Table 1. Fungal organisms and their respective population (%) isolated from Shilajit rocks at Jaurasi area (Almora)

Fungal organisms	Population occurrence (%)	Fungal organisms	Population occurrence (%)
Aspergillus sydowii (Bainier & Sartory) Thom & Church	50	F. moniliforme var subglutinans (Wollenw & Reinking)	50
Aspergillus niger Van Tiegh	100	Hormoconis resinae (Lindau) Van Arx & do Vries	50
Aspergillus ochraceus (Whihelm)	50	Mrimbla ingelheimense (Van Beyma) Pitt	50
Aspergillus ustus (Bainier) Thom & Church	25	Penicillium aurantiogriseum (Dierck)	25
Alternaria alternata (Fr) Keeissler	50	Pestalotiopsis sp (Steyaert)	50
Absidia corymbifera (Conn) Sacc & A Trotter	50	Rhizoctonia sp D C Ex Fr (Sacc)	25
Botryodiplodia theobromae (Pat)	50	Sporomiella isomera Ahmed and Cain Dried Down.	50
Cladosporium oxysporum (Berk and M A Curtis)	75	Trichothecium roseum Link ex Fr. (acc)	75
Fusarium equisiti (Corda) Sacc	50	Ulocladium chartarum Preuss Simmons	75
F compactum (wollenw) W Gordon	50		

19 organisms which were later identified from CMI, England. Colony counts on the basis of total population of various fungi were recorded and calculated as follows:

$$\text{Population/cm}^2 = \frac{\begin{array}{c}\text{total number of the}\\\text{colonies of the organism}\\\text{appeared in the plates}\end{array}}{\begin{array}{c}\text{area of the washed}\\\text{surface}\end{array}} \times \frac{\begin{array}{c}\text{volume of}\\\text{surface}\\\text{washing}\end{array}}{\begin{array}{c}\text{number of}\\\text{samples}\end{array}}$$

It is apparent from Table 1 that the composition of mycoflora associated with the samples of Shilajit showed the presence of 19 fungal organisms. On the basis of population percentage, the epiphytic mycoflora has been grouped into four categories. Among them, one fungal form Aspergillus niger as 100%; three forms – Cladosporium oxysporum, Trichothecium roseum, Ulocladium chartarum as 75%; eleven fungal organisms – Aspergillus sydowii, A ochraceous, Alternaria alternata, Absidia corymbifera, Botryodiplodia theobromae, Fusarium moniliforme, F. equisiti, F. compactum, Merimbla ingelheimense, Pestalotiopsis sp. and Sporomiella isemera as 50% and the remaining four forms Aspergillus ustus, Hormoconis resinae, Penicillium aurantiogriseum and Rhizoctonia sp. as 35% were found in the association of Shilajit. It is interesting that no bacterial association could be seen.

The census of Shilajit mycoflora also depicted clearly that the major portion of fungal forms was constituted by members of Moniliales of the class fungi Imperfectii followed by Melanconiales and Sphaeropsidales of the class Ascomycetes. Therefore, it is presumed that the fungi belonging to Moniliales play an important role in proliferation of Shilajit from the rocks. The vegetation, such as Euphorbia royleans, Trifolium repens, Rhus

spp. and Ficus spp. was observed to grow around Shilajit-bearing rocks. The majority of plants have latex in them. In addition, nature of associated rocks, atmospheric conditions, rhythmic seasons, etc., may have also played vital roles in its formation. Nevertheless, the study of chemical composition of each fungal form is to be carried out to ascertain the chemistry of Shilajit.

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Incidence of three Mendelian traits in five endogamous populations of Purnia, Bihar

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Incidence of three Mendelian traits, viz ABO blood, Rh blood group and PTC taste ability was studied in randomly selected representative samples of five endogamous populations of Purnia, Bihar. Allelic

frequency was calculated and the biological distance between the pairs of populations estimated by Nei's formula. On the basis of genetic distance (D) two main clusters were found—one for Muslims and the other for non-Muslims (Rajput, Brahmin, Bania and Kayastha).

ON the basis of distribution and genetic analysis of a particular trait it can be concluded that the genes of all living mankind have been drawn from a common gene pool. Populations differ from one another relatively and not absolutely in respect of the frequency of one or more genes. Human biological variations are related to ethnic and geological background of a population[1]. Sympatric populations are supposed to have almost a similar gene pool structure[2]. But depending on their mode of origin, either by fusion or fission process some differences may be discernible on this point in various endogamous populations[3,4]. Existence of caste system in India and the practice of endogamy led to emergence of various gene pools of human populations. The aim of the present work is to know the extent of similarity or variation in the gene pool of five endogamous castes of Purnia district of Bihar, (India). These five castes were chosen because they are the major castes of this district.

