Theor Appl Genet (1991) 81:139

Letter to the Editor

Comment on "Selection system efficiencies for computer-simulated progeny test field designs in loblolly pine"
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Received July 1, 1990; Accepted July 19, 1990
Communicated by R. D. Burdon

Summary. Loo-Dinkins et al. reported relatively poor 'realized' gains from selecting individuals on departures from the means of small multi-tree plots. This could be largely attributed to disregarding a heritability of plot effects.

Key words: Forwards selection – Within-family selection – Genetic gain – Selection accuracy – Field layout

Loo-Dinkins et al. (1990) made a simulation study of the efficiency of alternative progeny test field designs, and selection procedures therefrom, for choosing individual offspring from within the tests (i.e., 'forwards' selection).

The simulations assumed certain variance structures, as well as fixed number of families and total trees, so the main design variable involved a trade-off between block replicate numbers and trees per plot. Two trees from each of the ten top-ranked families were selected. Selection of trees within families was based alternatively on departures from: block means, neighborhood means, or plot means. The outcomes of such selection were compared among selection procedures and with 'expected' gains based on family-mean and within-family heritabilities (Eq. 4).

A consistent result was that, with multi-tree plots, selection of individuals on the basis of departures from plot means gave lower 'realized' gains than the other selection procedures, particularly when the plots were small. The authors suggested, as an explanation, that this stemmed from the fact that "... the sample size being compared for selection was very small." This is effectively invoking the reduced variance associated with comparisons within finite subgroups, i.e., the plots (see Burdon 1982: Eq. 12), which appears valid in itself.

There is, however, another, associated factor that would contribute to the result in question. As I have shown (Burdon 1982; Eq. 25), plot means or plot effects have a heritability stemming from sampling error for within-family genetic variance, and this effectively compensates for the reduced variance within plots. Such a heritability can clearly become appreciable as multi-tree plots become small, two-tree plots being the limiting case. It appears that the particular selection procedure simulated by Loo-Dinkins et al. (1990) did not take account of such a heritability, and could thus be expected to show less than the potential efficiency of the field layout.

As I noted, however, accommodating the heritability of plot effects in selection could be very cumbersome, which still leaves in question the inherent suitability of small, multi-tree plots for forwards selection.

References

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