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INTERNATIONAL BOARD FOR PLANT GENETIC RESOURCES

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PREFACE

IBPGR INITIATED THE SERIES *Systematic and Ecogeographic Studies on Crop Genepools* in 1985. It was especially designed to provide an avenue to publish surveys conducted by IBPGR at a global level of the genepools of specified crops. The crop genepool was defined in the widest sense, including wild relatives whose contribution to the genepool of the cultivated crop may be potential rather than real. Two titles were published in the original format.

Henceforth the series will reflect a much wider range of approaches to its subject. Any substantial study of the systematics and/or ecogeography of a crop genepool, whether global or regional in scope, will be considered for publication provided that it makes a significant contribution to the understanding of the genepool and hence to promoting its conservation. Contributions will be accepted for publication in English. Subject to funds being available they will also be published in the major languages most appropriate to the subject.

It is a pleasure to welcome Dr Ivan Geric and his collaborators as the contributors to this volume number 3, which is the first to be published in the restructured series in this new format.

Alison McCusker
Head of Research, IBPGR

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SUMMARY

YUGOSLAV CORN COLLECTIONS contain about 2000 accessions (each representing a population) originating from Yugoslavia. These populations were classified in 18 groups (races) mainly on the basis of morphological characters. Genetic variability and diversity of about 300 of these populations were studied.

Isozymes were used as gene markers in the study of genetic characters of the populations. Isozymes from 12 enzymic systems, controlled by 21 loci, were analyzed. The population variability was estimated on the basis of the number of alleles determined and the polymorphism and heterozygosity of the loci. Genetic diversity among the populations was estimated on the basis of genetic distances.

All of the analyzed loci were found to be polymorphic. Some loci (Acp1, Adh1, Cat3, Est8, Glu1, Idh2, Mdh2) were polymorphic very frequently and some quite seldom (Got1, Idh1, Mdh4). Locus Got3 was monomorphic for all populations except one.

Two to eight alleles were found at the loci analyzed. The largest number of alleles was found at locus beta-Glu1. Eighty-six alleles were distributed among the tested populations, four alleles per locus on average. Individual populations had 24 to 48 alleles. The average proportion of polymorphic loci ranged among the populations from 14 to 86%; the average expected heterozygosity ranged from 0.049 to 0.288.

All groups (races) were genetically heterogeneous with respect to variability and diversity of populations. Higher variability was found within rather than between the populations. Cluster analysis showed that all groups were more or less diverse. Montenegrin flints, derived flints, Romanian flints and southern dents were genetically closer than Bosnian early dents, northeastern 8-row flints and soft flints. In general, populations of Montenegrin flints had low variability and were fairly close, Bosnian early dents had high variability and were quite diverse, and southern dents had high variability but were genetically similar. Low genetic differentiation mainly corresponds to low diversity and *vice versa*.

A tendency was observed in populations which had stayed longer in the collection (as a small population) to be less variable and genetically more distinct than populations recently included in the collection.

The results obtained indicated that the Yugoslav corn collection features significant genetic variability and may serve as an important genetic source for corn breeding.

INTRODUCTION

CROP PRODUCTION IMPROVEMENT depends on the development of new genetic lines possessing improved agronomic traits. The development of new lines depends in its turn on source materials or, more precisely, on the variability present in source materials.

Populations with higher genetic variability, other conditions being the same, are superior source materials (Mišević, 1986).

The contemporary production of corn is based on the exploitation of heterosis as a biological phenomenon. Heterotic effect, believed to depend on parental diversity, is defined as a state of the maximum heterozygosity of an organism (Borojević, 1976).

Intensive breeding and development of uniform populations narrow down the genetic basis of breeding and commercial material of corn. New genetic sources, i.e. genes that confer desirable agronomic traits, are being intensively searched for. The main sources of new germplasm are original forms, old varieties and wild relatives of agricultural crops.

The use of exotic germplasm is definitely the most valuable method of increasing the genetic variability of corn breeding materials (Ivanović and Rosić, 1986). To be able to use these sources it is necessary to keep collecting, maintaining and studying natural genetic resources.

A sizable stock of source materials of corn has been gathered. Genebanks contain about 60 000 samples (Sprague, 1980). There are several large collections, e.g. one in Latin America with 25 000 samples (Lonnquist, 1974), another in Mediterranean countries (Brandolini, 1969), etc. Only a small portion of these samples has been systematized into over 250 races, most of them originating from the Americas (Nelson, 1972).

Only a small fragment of the available corn germplasm is exploited commercially (Sprague, 1980). A somewhat larger portion has been included in breeding programmes, but the major part is out of the reach of corn breeders.

The Yugoslav corn collection is counted in the group of large collections. It comprises about 2000 populations and varieties which have been gathered on the territory of Yugoslavia (Radović, 1985).

Corn has been grown in Yugoslavia for more than 400 years and it came from different directions. It is believed that corn was first grown in Dalmatia, around 1570 (Radić, 1875), and that it was introduced from the west. The Turks reintroduced it from the east at the time of their expansion into Europe and the conquest of the Balkans.

The earliest introduced corn races were flints from the Caribbean, then flints from the Andes and Mexico, and then flints from North America. Dents from the Corn Belt, introduced at the end of the last century, promoted the

production of corn not only in the Balkans but in Europe in general (Radović and Gerić, 1986).

Therefore, the old corn types in Yugoslavia draw origin from American races although there are indications that some of the Yugoslav collection came from the Far East (Leng *et al.* 1962).

The populations and varieties in the Yugoslav collection are divided into groups (races) according to the natural classification adopted by Anderson and Cutler (1942), i.e. mostly according to the morphological characters of the plant and the ear and kernel. Sixteen groups were originally formed (Pavličić and Trifunović, 1966). The classification was amended by separating two additional groups containing populations developed by hybridization.

Presently, there are 18 groups in the collection. The largest group comprises Corn Belt dent types (group 13). Although this type was the latest to be introduced, numerous dent type forms were developed because of their economic importance. According to Trifunović (1978), the varieties typical of the European Corn Belt have developed by spontaneous crossings between dents and flints. The other two large groups are groups 1 and 6: Montenegrin flints and derived flints, respectively. The least numerous groups are groups 8, 10, and 11: small-kernel flints, Romanian flints, and large-ear dents, respectively. Most groups were divided into subgroups on account of their heterogeneity. Group 6, derived flints, is the most heterogeneous.

The distribution of the collected corn types in the territory of Yugoslavia is highly variable. Although Montenegrin flints comprise a sizable group, they all come from a small area; the populations gathered in the central part of Montenegro are considered to be the closest to the original races. Likewise, Bosnian early dents were gathered mostly in Western Bosnia, Kosmet semi-flints mostly in the region of Kosovo Province, Macedonian flints were grown almost exclusively in Macedonia, and white dents on the territory of Serbia Proper. On the other hand, eight-row flints and derived flints were grown over a large area, in the mountainous regions from Serbia to Slovenia. Different dents (Corn Belt type dents, southern dents, soft dents) were grown mostly in the fertile plains of Serbia, Vojvodina Province, and Slavonia. Mediterranean dents were grown along the Adriatic coast, from Slovenia to Montenegro.

Although the Yugoslav corn types draw origin from American races, they developed differences from the original forms because they were grown for centuries in large or small isolated populations and in the variety of Yugoslav ecological and geographical conditions. There developed populations, varieties, and biotypes which differ to a variable degree from their progenitors as well as among themselves, but which became adapted to the local conditions. The Yugoslav corn collection is considered an important asset for further improvement of corn production. Studying Southeastern European corn populations, Leng *et al.* (1962) declared them an important source of conserved and divergent corn germplasm.

In spite of its size, the Yugoslav corn collection has not been studied

intensively and its actual value has not been assessed. Radović (1980) and Radović and Mišević (1985) emphasized the diversity of the populations in the collection and their importance for breeding. Tavčar (1961), Zečević (1970, 1973) and Zečević et al. (1975, 1982) conducted a limited study of genetic characters of the populations; they studied mostly the chromosomal nodules. Isozymic variation has recently been studied in a limited number of populations (Tucić and Tucić, 1980, 1983; Gerić *et al.* 1983a, b).