Five endogamous populations selected for the present study were Brahmin, Rajput, Kayastha, Bania and Muslims. The data were collected from door-to-door survey method. In no case were two persons belonging to the same family subjected to test. Mendelian traits viz., ABO blood groups Rh and PTC taste ability were studied. The standard methodology was followed for estimation of specific phenotypes as given below: [A] ABO blood groups: by slide agglutination method using antisera A and antisera B. [B] Rh blood: by slide agglutination method by using antisera Rh(D). [C] PTC taste ability by using the method of Harris and Kalmus[5]. The allelic frequency was calculated by maximum likelihood method.

(a) *ABO blood group*

All five populations have different patterns of the incidence of various blood groups (Table 1). Among Brahmins, group A is most prevalent (38%), the next

Table 1. Frequency (%) of ABO blood groups, Rh, PTC taste blind in the population surveyed

		Blood group				PTC taste blind
Population	A	B	AB	O	Rh⁻	
Brahmin	38	27	7	28	1	29
Kayastha	40	15	15	30	0	28
Rajput	40	30	20	10	2	31
Bania	20	45	15	20	2	35
Muslim	10	25	10	55	4	34

1. Brahmin
2. Rajput
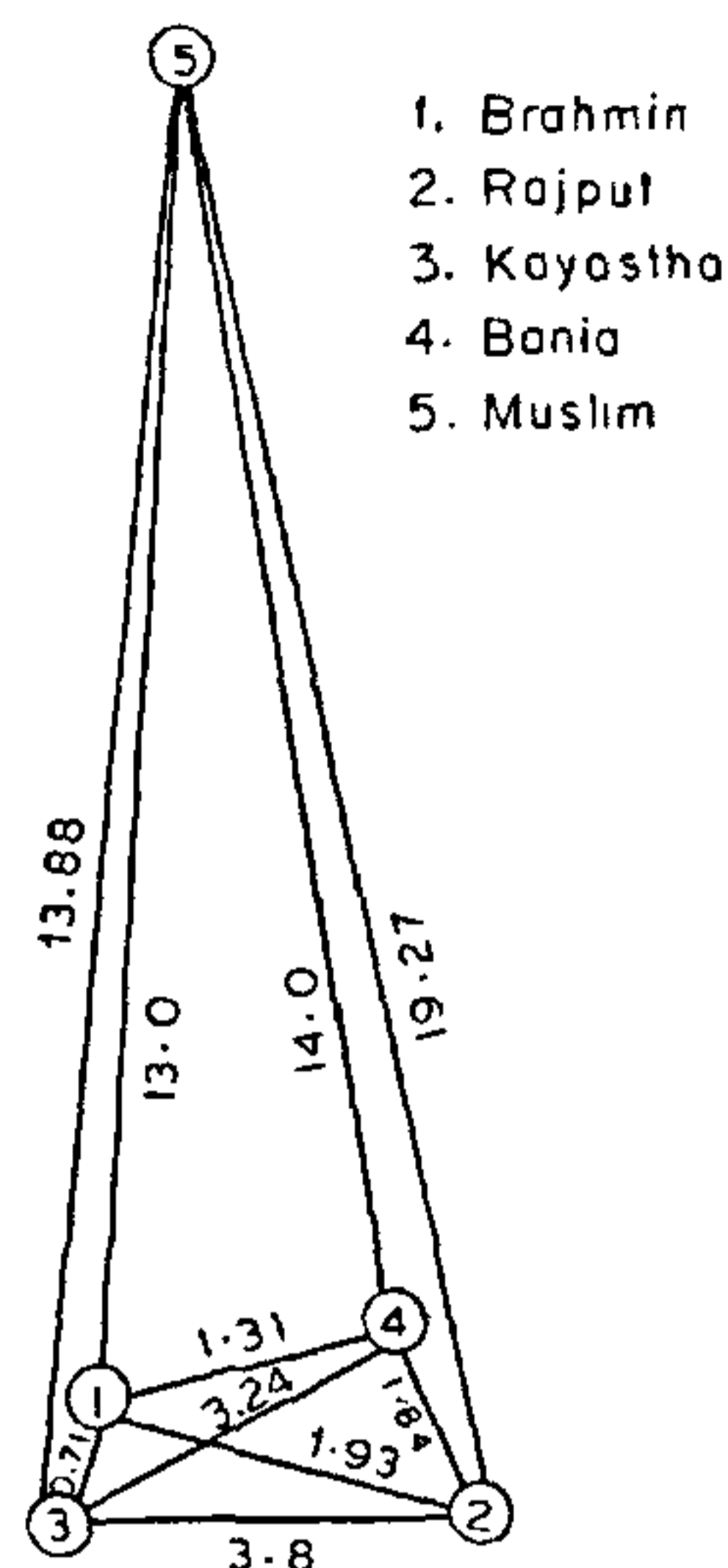3. Kayastha
4. Bania
5. Muslim

Figure 1. A diagrammatic representation of genetic distance among five population groups of Purnia, Bihar

common group is O (28%) followed by B (27%) and AB (7%). Among Kayastha group A is more frequent (40%) followed by O (30%) and B (15%). Among Rajputs also group A is more prevalent (40%) followed by B (30%) and AB (20%). The least common group in this population is O (10%). Among Bania group B is more frequent (45%). Group O and A are in equal distribution (20% each) and AB (15%). Among Muslims group O is more frequent (55%) followed by B (25%). Groups A and AB are in equal distribution (10% each). Group AB is comparatively least frequent in almost all five populations.

