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# Character association and path analysis studies in tamarind (*Tamarindus indica* L.) genotypes

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### Abstract
The present study was carried out at HRES, Hidkal Dam, Belagavi district, Karnataka during the year 2019-2020, to investigate the character association, direct and indirect effect of pod traits on tree yield among various genotypes of tamarind. The analysis of variance found to be highly significant among genotypes for all the yield parameters. Pod yield per tree (kg/tree) had highly significant and positive correlation with all the characters studied such as pod length, pod width, pod girth, pulp weight, shell weight, seed weight, vein weight, number of seeds, pod weight, pulp per cent and vein per cent except seed per cent and shell per cent. Path analysis studies revealed that seed weight, pod length, number of seeds and vein weight had positive direct effect on pod yield per tree.

**Keywords:** Genotypic correlation, phenotypic correlation, genotypic path analysis, phenotypic path analysis

### Introduction
Tamarind (*Tamarindus indica* L.) is a hardwood evergreen monotypic genus, multipurpose tree species belongs to dicotyledonous family Leguminosae and sub-family Ceasalpinae. It is a diploid species with somatic chromosome number of 2n=24 (Kumar *et al.*, 2015) [9]. The species is natural to tropical Africa, it has a broad geographical distribution throughout the world in tropical, subtropical and semi-arid zones with a prime concentration in India, apart from western dry regions and Himalayas. The term tamarind is derived from the Arabic word "Tamar-E-Hind" meaning "Date of India" (Pooja *et al.,* 2018) [14].

It has been acclimatized to many places of the world and extensively cultivated in Bangladesh, India, Malaysia, Myanmar, Thailand, several African, European and central American countries (Rao and Mathew, 2012) [15]. It is predominantly found in the Indian states of Andhra Pradesh, Maharashtra, Karnataka, Madhya Pradesh, Tamil Nadu, West Bengal, Bihar and Chhattisgarh. Pulp was the most exported product of tamarind, India is the main producer of tamarind in the world with the yearly production of 3 lakh tons, of which 1.15 lakh tons of pulp per annum exported to various countries *viz.* USA, Australia, Sri Lanka, Malaysia, Pakistan beside some European countries etc. (Sinha *et al.,* 2015) [17].

Tamarind conventionally grown mainly for its pulp since ages, which is a chief culinary ingredient. Virtually whole tree has some specific use, but the utmost useful part is the pod (fruit). Fruit encompasses a sweetish, acidic pulp, which is commonly used for souring curries, sauces, chutneys and certain beverages. It is an ironic source of vitamins, minerals and similarly contains more of calcium than any other fruit. Hence, it has a potential and commercial future in the post-harvest products like pickles, candy, juices, soft drinks, jams and confectioneries. The pulp comprises a small amount of carotene, thiamine, nicotinic acid which is used to cure dysentery and it also have some other medicinal values (Pooja *et al.,* 2018) [14]. In traditional medicine, it is used in wound healing, abdominal pain, dysentery, diarrhoea, parasitic infestation, malaria, fever and respiratory problems because of its fungicidal and bactericidal properties. It is typically used in tropical countries because of its laxative, carminative, refrigerant and aphrodisiac properties (Kuru, 2014) [10].

Tamarind is highly cross-pollinated crop, heterozygous and it is grown as backyard, roadside tree even in waste and barren lands with seedling origin trees. Seedlings exhibit a wide range of variation which aids in the selection of the superior desirable genotypes. The plants show high degree of variations found in natural population as the trees are generally cross pollinated, hence they show wide range of heterozygosity. The variation primarily is observed for characteristics such as growth, pod weight, pod shape, pulp colour and fruit yield. So, it is very essential to study the existence of variability among several genotypes based on morphological difference and also by using markers to select the genotypes with superior characteristics for better yield and quality fruits.

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To identify elite genotype and to know the amount of diversity exist in tamarind crop, the present study was undertaken with a following objective to study the "Character association and path analysis studies for yield contributing traits in tamarind".

