

Sorting of Puccinia recondita:Triticum infection-type data sets toward the gene-for-gene model.

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Author(s) : [Browder, L. E.](#) ; [Eversmeyer, M. G.](#)

Author Affiliation : USDA, Kansas State Univ., Manhattan, USA.

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Abstract : Infection-type data, derived from inoculating 14 randomly arranged host lines with 7 randomly arranged cultures of *P. recondita*, were machine sorted sequentially by first rearranging culture order (data columns) according to ascending values of infection-type codes to each host line (data rows). Host-line order (data rows) was then

sequentially rearranged according to descending values of infection-type culture (data columns). This sorting resulted in a table in which lines and cultures were arranged with a generally increasing number of low infection types from top to bottom and a generally increasing number of high infection types from left to right, theoretical gene-for-gene model. Lines were sorted so that a given line could not have all the genes for low reaction carried by any line listed below it in the table. This has direct application in comparing host lines with unknown reaction genotypes with lines with known reaction genotypes. Lines with similar reaction genotypes and cultures with similar pathogenicity genotypes occur together within the table. The data were retained in the original form so that visual analysis of the data could easily be made. The data were arranged so that low infection types produced by corresponding gene pairs occurred diagonally left to right and top to bottom in the table.

ADDITIONAL ABSTRACT: Fourteen wheat lines were inoculated with seven *P. recondita* cultures. The infection-type (IT) data, in a matrix, were sorted by a computer programme that rearranged culture order according to ascending values of IT on each host line (data columns) and then rearranged host line order according to descending values of IT to each culture (data rows). In the resulting table, lines and cultures were arranged with a generally increasing number of low ITs from top to bottom and a generally increasing number of high ITs from left to right, theoretical gene-for-gene model. A given line could not have all the genes for low IT carried by any line listed below it in the table. Low ITs produced by different combinations of genes occurred diagonally from left to right and from top to bottom in the table. The method is considered useful for establishing that new sources of wheat have genes for low IT which differ from those of sources used previously, for demonstrating that a given line does not carry certain genes for low IT and for hypothesising that particular host lines have certain resistance genes. In the present paper it is suggested that Chiccoro "S" carries Lr1 and one or more other genes for low IT and that Waldron carries Lr2a and an additional gene for low IT and that Era carries Lr1.

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