Molecular polymorphism and allozymes as genetic markers, discovered in animals and plants quite recently, are nowadays used as an efficient tool in various studies of plant species, especially in the assessment of genetic resources.

Simpson and Withers (1986) reviewed and cited numerous publications on the characterization of genetic resources by isozymes. The review papers of Allard *et al.* (1975) and Brown (1978) considered the importance of isozymes in the studies of genetic characters of populations, genetic structure, and conservation. Moore and Collins (1983) considered the feasibility of using biochemical markers in the studies of variability, plant breeding, seed production and breeders' rights.

There is a fair number of experimental results of isozyme studies of corn: on genetic control of isozyme formation (Goodman and Stuber, 1983), on the use of isozymes in the identification of lines and hybrids (Goodman and Stuber, 1980; Stuber and Goodman, 1983), on allozymic variability in corn and related species (Doebley *et al.* 1984), etc.

The importance of molecular polymorphism and its relation to the morphological variability and adaptability of plants have also been studied (Hedrick and McDonald, 1980; Gottlieb, 1981; McDonald, 1983). The survival of plants in certain ecological conditions depends on the capacity of certain genotypes to become adapted to the prevailing conditions of the site. Some studies (Doebley *et al.* 1983; Salanoubat and Pernes, 1986) have indicated a relationship between isozymes and the geographic position of populations. Damerval *et al.* (1987) found high correlations between quantitative differences (amount of certain proteins) and morphological variability and low correlations between qualitative (isozymes) and morphological characters. They concluded that the regulatory (post-translational) processes are of primary importance for morphological variability.

The quantitative characters, especially the yield, are the essential agronomic characters of the grown plants. The genetic regulation of the expression of quantitative characters is a complex problem since the important agronomic characters are usually controlled polygenically. The use of enzymic loci and isozymes in the identification of genes for quantitative characters is based on gene linkage. Some studies hinted that the allozymic diversity of parental components is connected with the performances of their hybrids only when the parental components are of similar origin (Frei *et al.* 1986a); moreover the selection for allozymes does increase yield, but with a low effect (Frei *et al.*

1986b). Recently published studies (Edwards *et al.* 1987; Stuber *et al.* 1987; Kahler and Wehrhahn, 1986) indicate the existence of correlation between allozymes as gene markers and quantitative characters. No connection has been established between the important agronomic characters and the heterozygosity of enzymic loci in corn hybrids (Polak and Gardner, 1986).

The examples given above illustrate the scope of application of molecular markers not only for the assessment of genetic resources but also in breeding programmes. This is only one of the modern approaches to plant genetics and breeding, however it is an efficient instrument based on most recent findings especially in the field of biochemical genetics.

The target of the present study is to carry out an extensive investigation in order to produce data on some genetic characters of the collected materials. Using isozymes as gene markers, controlled by several enzymic loci, and analysing a large number of populations from each group, we shall be able to draw conclusions on genetic variability and diversity of the Yugoslav corn collection.

MATERIAL AND METHOD

POPULATIONS FROM 18 GROUPS were studied. A list of the analyzed populations and their collection numbers are given in Table 1 (p.26). Approximate locations of the analyzed populations show that these populations originated from the whole territory of Yugoslavia.

Locations could not be determined for several populations (group 1: C1304; group 2: C1367 and C1373; group 4: C103 and C150; group 5: C83 and C170; group 6: C182 and C897; group 7: C926 and C1308; group 8: C161, C166 and C1822; group 9: C1804; group 11: C984; group 13: C236, C258 and C278; group 14: C231; group 15: C233 and C252; group 16: C280 and C683). Accession numbers from C289 to C365 of group 14 (derived dents) as well as C317 and C327 (of group 16) are different yellow dents selected in Novi Sad.

About 20 individuals from each population were analyzed. The limited number of individuals analyzed did not ensure detection of all alleles present at a low frequency but it allowed a larger number of populations to be analyzed, giving a better picture of genetic characters of the entire collection. Parts of the coleoptile of etiolated seedlings 7-8 days old were analyzed.

The variability and diversity of the analyzed populations were assessed on the basis of isozymes from 12 enzymic systems, controlled by 21 loci (Table 2, p.27).

Enzymic variants were separated by the method of electrophoresis on starch gel. The electrophoresis and staining were mostly done using the methods of Cardy *et al.* (1981). Isozymes from various enzymic systems were designated as in the laboratory of the cooperating scientist, C.W. Stuber (North Carolina State University, Department of Genetics). Details of the entire procedure of analysis and designation are presented in a paper by Gerić *et al.* (1986). Hybrid R35 x R12, of known genetic constitution, was used as the standard for the identification of enzymic variants. Other standards were used in several instances; some rare variants were identified after consultation with the United States laboratory mentioned above.

Since variants MDH1-6 and MDH2-6 have the same migration pattern and the same position, similarly to variants MDH4-12 and MDH5-12, and since variants MDH1-6 and MDH5-12 stain poorly, it is not possible to detect them reliably in the presence of MDH2-6 and MDH4-12, respectively. A reliable detection is possible only in the absence of variants MDH2-6 and MDH4-12, the light staining at the expected positions indicating the presence of the former variants. However, since variants MDH1-6 and MDH5-12 usually are present in corn plants, it was decided to register the pairs of variants (MDH1-6 and MDH2-6; MDH4-12 and MDH5-12) whenever intensively stained bands appeared at the expected positions. Variants PGM1-9 and PGM2-4 also migrated together and the presence of both variants was registered.

The presence of allelic genes controlling the formation of variants and the polymorphic-monomorphic state of the loci were established on the basis of the detected and identified variants. The detected alleles and their frequencies were the basic information for further analyzing of genetic characters of the examined populations.

Expected heterozygosity of the populations was calculated on the basis of allelic frequencies; genetic diversity was estimated on the basis of standard genetic distance after Nei (1978).

RESULTS

Alleles and their frequencies

The loci controlling the formation of variants within the 12 analyzed enzymic systems differed in their polymorphism. The detected alleles are presented in Table 3 (p.27). The locus for beta-glucosidase was most polymorphic, with eight alleles detected in it. The loci for ACP and some loci for MDH were fairly polymorphic.

The polymorphism of the loci and the number of detected alleles varied considerably among the examined populations. Table 4 (pp. 28-34) shows the number of the detected alleles per locus in the analyzed populations. Although all loci were polymorphic and although several alleles were found at many loci, a large number of populations with a variable number of monomorphic loci was registered because of the uneven distribution of the detected alleles.

Taking into consideration individual populations, the largest number of alleles was detected at locus Glu1. Population C1373, from the group of Bosnian early dents, had seven alleles at that locus. Conversely, the locus was found to be monomorphic in three populations from group 5 (northeastern 8-row flints). Due to the differences in the distribution of individual alleles (many alleles were rare or very rare), the loci known to have several alleles were frequently found to be monomorphic. For example, five alleles were found at locus Got1 but only one allele was regularly detected; the others were rare or very rare, making the locus monomorphic in the majority of the populations examined. On the other hand, three alleles were found at locus Idh2 but two of them were very frequent, making the locus polymorphic in the majority of the populations (usually with two alleles).

The following loci were polymorphic in the majority of the populations: Acp1, Adh1, Cat3, Enp1, Est8, Glu1, Idh2, Mdh1, Mdh2, and Pgd1; the loci Got2, Mdh3, Mdh5, Pgm2 and Phi1 were less frequently polymorphic; Got1, Idh1, Mdh4, Pgm1 and Pgd2 were seldom polymorphic, the alleles Got1-4, Idh1-4, Mdh4-12, Pgm1-9 and Pgd2-5 were usually fixed; Got3 was monomorphic for all populations except one.

The number of alleles found in individual populations varied considerably because the populations differed in both the number of polymorphic loci and the level of polymorphism of the loci. The smallest number of alleles (24) was found in population C167 from the group of Mediterranean flints in which only three out of 21 loci were polymorphic. The largest number of alleles (46) was found in population C1516 from the group of southern-type dents in which 18 out of 21 loci were polymorphic. There were several populations with more than 40 alleles, their number indicating that the majority of the loci were polymorphic. Also, 11 populations were found to have less than 30 alleles which indicated that most of their loci were monomorphic. A regular pattern

could be discerned in the distribution of polymorphic loci among the populations. In that respect, all groups were quite heterogeneous.

