Research Papers

Government Brennen College

Dharmadam, Thalassery
brennencollege@gmail.com
brennenclg.dce@kerala.gov.in

High density equation of state and condensation of ideal Bose gas using Mayer's generating function

Suresh THELAKKADAN PUTHIYAVEETTIL[1], **Udayanandan KANDOTH MURKOTH**[2,*]

[1]School of Pure and Applied Physics, Kannur University, Kerala, India
[2]Nehru Arts and Science College, Kanhangad, Kerala, India

Abstract: The equation of state of an ideal collection of bosons in the low-density and high-density regime are found using the method of cluster expansion with Mayer's generating function. The saturation density and the other thermodynamic properties are calculated by the application of Mayer's convergence of the partition function. By calculating the value of saturation density from the singularity of the partition function series, the differences between the Mayer series convergence and the virial series convergence for ideal bosons are also established.

Key words: Equation of state, Mayer's convergence, Bose–Einstein condensation

1. Introduction

The equation of state and hence the thermodynamic properties of the ideal quantum systems, like Bose or Fermi, show significant deviation from the ideal behavior [1]. This can be explained with the help of the quantum statistical method by considering the symmetric and antisymmetric properties of the wave functions. Bosons show a peculiar attractive spatial correlation, which can lead to a condensation [2,3] due to the symmetric nature of the wave functions, and fermions show repulsive spatial correlations due to the antisymmetric wave functions. Hence, the equation of state of these systems has the nature of the virial series [4,5]. The radius of

Research Article

Study of heritability, genetic advance and variability in *scoparia dulcis* L.

Abstract

Background: The capacity of genotype to express different phenotypes in different environments is phenotypic plasticity and for any crop improvement it depends on magnitude of genetic variability present in base population. Environmental effects influence the total observable variations of quantitative traits. Therefore, partitioning of overall variance due to genetic and non–genetic causes becomes necessary for effective breeding programme. The heritability, genetic advance and variability of the medicinally important plant *Scoparia dulcis* L. was studied presently. All the traits studied in the case of *S. dulsis* excluding leaf area showed significant variation at 1% level of significance showing the significance of variation between them in the case of the characters. Genotypic coefficients of variation were also lower in all the cases of significant variation when compared to phenotypic coefficients of variation showing the different levels of influence of environmental factors on the expression of the traits under study. In the case of growth traits, the highest heritability were shown by leaf area and the genetic advance was found to be the highest in inter nodal length.

Keywords: *Scoparia dulcis* L., phenotypic variance, genotypic variance, genetic advance, heritability

Chandramohanan KT, Neethu Narayanan

Post Graduate Department of Botany, Government Brennen College, India

Correspondence: Chandramohanan KT, Post Graduate Department of Botany, Government Brennen College, Thalassery, Kerala, India, Tel +9194 4754 7217, Email chandrubrennen@gmail.com

Introduction

Individual organisms can alter their development, physiology and life history depending on environmental conditions. These environmental responses are both trait and resource specific, and represent evolved characteristics that vary among genotypes, populations and species.[1] The capacity of genotype to express different phenotypes in different environments, phenotypic plasticity and for any crop improvement it depends on magnitude of genetic variability present in base population.[2] Environmental effects influence the total observable variations of quantitative traits. Therefore, partitioning of overall variance due to genetic and non–genetic causes becomes necessary for effective breeding programme. The genotypic coefficient of variation estimates the heritable variability, whereas phenotypic component measures the role of environment on the genotype. High phenotypic coefficient of variation and low genotypic coefficient of variation for a character indicated high influence of environment in its expression. The phenomenon of transmission of characters from parents to offspring is usually measured in terms of heritability. Therefore the estimates of heritability and genetic advance would help to formulate a sound breeding programme. The heritability, genetic advance and variability of the medicinally important plant *Scoparia dulcis* L. of the family Plantaginaceae was studied presently.

The plant selected for the present study is *S. dulcis*. It is native to South America and it was introduced in to India in 1843. It is a perennial herb found in almost all localities, mainly distributed in the tropical and sub tropical region. The plant grows abundantly in rainy season. The plant has been reported to have weed status also. The plant has short life cycle, it takes nearly three months. The plant has high power to overcome environmental stress. It is distributed on road side, pathways, salty areas, marshy and wet lands. The plant reproduces vegetatively and sexually. In wet areas the root system of the plant always active so new leafy branch arises from the base of the stem. As a result of sexual reproduction numerous seeds may form. These plants have high medicinal importance. The plant of *S. dulcis* is known to possess anti–diabetic activity, anti–ulcer activities antioxidant activity, anti–kidney stone activity, anti–malarial activity, sedative, hypnotyic, antioxidant, antitumor, which supports the therapeutic effects claimed by traditional practitioners. The active principles present in *S. dulcis* have been shown to exhibit cytotoxic and antitumor activity. Traditionally the plant widely used for the treatment of kidney stone in the indigenous peoples of Kerala like Kurichyas. Study of folk medicine was largely conducted in Bangladesh, toothache and stomach trouble, bronchitis, gastric disorder, haemorrhoids, insect bite, skin wound and hypertension *etc*. High medicinal importance of the plant is due to the presence of various chemical compounds like terpenoids, phenols, steroids, coumarins, phenols, saponins, tannins, amino acids, catecholamine, noradrenaline, adrenaline (having sympathomimetic effects), acacetin, amyrin, apigenin, benzoxazin.[3] In Sanskrit literature it is mentioned for the treatments of kidney stone, and so it is commonly known in Malayalam as *kallurukki*.

