CORRELATION AND PATH COEFFICIENT ANALYSIS IN RHODODENDRONS FROM WOKHA DISTRICT, NAGALAND

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SUMMARY The morphological traits [plant height (ph), leaf length (ll), leaf breadth (lb), petiole length (ptl), number of flowers and its distribution pattern (nofdp), petal length (pl), anther breadth (ab), carpel length (cl) and altitude (alt)] were selected after normality test for approximate normal distribution of the characters and calculated correlation and path coefficient analysis of *Rhododendron* genotypes at mean (1862 ± 49.81 masl) altitude of the Wokha district of Nagaland. Interrelationships among related characters and traits and their contributions towards number of flowers and distribution pattern (nofdp) have been studied. The significant associations were found in the quantitative traits such as plant height, petiole length, leaf length, leaf breadth, petal length and carpel length at probability level (p 0.01 and p 0.05) of two tailed Pearson correlation coefficient respectively. The highest Pearson correlation coefficient was recorded between leaf length and leaf breadth (0.688**) at the probability level p 0.01. The characters were analyzed for conventional (model 1) and sequential path (model 2) coefficients and the trait petal length has explained only 18.6% variation for anther breadth and carpel length in model 2. The direct effect of variables was recorded insignificant in both model 1 and model 2 analyses. The measures of colinearity tolerance (T) and variation inflation factor (VIF) values showed noncolinearity among the characters. Path coefficient analysis (conventional and sequential) suggested that characters were found insignificant and unsatisfactory and none of the traits could be differentiated as selection criterion for nofdp.

Keywords: Morphological traits, Nagaland altitude, path coefficient analysis, *Rhododendron*.

INTRODUCTION

Rhododendron L. comprises about 850 species worldwide (Mabberley 2008). It is mainly confined to regions of higher altitudes. Rhododendrons are characterized by shrubby to small and large trees ranging in size from 10—100 cm to 30 m (Linnaeus 1753, Mao & Gogoi 2012). In India, this genus is represented by about 80 species of which 98% are found in the Himalayan region among which 72% are inhabited in Sikkim. Species availability shows a drastic decrease from 4500 mean altitude above sea level (masl) to 2500 masl (Bhattacharyya & Sanjappa 2008, Singh et al. 2003).

Rhododendrons have been known for bearing beautiful, attractive and colourful clusters of

flowers and even recognized as State flower of both Himachal Pradesh and Nagaland States of Northeast India. In addition, certain tree species have been recognized as State trees. Whereas Sikkim honoured *R. niveum*, Uttarakhand State named *R. arboreum* as their State trees respectively (Bhattacharyya 2011, De Milleville 2002, Mao et al. 2009).

Nagaland state involves the former Naga Hills district of Assam situated at the extreme north-eastern part of India carrying an area of 16,527 sq km. It is mostly covered by high altitude mountains with average height of the peaks between 900 and 1200 masl. It consists of 11 districts with different altitudes, lowest being Dimapur with 260 masl and Kiphire with 3840 masl as the highest (Kant 2004, Kharwal & Rawat 2013, Pradhan 1985).

A perusal of literature pertaining to Rhododendrons of Nagaland reveals that barring inventory on taxonomy and distribution (Clinton et al. 1994, Keeley 1988, Laloo et al. 2006, Srivastava 2012, Watt 1890) data on morphological and genetic variations in relation to tree improvement programme are very meager (Ajay et al. 2001, Kuttapetty et al. 2014, Latham et al. 1996, Paul et al. 2019, Sharma & Rikhari 1997, Sekar & Srivastava 2010, Yumnam 2008).

The survey of *Rhododendron* species at different altitudes of Nagaland suggests that most of the species are placed under RET and red-listed. *R. formosum* var. *formosum*, *R. formosum* var. *inaequale*, *R. ellioti*, *R. macabeanum* and *R. wattii* are red-listed under IUCN categories from the State (Gibbs et al. 2011). The latter is the most critical species and is represented by a single tree

located from Dzukou Hill (Mao & Gogoi 2007). The *Rhododendron* species endemic to Nagaland are, *R. elliottii*, *R. macabeanum*, *R. triflorum* var *bauhiniflorum*, *R. wattii*, *R. johnstoneanum*, *R. formosum* var *inequale* and *R. arboreum* (World's largest *Rhododendron*) and they require immediate conservation (Mao 2010, Kingdom-Ward 1949, 1960).

In *Rhododendron*, the number of flowers and its distribution pattern (nofdp) is a complex quantitative trait and is highly affected by the environmental factors. It is indirectly related to formation of seeds through interaction of pollen from anthers to stigma, and hence the growth of the tree genotype, as well as the collection of the genotype germplasm. Simple correlation analysis that relates to the number of flowers and its distribution pattern to a single variable may not provide a complete understanding about the importance of each component in determining nofdp. Path coefficient analysis is a statistical technique of splitting the correlation coefficients into its direct and indirect effects, and the contribution of each character or component to nofdp could be estimated. The objective of the present study is to determine the inter-relationships among related components to nofdp in Rhododendrons.

In situ and ex situ conservation of Rhododendrons could be popularized. In situ conservation includes the establishment of national parks, biosphere reserves, gene sanctuaries, and protected area network. Besides this, awareness about the importance of the *Rhododendron* species among local people and their active participation, complete ban on grazing or forest fire for jhum or terrace

cultivation in protected areas, may be helpful. Ex situ conservation involves cultivating the species in botanic gardens and parks of suitable climatic conditions in hilly areas using vegetative cuttings, seeds or by tissue culture techniques. Most importantly, government should fund the projects to conserve as well as to study the chromosomal diversity of these RET and vulnerable trees in the State for the prediction of plant breeding programmes.