Within the groups, too (Table 5, p. 35), the most polymorphic was locus Glu1, where 6-8 alleles have been found. Locus Acp1 was also very polymorphic, with 3-5 alleles. By contrast, locus Got3 was practically monomorphic. Locus Idh1 was also monomorphic but in the groups where it was polymorphic only two alleles were detected. All other loci were polymorphic in all groups. In individual groups alleles ranged from 51-62. In group 13 (Corn Belt dents) many populations have been analyzed and 61 alleles detected; in groups 2 (Bosnian early dents) and 6 (derived flints) less populations were tested but 62 and 60 alleles were detected, which indicates the increased polymorphism of loci in those two groups.

The populations differed in the frequency of the detected alleles (Tables 6-23, pp. 36-73). Some alleles were common to all populations and some were rare or very rare. The alleles referred to as common could be found in all or the majority of the populations, in high frequencies; the rare alleles were those found in several populations in low frequencies; very rare alleles were those found only in individual populations in low frequencies.

For example, Got1-4 was a common allele. It was found in all populations and its frequency was high, up to 1.00. On the other hand, Got1-6 was a rare allele. It was found in several populations, mostly in group 15 (southern-type dents) but its frequency was regularly low with the exception of populations C118, C692, and C236 in which its frequency ranged from 0.34 to 0.62. The loci controlling the formation of the GOT variants contained several very rare alleles, e.g. Got1-1, Got1-5.8, and Got1-8. The first two alleles were found in one or two populations and their frequencies were low. Got1-8 was found in two populations, in higher frequencies.

The loci controlling the formation of the MDH variants contained several common alleles as well as several rare or very rare alleles. Mdh1-1 and Mdh1-6 were common in locus Mdh1; Mdh2-3, Mdh2-3.5 and Mdh2-6 in locus Mdh2; Mdh3-16, Mdh4-12, and Mdh5-12 in loci Mdh3, Mdh4, and Mdh5, respectively. Some of Mdh's alleles were high. Allele Mdh2-4 was found only for population C492 but with a frequency of 0.35; allele Mdh2-5.6 was found for two populations, but with a frequency of 0.83 for one of them (C177). Allele Mdh4-8 was found at locus Mdh4 in several populations. The allele was found in three populations (C895, C103 and C1823) in group 6 (derived flints) at high frequencies from 0.28 to 0.44. This is an indication that these populations and the group in general are functionally specific from a biochemical point of view. Allele Mdh5-15 was detected at locus Mdh5 in several populations but at low frequencies. The allele was predominantly in groups 7 and 11. Its frequencies were high in only two populations, C558 and C394. Several rare alleles were found at loci Mdh1 and Mdh2.

Two alleles were detected at locus Pgm1. One of them, Pgm1-9, was detected in all populations at high frequencies, up to 1.00. The other one,

Pgm1-6, was detected in several populations but as a rule at very low frequencies. The latter allele was found primarily in groups 11, 13 and 15. Its frequencies were high (0.27 to 0.47) in a limited number of populations, e.g. C233, C258, and C278 from group 13. This was another indication that this group, and these populations in particular, feature some specific functional characteristics.

Several alleles were detected at locus Pgd2. Pgd2-5 was the dominant one. Pgd2-2.8 and Pgd2-10 were found in several populations; their frequencies were usually low with the exception of Pgd2-2.8 for C858 and Pgd2-10 for C33 where the frequencies were 0.56 and 0.45, respectively.

The analyses were generally aimed at singling out populations with specific characteristics. Genotypical characteristics of the populations indicate their origin, i.e. races they spring from, as well as the extent of changes they had undergone in consequence of the local ecological conditions and the intervention of growers.

So far, limited data have been gathered on physical and chemical properties and specific functional characteristics of enzymic variants, even those that were detected. It is still not possible to draw reliable conclusions either on the kind of functional specificity observed or its agronomic importance.

The analyzed groups, formed principally on the basis of the morphological characteristics of the populations comprising them, were quite heterogeneous with respect to allozymic variability. It was thus difficult to define common characteristics of populations in individual groups. Nevertheless some specific characteristics of individual groups could be discerned on the basis of average frequencies of characteristic alleles at several loci (Table 24, p. 74). Group 1 (Montenegrin flints) could be distinguished in that respect. The highest average frequencies of alleles Adh1-4, Idh2-4, and Pgd1-2 were registered in this group. Not a single Montenegrin flint contained allele Pgm1-16. Monomorphic locus Pgm1 was found only in groups 1 and 7. Allele Glu1-2 was at the highest frequency and Glu1-N had the lowest average frequency for the group of Montenegrin flints. The situation was reversed in group 11 for which alleles Idh2-6 and Pgd1-3.8 were at considerably high average frequencies, Adh1-6 was at high frequency and Pgm1-16 was at relatively high frequency. These findings indicate possible biochemical and functional specificities on the level of the groups.

Genetic variability of populations

Over the centuries of corn growing on the territory of Yugoslavia, the introduced races changed under the effect of ecological conditions. The growers kept selecting their corn crops for agronomically superior varieties and genotypes. Thus, the populations we studied carry both genetic characters of their progenitors and changes induced by the environment and growers. All three factors are reflected in the variability and diversity of the studied populations.

Variability of populations depends on the polymorphism of the loci, number of alleles per locus, and the frequency of the alleles. The polymorphism of individual loci and the frequency of the detected alleles were used to estimate the proportion of the polymorphic loci and the average heterozygosity of the populations (Table 25, pp. 75-77).

Populations in all groups differed with respect to their variability. However, if the populations with extreme values are disregarded, the polymorphism of loci and the lowest average heterozygosity were detected for population C167 from the group of Mediterranean flints. Low values were also detected for C34 and C1184 from the group of Montenegrin flints, C64 from the group of 8-row flints and C737 from the group of 8-row soft dents. For these populations, almost all loci were monomorphic.

High or very high variability were established for several populations. These populations had a high average proportion of polymorphic loci and high heterozygosity, e.g. C1380 from group 2, C1796 and C1815 from group 3, C1537 and C1804 from group 9, C1520, C1549 and C1552 from group 10, C1517 and C1561 from group 13, C296 from group 14, C1516 from group 15. For these populations almost all loci were polymorphic and only 3 to 5 loci were monomorphic.

Figures 1-18 (pp. 82-90), showing intrapopulation variability depending on the average proportion of polymorphic loci and average heterozygosity, also prove that the examined groups were heterogeneous regarding the variability of their populations. In addition to the heterogeneity within the groups, the figures show that differences also existed among the groups. Groups 1 and 16 contain a fair number of populations with low values which is an indication that those groups tend towards low intrapopulation variability. On the other hand, groups 2, 3, 10, 11 and 15 contain a fair number of populations with values indicating that the groups tend towards high intrapopulational variability. In groups 6, 9, 12 and 14 the values of variability were mostly medial, while groups 4, 5, 7, 8, 13, 17 and 18 were widely heterogeneous in that respect.

Genetic diversity

Genetic proximity and distance were assessed only for populations within groups, not for populations from different groups. The cluster analysis and dendrograms in Figures 19-36 (pp. 91-108) illustrate the genetic proximity and distance among the populations in the analyzed groups. It may be seen in the figures that some groups were more homogeneous than the others, i.e. their populations were genetically closer. In the more heterogeneous groups, some populations were similar but there were also those which were considerably distant.

Montenegrin flints (group 1), Kosmet semi-flints (group 3), derived flints (group 6), Romanian flints (group 10) and southern dents (group 15) were fairly homogeneous groups with populations which are genetically close. Group 10 is small and its populations have been grown in a narrow area and

in a kind of seclusion which explains why these populations were found to be genetically close. On the other hand, group 6 was large, fairly heterogeneous from a morphological viewpoint (it had the largest number of subgroups), and it comprised populations collected in different parts of Yugoslavia. It is difficult to explain why the populations in this group were relatively close. These populations come from mountain regions and perhaps similarities in ecological conditions brought about genetic similarities.