When compared to other medicinal plant, this plant may show wide distribution. This phenotypic plasticity is influenced by both genetic and phenotypic traits. The main aim of the present study is to analyse the variation present within the species of *S.dulcis* understanding the source of phenotypic variation and response of organism with the environment. Variation in the phenotypic traits may be a product of current environmental differences between sites (phenotypic plasticity), a product of heritable differences (genotype differences=ecotypes) between the subpopulations at different sites, or a combination of both.[4]

Materials and methods

The area of the present study is extended mainly in three North Malabar districts of Kerala, India: Kasargod, Kannur and Kozhikode (Table 1). These three districts are characterised by the presence of Malabar Coast, influence of Western Ghats and the tropical climatic condition.

Table 1 Accessions collected for the present study.

Accession number	Place of collection	Panchayat/municipality	District
BR 1	Dharmadam,	Dharmadam grama panchayat	Kannur
BR 2	Chettipeedika,	Puzhati grama panchayat	Kannur
BR 3	Kanayanoor,	Chemilode grama panchayat	Kannur
BR 4	Mayyil	Mayyil grama panchayat	Kannur
BR 5	Chelora,	Chelora grama Panchayat	Kannur
BR 6	Kadamboor,	Kadamboor grama panchayat	Kannur
BR 7	Panerichal,	Peralassery grama panchayat	Kannur
BR 8	Kadachira,	Kadamboor grama panchayat	Kannur
BR 9	Panayathamparamba,	Anjarakandy grama panchayat	Kannur
BR 10	Marakkarkandi,	Kannur coorporation	Kannur
BR 11	Karivallur,	Peralam grama panchayat	Kasargod
BR 12	Kalikkadavu,	Pilicode gramapanchayat	Kasargod
BR 13	Kulam,	Cheruvattur panchayath	Kasargod
BR 14	Kanjangad,	Kanjangad block panchayat	Kasargod
BR 15	Cheruvathoor,	Cheruvathur grama panchayat	Kasargod
BR 16	Nileswaram,	NileswaramMunicipality	Kasargod
BR 17	Railway station ,	Kasarkode municipality	Kasargod
BR 18	KSRTC bus stand,	Kasarkode municipality	Kasargod
BR 19	Cherkkala,	Cherkala gramapanchayat	Kasargod
BR 20	Madur	Madur grama panchayat	Kasargod
BR 21	Ramanattukara	Ramanattukara grama panchayat	Kozhikode
BR 22	Medical college	Kozhikode corporation	Kozhikode
BR 23	Kunnamangalam,	Kunnamangalam grama panchayat	Kozhikode
BR 24	Civil station	Kozhikode corporation	Kozhikode
BR 25	Mananchira	Kozhikode corporation	Kozhikode
BR 26	Beypur	Nallalam grama panchayat	Kozhikode
BR 27	Meenchanda	Kozhikode corporation	Kozhikode
BR 28	Railway station	Kozhikode coorporation	Kozhikode
BR 29	Farok	Farok municipality	Kozhikode
BR 30	Idimuzhikkal	Farok municipality	Kozhikode

For the present study the fields were frequently visited and the observations were made on required aspects. Plants from thirty accessions (Table 1), ten accessions each from Kasargod, Kannur and Kozhikode districts were collected and analysed. Nine plants were collected from each accession randomly. Data were collected for three consecutive growing seasons of 2016–17. Nine genetically stabled morphometric characters *viz* length of tap root, number of secondary roots, length of main shoot, number of primary branches, length of primary branch, number of secondary branches, number of nodes on primary branches, inter nodal length and leaf area were studied.