MATERIALS AND METHODS

The morphological quantitative data such as plant height (ph), number of branches (nbr), girth of the tree (g), number of internodes (in), node length (nl), leaf length (ll), leaf breadth (lb), petiole length (ptl), peduncle length (pdl), pedicel length (pcl), number of flowers and its distribution pattern (nofdp), petal length (pl), petal breadth (pb), stamen length (sl), anther breadth (ab), and carpel length (cl) were collected which served as morphometric quantitative traits for the present purpose. The morphological quantitative traits, ph and g were measured in meters (m), traits, nbr, in, nofdp were measured as counts and the traits, nl, ll, lb, ptl, pdl, pcl, pl, pb, sl, ab and cl were measured in centimeters (cm).

The data collection and measurement of the traits had been done from three different altitudes (alt), (alt 1780, 1854, 1952 masl) and *Rhododendron arboreum* species of Wokha district of Nagaland. The species is highly distributed at all the altitudes of the Wokha district.

The morphological quantitative data were processed for the Normality test (SPSS ver. 16) as most of the parametric tests could be reliable only when the data are normally distributed. The normal distribution peaks in the middle is symmetrical about the mean, but data do not need to be normally distributed for the test to be reliable. The following are the parameters (ph, ll, lb, ptl, nofdp, pl, ab, cl and alt) which passed the normality test for further analysis.

The quantitative data showed approximate normal distribution analyzed for Pearson correlation coefficients (p 0.05 and 0.01) for the positively and negatively associated traits. The data was analyzed for conventional and stepwise path coefficient (standardized β coefficient) with measures of colinearity of tolerance (T) and variance inflation factor (VIF) value. The data were analyzed initially for the conventional (Enter) method but in this method the β coefficient value was not standardized so to get the standardized β coefficient used the stepwise path coefficient method for the dependent variable (DV) as nofdp and independent variables (IV) as ph, ll, lb, ptl, pl, ab, cl and alt.

The tolerance value is the amount of variability of the selected independent variable not explained by the other independent variables (1- R^2i, where R^2i is the coefficient of determination for the prediction of variable i by the predictor variable). VIF indicates the extent of effects of other independent variables n the variance of the selected independent variables [VIF=1/(1- R^2i)]. Thus, very small tolerance value (below 0.1) and large variance inflation factor value (above 10) indicate high colinearity.

The standardized regression coefficient (β) value acts as direct effect or value (DV) of the variables on the nofdp. The indirect effect is

possible to calculate as the correlation coefficient value is the sum of direct and indirect value [therefore, Correlation (r) = direct (β) + indirect value (α)]. The proportion of the direct effect might be estimated by dividing the value of standardized regression coefficient (β) by its correlation (r) value. Similarly, the proportion of the indirect effect could be estimated by 1-β/r. The product (β × r) and summed across each variable with the direct variable into the dependent variable is R^2. The subtraction $1 - R^2$ is the value of dependent variable. Sequential Path coefficient diagram was drawn by MS Office (publisher) software.

OBSERVATIONS

Pearson correlation coefficient (2 tailed) computed between the different pairs of characters and significant relationship among studied traits was recorded (Table 1). Altitude is negatively and significantly correlated (−0.551**) with plant height at p 0.01. Plant height is positively and significantly correlated with petiole length (0.326*) at p 0.05. Leaf length positively and significantly correlated with leaf breadth (0.688**) and petiole length (0.450**) at p 0.01. Leaf breadth is positively and significantly correlated with petiole length (0.424**) at p 0.01. Petiole length significantly and positively correlated with the carpel length (0.448**) and nofdp (0.437**) at p 0.01.

The direct effects of the traits were analyzed by conventional path coefficient method, where all the predictor variables (ph, ll, lb, ptl, pl, ab, cl and alt) considered as first order variables over nofdp as response variable and measures of colinearity were recorded (Table 2).

Sequential path coefficient analysis was performed for better understanding the predictor variables (ph, ll, lb, ptl, pl, ab, cl and alt) and their relative contribution to dependent variable (nofdp) (Table 3). The direct and indirect contribution of independent variables (ph, ll, lb, ptl, pl, ab, cl and alt) on dependent variable (nofdp) computed and represented in the form of a line diagram (Fig. 1).

DISCUSSION

Pearson correlation coefficient (2-tailed) among the traits selected showed association either positive or negative for the growth and development of the *Rhododendron* trees at an altitude of 1862 ± 49.81 masl of the Wokha district of Nagaland. The significant associations were observed in the quantitative traits, plant height, petiole length, leaf length, leaf breadth, petal length and carpel length of Rhododendrons of Wokha altitude at p 0.01 and p 0.05 respectively. The quantitative trait, plant height is negatively and significantly correlated (− 0.551**) with altitude at p 0.01 and positively and significantly correlated with petiole length at p 0.05. Leaf length positively and significantly correlated with leaf breadth (0.688**) and petiole length (0.450**) at p 0.01. Leaf breadth is positive and significantly correlated with petiole length (0.424**) at p 0.01. Petal length positively and significantly correlated with the carpel length (0.448**) and nofdp (0.437**) at p 0.01 respectively. The highest correlation was recorded between leaf length and leaf breadth (0.688**) at P 0.01 (Table 1). The present findings are in agreement with the works of others (Allen et al. 2015, Asmare et al. 2017, Berry et al. 2018, Koyama et al. 2015, Latte et al. 2015, Sidor et al.

TABLE 1: Correlation coefficient between the morphological quantitative traits of *Rhododendron*.

	alt	ph	ll	lb	ptl	pl	ab	cl	nofdp
alt	1	−0.551**	−0.059	−0.269	−0.305*	−0.044	0.016	−0.005	−0.239
ph		1	0.147	0.227	0.326*	0.086	0.019	0.073	0.132
ll			1	0.688**	0.450*	0.102	0.000	0.198	0.239
lb				1	0.424**	0.103	0.056	−0.022	0.289
ptl					1	0.016	0.064	−0.011	0.056
pl						1	0.022	0.448**	0.437**
ab							1	−0.284	0.109
cl								1	0.100
nofdp									1

** Correlation is significant at the 0.01 level (2-tailed).
*Correlation is significant at the 0.05 level (2-tailed).
alt: Altitude, ll: Leaf length, ab: Anther breadth, pl: Petal length, ptl: Petiole length, ph: Plant height, lb: Leaf breadth, cl: Carpel length, nofdp: Number of flowers and distribution pattern.