Macedonian flints (group 4), small-grain flints (group 8), 8-row soft dents (group 9), large-eared flints (group 11), white semi-dents 'moravac' (group 12), derived dents (group 14), Serbian dents (group 16) and hard dents (group 17) were less similar. Although group 14 is composed entirely of yellow dents selected mainly in Vojvodina Province, the group may be divided into two subgroups with two populations (C225 and C343) genetically distant from the other members of the groups.

Bosnian early dents (group 2), northeastern 8-row flints (group 5), Mediterranean flints (group 7), Corn Belt dents (group 13) and soft flints (group 18) were the most heterogeneous groups. These groups contained similar, but at the same time very diverse, populations.

Cluster analysis, based on allozyme data and distances, showed that in each group the studied populations are grouped according to genetic similarity thus forming the subgroups. The studies showed that in group 2 (Bosnian early dents), one large subgroup is formed, that 4 populations are diverse, of which two (C490 and C771) are highly diverse. It is almost the sane with group 5 (northeaster 8-row flints) and group 9 (Mediterranean flints). In Corn Belt dents (group 13) several subgroups occurred, with populations which were mutually very similar, while one population was very distant from the rest. The cluster analysis showed that the several populations of Corn Belt dents (from C1444 to C1561) collected in the western part of the country were close and at the same time fairly distant from other members of the group which had been collected in the northeastern lowlands, but three populations from the northeastern region (C243, C426 and C761) were close to the populations from the west.

Similarity and diversity among certain populations are difficult to explain. It may be assumed that they have been generated from different directions of breeding and from possible differences in the source materials.

Characters of the groups are also illustrated by the genic differentiation within and among populations in the groups (Table 26, p. 79.). Of the total difference in genes (H_T), the major part consists of genic differences within populations (H_S) and a small part of genic differences among populations (D_{ST}).

It was characteristic for Montenegrin flints (group 1) that both total genic difference and genic differentiation within and among the populations were low. This is in agreement with the previously mentioned findings that these populations have a low variability and that they are genetically similar. On the other hand, genic differentiation within and among populations was high for

Bosnian early dents (group 2). Kosmet semi-flints (group 3) and Romanian flints (group 10) were found to have differentiation within populations and a small difference among high populations. In the case of white semi-dents (group 12), differentiation was low within and high among populations. In group 13, which is a large and important group, the values for the above indicators were high but not the highest. This is another indication of populational variability and genetic diversity of that group.

The differentiation of genes within the groups (races), as illustrated by differentiation coefficients (G_{ST}), was very low in group 10 (Romanian flints) and high in several groups, e.g. group 12 (white semi-dents), group 5 (northeastern 8-row flints), and also in group 13 (Corn Belt dents). This study revealed a larger gene differentiation than was the case in the study of Tucić and Tucić (1980) which had included a small number of populations of the Yugoslav maize collection.

DISCUSSION

THE ULTIMATE GOAL OF collecting, maintaining, and studying genetic resources is the improvement of that portion of germplasm which is used in breeding. The magnitude of variability within and among populations is extremely important for breeding. Studies of germplasm of corn and other crops have shown that variability is, as a rule, larger within than among populations (Tucić and Tucić, 1983; O'Malley *et al.* 1979; Loukas *et al.* 1983; etc.).

The most important new sources of genes and new genetic variability are races, old varieties, isolated populations, and wild relatives of agricultural crops. The variability of various genetic sources is shown in Table 27 (p. 79). The total variability was measured only on the basis of the average number of alleles per locus. The number of alleles detected in given germplasm depends on both the number of analyzed populations and the number of analyzed individuals per population. The studies described here were concerned mainly with the same enzymic loci, which makes their results comparable. Although they differed in the number of analyzed populations and individuals, their results are a good illustration of total variability and the extent of use of genetic resources of corn.

Corn races, ancestors of modern varieties and hybrids, have the highest variability, 4 to 5 alleles per locus (Goodman and Stuber, 1983; Doebley *et al.* 1983). In the present study, open-pollinated populations in the studied groups had a stable average number of alleles per locus (about 2.5 alleles). Similar values were obtained by other authors (Kahler *et al.* 1986; Smith, 1986). We studied about 15 populations from each group. However, taking into account all alleles detected in all populations of the Yugoslav collection that have been analyzed so far (almost 300 of them), the total variability in the collection will be larger (about 4 alleles/locus, Gerić *et al.* 1986, 1987) approaching those found in some source populations. Analyses of a large number of corn inbreds (over 400), which had been grown in the United States, indicated that this collection too has a significant variability (Stuber and Goodman, 1983; Smith *et al.* 1985).

In addition to the maintenance of genetic resources, another important aspect is the use of available germplasm in breeding programmes. According to the previously cited authors and other literature, the most commonly used lines in the United States (Smith *et al.* 1985) and over 100 SC corn hybrids (Smith, 1984) have 2.2 alleles/locus on average; the most common Yugoslav hybrids have only 1.8 alleles/locus (Gerić *et al.* unpublished). The number of detected alleles was very small probably because only 20 SC hybrids were analyzed.

These as well as other data show that the corn germplasm used by breeders is genetically narrow. Having analyzed molecular polymorphism (allozymes)

in several historically important American inbred lines, Smith et al. (1985a) concluded that the genetic basis of corn is not as narrow as might be expected from the fact that there are, in practice, only two races in the genetic basis of the available commercial corn hybrids. The 70 historically important inbred lines contained about 50% of the alleles detected in 30 races from Bolivia. The authors explained the finding by a possible heterogeneity of the races. Fifty plants of an exotic race contain as many alleles as all of 70 American inbreeds. Our data indicate that the groups (races) are heterogeneous: the populations in each group differ in the number of alleles; they differ even more in their frequencies.

A study of the germplasm of the most popular corn inbred lines in the United States, conducted in the period 1970-1980, indicated a decreased variability but increased genetic diversity (Smith *et al.* 1985b).

The importance of the incorporation of exotic germplasm into adapted materials has also been considered (Ivanović and Rosić, 1986). When crossing Corn belt dents and populations with exotic germplasm, the heterotic effect was lower than the varietal heterotic effect (Cross *et al.* 1987).

Although the genetic basis of germplasm has not yet become a limiting factor in corn breeding programmes, the necessity of introducing exotic germplasm in the process of breeding as a long-term target is proposed. The maintenance and study of the available genetic resources is the essential prerequisite for their better use in corn breeding programmes.

The quantitative characters, especially the yield, adaptation to the environment, and resistance, are important agronomic features of agricultural crops. It is supposed that the natural, and still unexploited, genetic resources contain an abundance of desirable genes. Detailed studies of material in genebanks should be undertaken in order to find these genes.

As the populations in the Yugoslav corn collection were divided into groups mostly according to their morphological characters, it follows that the groups are morphologically homogeneous. Our results indicated that the groups were more or less heterogeneous regarding the studied isozymes; thus it seems that there is no relationship between loci for these morphological traits and loci controlling enzymes.

Isozymic data may also be used to detect the origin of material and changes in it induced by natural and artificial selection. An analysis was conducted on the presence of several alleles in different genetic sources (Table 28, p. 80) and the following distinction was observed: there are usually two alleles at locus Adh1 but only one of them (Adh1-4) is dominant. However, the other allele (Adh1-6) is found with increased frequencies for some groups and in the group of Northern flints it is dominant over Adh1-4. In general, allele Adh1-6 is fairly frequent in the Yugoslav corn collection. Another distinction was observed for Bolivian races which have a higher average frequency of Got1-6 than Got1-4; in the Yugoslav and American populations, Got1-6 is at low frequency. Also, two alleles are mostly detected at locus Idh2, both with high frequencies.

However, the average frequency of Idh2-6 is very low for the Bolivian races as well as for the Montenegrin flints. Finally, two alleles are frequently found at locus Pgd1, Pgd1-3.9 allele usually being dominant. In the case of the northern flints, this locus is virtually monomorphic (with Pgd1-3.8); this allele is detected at high frequency for Yugoslav SC hybrids indicating probably an increased influence of the Northern flints on Yugoslav commercial germplasm. The other allele, Pgd1-2, is dominant only for the Montenegrin flints.

