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K **:** Generation mean analysis; inheritance; agronomic traits; additive; dominance

I

Tomato constitutes 7% of total horti167[ture produce in Kenya and agronomic traits including leaf, oral, growth habit, crop yields and yield components provide valuable information for crop improvement programmes [9, 10] revealed that morphological and agronomic traits not only provide consumer satisfaction and quality raw materials for the processing industry but also enhance the competitiveness of tomato crop in horticultural sector. Knowledge on the relative contribution of various traits to yields can signi cantly facilitate identi cation of high yielding genotypes from a population of varying genotypes [11]. Study nding of Adelana, (1975) as reported by attributed poor tomato yields as a result of owers not developing into fruits [12]. ere are limited tomato technologies, innovations and management practices in Kenya and most African countries [1, 13]. Moreover, breeding programs in Kenya have only focused on cereals, pulses, root and beverage crops, an elevation of 1820m above sea level (ASL) which is at agro-ecological zone (AEZ) III. It has a bimodal rainfall of 1059 mm per year distributed in two seasons which are the long rains (March to May) and short rains (October to December). Temperature ranges from 12.3 to 22.5°C and soils are humic nitisols that are deep and well-drained with a pH of 5.0 to 5.4 [17].

Mwea Research Station is located at 0°41'S; 037°21'E with an elevation of 1247m ASL which is at agro-ecological zone II. e area has a bimodal rainfall regime of 973 mm annually with long rains (March to May) and short rains (October to December). Temperature ranges from 15.6 to 28.6°C and soils are Niti-rhodic ferrosols with a pH of about 5.1 [18].

E

e experiment involved development of study populations and eld evaluations of progenies and their parents. Study populations were developed at Kabete Field Station (April and September 2018) using a randomized complete block design with three replicates. Hybridization of 5 parental lines in 10 x 10 half diallel mating design excluding reciprocals was carried out from April-August 2018 and backcrosses to both parents from September-December 2018 at Kabete Field Station following a modi ed protocol of [19].

e study used 5 tomato genotypes, i.e., 3 breeding genotypes from the World Vegetable Centre (AVRDC) in Taiwan namely; AVT01424, AVT01429 and AVT01314, a commercial cultivar from Continental Seeds Company Limited known as Roma VF, and Valoria selection from farmers in Kirinyaga County. Genotypes AVTO1424 and ATO1314 are semi-determinate and AVTO1429 is indeterminate that matures and owers early suitable for open eld cultivation. However, performances of these genotypes and productivity in terms of yields have not been determined in Kenya [13]. Commercial variety Roma VF is a determinate pure-line that owers and matures early. Moreover, this variety is low yielding, require staking, lacks trait for resistance to bacterial wilt and insect pests [1]. Valoria selection is a determinate line preferred by farmers in Central Kenya and requires staking. Besides, the selection is low yielding, late owering, late maturing, and their traits have not been validated.

D

Four bi-parental crosses were developed from Roma VF and AVTO1429, AVTAO1424, AVTO1314 and Valoria Select giving F

Segregation ratios were subjected to chi-square tests to establish goodness-of-fit for observed ratios. The outcome was compared with the observed results to determine whether the differences are because of chance or other traits hence:-

Chi-square= (Observed- Expected)^2 / Expected

Hence, $x^2 = \sum [(O-E)^2 / E]$

The calculated chi-square value was used to determine P (probability) value from the chi-square table. If *P*-value obtained <5%, Due to insigni cant di erence (P≤0.01) on additive, dominance, additive x additive interaction, and additive x dominance interaction

followed closely BC_1P_2. Di erences among the generations for each trait were signi cant.

From the 6-parameter model, the combined gene e ects (3.6) were higher than the interaction components (2.29) put together. Duration to owering and maturity was controlled by dominance gene e ects (2.69**) and the interactions of additive x additive e ects (5.24**) and dominance x dominance interactions (-4.49**). ese

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