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Abstract

As a result of two crosses among three local varieties of wheat, five populations (P_1, P_2, F_5, F_6 and F_7) were used as parents and grown during two successive seasons; 2016/2017 and 2017/2018. To estimate five types of gene action (e.g., mean effects, additive, dominance, additive × additive, and dominance × dominance), five formulas were developed from with algebraic solution, algebraic proof, and mathematical proof. Besides, to test adequate of a simple additive-dominance model, three formulas A, B, and C scaling test were developed. The path analysis method by PROCESS Macro, AMOS, and Bootstrapping was employed to assess the relationships between grain yield/plant (GYP) as the dependent variable and each one of the number of spikes (NS) and 1000-grain weight (TW) as the independent variables. The results show that there are eight validated equations used to estimate the scaling test (A, B and C) and five types of gene effects (m, a, D, I and L), respectively. Confidence interval using Bootstrapping results indicate that TW was played as the partial mediator between NS as an exogenous variable and GYP as an endogenous variable. Generation means analysis is a relatively simple and

statistically reliable tool suitable for the fundamental estimation of different genetic influences.