QUANPLUS: A Spreadsheet for Calculation of Heritability and Generation Mean Separation

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Quantitative traits are often time-consuming to analyze. A spreadsheet has been designed for computers running MS-DOS to quickly estimate heritabilities and additive genetic variance of a quantitative trait for an inheritance study (Ozminkowski et al., 1990). It is also useful for educational purposes. It is based on a six-generation analysis that includes two inbred lines as parents, one with the trait in question (P1) and the other without (P2), the F_1 hybrid (F1), a backcross of the F_1 to each parent (BC1, BC2), and the F_2 population (F2).

The spreadsheet requires Lotus 123, ver. 2 (Cambridge, Mass.), or a compatible spreadsheet program. QUANPLUS can analyze discrete or continuous data. Raw data are entered for discrete variables (e.g., subjective ratings, percentages). Figure 1 shows an analysis of discrete data collected on a 1 to 5 rating scale. In analysis of discrete variables, values entered into the data matrix must be the quantity of plants given each rating value [i.e., 11 P1 plants given a 4 rating (Fig. l)]. Sample variances of discrete data are calculated in hidden columns without the @var subroutine of 123. The data matrix for discrete analysis can be adjusted to accommodate other rating scales or whole number percentages. Analysis of a continuous variable (e.g., yield) requires the number, means, and variances of samples,

The arithmetic mean of the variances of the inbred parents and F_1 samples serves to estimate the environmental variance (@SQR E). The F_2 variance represents the phenotypic variance (sVar F2). The genotype-environment interaction is assumed to be zero. This assumption allows estimation of the ge-netic variance (@SQR G = sVar F2 - @SQR E) (Wright, 1968). The additive component of the genotypic variance (@SQR A) is estimated using the variances of the F_2 and two backcross generations (Warner, 1952). Narrow- and broad-sense heritabilities are calculated as described by Warner (1952) and Fehr (1987), respectively. If backcross generations are unavailable, all parameter estimates, except those of @SQR A and narrow-sense heritability, remain valid.

Means of each generation are compared using a Student's *t* test with unequal variances (Steel and Torrie, 1980). The F_1 vs. mid-parent, F_2 vs. mid-parent, and F_2 vs. the mean of both backcrosses are also tested as verification of complete additivity of the trait (Wright, 1968). Effective degrees of free-dom are calculated, but significance must be determined manually using a Student's t table (Steel and Torrie, 1980)

Another scaling spreadsheet, JNTSCALE (Ng, 1990), is available, but means are not separated and population (not sample) variances must be entered; population variances are also produced by QUANPLUS for use in JNTSCALE. QUANPLUS.WK1 is available for R.H.O. or R.G.G. for a nominal charge or on HortLine, the ASHS BBS (703/836-2418). The spreadsheet is also available for use with Microsoft Excel (Redmond, Wash.) on a Macintosh (Apple Corp., Cupertino, Calif.) microcomputer (from R.H.O).

Literature Cited

Fehr, W.R. 1987. Principles of cultivar development. vol. 1. Macmillan, New York. p. 95-105,

Ng, T.J. 1990. Generation means analysis by microcomputer. HortScience 25:363.

Ozminkowski, R.H., Jr., R.G. Gardner, R.H. Moll, and W.R. Henderson. 1990. Inheritance of prostrate growth habit in tomato. J. Amer. Soc. Hort. Sci. 115:674-677.

Steel, R.G.D. and J.H. Torrie. 1980. Principles and procedures of statistics. 2nd ed. McGraw-Hill, New York. p. 106, 577.

Warner, J.N. 1952. A method for estimating heritability. Agron. J. 44:427-430.

Wright, S. 1968. Evolution and the genetics of populations. Vol. 1: Genetic and biometric foundations. University of Chicago Press, Chicago. p. 391-403.

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                     QUANPLUS 3.0 D
            For Discrete Data (e.g. percentage or ratings)

            <Alt> M for        Press F9 to          <Alt> T for
               Menu            RECALCULATE           Terminology

    Data Matrix                  GENERATIONS
                      === NON-SEGREGATING ===   ===== SEGREGATING =====
    Rating or %]      P1      P2        F1         F2      BC1       BC2
        1.00 ]         0      17         0         31        0        40
        2.00 ]         0       6         5         47        5        46
        3.00 ]         4       1        12         82       26        25
        4.00 ]        11       0         5         52       40         9
        5.00 ]         9       0         1         28       46         0
        0.00 ]         0       0         0          0        0         0
    ===========================================================================
               ]      P1      P2        F1         F2      BC1       BC2
      N        ]      24      24        23        240      117       120
      Sum      ]     101      32        71        719      478       243
      Mean     ]    4.21    1.33      3.09       3.00     4.09      2.03
      Sum SQR  ]     437      50       233       2489     2044       593
      CF       ]  425.04   42.67    219.17    2154.00  1952.85    492.08
      cSS      ]   11.96    7.33     13.83     335.00    91.15    100.93
      sVar     ]   0.520   0.319     0.628      1.402    0.786     0.848
    SE(Mean)   ]   0.147   0.115     0.165      0.076    0.082     0.084
      pVar     ]   0.498   0.306     0.601      1.396    0.779     0.841
    ===========================================================================

    Parameter     Value Std Error     Heritability   Value
    @SQR E        0.489    0.083          Broad       0.651
    @SQR G        0.913    0.153          Narrow      0.834
    @SQR A        1.169    0.296
    ===========================================================================

          Generation Mean Comparison by Student's t Test
                (with unequal variances)    (Steel & Torrie)

                       S(M1-M2)    M1-M2   t' Value  Effective df
    P1 vs. P2            0.187     2.875    15.379      43.5
    P1 vs. F1            0.221     1.121     5.066      44.2
    P1 vs. F2            0.166     1.213     7.311      36.8
    P1 vs. BC1           0.168     0.123     0.729      38.7
    P1 vs. BC2           0.170     2.183    12.881      39.6
    P2 vs. F1            0.202     1.754     8.702      39.6
    P2 vs. F2            0.138     1.663    12.021      46.8
    P2 vs. BC1           0.141     2.752    19.460      49.6
    P2 vs. BC2           0.143     0.692     4.848      51.4
    F1 vs. F2            0.182     0.091     0.500      32.3
    F1 vs. BC1           0.184     0.999     5.412      33.8
    F1 vs. BC2           0.185     1.062     5.726      34.4
    F2 vs. BC1           0.112     1.090     9.724     296.6
    F2 vs. BC2           0.114     0.971     8.545     296.2
    BC1 vs. BC2          0.117     2.060    17.551     235.0
    F1 vs. P1 & P2       0.190     0.316     1.665      22.6
    F2 vs. P1 & P2       0.121     0.225     1.864     259.3
    F2 vs. BC1 & BC2     0.096     0.046     0.481     241.4
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Fig. 1. Sample output from QUANPLUS.WK1 with a discrete variable.