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**Genetic Statistical Model to Estimate Epistasis, Additive and Dominance Genetic Effects Using Advanced Populations. (2017).
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Abstract

Estimating gene effects contributing to metric traits has been investigated in several studies. Most estimation methods focused on means of earlier filial (\bar{F}_1 and \bar{F}_2) and backcross populations (\overline{BC}_{11} and \overline{BC}_{12}). In this paper, a novel approach is proposed to estimate gene effect using the data generated from advanced filial ($\bar{F}_3, \bar{F}_4 \dots \bar{F}_n$) and backcross populations (\overline{BC}_{n1} and \overline{BC}_{n2}). Where the following set of equations is derived by algebraic solution of $\bar{P}_1, \bar{P}_2, \bar{F}_3, \bar{F}_4, \overline{BC}_{31}$ and \overline{BC}_{32} means:

$$\text{Mean (M)} = \frac{1}{98} (49 \bar{P}_1 + 49 \bar{P}_2 - 64 \overline{BC}_{31} - 64 \overline{BC}_{32} + 128 \bar{F}_4),$$

$$\text{Additive effect (D)} = \frac{1}{2} (\bar{P}_1 - \bar{P}_2),$$

$$\text{Dominance effect (H)} = \frac{1}{49} (384 \overline{BC}_{31} + 384 \overline{BC}_{32} - 196 \bar{F}_3 - 294 \bar{P}_1 - 294 \bar{P}_2 + 16 \bar{F}_4)$$

Three types of epistasis:

$$\text{Additive x additive effect (I)} = \frac{32}{49} (\overline{BC}_{31} + \overline{BC}_{32} - 2 \bar{F}_4),$$

$$\text{Additive x dominance effect (J)} = \frac{1}{7} (32 \overline{BC}_{31} - 32 \overline{BC}_{32} - 28 \bar{P}_1 + 28 \bar{P}_2) \text{ and}$$

Dominance x dominance effect (L) = $\frac{16}{49} (98 \bar{F}_3 - 68 \bar{F}_4 + 49 \bar{P}_1 + 49 \bar{P}_2 - 64 \overline{BC}_{31} - 64 \overline{BC}_{32})$ 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 $\bar{P}_1, \bar{P}_2, \bar{F}_3, \bar{F}_4, \overline{BC}_{31}$ and \overline{BC}_{32} .