TABLE 2: Direct effects of first order predictor variables on nofdp and measures of colinearity in model 1 (all predictor variables as first order variables over nofdp as response variable) in *Rhododendron* population.

Predictor variables	Phenotypic correlation with nofdp as response variable	Direct effect (β)	Indirect effect (r=β+α)	Proportion direct effect (β/r)	Proportion indirect effect (1-β/r)	R^2	Tolerance	VIF
alt	−0.239	−0.252	0.013	1.05	−0.05	0.060	0.627	1.595
ll	0.239	0.211	0.028	0.88	0.12	0.050	0.415	2.410
ab	0.109	0.074	0.035	0.68	0.32	0.008	0.884	1.131
pl	0.437	0.453	−0.016	1.03	−0.03	0.198	0.753	1.328
ptl	0.056	−0.157	−0.101	−2.80	3.80	−0.009	0.688	1.454
ph	0.132	−0.040	0.172	0.30	0.70	−0.005	0.661	1.512
lb	0.289	0.097	0.192	0.34	0.66	0.028	0.436	2.295
cl	0.100	−0.122	0.222	−1.22	2.22	−0.012	0.636	1.572

Method: Enter; Dependent variable: nofdp; Independent variables: alt, ll, lb, ab, pl, ptl, ph, cl.
alt: Altitude, ll: Leaf length, ab: Anther breadth, pl: Petal length, ptl: Petiole length, ph: Plant height, lb: Leaf breadth, cl: Carpel length, nofdp: Number of flowers and distribution pattern.

TABLE 3: Direct effects, tolerance and variance inflation factor (VIF) values for the predictor variables in model 2 in *Rhododendron* population.

Response variables	Predictor variables	Phenotypic correlation (r)	Adjusted R2	Direct value (β)	Indirect value (r=β+α)	Proportion direct value (β/r)	Proportion indirect value (1-β/r)	Tolerance	VIF
alt	ph	−0.551**	0.035	0.001	−0.552	−0.00	1.0018	0.697	1.435
	ll	−0.059		0.225	−0.284	−3.81	4.81	0.997	1.003
	lb	−0.269		0.242	−0.511	−0.90	1.90	0.928	1.078
	ptl	−0.305*		−0.018	−0.287	0.06	0.94	0.907	1.103
	pl	−0.044		0.427	−0.471	−9.70	10.70	0.998	1.002
	ab	0.016		0.113	−0.097	7.06	−6.06	1.000	1.000
	cl	−0.005		0.099	−0.104	−19.80	20.80	1.000	1.000
ph	ll	0.147	0.012	0.230	−0.083	1.56	−0.56	0.978	1.023
	lb	0.227		0.244	−0.017	1.07	−0.07	0.919	1.088
	ptl	0.326*		−0.019	0.345	−0.06	1.06	0.871	1.148
	pl	0.086		0.429	−0.343	4.98	−3.98	0.993	1.008
	ab	0.019		0.113	−0.094	5.94	−4.94	0.999	1.001
	cl	0.073		0.099	−0.026	1.35	−0.35	0.993	1.007
ll	lb	0.688**	0.043	0.153	0.535	0.22	0.78	0.474	2.109
	ptl	0.450**		−0.156	0.606	−0.35	1.35	0.703	1.422
	pl	0.102		0.412	−0.310	4.03	−3.03	0.984	1.016
	ab	0.00		0.114	−0.114	0.00	0.00	0.999	1.011

Method: Enter; Dependent variable: nofdp; Independent variables: alt ,ll, lb, ab, pl, ptl, ph, cl.
ph: Plant height, ll: Leaf length,lb: Leaf breadth, ptl: Petiole length, nofdp: Number of flowers and distribution pattern, pl: Petal length, ab: Anther breadth, cl: Carpel length.
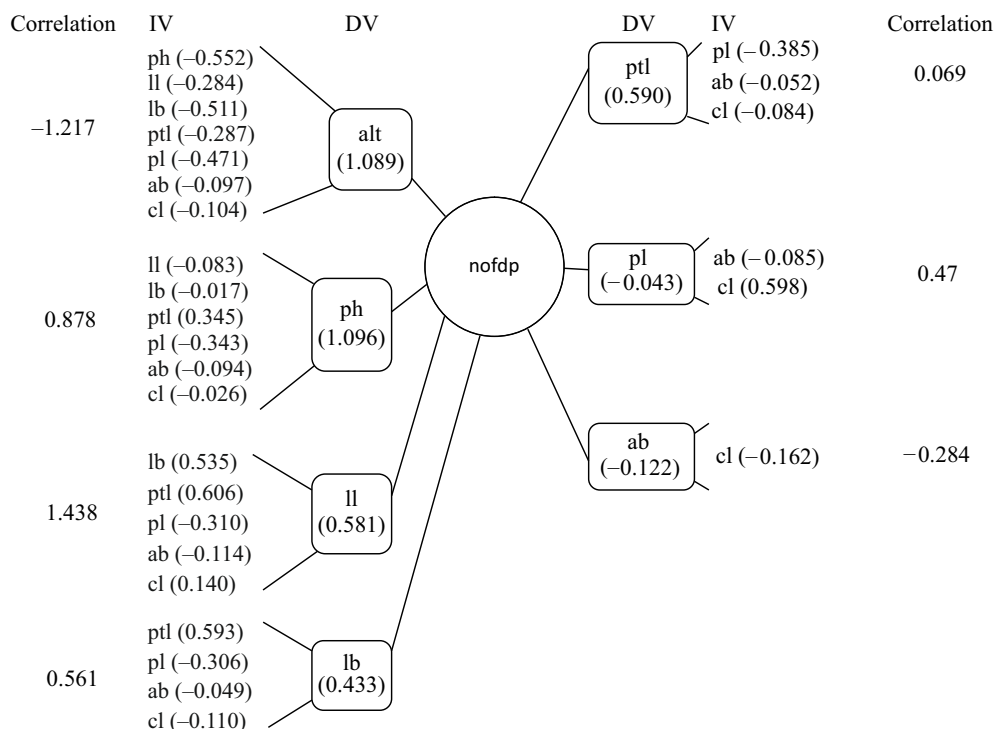
Fig. 1: Estimation of direct (DV) and indirect (IV) effects on nofdp by the characters ph, ll, lb, ptl, pl, ab and cl.

