Mora-Aguilera G and Acevedo-Sánchez G. 2021. A retrospective analysis of plant and human epidemics for COVID-19 comprehension. *Mexican Journal of Phytopathology* 39(4). <https://doi.org/10.18781/R.MEX.FIT.2021-27> |

**ABSTRACT**

**Objective/Background.** Research objective was to assess phytosanitary response and epidemiological behavior associated with *Alternaria* spp. and virus symptoms among 12 *Phaseolus vulgaris* genotypes.

**Materials and Methods.** During 2020, assessments were conducted at flowering (June) and fructification (August). Severity was evaluated *in situ* with a 6-class logarithmic-diagrammatic scale setup in App-Monitor® v1.1. Genotype health was determined using Integrated Damage Index (IDI), weighted and adjusted for disease intensity and plant vigor (IV), which was estimated with images (RGB, 14mpx) captured with Phantom-3 at 5 m from genotype centroid. In SAS v9.4, an ANOVA (Tukey, *p*<0.05) in randomized blocks was performed. In SURFER v10, spatial patterns were obtained with kriging and omnidirectional variograms. Forty-three total samples for isolation, pathogenicity testing and molecular identification were performed with universal primers ITS-*Alternaria* and NIb/BL1-Virus. Final data matrix included 22 variables, 859 observations and 18,898 metadata.

**Results.** *Alternaria alternata* (AL) and *Bean common mosaic virus* (BCMV) with 99% homology were identified in 100% of samples analyzed. *Vaquita Negro*, *Garrapato* and *Canario* were statistically (*p*<0.05) most susceptible genotypes (37.3-58%) for BCMV, meanwhile *Canario* and *Tipo Flor de Mayo* (41.4-42.7%) for AL. Spatially, random and aggregate spreading patterns were reported for BCMV. *Vaquita Negro* showed uniform spread at high-intensity, associated with transmissibility by seed. AL, in contrast, reported multiple or aggregate foci patterns. *Tipo Flor de Mayo* and *Canario* exhibited coalescent aggregate foci since flowering due to climatic inductivity optimal for mycelial growth and sporulation. *Oti* and *Negro Perla* had higher climatic adaptability and sanitary tolerance with IV > 0.7 and IDI < 0.43.

**Conclusion**. This approach allows the generation and validation of tools capable of integrating a comprehensive multidisciplinary strategy to improve genetic improvement programs for *P. vulgaris*.

**Keywords:** *Alternaria alternata*, *Bean common mosaic virus*, severity, genotype, common bean

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**Acknowledgments**

In this section, you can acknowledge any support given which is not covered by the author contribution or funding sections.

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| **Results** | SM | - | SM | SM | - | SM |
| **Discussion** | SM | - | SM | SM | - | SM |
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| **Limitations** | SM | Optional | SM | SM | - | SM |
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