## Materials and Methods
The experimental materials for the present study consists of 61 tamarind genotypes, which are of 20 years old plants at Horticulture research experimental station, Hidkal Dam. The observations on 15 quantitative parameters like pod length (cm), pod width (cm), pod girth (cm), pulp weight (g), shell weight (g), seed weight (g), vein weight (g), number of seeds, pod weight (g), pulp per cent (%), shell per cent (%), seed per cent (%), vein per cent (%), pulp to shell ratio and pod yield per tree (kg/tree). In the present study each genotype was considered as a treatment, 10 fruits from one tree were collected and 5 fruits are grouped as one replication hence, 2 replications are made (61 treatments and 2 replications). The data was analysed through Randomized Complete Block Design using the mean values of 15 traits to find out the significance of genotypes. Genotypic and phenotypic correlation between fourteen quantitative traits was estimated following the method given by Aljibourie et al., 1958; whereas genotypic and phenotypic path coefficient analysis was done by method given by Dewey and Lu (1959) [5]

## Results and Discussion
### Character association
Correlation studies specify the degree of inter-relationship of plant traits for improvement of yield and yield attributing characters in any breeding program. Hence, comprehension of the inter-relationship between fruit yield per plant and yield attributing characters is vital importance for effective selection and improvement of any yield characters. Correlation is an estimate of degree of relationship between two traits. In the present study both genotypic and phenotypic correlation were performed for yield per plant and its attributing characters. Generally genotypic correlation is higher than phenotypic correlation for most of characters analyzed. Genotypic correlation indicates the inherent association between genes controlling any two traits thus helps in effective selection scheme.

Phenotypic correlation and genotypic correlation data was presented in table-1 and table-2 respectively. Pod yield per plant showed highly significant and positive association with pod length, number of seeds, pod weight, seed weight, vein weight per pod, pulp weight, pod width, shell weight. Significant positive association with pulp per cent, vein per

cent pod girth and positively non-significant association with seed per cent at both phenotypic and genotypic levels which indicates that these traits suggest effective selection for increased yield. Similar results are reported by Bhogave et al. (2018) and Mayavel et al. (2018) [3, 12].

### Path coefficient analysis
Yield is a complex trait and is composed of dependent and independent characters which contribute directly as well as indirectly through each other. Selection based on only correlation study for high yield would be misleading. Since a trait may not be directly associated with yield may be depend on other traits. Through path analysis, it is possible to find out the direct and indirect influence of component characters on the yield. This technique was developed by Wright (1921) [19] and demonstrated by Dewey and Lu (1959) [5] helps in dividing correlation coefficient into direct and indirect association of different characters on the yield.

In the present study, path analysis between the components of pod yield per plant in tamarind was calculated. As the only genotypic correlations are inherent, so the path analysis is discussed only at genotypic level. In the current research, among 14 traits chosen for path analysis which revealed that, seed weight, pod length, number of seeds and vein weight had maximum positive direct effect on pod yield per tree (Table-4). Similar findings were reported by Divakara (2008) [6], Pooja et al. (2018) [14], Agasimani et al. (2019) [1]. So direct selection of plant based on any of these independent traits leads to improvements of genotypes for tamarind pod yield per tree. Whereas, maximum negative direct effect on pod yield per tree was observed by pulp weight, pod weight, pod girth, pod width, seed per cent, shell weight, so these traits do not contribute to the selection of genotypes for improvement of yield. Similar findings were reported by Singh and Nandini (2014) [16], Agasimani et al. (2019) [1], Mayavel et al. (2018) [12].

## Conclusion
Pod yield per plant showed highly significant and positive association with pod length, number of seeds, pod weight, seed weight, vein weight per pod, pulp weight, pod width and shell weight which indicates that these traits suggest effective selection for increased yield. path analysis which revealed that, seed weight, pod length, number of seeds and vein weight had maximum positive direct effect on pod yield per tree, so direct selection of plant based on any of these independent traits leads to improvements of genotypes for tamarind pod yield per tree.