The calculated frequencies of certain alleles indicated that there existed considerable differences between US Northern flints and US Southern dents (Doebley *et al.* 1986, 1987). According to these authors, 11 loci distinguish the populations of these two corn races in the United States. Table 28 (p. 80) shows that the most striking differences occurred in the following loci: Acp1, Adh1, Mdh2 and Pgd1. In the Yugoslav collection, the populations in group 5 have been defined as Northerneastern 8-row flints; according to Leng *et al.* (1962), these populations correspond to US Northern flints. Our results show (Table 28, p. 80; Table 10, pp. 44-45) that the average frequencies of the characteristic alleles in this group correspond only in part to the frequencies of US Northern flints. Some populations from our group are similar to US Northern flints in the frequencies of alleles at particular loci, but other populations are quite different. This is in agreement with the statement of Leng *et al.* (1962) that the American flints intercrossed with other flint and dent varieties in southeastern Europe, thus generating a variety of hybrid products.

Greater similarity exists between US Southern dents and the dents in group 15 of the Yugoslav collection. Therefore, differences between group 5 (northeastern or northern flints) and group 15 (southern dents) of the Yugoslav collection are much smaller than stated by Doebley *et al.* (1986, 1987) for the American Northern flints and Southern dents. The greater differentiation between the two American races is most likely due to greater isolation, which in turn means that the American populations are closer to the original forms than the Yugoslav, which had been grown in a smaller area with less isolation.

The results of this study indicate yet another tendency. Populations maintained in the collection for a long time, i.e. those with small accession numbers, have in several instances a lower populational variability and larger genetic distances than the recently included populations (see figures). The reduction in the populational variability in the course of maintenance is most probably due to inbreeding in a small population; according to these results, the maintenance led to increased genetic differentiation.

The study of genetic resources by various methods, including the use of isozymes as gene markers in the analysis of genetic variability and diversity, is focused on the discovery of new genes for desirable agronomic traits and on an increased use of the available germplasm in corn breeding programmes. These analyses may reveal the value of certain sources and individual populations which may then be used as source materials in breeding superior corn genotypes.

CONCLUSIONS

THIS IS THE most extensive and the most complete study of genetic characteristics of populations in the Yugoslav corn collection conducted so far, using isozymes as gene markers.

The collection includes over 2000 populations which have been collected in different parts of Yugoslavia. The populations are classified into 18 groups (races), mostly on the basis of the morphological characters of the plant, ear and grain. A total of 277 populations from 18 groups have been studied so far.

The present study showed that the collection possessed considerable genetic variability and that the populations in it were more or less diverse.

According to the isozymic data, each group in the collection is genetically heterogeneous. Larger differences were found among populations within groups than among the groups. The variability was larger within the populations than among them.

Considering the extent of genetic variability detected, the collection should become an important genetic source for the improvement of the sum of genetic variability in the materials used in corn breeding.

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TABLES 1-28

Table 1. List of analyzed populations (Accession number)

Group1: Montenegrin flints	Group 4: Macedonian flints	Group 7: Mediterranean flints
1. C34	1. C103	1. C167
2. C1184	2. C150	2. C189
3. C1194	3. C592	3. C191
4. C1229	4. C593	4. C510
5. C1239	5. C594	5. C848
6. C1259	6. C597	6. C851
7. C1263	7. C600	7. C901
8. C1265	8. C666	8. C920
9. C1266	9. C892	9. C926
10. C1268	10. C893	10. C934
11. C1286	11. C895	11. C1218
12. C1287	12. C1802	12. C1223
13. C1291	13. C1816	13. C1308
14. C1302	14. C1821	14. C1309
15. C1304	15. C1823	15. C1337

Group 2: Bosnian early dents	Group 5: Northeastern US 8-row types	Group 8: Small-grain flints
1. C162	1. C62	1. C159
2. C444	2. C64	2. C161
3. C462	3. C72	3. C163
4. C480	4. C83	4. C166
5. C488	5. C118	5. C558
6. C490	6. C125	6. C900
7. C771	7. C132	7. C935
8. C847	8. C170	8. C1475
9. C858	9. C177	9. C1497
10. C877	10. C184	10. C1822
11. C1365	11. C527	
12. C1373	12. C1545	
13. C1375	13. C1550	
14. C1377	14. C1559	
15. C1380	15. C1751	

Group 3: Semi-flints from Kosmet	Group 6: Derived flints	Group 9: 8-row soft dents
1. C33	1. C182	1. C69
2. C48	2. C391	2. C582
3. C389	3. C492	3. C602
4. C394	4. C494	4. C737
5. C401	5. C528	5. C762
6. C419	6. C532	6. C796
7. C570	7. C897	7. C1481
8. C576	8. C899	8. C1489
9. C1789	9. C1330	9. C1496
10. C1791	10. C1471	10. C1506
11. C1794	11. C1472	11. C1507
12. C1796	12. C1520	12. C1524
13. C1803	13. C1521	13. C1537
14. C1811	14. C1523	14. C1583
15. C1815		15. C1804

Group 10: Romanian flints	Group 11: Large eared flints	Group 12: White semi-dents "Moravac"
1. C676	1. C138	1. C58
2. C690	2. C141	2. C90
3. C692	3. C715	3. C198
4. C700	4. C832	4. C385
5. C1528	5. C838	5. C435
6. C1530	6. C918	6. C539
7. C1549	7. C922	7. C654
8. C1552	8. C984	8. C669
9. C1592	9. C1544	9. C724
	10. C1577	10. C799
	11. C1717	11. C802
	12. C1729	12. C804
	13. C1744	13. C870
	14. C1833	14. C882
		15. C887

Group 13: US corn belt-type dents	Group 14: Derived dents	Group 15: Southern US type dents
1. C196	1. C225	1. C222
2. C216	2. C231	2. C232
3. C233	3. C289	3. C245
4. C236	4. C296	4. C252
5. C243	5. C309	5. C262
6. C258	6. C320	6. C266
7. C273	7. C321	7. C914
8. C278	8. C325	8. C1480
9. C284	9. C336	9. C1488
10. C384	10. C337	10. C1492
11. C426	11. C343	11. C1509
12. C482	12. C347	12. C1516
13. C559	13. C348	13. C1565
14. C566	14. C359	14. C1588
15. C577	15. C362	
16. C638	16. C365	
17. C645	17. C717	
18. C694		
19. C761		
20. C1444		
21. C1467		
22. C1478		
23. C1505		
24. C1517		
25. C1561		

Group 16: Serbian dents	Group 17: Hard dents	Group 18: Soft flints
1. C210	1. C22	1. C74
2. C228	2. C31	2. C114
3. C280	3. C55	3. C124
4. C317	4. C60	4. C127
5. C327	5. C76	5. C139
6. C611	6. C110	6. C211
7. C672	7. C133	7. C235
8. C680	8. C214	8. C326
9. C683	9. C244	9. C330
10. C721	10. C282	10. C356
11. C827	11. C369	11. C360
12. C828	12. C380	12. C387
13. C864	13. C382	13. C393
14. C865	14. C432	14. C398
	15. C433	15. C454
	16. C569	16. C533
	17. C616	17. C575
	18. C632	18. C612
	19. C659	19. C620
	20. C829	20. C647

Table 3. Alleles detected in examined populations

Loci	Allele - designated	Total
1. Acp 1	1,2,3,4,6	5
2. Adh 1	2,4,6	3
3. Cat 3	7,9,12,N	4
4. Enp 1	4,6,7,8,10	5
5. Est 8	4,4.5,5,6,N	5
6. Glu 1	1,2,3,6,7,8,10,N	8
7. Got 1	1,4,5.8,6,8	5
8. Got 2	2,4,10,N	4
9. Got 3	4,N	2
10. Idh 1	4,6,N	3
11. Idh 2	4,6,8	3
12. Mdh 1	8.5,1,6,9,10.5,N	6
13. Mdh 2	3,3.5,4,4.5,5,5.6,6,N	7
14 Mdh 3	16,16.3,16.9,18,N	5
15. Mdh 4	8,12	2
16. Mdh 5	12,15	2
17. Pgm 1	9,16	2
18. Pgm 2	2,3,4,8	4
19. Pgd 1	1,2,3.8,7,N	5
20. Pgd 2	2.8,5,6,10	4

Table 2. Enzymes studied, their loci and location on corn chromosomes (from Stuber and Goodman, 1983)