2015, Sukhodolskaya & Ananina 2017, Xu et al. 2017, Zvarikova et al. 2016).

Pearson correlation coefficient was based on the association between a pair of traits with regard to the growth and development of both the traits simultaneously either positively or negatively or in opposite directions. Therefore, to observe the relative significance of the paired traits conventional path coefficient analysis was performed, which is a statistical technique to split the correlation coefficient into its direct and indirect effects or value. Mostly, the technique allows estimating the contribution of each trait or character on the yield of a crop, or on a particular trait or character in study other than crop plant.

Direct effects were estimated through conventional path coefficient analysis, where all the traits were considered as the first order variables over nofdp as response variable (model 1) and measures of multicolinearity (Tolerance and VIF). Generally, the value of tolerance less than 0.1 and value of VIF more than 10 suggested high colinearity of the trait and should be removed from the first order variables, if any. At present, all the variables in the study were taken as first order variables showed tolerance of more than 0.1 and less than 10 VIF value. Therefore, none of the traits was removed from the first order variables and processed for further analysis (Table 2).

Stepwise sequential path coefficient analysis (model 2) of traits under study has provided a better understanding of the interrelationships between the various traits and their relative contribution to nofdp. The results of tolerance and VIF values for predictor variables suggested not much difference from values in model 1. Sequential path analysis could be used in minimizing the colinearity problems and identifying factual contributions of each trait or character in different path components. The direct effect of the trait, pl has contributed maximum variation (0.186) for the predictor variables ab and cl and rest of the direct effects were recorded negligible (Table 3). The direct effects and contributions of selected characters were insignificant in both models 1 and 2. Therefore, the present study is inconsistent with both models 1 and 2, but both the methods were used in other crops to differentiate contributions of each variable on a particular trait or yield (Berry et al. 2018, Burridge et al. 2016, Du et al. 2018, Epps et al. 2015, Fidan & Sirin 2016, Georgian et al. 2015, Huang et al. 2017, Jing et al. 2015a, 2015b, Kuang et al. 2015, Li et al. 2015, Lynch 2015, Ma et al. 2015, Melo et al. 2016, Miguel et al. 2015, Said et al. 2017, Shrestha et al. 2017, Velho et al. 2017, Wu et al. 2017).

Although both the models were insignificant, a line diagram of sequential path coefficient analysis was drawn to indicate the interrelationship between variables and their contributions in the form of direct and indirect values towards the nofdp (Fig. 1). The advantage of sequential path coefficient analysis over conventional path coefficient analysis was the understanding and contribution of direct and indirect effects of different traits over yield or any particular traits as response variable. Unfortunately, none of the traits was differentiated as selection criterion for nofdp.

ACKNOWLEDGEMENTS

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RESEARCH ARTICLE

CONSANGUINITY STUDY IN THE KNANAYA CATHOLIC CHRISTIAN COMMUNITY OF KOTTAYAM DISTRICT, KERALA I. PATTERNS, FREQUENCY AND EFFECTS

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SUMMARY Consanguinity study was carried out in the Knanaya Catholic Christian community of Kottayam district, Kerala. Aspects such as consanguinity patterns, frequency and effects in terms of couple fertility and pre-reproductive mortality and morbidity assessed with consanguinity in the community were assessed. Closer degree spousal alliances were absent and the observed degrees are second cousin (very low) and more distant third cousin marriages (3C) which together constituted 15.4%. The couple fertility and pre-reproductive mortality profiles were low and there differentials not significant, while the associated morbidity incidence, especially of the sensory types (blindness, deaf and dumb) fairly high and differentially significant. Paucity of closer degree spousal alliances may be due to large size of the group which readily facilitates less related (3C) and unrelated alliances despite the community still pursuing tight endogamy. It is presumed that closer degree alliances and associated high risk effects could have been prevalent in the community in times when it was made smaller in size.

Keywords: Consanguinity, Knanaya, Christian, Kottayam, Kerala.

INTRODUCTION

Consanguinity or human inbreeding is referred to as the phenomenon of marital union between spouses who are related to each other by common ancestry. The probability of two related spouses possess the same genes inherited from the common ancestor would be pretty high, and inbreeding would bring them together resulting in higher frequencies of homozygous offspring in blood related families. Detrimental effects of inbreeding arise as a consequence of genetic homozygosis of lethal or sublethal recessive genes and the homozygous children are likely to meet with developmental hazards in utero or after birth (Mathew 2017), and become nonviable leading to mortality at various pre-reproductive stages and morbid conditions of genetic predisposition, and succumb to various genetic diseases and congenital defective condition. The magnitude of consanguinity related risk effects is dependent primarily on the nature, number and frequency of deleterious recessive genes present in the population and the degree, level and duration of inbreeding (Mathew & Jyothilekshmi 2017). The earliest consanguinity study in Kerala are those of Kumar et al. (1967) and Abraham &

Mathew (1969). Many castes and communities and tribals in the state have been practising close-kin marriage alliances as part of their social custom for centuries. However, all Episcopal Christian church in the state exercise uncompromising church ban prohibiting alliances between close relatives up to second cousin. Contrary to this, a particular Christian group, the Knanayas who have been pursuing endogamy since their origin in the early Christian era, by which mate selection is exclusively from within their closed community, and hence marriage alliance in them are prone to the near obligatory between related spouses. There are two distinct Knanaya communities in Kerala, the Catholic and Jacobite, and the present consanguinity study concern the Catholic Knanayas of Kottayam District with emphasis in the patterns, frequency and effects of the phenomenon.