**Table 1:** Phenotypic correlation coefficients among pod traits in tamarind genotypes

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1.000 | 0.535** | 0.437** | 0.632** | 0.629** | 0.634** | 0.507** | 0.518** | 0.698** | 0.192* | -0.220* | -0.011 | 0.091 | 0.577** |
| 2 | | 1.000 | 0.446** | 0.790** | 0.558** | 0.629** | 0.442** | 0.352** | 0.758** | 0.461** | -0.396** | -0.117 | -0.032 | 0.306** |
| 3 | | | 1.000 | 0.550** | 0.503** | 0.499** | 0.502** | 0.417** | 0.586** | 0.300** | -0.291** | -0.093 | 0.121 | 0.180* |
| 4 | | | | 1.000 | 0.648** | 0.790** | 0.556** | 0.541** | 0.944** | 0.649** | -0.570** | -0.161 | -0.030 | 0.424** |
| 5 | | | | | 1.000 | 0.684** | 0.488** | 0.486** | 0.804** | 0.002 | 0.126 | -0.149 | -0.004 | 0.268** |
| 6 | | | | | | 1.000 | 0.551** | 0.787** | 0.920** | 0.166 | -0.527** | 0.395** | -0.028 | 0.433** |
| 7 | | | | | | | 1.000 | 0.433** | 0.631** | 0.159 | -0.327** | -0.074 | 0.763** | 0.429** |
| 8 | | | | | | | | 1.000 | 0.673** | 0.104 | -0.470** | 0.383** | 0.047 | 0.463** |
| 9 | | | | | | | | | 1.000 | 0.390** | -0.458** | 0.020 | 0.018 | 0.443** |
| 10 | | | | | | | | | | 1.000 | -0.648** | -0.485** | -0.093 | 0.221* |
| 11 | | | | | | | | | | | 1.000 | -0.304 | -0.047 | -0.340** |
| 12 | | | | | | | | | | | | 1.000 | -0.150 | 0.050 |
| 13 | | | | | | | | | | | | | 1.000 | 0.196* |

* significant at 5 per cent ** significant at 1 per cent Table 'r' at 5% 0.177 at 1% 0.232

| | |
|---|---|
| 1. Pod length (cm) | 5. Shell weight (g) |
| 2. Pod width (cm) | 6. Seed weight (g) |
| 3. Pod girth (cm) | 7. Vein weight (g) |
| 4. Pulp weight (g) | 8. Number of seeds |

9. Pod weight (g) — 13. Vein per cent (%)
10. Pulp per cent (%) — 14. Pod yield (kg/tree)
11. Shell per cent (%)
12. Seed per cent (%)

**Table 2:** Genotypic correlation coefficients for pod traits in tamarind genotypes

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1.000 | 0.668** | 0.523** | 0.815** | 0.865** | 0.837** | 0.634** | 0.776** | 0.907** | 0.270** | -0.294** | -0.037 | 0.096 | 0.710** |
| 2 | | 1.000 | 0.477** | 0.917** | 0.649** | 0.758** | 0.492** | 0.447** | 0.877** | 0.590** | -0.501** | -0.139 | -0.047 | 0.336** |
| 3 | | | 1.000 | 0.668** | 0.609** | 0.605** | 0.607** | 0.512** | 0.699** | 0.445** | -0.393** | -0.156 | 0.171 | 0.208* |
| 4 | | | | 1.000 | 0.689** | 0.831** | 0.574** | 0.599** | 0.956** | 0.708** | -0.617** | -0.169 | 0.005 | 0.461** |
| 5 | | | | | 1.000 | 0.706** | 0.574** | 0.494** | 0.823** | 0.100 | 0.028 | -0.203* | 0.124 | 0.307** |
| 6 | | | | | | 1.000 | 0.595** | 0.812** | 0.931** | 0.318** | -0.604** | 0.330** | 0.044 | 0.487** |
| 7 | | | | | | | 1.000 | 0.525** | 0.666** | 0.161 | -0.315** | -0.109 | 0.783** | 0.466** |
| 8 | | | | | | | | 1.000 | 0.704** | 0.271** | -0.612** | 0.345** | 0.182* | 0.571** |
| 9 | | | | | | | | | 1.000 | 0.493** | -0.523** | -0.026 | 0.091 | 0.485** |
| 10 | | | | | | | | | | 1.000 | -0.709** | -0.392** | -0.179* | 0.267** |
| 11 | | | | | | | | | | | 1.000 | -0.322** | 0.025 | -0.392** |
| 12 | | | | | | | | | | | | 1.000 | -0.170 | 0.051 |
| 13 | | | | | | | | | | | | | 1.000 | 0.228* |