Locus	Enzyme	Chromosome location
Acp 1	Acid phosphatase 1 (ACP1)	9
Adh 1	Alcohol dehydrogenase 1	1L
Cat 3	Catalase 3 (CAT3)	?
Enp 1	Endopeptidase 1 (ENP1)	6L
Est 8	Esterase 8 (EST8)	3S
Glu 1	Beta-glucosidase 1 (GLU1)	10L
Got 1	Glutamateoxaloacetate transaminase 1 (GOT1)	3L
Got 2	" " 2 (GOT2)	5L
Got 3	" " 3 (GOT3)	5S
Idh 1	Isocitrate dehydrogenase 1 (IDH1)	8
Idh 2	" " 2 (IDH2)	6L
Mdh 1	Malate dehydrogenase 1 (MDH1)	8
Mdh 2	" " 2 (MDH2)	6L
Mdh 3	" " 3 (MDH3)	3L
Mdh 4	" " 4 (MDH4)	1L
Mdh 5	" " 5 (MDH5)	5S
Pgd 1	Phosphogluconate dehydrogenase 1 (PGD1)	6L
Pgd 2	" " 2 (PGD2)	3L
Pgm 1	Phosphoglucomutase 1 (PGM1)	1L
Pgm 2	" " 2 (PGM2)	5S
Phi 1	Phosphohexose isomerase 1 (PHI1)	1L

Table 4. Number of alleles per locus detected in populations of the collection

Group 1: MONTENEGRIN FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
1. C34	3	1	3	1	1	3	1	1	1	1	1	2	3	1	1	1	1	1	2	1	1	31
2.C1184	3	1	2	1	2	4	1	1	1	1	1	2	3	1	1	1	1	1	2	1	1	32
3.C1194	3	2	3	2	1	3	1	1	1	1	1	2	2	1	1	1	1	2	2	1	1	33
4.C1229	3	2	3	2	1	4	1	3	1	1	2	1	2	1	1	1	1	1	2	1	1	35
5.C1239	3	2	3	1	1	3	1	1	1	1	2	2	2	1	1	1	1	1	2	1	1	32
6.C1259	3	2	3	2	3	5	2	2	1	1	2	3	2	2	1	1	1	2	2	2	1	43
7.C1263	3	1	2	2	1	4	1	1	1	1	2	3	2	2	2	1	1	1	2	2	1	36
8.C1265	2	2	3	2	2	5	1	2	1	1	2	2	2	1	1	1	1	1	2	1	1	36
9.C1266	2	2	3	2	2	4	1	1	1	1	2	2	2	2	1	1	1	1	2	1	1	35
10.C1268	2	2	3	2	2	4	1	1	1	1	2	2	2	1	2	1	1	1	2	1	1	35
11.C1286	3	2	1	1	3	4	1	1	1	2	1	1	2	1	1	1	1	2	2	1	1	33
12.C1287	4	2	1	2	2	2	1	1	1	2	1	1	3	1	1	2	1	2	1	1	1	33
13.C1291	4	2	3	2	3	4	1	1	1	1	2	2	3	1	1	2	1	2	2	2	2	42
14.C1302	3	2	3	2	2	4	1	1	1	1	2	2	3	2	1	2	1	1	2	2	1	39
15.C1304	2	1	3	2	2	4	1	2	1	1	2	2	2	2	1	2	1	2	2	2	1	38

Group 2: BOSNIAN EARLY DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
16. C162	3	1	1	1	2	3	1	1	1	1	2	2	1	1	1	1	1	2	1	1	1	29
17. C444	3	2	3	2	2	3	2	1	1	2	2	2	2	1	1	1	1	2	2	1	1	37
18. C462	3	2	3	2	2	3	1	1	1	2	3	3	2	1	1	1	1	2	2	2	2	40
19. C480	1	2	1	1	2	1	2	1	1	1	2	1	2	1	1	1	1	2	2	1	2	29
20. C488	1	2	2	2	2	4	1	1	1	1	2	2	3	2	1	1	1	2	2	1	1	35
21. C490	1	2	1	1	2	3	1	1	1	1	2	1	2	1	1	1	1	1	1	1	1	27
22. C771	1	2	2	2	2	3	1	1	1	1	2	1	2	2	1	2	1	1	2	1	1	32
23. C847	2	2	2	2	2	3	1	1	1	1	2	2	1	1	1	1	2	1	2	3	1	34
24. C858	2	2	2	1	2	2	2	2	1	1	2	1	1	1	1	1	2	2	2	2	1	33
25. C877	2	2	2	2	4	4	1	2	1	1	2	3	2	2	1	1	1	1	2	1	1	38
26.C1365	4	2	2	2	3	5	1	2	1	1	2	2	3	3	1	2	1	2	2	1	2	44
27.C1373	3	2	3	2	3	7	1	2	1	1	2	2	3	2	1	2	1	2	2	1	2	45
28.C1375	4	2	3	2	2	5	1	2	1	1	2	3	3	1	1	2	1	2	2	1	2	43
29.C1377	3	2	3	1	2	6	1	2	1	1	2	2	3	1	1	2	1	2	2	1	1	40
30.C1380	3	2	3	2	2	6	1	2	1	2	2	3	3	2	1	2	2	3	2	2	2	48

Group 3: SEMI-FLINTS FROM KOSMET

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
31. C33	3	2	3	2	2	4	1	1	1	1	2	2	2	1	2	1	1	3	2	2	1	39
32. C48	1	2	3	2	2	3	1	2	1	1	2	1	2	1	1	2	1	2	2	1	2	35
33. C389	2	2	4	1	2	4	2	1	1	1	2	1	2	1	1	1	1	2	1	1	1	34
34. C394	3	2	4	1	3	3	1	2	1	1	2	2	2	1	1	2	1	2	1	1	1	37
35. C401	1	2	2	2	2	2	1	2	1	1	2	2	2	1	1	2	1	2	2	1	1	33
36. C419	2	2	2	1	2	3	1	2	1	1	2	2	3	2	1	1	1°	1	2	1	2	35
37. C570	2	2	3	2	2	3	1	2	1	1	2	1	1	1	1	1	1	2	2	1	1	33
38. C576	3	2	2	2	2	3	1	2	1	1	2	1	1	1	1	2	2	2	1	1	2	35
39.C1789	3	2	4	2	2	5	1	1	1	1	2	2	3	1	1	2	2	2	3	1	1	42
40.C1791	4	2	4	2	2	4	1	1	1	1	2	2	3	2	1	2	2	2	2	1	2	43
41.C1794	3	2	3	2	5	5	1	2	1	1	2	2	3	1	1	2	1	3	2	1	2	45
42.C1796	3	2	3	3	2	4	1	2	1	1	2	2	3	2	1	2	2	3	2	2	1	44
43.C1803	2	2	3	1	4	5	1	1	1	1	2	3	2	1	2	2	1	2	2	1	2	41
44.C1811	3	2	3	2	2	5	1	2	1	1	2	2	3	2	1	1	2	2	2	1	2	42
45.C1815	3	2	3	2	2	4	2	2	1	1	2	3	3	2	1	2	2	2	2	1	2	44

Table 4. continued

Group 4: MACEDONIAN FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
46. C103	3	2	2	2	2	3	2	2	1	2	2	1	2	1	2	1	1	1	2	1	1	36
47. C150	3	2	2	2	2	2	1	1	1	1	2	2	2	1	1	1	1	1	2	1	2	33
48. C592	2	2	3	2	2	2	1	1	1	1	2	2	1	1	1	1	1	2	2	1	1	32
49. C593	2	2	2	2	2	4	1	2	1	1	2	4	2	1	1	1	1	1	2	1	1	36
50. C594	2	2	3	1	2	4	1	1	1	1	1	2	2	1	1	1	1	1	2	1	1	32
51. C597	3	2	2	2	2	4	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	33
52. C600	1	2	2	1	2	2	1	1	1	1	1	2	2	1	1	1	1	1	2	1	2	29
53. C666	2	2	2	2	2	3	1	1	1	2	2	3	2	1	1	2	1	1	2	1	2	36
54. C892	2	2	3	2	2	3	1	1	1	1	1	2	2	1	1	1	1	1	2	1	1	32
55. C893	2	2	3	2	2	2	2	2	1	1	1	2	1	1	2	2	1	1	2	1	1	34
56. C895	1	2	3	2	2	2	1	2	1	1	2	2	1	1	2	1	1	1	2	1	2	33
57.C1802	3	2	3	2	2	4	1	1	1	1	2	3	2	1	2	1	1	1	2	1	1	37
58.C1816	3	2	3	2	2	6	2	2	1	1	2	2	3	2	1	1	2	2	2	1	2	44
59.C1821	3	2	3	2	2	4	1	2	1	1	2	3	3	1	2	1	2	2	2	2	2	43
60.C1823	3	2	3	2	2	5	1	2	1	1	2	3	3	1	2	2	2	1	2	1	1	42