MATERIALS AND METHODS

The 'Knanaya' Christian of the Kerala region belongs to two distinct denominations such as (1) the Vijayaparam Catholic Diocese of Kottayam district and (2) a Jacobite group mostly resident in Ranni (Pathanamthitta Dist.), Chigavanam (Kottayam Dist.) and Thiruvanthapuram city (Thiruvanthapuram Dist.). The Knanayas of the Kottayam District are reflecting a large group while the Jacobite group is a smaller fraction. Consanguinity data were collected by census method by door-to-door visit, from a random sample of 565 families (the sample size is roughly 10%) using a comprehensive questionnaire which includes a variety of socio-economic demographic reproductive and genetic parameters. The patterns of consanguinity commonly practised in inbreeding communities are (1) Uncle-Niece (UN)/Aunt-Nephew (AN), (2) Double first cousin (DFC) who are offspring of sibs married to related sibs, (3) First cousin (IC) who are

offsprings of sibs married to unrelated spouses (4) First cousin once removed (1.5C) which is relation between an individual and the daughter of one his first cousins (5) Second cousin (2C) who are children of first cousins and (6) Third cousins (3C) who are children of second cousins. Mating beyond 2C is conventionally reckoned as non-consanguineous in most studies.

The basic measures of consanguinity applied for describing and quantifying genetic relationships are, (1) the frequency of consanguinity, which is the rate at which all the different patterns together occur, calculated as the percentage of the sample, (2) the coefficients of consanguinity (F), it is the probability that a consanguineous offspring in an identical homozygote. The mean coefficient of inbreeding was computed by the path coefficient method following Wright (1922).

The coefficient of consanguinity for various degrees of spousal relationships are, 1/8 for UN/AN, 1/16 for IC, 1/32 for 1.5C, 1/64 for 2C and 1/128 for 3C. The coefficient of unrelated marriage is F = 0. For assessment of the reproductive outcome, various parameters are used such as (a) Couple fertility, measured in terms of three parameters such as conception, live birth and child survival. A woman who missed normal monthly period for one or more considered pregnant. A pregnancy that does not terminate in a viable birth is foetal loss or prenatal mortality which includes abortion (loss before 28th wks of gestation) and still birth (loss after 28th wk). Neonatal mortality refers to the death between 28 d of birth and one y. Infant mortality is the sum of neonatal and postneonatal. Child mortality refers to non-accidental death of a child between 1 and 10 of life and those between 10 and 20 as juvenile mortality. Mortality after birth at various stages together forms postnatal mortality. Total mortality is the sum of all losses from abortion to juvenile death. Morbidity data were

collected under two main types such as (1) congenital defects of which three categories (a) physical defects (b) sensory defects and (c) mental defects and (2) diseases. Since individual morbid conditions were not large enough, all conditions were pooled and the total analysed against the total live-birth. Appropriate statistical methods were used to determine the significance levels of association.

OBSERVATIONS

The patterns of mating and the frequency of consanguinity in the group are furnished in Table 1. Closer degree alliances like UN, IC or 1.5C were absent and even the 2C relationship was rare (2 in the sample), while the dominant mating type was 3C, and then together constitute 15.4%, the mean F was very low (0.0013). Prenatal mortality was 5.69% and the difference was less significant, while postnatal mortality was very low which was not significant in the community (1.51) and NC group (1.86). Total mortality was 7.11%, the differential was not significant. Morbid conditions of various kinds (physical, sensory and mental) together constitute 10.55% and the difference was significant. Most common morbid conditions noticed were the sensory, especially blindness followed by deaf and dumb.

TABLE 1: The pattern, frequency and mean F of consanguinity in the Knanayas of Kottayam district.

Pattern	Frequency	
	No.	(%)
Second cousin	2	0.35
Third cousin	85	15.04
Consanguineous	87	15.40
Nonconsanguineous	478	84.60
Total	565	100
Mean coefficient of inbreeding	0.0013	

DISCUSSION

The patterns of consanguinity prevalent commonly in diverse population groups globally are, Uncle-niece (UN), first cousin (IC), first cousin once removed (1.5C) and second cousin (2C), of which the IC type is the most prevalent. In all the Kerala communities previously studied also the same trend exists (Mathew et al. 2006, Mathew & Jyothilekshmi 2017). But in the present Catholic Knanaya community, closer degree alliances were absent, and even the 2C frequency was very rare, with the related alliances mostly restricted to the 3C degree still the group pursuing tight endogamy. In most endogamous population and racial isolates the world over, consanguineous unions of closer degree are frequent and mere obligatory, especially inevitable when the population size is small (Bittles 2012). In the present ecclesial endogamous Catholic faction of Knanayas, widespread closer degree spousal alliances could have existed in the earlier centuries of its existence when the population size was small. But, with the passage of time as the population becomes large, the existing situation could have facilitated mate selection possible mostly between less related (3C) and unrelated spouses. Unpublished data of the Jacobite faction of the Knanayas of the State appear to offer evidence of this possibility. Preliminary observations in this smaller fraction showed prevalence of closer degree spousal relations like IC and 1.5C.

The level of inbreeding is measured in terms of two parameters, the frequency and coefficient of inbreeding, of which the former is the frequency with which the different patterns together occur, calculated as the percentage of the total sample, while the latter is defined as the probability that the consanguineous offspring in

an identical homozygote. The frequency in the present Catholic faction of the Knanayas calculated with existing 2C and 3C together is 15.40% and because of the most predominant weaker spousal degree relationships (3C) in the group and the mean F is very low (0.0013). A wide range of consanguinity levels exist in the world population groups, ranging from less than 0.5% to as high as above 90%. The low levels occur mostly in USA and most European Christian nations in which the very low rates are attributable to the impact of church ban on close degree alliances up to second cousin, coupled with increased mobility industrialization and urbanisation (Bittles 2012, Mathew 2018). The frequency in the Kerala group of communities earlier studied range from 1.55% (Christian Maliarayan) to a very high over 70% as in many tribal groups of Palakkad district (Joseph & Mathew 1991, 2005), and the frequency reached a peak of over 90% in the tribals of the Idukki district, of which the highest ever reported, in the Kurumba Pulaya tribe (Sindu et al. 2001). The consanguinity rates and the mean F in the Kerala community have revealed a clear and a consistent gradient very much associated with the socio-economic covariables and literacy factor (Mathew & Jyothilekshmi 2017).