Collected data were statistically analysed for variability of traits by using Analysis of variance (ANOVA). Analysis of variance (ANOVA) was carried out to test the significance of variations in terms of the different characters studied presently. F value was calculated for the purpose and Test of significance was done with reference to standard F–Table.[5] CD was calculated with the formula:

$$CD = t_{0.05} \, x \sqrt{2VE/r}$$

Where $t_{0.05}$ is $t_{0.05}$ for error degree of freedom; VE is the error mean square and r the number of replications. Phenotypic and genotypic variances for the different characters were estimated as per Singh & Choudhary[6] using the formula:

$$Genotypic\ Variance(\sigma^2 g) = \frac{MSS\ for\ treatment - MSS\ for\ error}{Number\ of\ replications.}$$

$$Phenotypic\ Variance\ (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where $\sigma^2 e$ is the error variance. Coefficients of variation provide information on the extent of variability of characters as percentage of the corresponding mean values of the characters. Phenotypic and genotypic coefficients of variation were estimated following Burton & Devane.[7]

$$Genotypic\ coefficient\ of\ variation\ (GCV) = \frac{\sigma g\ x\ 100}{\overline{X}}$$

Where σg = the genotypic standard deviation and $\overline{X}$ =grand mean of the character.

$$Phenotypic\ coefficient\ of\ variation\ (PCV) = \frac{\sigma p\ x\ 100}{\overline{X}}$$

Where σp =the phenotypic standard deviation.

Heritability (broad sense) is estimated as the percentage of genotypic variance over phenotypic variance.[8] Genetic advance is the genetic improvement of the progeny possible through selection over the original population. Genetic advance was calculated using the following formula:[7]

$$GA = \frac{KH^2 \sigma p}{\overline{\overline{X}}}$$

Where H^2=heritability (broad sense); σp =phenotypic standard deviation; K=selection differential which is 2.06 at 5% intensity of selection in large samples.[9]

Results and discussion

The existence and progression of a genetic stock is governed by the magnitude of genetic variability accessible in terms of heritable traits. Genetic improvement is generally accomplished by selecting the genotypes with desirable qualities from the available populations.

Analysis of variance is a statistical procedure to compare the extent of variations between populations with the extent of variations within populations so as to determine the significance of variability between populations or accessions.[10] All the traits studied in the case of *S. dulsis* excluding leaf area showed significant variation at 1% level of significance showing the significance of variation between them in the case of the characters. However, leaf area showed no significant variation showing that their variation is narrow between the accessions. The reason of this variability may be both genetic as well as environmental. Genotypic variation between cultivars or populations is the expression of their genetic differences and phenotypic variation is the result of interaction between genetic differences and environment. Genotypic and phenotypic variations have been studied presently in the case of 30 accessions of *S. dulsis* on genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation Table 2.

Table 2 Genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense) and genetic advance in the case of 9 characters of *Scopariadulcis* L.

Characters					
Genotypic variance	**Phenotypic variance**	**GCV (%)**	**PCV (%)**	**Heritability**	**Genetic advance**
1. Length of tap root					
2.8	5.89	15.45	22.16	48.59	22.18
2. No. of secondary root					
4.52	18.42	13.8	27.85	24.56	14.09
3. Length of main stem					
18.65	61.2	16.17	16.17	30.48	18.39
4. No. of primary branches					
1.83	7.6	24.96	50.85	24.09	25.23
5. No. of secondary branches					
2.86	16.65	28.05	67.68	17.18	23.96
6. Length of primary branch					
4.68	37.65	12.68	35.95	12.45	9.21
7. No.of nodes					
4.36	12.69	13.83	23.59	34.38	16.71
8. Inter nodal length					
2.32	5.5	71.88	90.6	42.25	96.24
9. Leaf area					
0.63	1.29	53.12	76.19	48.61	76.3

In *S. dulsis*, in all the cases of significant variation, phenotypic variance was higher than genotypic variance indicating the polygenic nature of the traits under study and also the involvement of additive genes in the control of the characters. Genotypic coefficients of variation were also lower in all the cases of significant variation when compared to phenotypic coefficients of variation showing the different levels of influence of environmental factors on the expression of the traits under study. Among the growth traits the highest GCV and PCV were shown by inter nodal length (71.9 % and 90.6 % respectively) followed by leaf area (52.1% and 76.2% respectively) and number of secondary branches (28.0% and 67.7% respectively) showing the wide variability of these traits among the accessions studied.

Heritability (broad sense) is the ability of a trait to get inherited to the progeny. Oligogenic traits show high heritability whereas the heritability of polygenic trait is controlled by the number of polygenes involved and the involvement of the environment on their expression. Most of the agronomic traits of *S. dulsis* are polygenic in nature and they show different levels of significance. In the case of *S. dulsis*, among the growth traits, the highest heritability were shown by leaf area (48.6) followed by length of tap root (48.6) and intermodal length (42.3%). Heritability of number of primary branch and number of secondary branches was comparatively low thus showing the influence of environment on the expression of these traits.

Percentage of genetic advance possible under selection is a measure of the quantum of improvement possible and a parameter that can be used to find out the utility of characters in crop improvement programmes. In *S. dulsis*, among the growth characters studied, genetic advance was found to be the highest in inter nodal length (96.2%) followed by leaf area (76.3%). This shows that these characters can be effectively used for selecting superior genotypes.

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Conflict of interest

Authors declare there is no conflict of interest.

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