Group 5: NORTHEAST US 8-ROW TYPES

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
61. C62	2	1	3	3	2	1	1	1	1	1	2	1	3	2	1	1	1	2	2	1	2	34
62. C64	1	2	2	2	2	1	1	1	1	1	2	1	2	1	1	1	1	1	2	1	1	28
63. C72	2	2	2	3	2	1	1	1	1	1	2	2	3	2	1	1	1	2	2	1	2	35
64. C83	1	2	1	1	2	2	1	2	1	1	1	1	2	1	1	1	1	1	1	1	1	26
65. C118	3	2	1	2	2	3	2	1	1	1	2	2	3	1	1	2	1	1	1	1	2	35
66. C125	1	1	1	2	2	4	1	2	1	1	2	2	3	1	1	1	2	1	2	1	1	33
67. C132	2	2	2	1	2	3	2	1	1	1	2	2	2	1	1	1	1	2	2	2	1	34
68. C170	3	2	3	2	2	4	1	1	1	1	2	1	1	1	1	2	2	1	2	1	1	35
69. C177	3	2	1	1	3	4	1	2	1	1	1	3	3	1	1	1	1	1	2	1	1	35
70. C184	4	2	1	2	2	2	2	2	1	1	2	1	1	2	1	1	1	1	2	1	1	33
71. C527	1	2	3	2	4	2	1	1	1	1	2	2	2	1	1	1	1	2	2	2	1	35
72.C1545	3	2	3	2	3	4	1	1	1	1	2	2	3	1	1	1	2	2	2	1	2	40
73.C1550	4	2	2	2	2	3	1	2	1	1	2	2	3	1	1	2	1	3	2	1	2	40
74.C1559	3	2	3	2	2	4	1	2	1	1	2	2	3	2	1	1	1	2	2	1	2	40
75.C1751	3	2	3	2	3	5	2	2	1	1	2	2	2	1	1	1	1	2	2	2	2	42

Group 6: DERIVED FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
76. C182	3	2	4	2	2	3	1	2	1	1	2	2	2	1	1	1	1	1	2	2	1	37
77. C391	2	2	2	2	2	4	1	1	1	1	2	1	3	1	1	1	1	1	2	1	1	33
78. C492	2	2	3	2	2	4	1	2	1	1	2	1	2	1	1	1	1	2	2	1	2	36
79. C494	2	2	3	1	2	4	1	1	1	1	2	2	1	1	1	1	1	1	3	3	1	35
80. C528	2	2	3	2	2	5	1	2	1	1	2	3	3	2	1	1	1	2	2	1	1	40
81. C532	3	2	3	2	2	3	1	2	1	1	2	1	2	1	1	2	1	1	1	1	1	34
82. C897	4	2	3	2	2	3	1	2	1	1	2	2	1	1	1	1	1	2	2	1	1	36
83. C899	2	2	3	2	2	2	2	1	1	1	2	2	2	1	1	2	1	2	2	1	1	35
84.C1330	2	2	3	2	2	3	1	1	1	1	2	3	3	1	2	2	1	1	2	2	2	39
85.C1471	3	2	3	2	2	5	2	1	1	1	2	2	3	2	1	1	1	2	2	1	2	41
86.C1472	2	2	3	2	2	3	1	2	1	1	2	2	4	2	1	2	2	2	2	1	2	41
87.C1520	3	2	3	2	2	3	1	2	1	1	2	2	3	1	1	2	1	1	1	1	1	36
88.C1521	3	2	3	2	4	2	1	1	1	1	2	2	2	1	1	1	1	1	2	1	1	36
89.C1523	3	2	3	2	2	4	2	2	1	1	1	3	3	2	1	2	2	1	2	2	1	42

Table 4. continued

Group 7: MEDITERRANEAN FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
90. C167	2	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	24
91. C189	2	2	2	2	2	3	1	2	1	1	2	3	3	2	1	2	1	3	2	2	2	41
92. C191	2	2	3	3	2	2	1	1	1	1	2	2	2	1	1	2	1	2	2	2	2	37
93. C510	2	2	1	2	2	3	1	2	1	1	2	1	2	2	1	1	1	2	2	1	1	33
94. C848	3	2	2	2	2	3	2	2	1	1	1	3	2	1	1	2	1	1	2	1	1	36
95. C851	2	2	2	2	2	3	1	2	1	1	2	1	1	1	1	1	1	3	2	2	1	33
96. C901	2	2	3	2	2	3	1	1	1	1	2	2	1	1	1	2	1	1	2	1	1	32
97. C920	3	2	1	1	2	2	1	1	1	1	2	3	2	1	1	2	1	2	2	1	1	32
98. C926	1	2	3	1	2	3	1	2	1	1	2	2	2	1	2	2	1	1	2	1	1	33
99. C934	2	1	2	2	3	3	1	1	1	1	2	2	1	1	1	1	1	2	2	1	2	32
100.C1218	2	2	2	2	2	3	1	2	1	1	2	1	2	1	1	2	1	2	2	2	1	34
101.C1223	2	2	3	2	2	3	1	1	1	1	2	2	2	1	1	1	1	2	2	1	1	33
102.C1308	2	2	2	2	2	3	1	2	1	1	2	2	2	2	2	2	1	1	2	1	1	35
103.C1309	2	1	2	3	2	4	2	2	1	1	2	3	3	1	1	2	2	2	2	2	1	40
104.C1337	3	1	3	2	2	5	1	1	1	1	2	3	3	2	1	1	1	2	2	2	2	40

Group 8: SMALL-GRAIN FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
105. C159	2	2	3	2	2	1	1	1	1	1	2	2	1	1	1	1	1	1	2	1	1	30
106. C161	2	2	2	2	2	1	1	1	1	1	1	2	1	1	1	1	1	2	2	1	2	30
107. C163	1	2	1	2	3	2	1	1	1	1	2	2	1	1	1	1	1	1	2	1	1	29
108. C166	2	1	3	3	2	2	1	2	1	1	2	1	1	1	1	1	1	1	2	1	1	31
109. C558	2	2	3	2	2	2	1	2	1	1	2	2	2	1	1	2	1	1	2	1	1	34
110. C900	3	2	3	2	2	4	2	1	1	1	1	2	2	2	1	2	1	2	2	1	1	38
111. C935	2	2	2	3	2	3	1	1	1	1	1	2	1	1	1	2	2	1	2	1	1	33
112.C1475	5	2	2	2	2	4	1	1	1	1	2	2	3	2	1	1	2	2	2	1	1	40
113.C1497	2	1	3	2	2	3	1	2	1	1	2	2	3	2	1	1	1	2	2	1	1	36
114.C1822	4	2	3	1	2	6	1	2	1	1	2	2	3	2	1	1	1	2	2	1	1	42