* significant at 5 per cent ** significant at 1 per cent Table 'r' at 5% 0.177 at 1% 0.232

| | | | |
|---|---|---|---|
| 1. Pod length (cm) | 5. Shell weight (g) | 9. Pod weight (g) | 13. Vein per cent (%) |
| 2. Pod width (cm) | 6. Seed weight (g) | 10. Pulp per cent (%) | 14. Pod yield (kg/tree) |
| 3. Pod girth (cm) | 7. Vein weight (g) | 11. Shell per cent (%) | |
| 4. Pulp weight (g) | 8. Number of seeds | 12. Seed per cent (%) | |

**Table 3:** Phenotypic path analysis for yield traits in tamarind genotypes

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | rP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 0.523 | -0.002 | -0.107 | 2.116 | 0.785 | 1.774 | 0.568 | 0.159 | -5.214 | -0.274 | 0.305 | 0.016 | -0.072 | 0.577 |
| 2 | 0.28 | -0.004 | -0.109 | 2.645 | 0.697 | 1.76 | 0.495 | 0.108 | -5.657 | -0.657 | 0.551 | 0.172 | 0.025 | 0.306 |
| 3 | 0.228 | -0.002 | -0.244 | 1.841 | 0.628 | 1.397 | 0.562 | 0.128 | -4.374 | -0.428 | 0.404 | 0.136 | -0.096 | 0.180 |
| 4 | 0.331 | -0.003 | -0.134 | 3.347 | 0.809 | 2.211 | 0.623 | 0.166 | -7.051 | -0.926 | 0.792 | 0.235 | 0.024 | 0.424 |
| 5 | 0.329 | -0.002 | -0.123 | 2.168 | 1.249 | 1.914 | 0.546 | 0.15 | -6.005 | -0.003 | -0.176 | 0.218 | 0.003 | 0.268 |
| 6 | 0.332 | -0.002 | -0.122 | 2.646 | 0.854 | 2.797 | 0.617 | 0.242 | -6.87 | -0.237 | 0.732 | -0.578 | 0.022 | 0.433 |
| 7 | 0.265 | -0.002 | -0.123 | 1.861 | 0.609 | 1.542 | 1.119 | 0.133 | -4.709 | -0.227 | 0.455 | 0.108 | -0.604 | 0.430 |
| 8 | 0.271 | -0.001 | -0.102 | 1.811 | 0.607 | 2.201 | 0.485 | 0.307 | -5.022 | -0.148 | 0.653 | -0.561 | -0.037 | 0.463 |
| 9 | 0.365 | -0.003 | -0.143 | 3.161 | 1.004 | 2.574 | 0.706 | 0.207 | -7.466 | -0.556 | 0.637 | -0.03 | -0.014 | 0.443 |
| 10 | 0.101 | -0.002 | -0.073 | 2.173 | 0.002 | 0.465 | 0.178 | 0.032 | -2.912 | -1.426 | 0.9 | 0.71 | 0.074 | 0.221 |
| 11 | -0.115 | 0.002 | 0.071 | -1.908 | 0.158 | -1.474 | -0.366 | -0.144 | 3.421 | 0.924 | -1.39 | 0.445 | 0.037 | -0.340 |
| 12 | -0.006 | 0.0001 | 0.023 | -0.538 | -0.186 | 1.104 | -0.082 | 0.118 | -0.151 | 0.691 | 0.422 | -1.465 | 0.119 | 0.050 |
| 13 | 0.048 | 0.0001 | -0.03 | -0.1 | -0.005 | -0.077 | 0.854 | 0.014 | -0.133 | 0.132 | 0.065 | 0.219 | -0.792 | 0.196 |