Effects

The practice of blood-related alliances has implications on various realms of human life which include social effects, reproductive effects in term of fertility or fecundity, and genetic effects in terms of pre-reproductive mortality and morbidity of which the latter two directly concern human survival in public health (Mathew 2018).

Fertility effects

Human fertility is conventionally measured in terms of three reproductive parameters such as conception, live-birth and child survival. Available information has projected three trends of association between consanguinity and human fertility such as (a) lower fertility differentials among inbreeds (Lazo et al. 1996) (b) significant higher association (Bener & Ali 2006) and (c) no clear association (Rao & Inbaraj 1977). The present Knanayas of Kottayam district registered fairly low fertility mean and insignificant differentials (Table 2). The overall fertility profile in the Kerala communities studied earlier showed significant differentials between the consanguinity and NC groups (Mathew & Jyothilekshmi 2017). A range of proximate determinates exert direct influence on fertility which include age at menarche and menopause, sterility/fecundity and lactational amenorrhoea (Wood 1989). Reproductive compensation through quick replacement of an infant dying early provides another convincing explanation for the positive association between consanguinity and fertility (Mathew 2018). A number of social and demographic factors are also implicated for the greater fertility profile. The low fertility profile and insignificant fertility differential in the present community could be a reflection of little reproductive compensation and lesser reproductive span due to relatively higher age at marriage, rather than representing any underline biological difference in fecundity ascribable to consanguinity.

Mortality effects / Morbidity effects

Mortality in humans is the loss of progeny from early stage to the pre-reproductive juvenile stage. Various genetic and nongenetic reasons have been implemented for the consanguinity related mortality/morbidity. The detrimental effects associated with consanguinity are caused by the expression of lethal/sublethal recessive genes

TABLE 2: Effect of Consanguinity on mortality, morbidity and couple fertility in the Knanayas of Kottayam district.

| Parameter | No. of cases | Consanguineous | | | | | | Nonconsanguineous | |
| | | 2C | | 3C | | Total | | No. | % |
		No.	%	No.	%	No.	%		
Abortion	43	1	25	9	4.35	10	4.78	33	3.09
Still-birth	12	0	0	2	0.97	2	2.3	10	2.1
Prenatal mortality	55	1	25	11	5.31	12	**5.69***	43	**4.03**
Neonatal	7	0	0	2	1	2	1	6	0.58
Post-neonatal	5	0	0	1	0.59	1	0.59	11	1.08
Child	2	0	0	0	0	0	0	2	0.2
Juvenile	0	0	0	0	0	9	0	0	0
Post-natal mortality	14	0	0	3	1.51	3	**1.51**	19	**1.86**
Total mortality	69	1	25	14	6.76	15	**7.11**	62	**5.82**
Physical defects	10	0	0	4	2.01	4	2.01	6	0.58
Sensory defects	19	0	0	8	3.57	8	4.02	11	1.08
Mental defects	0	0	0	0	0	0	0	0	0
Diseases	22	1	33.33	8	4.08	9	4.52	13	1.27
Morbidity*	51	1	33.33	20	10.20	21	**10.55****	30	**2.93**
Total pregnancy	1277	4		207		211		1066	
Total live-birth	1222	3		196		199		1023	

**Significant ($p<0.01$), *Significant ($p<0.05$).

inherited from the common ancestor, and such unions are expected to elevate the frequency of affected recessive homozygotes, the effect being more conspicuous when the genes are rare (Mathew & Jyothilekshmi 2017). Most studies have suggested significant levels of adverse effects, others marginal and still others no effect and still others even beneficial. But there is a strong view that homozygosity for deleterious recessive genes does reflect in offspring which becomes nonviable leading to loss by mortality at both prenatal and postnatal stages, and also by diverse morbid conditions (Bittles 2008, 2012).

Prenatal mortality refers to pregnancy wastage by foetal loss at various stages before birth such as early (abortion), intermediate (miscarriage) and late (still-birth) stages. The effects of consanguinity on prenatal mortality includes failure of conception and deleterious effect in embryonic developments. In consanguineous unions, the foetuses produced are at an

increased risk of getting aborted due to high homozygosity of alleles and there are also higher risk of premature birth and child being underweight. Several factors are known to contribute to increased prenatal loss in consanguineous families such as (a) increase of homozygosity of lethal genes, (b) effect of addictively active polygenes, (c) increased antigenic difference between the mother and the foetus (Mathew & Jyothilakshmi 2017). In the present Knanayas community, the pregnancy wastage at prenatal stage noticed was 5.69% in the consanguineous group, which was marginally higher than in the non-consanguineous families (4.03%). Postnatal mortality refers to loss of offspring at different stages after birth (neonatal, postnatal, infant, child, juvenile). The observed frequency is very low, both in the consanguineous (1.5%) and non-consanguineous (1.86%) almost evenly poised. The total mortality profile was 7.11% in the consanguineous groups against 5.82% in the non-consanguineous and the differential is not significant.

Morbidity refers to various kinds of diseases and congenital defects and abnormalities commonly classified as sensory, physical and mental. Severe morbidity causes death during the postnatal stages and may handicap the bearer impairing functions of various organs. The morbid conditions noticed in the present communities are, physical (2.01%), sensory (4.02%) and mental (0%) and diseases (4.52%). The pooled data of all the morbid conditions constituted 10.55% against the 2.93% in the non-consanguineous group and the differential was highly significant. Most common morbid condition was the sensory type especially, blindness followed by deaf and dumb.

