

Article Title No. 1	Genetic Statistical Model to Estimate Epistasis, Additive and Dominance Genetic Effects Using Advanced Populations.
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Abstract

Most investigations for estimating gene effects contributing to metric traits has been exclusively focused on means of earlier filial (F_1 and F_2) and backcross populations (BC_{11} and BC_{12}). In this paper a novel approach is suggested using data generated from advanced filial ($F_3, F_4 \dots F_n$), and backcross populations (BC_{n1} and BC_{n2}). The following set of equations is derived by algebraic solution of P_1, P_2, F_3, F_4 , and $BC_{32} BC_{31}$ means:

$$\text{Mean (M)} = 1/98(49P_1 + 49P_2 - 64BC_{31} + 128F_4),$$

$$\text{Additive effect (D)} = 1/2(P_1 - P_2),$$

$$\text{Dominance effect (H)} = 1/49(384BC_{31} + 384BC_{32} - 196F_3 - 294P_1 - 294P_2 + 16F_4)$$

Three types of epistasis

$$\text{Additive x additive effect (I)} = 32/49(BC_{31} + BC_{32} - 2F_4),$$

$$\text{Additive x dominance effect (J)} = 1/7(32BC_{31} - 32BC_{32} - 28P_1 + 28P_2) \text{ and}$$

$$\text{Dominance x dominance effect (L)} = 16/49(98F_3 - 68F_4 + 49P_1 + 49P_2 - 64BC_{41} - 64BC_{32})$$

The proposed equations have been proved by means of algebra, in addition to mathematical proof using real data. The results suggest that, the model can serve as a viable particularly to estimate epistasis, additive and dominance genetic effects using the data generated from advanced filial and backcross populations $P_1, P_2, F_3, F_4, BC_{31}$ and BC_{32} .