Residual = 0.7308

* significant at 5 per cent ** significant at 1 per cent rP- Pod yield per tree (kg/tree)

| | | | |
|---|---|---|---|
| 1. Pod length (cm) | 5. Shell weight (g) | 9. Pod weight (g) | 13. Vein per cent (%) |
| 2. Pod width (cm) | 6. Seed weight (g) | 10. Pulp per cent (%) | |
| 3. Pod girth (cm) | 7. Vein weight (g) | 11. Shell per cent (%) | |
| 4. Pulp weight (g) | 8. Number of seeds | 12. Seed per cent (%) | |

**Table 4:** Genotypic path analysis for yield traits of tamarind genotypes

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | rG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 0.471 | -0.282 | -0.33 | -0.055 | -0.652 | 1.146 | 1.436 | 0.353 | -1.224 | -0.251 | 0.217 | 0.057 | -0.177 | 0.710 |
| 2 | 0.315 | -0.422 | -0.301 | -0.062 | -0.489 | 1.038 | 1.113 | 0.204 | -1.183 | -0.55 | 0.369 | 0.218 | 0.086 | 0.336 |
| 3 | 0.246 | -0.201 | -0.631 | -0.045 | -0.459 | 0.828 | 1.374 | 0.233 | -0.943 | -0.415 | 0.29 | 0.245 | -0.314 | 0.208 |
| 4 | 0.384 | -0.386 | -0.421 | -0.068 | -0.52 | 1.138 | 1.300 | 0.273 | -1.29 | -0.66 | 0.455 | 0.265 | -0.008 | 0.461 |
| 5 | 0.408 | -0.273 | -0.384 | -0.047 | -0.754 | 0.967 | 1.300 | 0.225 | -1.11 | -0.093 | -0.021 | 0.318 | -0.228 | 0.307 |
| 6 | 0.395 | -0.32 | -0.382 | -0.056 | -0.532 | 1.369 | 1.348 | 0.37 | -1.256 | -0.296 | 0.445 | -0.517 | -0.081 | 0.487 |
| 7 | 0.299 | -0.207 | -0.383 | -0.039 | -0.433 | 0.815 | 2.264 | 0.239 | -0.899 | -0.15 | 0.232 | 0.17 | -1.442 | 0.466 |
| 8 | 0.366 | -0.189 | -0.323 | -0.041 | -0.372 | 1.112 | 1.188 | 0.456 | -0.95 | -0.252 | 0.451 | -0.541 | -0.335 | 0.571 |
| 9 | 0.428 | -0.37 | -0.441 | -0.065 | -0.62 | 1.275 | 1.508 | 0.321 | -1.349 | -0.459 | 0.385 | 0.041 | -0.167 | 0.485 |
| 10 | 0.127 | -0.249 | -0.281 | -0.048 | -0.076 | 0.435 | 0.365 | 0.123 | -0.665 | -0.932 | 0.522 | 0.614 | 0.33 | 0.267 |
| 11 | -0.139 | 0.211 | 0.248 | 0.042 | -0.021 | -0.827 | -0.714 | -0.279 | 0.705 | 0.66 | -0.737 | 0.504 | -0.046 | -0.392 |
| 12 | -0.017 | 0.059 | 0.099 | 0.011 | 0.153 | 0.451 | -0.246 | 0.157 | 0.035 | 0.365 | 0.237 | -1.567 | 0.314 | 0.051 |
| 13 | 0.045 | 0.02 | -0.108 | 0.0003 | -0.093 | 0.06 | 1.772 | 0.083 | -0.122 | 0.167 | -0.018 | 0.267 | -1.843 | 0.228 |

Residual = 0.5779

* significant at 5 per cent ** significant at 1 per cent rG- Pod yield per tree (kg/tree)

| | | | |
|---|---|---|---|
| 1. Pod length (cm) | 5. Shell weight (g) | 9. Pod weight (g) | 13. Vein per cent (%) |
| 2. Pod width (cm) | 6. Seed weight (g) | 10. Pulp per cent (%) | |
| 3. Pod girth (cm) | 7. Vein weight (g) | 11. Shell per cent (%) | |
| 4. Pulp weight (g) | 8. Number of seeds | 12. Seed per cent (%) | |

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