Letter to the Editor

Some Additional Comments on Sorting Infection-Type Data Sets

D. R. Knott and R. Johnson

Professor, Crop Science Department, University of Saskatchewan, Saskatoon, Canada S7N 0W0, and principal scientific officer, Plant Breeding Institute, Cambridge, England CB2 2LQ, respectively.

Browder and Eversmeyer (1) outlined a procedure for computerized sorting of sets of data consisting of infection types (ITs) from interactions between lines of *Triticum aestivum* L. emend. Thell and cultures of *Puccinia recondita* Rob. ex. Desm. In 1981, we (3) pointed out that the sorting procedure produced different results for the same data, depending on the order of the host and pathogen lines in the original, unsorted data. Browder and Eversmeyer (2) agreed that their "previously described program was, in fact, inadequate," and stated that they had revised their sorting program. However, their description of the revisions is incomplete. Browder kindly provided the revised procedure, which involves considerably more cycles of sorting than the original. Based on limited tests with it, we agree that it does sort permutations of either a Person or a Person-Habgood model data set into an isomer of the Person-Habgood form as described by Robinson (6). Browder and Eversmeyer (2) use the premise "that different low ITs are effected by different CGPs" (corresponding gene pairs). Although different CGPs often result in indistinguishable ITs, this does not appear to upset the sorting procedure with regard to other CGPs.

Browder and Eversmeyer (2) claim that "Knott and Johnson's contention that we did not conclusively show five CGPs is the most important issue raised because their other questions seem to stem largely from this." Our major point, that their original sorting procedure did not do what was stated, did not arise from our contention concerning the number of CGPs. With regard to the latter, we pointed out that the evidence for a fifth CGP involving line LR24 (Agent) was incomplete, since all cultures gave an LIT on it. As pointed out by Loegering (4), the gene-for-gene concept "is based on the fact that a gene pair for pathogenicity in the pathogen corresponds to a gene pair for reaction in the host—the corresponding gene pairs." The presence of either a gene pair for pathogenicity in the rust pathogen or a gene pair for reaction in the host cannot be genetically demonstrated until two different ITs have been identified. Browder and Eversmeyer make the assumption that for each different LIT there must automatically be a CGP. While this is probably true in most cases, either resistance or virulence may occasionally be due to two or more genes. Several examples of two gene ratios have been reported in the literature on rust diseases. Furthermore, there is always the possibility that resistance may not be race specific.

Browder and Eversmeyer (2) challenged our statement that in their original procedure "the final order of the host lines and pathogen cultures depends largely on the differences among the ITs in the last row and last column of the unsorted data set." Unfortunately, we said last column when we meant the last column used in the sorting procedure, which is in fact the first column of the

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unsorted data set. The effect of the last row or column used in the sorting with their original procedure can most easily be demonstrated by an example. In one test that we did using a randomization of Browder and Eversmeyer's data (1), the order of cultures after sorting the second last row was 1,4,2,3,5,6,7, and after sorting the last row it was 1,2,7,4,6,5,3. Only culture 1 remained in its same position. While the last row or column used in the sorting does not necessarily change the order, in some cases it can have a major effect, which is to a large extent independent of the sorting of the preceding rows or columns. Browder and Eversmeyer's revised procedure involves repeated sorting. This means that the data are already partially sorted before the final sorting is done, and minimizes the effects of the last row and column used in the final sortings.

Browder and Eversmeyer's (2) statement that "Knott and Johnson apparently fail to recognize the validity and usefulness of this concept," (ie, that a 01C IT is different than a 23X IT) is clearly incorrect. If we had not recognized such differences, we could not have used their original sorting procedure on their unsorted data and obtained their Table 2, a step that we performed to be sure that we understood their procedure. Browder and Eversmeyer's (2) concluding statement that, "Knott and Johnson obviously are approaching IT data analysis from different perspectives than our own, especially as to the importance of IT phenotype differences and as to what is required to demonstrate a CGP," is not really the case. We certainly recognize and use phenotypic differences in ITs. We agree that the demonstration of a new LIT implies the presence of a new CGP, but final proof requires pathogen cultures that give both high and low infection types on the host line, and actual genetic studies of both the host and the pathogen.

The sorting of infection-type data is a way to put them into a form that makes it easier to inspect and analyze by the procedures described by Loegering and Burton (5). Now that Browder and Eversmeyer's method has been revised it appears to provide a useful way of sorting data for this purpose.

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