The frequency of gene p is high among three upper castes (Brahmin, Rajput and Kayastha). In Bania the frequency of gene q is high while in Muslim frequency of gene r is high (Table 2) which might be due to consanguinity (Table 2 and Figure 1).

(b) *Rh-blood group*

The incidence of Rh⁻ subjects in all the four populations is comparatively higher among Muslims (4%) and least in Kayastha (0%). Among Rajput and Bania it is 2% while in Brahmin it is 1% (Table 2).

(c) *PTC taste ability*

Taste sensitivity to PTC (phenyl thio carbamide) is well established as a population genetic marker. Human

Table 2. Allelic frequency with standard errors of concerned genes in the gene pool of the population surveyed

	Brahmin	Kayastha	Rajput	Bania	Muslim
			Populations		
p	0 28 ± 0 012	0 30 ± 0 010	0 38 ± 0 018	0 19 ± 0 015	0 07 ± 0 005
q	0 21 ± 0 016	0 13 ± 0.015	0.31 ± 0 016	0 36 ± 0 023	0 16 ± 0 018
r	0 51 ± 0 020	0 57 ± 0 021	0.31 ± 0 018	0 45 ± 0.017	0 77 ± 0 012
D	0 90 ± 0 016	1 00 ± 0 053	0 86 ± 0 018	0 86 ± 0 020	0 80 ± 0 021
d	0 10 ± 0 016	0 00 ± 0 053	0 14 ± 0 018	0 14 ± 0 020	0.20 ± 0 021
T	0 47 ± 0 026	0.47 ± 0 025	0 44 ± 0 026	0 41 ± 0.290	0 42 ± 0 026
t	0 53 ± 0 026	0 53 ± 0 025	0 56 ± 0 026	0 59 ± 0 290	0 57 ± 0 026

Table 3. Estimate of Nei's measure of genetic distance (D) among five population groups of Purnia, Bihar

	Brahmin	Kayastha	Rajput	Bania
Kayastha	0 0071			
Rajput	0 0193	0 0382		
Bania	0 0131	0 0324	0 0184	
Muslim	0 1300	0 1388	0 1927	0 1400

population on the basis of their ability to taste PTC have been classified as tasters and non-tasters. The distribution of PTC among the Brahmin, Kayastha, Rajput, Bania and Muslim was bimodal. The antimode in them lies between the solutions nos 5 and 6. The frequency of non-tasters gene in all the five populations was high (Table 2).

Genetic distance can be regarded as a function of the difference in gene frequencies. It is simply a tool to investigate the relationship among a set of population, but it may not necessarily establish any exact phylogenetic relationship among them[6]. Besides, the genetic distance is used to measure the degree of gene differentiation among local populations and sometimes it can be related to geographic distance, linguistic differences or historical pattern of migrations of populations and thereby one can study the mechanism of microevolution[7]. Out of several so-called 'genetic distance' measures available in the literature, the one proposed by Nei[8] has been employed in the present study, since it has a biological meaning. In the present study the lowest genetic distance (D) (0.0071) has been observed between Brahmin and Kayastha and highest (0.1927) between Rajput and Muslim (Table 3 and Figure 1). From the genetic distance (D) of the population surveyed it is quite clear that there are two main clusters i.e., one for Muslims and the other for non-Muslims (Rajput, Brahmin, Bania, and Kayastha). In spite of common ancestry Muslims form a separate group which might be due to consanguinity. Further on the basis of genetic distance it may be concluded that the Rajput, Bania, Kayastha and Brahmin differ from each other in their gene pool.

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Cytophotometric DNA estimation in *Luzula* species

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In situ DNA amount in eight species of *Luzula* is quite constant, ranging from 5.89 to 7.77 pg. The chromosome number in these species ranges from diploid $2n = 6$ to polyploid $2n = 48$. Evolution in these species has probably been due to transverse fragmentation of chromosomes as well as polyteny.

THE species of *Luzula* do not have a centromere of the normal type in their chromosomes. The centromere is diffused or of multipolar type[1]. This characteristic of *Luzula* spp makes it an interesting case in the study of in