In almost all the inbreeding conditions of Kerala studied earlier, the magnitude of harmful effects in terms of consanguinity-related mortality/morbidity was highly significant, and positively correlated with the rate of consanguinity, which in turn negatively with socio-economic co-variables, especially the literacy factor. The relatively low profiles of harmful effects especially mortality, noticed in the present Knanaya community must be the reflection of relatively weaker degree of spousal relationship existing in the group at present, the spousal relationships mostly confined to distant relations (3C). It is well-nigh possible that closer degree alliances might have been inevitable and readily prevalent in this tightly endogamous community yester times when the population size was much smaller.

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RESEARCH ARTICLE

GENETIC DIVERGENCE IN FORAGE MAIZE (ZEA MAYS L.)

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SUMMARY Based on nonhierarchical Euclidean cluster analysis, 100 forage maize accessions and a known forage maize variety African Tall were grouped into eight clusters for fodder as well as kernel yielding traits, in combined form based on 20 metric traits. Cluster III composed of 26 accessions was the largest group with average response of each trait and cluster IV was monogenotypic with high yield. Wide range of means was observed for all the traits. The maximum intercluster distance was observed between cluster IV and V. Cluster IV was more divergent than the other clusters. The study showed that the cross between cluster IV and II with high and low cluster means for majority of characters will help to improve fodder and kernel yield as well as quality in forage maize.

Keywords: Forage maize, genetic divergence, variability, kernel, *Zea mays.*

INTRODUCTION

The diversity and utility of forage maize has been a subject of appreciation since long. Maize stands out as one of the most important cereal crops in the world with enormous role in food, fodder and nutritional security. From tassel to root, the maize plant is valuable. The stem, leaves, silk cob and kernels all have a commercial value. The use of maize as an animal feed is well known. It is the cheapest and most palatable carbonaceous for animals such as cattle, sheep, pig and poultry. It forms an excellent forage and better than all other forage crops in average yield of dry matter and digestible nutrients per hectare (Perry 1988). Being a C_4 plant it has very high production potential. Most of the maize crop is fed to livestock as grain, silage or fodder. Forage maize

leaves are particularly high in crude protein (11%) and rich in calcium and phosphorus for high milk yield. Forage maize plant does not have problems of prussic acid or hydrocyanic acid and therefore, it can be used as fodder even before flowering or in dry weather. Quite often maize crop is grown for a dual purpose for both fodder and grain. The diversity of environment under which maize is grown is unmatched by any other crop. The future of forage maize depends on the careful screening of the genotypes from the germplasm collection. Singh et al. (2005) have made core collections of forage maize from different geographical regions of India through many exploration programs and these accessions were preserved in National Gene Bank (National Bureau of Plant Genetic Resources, New Delhi).

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The accessions were evaluated and grouped for various fodder and kernel traits.

In view of the above, present study on the evaluation of accessions of forage maize, which is used as dual purpose crop in India was taken up. Genetic divergence is an essential requirement for any crop improvement programme because genetically diverse parents when crossed can bring together diversity of gene combinations either to exploit heterosis or to obtain superior recombinants. In maize, it is well known that adequate genetic diversity is necessary in breeding programme for development of high yielding varieties. Multivariate analysis is a useful tool for quantifying the degree of divergence between biological population at accession level and assessing relative contri-bution of different components to the total diver-gence at both inter- and intracluster levels (Murty & Arunachalam 1966). Therefore, an attempt has been made to evaluate the magnitude of genetic divergence among 101 accessions of forage maize including African Tall.

MATERIALS AND METHODS

Materials for the present study comprised of 100 accessions of forage maize collected from different parts of India mainly Madhya Pradesh, Rajasthan and Uttar Pradesh. The accessions were evaluated with known forage maize variety namely, African Tall in randomised block design with three replications for three consecutive years, 2001−2003. Each accession was evaluated in a plot of two rows of 4 M length at 0.4 M apart. In order to maintain the genetic purity and to avoid cross pollination, selected plants were bagged till pollination was over. Observations were recorded on 20 metric traits at 50% silking stage and at the maturity of the crop. Crude

protein content was determined by the conven-tional Kjeldal method. The metric traits data were analysed statistically using non-hierarchical Eucledean cluster analysis of grouping of genotypes proposed by Spark (1973). The replicated data were averaged over replicates and then cluster analysis was performed.

OBSERVATIONS

Means and genetic variance

The analysis of variance showed a wide range of variation and significant differences for all the traits. Estimation of the different quantitative parameters for fodder and kernel yield and their component characters over environments showed that amongst fodder, green fodder yield itself was highly variable. Similarly, the kernel yield per plant also exhibited maximum variation amongst the accessions followed by its contributing traits like number of kernels per row, thereby indicating the accessions under study were relatively more variable for these characters and provide an opportunity for selection. On the other hand crude protein content in leaf, stem and cob width showed low variation over the environment.

Genetic divergence

Based on nonhierarchical Euclidean cluster analysis the 101 accessions including African Tall were grouped into eight clusters, each having 15, 12, 26, 1, 2, 16, 19 and 10 accessions respectively (Table 1). The composition of clusters showed that accessions of a cluster originate from a wide range of ecogeographical areas, thereby suggested that genetic differences and similarities among the accessions were irrespective of the areas. This allows us to select parents for hybridization on the basis of genetic diversity and not merely on the basis of ecogeographical isolation.

TABLE 1: Composition of clusters for various fodder and seed yield characters in forage maize over three environments.

Cluster No.	Number of accessions	Accession number/ name
I	15	IC - 334821, 334889, 334904, 334920, 334947, 334989, 335051, 335056, 335062, 335069, 335079, 335082, 335086, 335144 and 335169.
II	12	IC - 334830, 334833, 334834, 334837, 334846, 334855, 334872, 334879, 334881, 334915, 334945 and 334949.
III	26	IC - 334826, 334955, 334973, 335028, 335045, 335053, 335089, 335098, 335103, 335109, 335110, 335111, 335112, 335115, 335120, 335128, 335131, 335138, 335141, 335149, 335156, 335158, 335164, 335173, 335178 and 335184.
IV	1	African Tall
V	2	IC - 335060, 335068.
VI	16	IC - 334836, 334838, 334841, 334853, 334863, 334864, 334867, 334869, 334871, 334876, 334877, 334880, 334884, 334943, 334954 and 334957.
VII	19	IC - 334825, 334974, 334996, 334999, 335000, 335009, 335017, 335024, 335025, 335043, 335048, 335050, 335092, 335094, 335116, 335117, 335122, 335128 and 335152.
VIII	10	IC - 334842, 334848, 334929, 334932, 334942, 334944, 335027, 335032, 335035 and 335041.

TABLE 2: Distance between cluster centroids among eight clusters of forage maize.

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	0.000							
II	6.098	0.000						
III	3.007	4.716	0.000					
IV	17.443	13.167	15.261	0.000				
V	4.739	10.302	7.322	20.971	0.000			
VI	5.508	3.176	4.490	13.357	9.349	0.000		
VII	4.589	5.437	2.824	14.227	8.402	4.094	0.000	
VIII	5.231	4.474	4.065	12.951	8.853	3.168	3.156	0.000

Cluster grouping

The average intercluster distance was zero for all possible pairs of combinations (Table 2). The average intercluster distance values ranged from 2.82 to 20.97. For all the traits, maximum inter-cluster distance was observed between cluster IV and V (20.97) followed by I to IV (17.44), III to IV (15.26), IV to VII (14.22), IV to VI (13.35) and II to IV (13.16). Cluster IV was more divergent to each cluster. The distribution pattern of clustering reveals considerable diversity among the accessions.

Cluster mean

The diversity in the present material was also supported by the appreciable amount of variation among cluster mean for different traits. The genetic lines belonging to cluster IV were performing better results for all the traits including dry fodder yield and kernel yield under study except leaf-stem ratio.

Being a cereal crop, forage maize is not rich in protein content (leaf + stem) however, cluster I had highest value percentile for crude protein. Therefore, this group will help in improving protein content in forage maize. Days to 50% silking and maturity were found early for cluster V having only two accessions explored from Hardoi district, Uttar Pradesh were showing lowest values for almost all the traits except leaf-stem ratio and number of kernel rows which were showing highest value (Table 3).

Late maturity promoted cob length, cob width, number of kernels per row, shank diameter, kernel length, kernel width and test weight which were recorded in cluster IV. Minimum values of cluster mean for cob width, number of kernels per row and shank diameter was found in cluster II. Kernel width was highest for cluster IV and lower for cluster I.

TABLE 3: Cluster means for different fodder and seed yield characters in forage maize.

Clusters	Days to 50% silking	Plant height (cm)	No. of leaves/ plant	Leaf blade length (cm)	Sheath length (cm)	Leaf width (cm)	Stem girth (cm)	Dry Fodder yield/plant (g)	Leaf-Stem ratio	Crude Protein (%)	Days to maturity	Cob length (cm)	Cob width (cm)	No. of kernel rows	Kernels /row	Shank diameter (cm)	Kernel length (cm)	Kernel width (cm)	Test weight (g)	Seed yield/ plant (g)
I	45.87	169.49	11.06	80.68	15.52	7.71	1.88	75.50	0.42	11.12	78.44	14.64	3.43	12.76	29.05	1.18	0.81	0.80	18.17	165.54
II	51.18	207.82	12.67	93.82	18.30	9.05	2.20	110.87	0.38	10.53	88.48	13.76	3.36	11.76	25.30	1.14	0.86	0.82	20.12	158.87
III	46.11	188.00	11.58	86.72	16.72	8.32	1.99	89.21	0.40	10.60	77.45	16.51	3.36	12.23	33.88	1.26	0.83	0.81	18.16	178.75
IV	59.22	268.93	17.44	104.81	20.54	10.21	2.94	170.29	0.47	8.66	119.33	21.34	3.71	13.17	39.26	1.62	0.94	0.90	25.73	261.61
V	45.11	152.87	10.04	69.30	13.55	6.96	1.54	44.74	0.54	11.10	73.00	12.76	3.51	13.91	26.67	1.22	0.83	0.78	17.09	165.17
VI	51.44	195.35	12.54	87.90	17.21	8.54	2.15	94.05	0.40	10.78	87.46	15.05	3.50	11.63	26.14	1.19	0.92	0.89	22.52	186.52
VII	45.80	190.58	11.65	87.60	16.47	8.22	2.03	99.26	0.35	10.78	78.11	16.99	3.60	12.41	33.95	1.38	0.88	0.86	20.72	214.61
VIII	49.94	196.18	12.81	85.11	16.93	8.78	2.14	100.63	0.40	10.93	84.32	16.41	3.69	13.48	31.68	1.26	0.93	0.83	21.32	194.42

DISCUSSION

The analysis of variance estimation for the accessions showed relatively high variations in the characters and provides good opportunity for their selection (Ertiro et al. 2013). Murty & Arunachalam (1966) reported that the genetic diversity among the genetic lines of common geographic origin could be due to factors like heterogeneity, genetic architecture of the population, past history of selection and developmental traits. The use of accessions in hybridization from these cluster groups having most of the desirable characters is likely to produce more transgressive segregants (Alom et al. 2003, Kant et al. 2001, Katiyar et al. 2000). Gupta et al. (1984) have recommended that fodder variety should be early growth and late flowering type while Srivas & Singh (2004) concluded that the improvement in characters like plant height, days to 50% silking, number of leaves per plant and stem girth will help to improve the fodder yield in maize both directly and indirectly. Clustering pattern could be utilized in choosing parents for cross combinations which may likely generate exploitable variability for the effective selection of various economic traits (Endang et al. 1971). As per earlier reports heterosis and better recombinants can be obtained by crossing between parents of clusters of high and low means (Usha Kumari et al. 2010). Therefore, for getting better heterosis the genetic lines from cluster IV and II with high and low cluster means for majority of characters respectively can be used for hybridization programme for improvement of yield in fodder and/or kernel in forage maize.

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