Group 9: 8-ROW SOFT DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
115. C69	3	2	2	3	2	2	1	1	1	1	2	1	3	1	1	1	1	2	2	1	3	36
116. C582	4	2	3	2	3	3	1	1	1	1	1	2	2	2	1	2	1	1	2	1	1	36
117. C602	2	2	2	2	1	5	2	1	1	1	2	2	2	1	1	1	1	2	2	1	2	36
118. C737	3	1	2	1	1	4	1	1	1	1	1	1	2	1	1	1	2	1	2	1	2	31
119. C762	3	2	2	1	2	3	1	1	1	1	2	2	3	1	1	1	1	2	2	1	3	36
120. C796	1	1	2	2	1	2	1	1	1	1	2	1	3	1	1	1	1	2	2	2	2	31
121.C1481	3	2	3	2	2	2	1	1	1	1	2	2	2	1	1	1	1	2	1	1	2	33
122.C1489	2	2	3	2	1	4	1	1	1	1	2	2	2	1	1	1	2	1	2	1	2	34
123.C1496	4	2	1	1	2	5	2	1	1	1	2	2	2	1	1	2	2	2	2	2	1	39
124.C1506	3	2	2	2	2	4	1	2	1	1	2	2	3	2	1	1	1	2	2	1	2	39
125.C1507	2	2	3	2	4	3	1	1	1	1	2	2	3	2	1	2	1	1	2	2	2	37
126.C1524	3	2	2	2	3	5	2	2	1	1	2	2	2	2	1	2	1	2	2	1	1	40
127.C1537	3	2	2	2	2	6	2	2	1	1	2	2	2	2	1	2	2	2	2	2	3	45
128.C1583	4	2	2	2	2	3	2	2	1	1	2	2	2	1	1	1	1	2	2	2	3	40
129.C1804	3	2	2	2	2	5	1	2	1	1	2	2	2	1	1	2	2	2	2	2	3	42

Table 4. continued

Group 10: ROMANIAN FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
130. C676	3	2	2	2	2	3	1	1	1	1	2	2	1	2	1	1	1	2	2	1	1	34
131. C690	2	2	2	2	2	4	2	2	1	1	2	2	2	1	1	1	1	2	1	2	1	36
132. C692	3	2	2	2	2	2	2	1	1	1	2	1	2	1	1	1	2	1	2	1	1	33
133. C700	3	2	3	2	2	2	1	2	1	1	2	2	2	1	1	1	1	1	2	2	2	36
134.C1528	3	2	3	2	2	6	1	2	1	1	2	2	3	2	1	1	1	2	2	1	1	41
135.C1530	4	2	3	2	2	4	1	2	1	1	2	3	3	2	1	2	1	2	2	1	2	43
136.C1549	3	2	3	2	3	4	2	2	1	1	2	2	3	1	1	1	2	2	2	2	2	43
137.C1552	3	2	3	2	2	6	2	2	1	1	2	2	3	2	1	1	2	2	2	2	2	45
138.C1592	3	2	3	2	2	5	1	2	1	1	2	3	3	2	1	1	1	2	2	2	1	42

Group 11: LARGE EARED FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
139. C138	4	2	3	2	4	3	2	1	1	1	2	1	1	1	1	1	2	2	2	1	1	36
140. C141	2	1	3	2	4	1	1	1	1	1	1	1	3	1	1	2	2	3	1	1	1	34
141. C715	3	3	2	2	2	4	1	2	1	1	2	2	2	1	1	2	1	2	1	1	2	36
142. C832	2	2	1	3	1	2	1	1	1	1	2	1	2	1	1	1	1	2	2	1	1	30
143. C838	4	2	3	2	2	2	1	1	1	1	2	1	2	1	1	1	1	2	2	2	1	35
144. C918	3	2	3	2	3	3	1	2	1	1	2	3	3	1	1	2	2	2	2	1	2	42
145. C922	4	2	2	2	3	3	1	2	1	1	2	2	2	1	1	2	1	2	2	2	2	40
146. C984	2	2	2	1	1	1	1	2	1	1	2	2	1	1	1	1	2	2	2	1	1	30
147.C1544	2	2	2	2	1	4	1	3	1	1	2	2	2	1	1	2	2	1	2	2	1	37
148.C1577	4	2	3	2	3	3	1	2	1	2	2	2	2	1	1	2	1	2	2	1	2	41
149.C1717	4	2	3	2	4	4	1	1	1	1	2	2	2	1	1	2	1	2	1	1	1	38
150.C1729	4	2	3	2	3	4	1	2	1	1	2	2	2	2	1	2	2	2	2	1	2	42
151.C1744	4	2	3	2	4	4	1	1	1	1	2	2	3	2	1	1	2	3	2	2	2	43
152.C1833	3	2	3	2	3	3	2	1	1	1	2	2	3	2	1	2	2	2	2	1	2	42

Group 12: WHITE SEMI-DENTS "MORAVAC"

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
153. C58	3	2	2	1	2	6	1	2	1	1	2	2	2	1	1	1	1	2	2	1	1	37
154. C90	3	2	3	2	2	3	1	1	1	1	2	1	1	1	1	2	1	1	2	1	2	34
155. C198	2	2	1	1	2	2	1	2	1	1	2	2	2	1	1	1	1	2	1	1	2	31
156. C385	2	2	2	1	2	4	1	1	1	1	2	2	2	2	1	1	1	1	2	1	1	33
157. C435	1	2	2	1	2	3	1	1	1	1	2	2	3	2	1	1	1	2	2	1	2	34
158. C539	2	2	2	1	2	5	1	1	1	1	2	1	2	1	1	1	1	2	2	1	1	33
159. C654	2	1	3	1	2	3	1	2	1	1	2	1	2	1	1	1	1	1	1	1	2	31
160. C669	2	2	1	1	2	3	2	2	1	1	2	1	2	2	1	1	2	2	2	1	2	35
161. C724	4	2	2	1	2	3	1	1	1	1	2	2	2	1	1	1	2	1	1	2	1	33
162. C799	3	2	3	1	2	3	1	2	1	1	2	2	2	1	1	1	2	2	2	2	2	36
163. C802	2	1	3	1	2	2	1	2	1	1	2	1	2	1	1	2	2	2	2	1	2	35
164. C804	2	1	1	1	3	4	1	1	1	1	2	2	3	2	1	1	1	2	2	1	1	34
165. C870	2	2	1	1	2	1	1	1	1	1	2	1	3	1	1	1	1	2	1	1	2	29
166. C882	2	1	1	1	2	4	1	2	1	1	2	2	2	1	1	1	2	2	2	1	2	34
167. C887	3	2	2	1	2	3	1	2	1	2	1	1	2	1	1	1	1	1	2	2	1	33

Table 4. continued

Group 13: US CORN BELT-TYPE DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
168. C196	2	2	3	1	2	2	1	1	1	1	2	3	3	1	1	1	1	1	2	1	2	34
169. C216	2	2	2	1	3	3	1	1	1	1	2	2	1	1	1	2	2	2	2	1	1	34
170. C233	3	2	2	1	2	2	1	1	1	1	2	1	2	2	1	1	2	1	2	1	1	32
171. C236	2	2	2	2	2	6	2	2	1	1	2	2	2	1	1	1	2	2	2	2	1	40
172. C243	3	2	2	1	2	4	1	2	1	1	2	2	2	3	1	1	1	1	2	1	2	37
173. C258	2	2	1	1	2	1	1	1	1	1	2	1	3	2	1	1	2	2	1	1	1	30
174. C273	2	2	2	1	2	4	1	2	1	1	2	2	2	1	1	1	1	1	2	1	1	33
175. C278	1	2	2	2	2	3	1	1	1	1	2	1	2	1	1	1	2	2	2	1	1	32
176. C284	1	2	1	1	2	3	1	1	1	1	2	2	2	1	1	1	1	1	1	1	2	29
177. C384	3	1	2	1	2	2	1	1	1	1	2	2	2	2	1	1	2	1	2	1	1	32
178. C426	3	2	2	1	2	4	1	2	1	1	2	3	3	2	1	1	2	2	2	1	2	40
179. C482	3	2	3	2	2	3	1	2	1	1	2	3	2	1	1	1	1	2	2	2	1	38
180. C559	1	1	3	2	2	3	1	1	1	1	2	2	2	1	1	1	1	3	2	1	1	33
181. C566	2	2	2	1	2	4	2	1	1	1	2	2	3	1	1	2	2	3	2	1	2	39
182. C577	2	2	4	1	2	4	1	1	1	1	2	2	1	2	1	1	1	2	1	1	1	34
183. C638	2	2	3	1	2	3	1	3	1	1	2	1	3	2	1	1	1	2	2	2	2	38
184. C645	2	2	2	2	2	4	2	2	1	1	2	2	2	1	1	1	1	1	1	1	2	35
185. C694	2	2	2	2	3	3	1	1	1	1	2	2	1	2	1	1	1	3	1	1	1	34
186. C761	3	2	1	1	1	3	1	2	1	1	2	2	3	1	1	1	2	1	2	1	2	34
186.C1444	4	2	3	2	2	4	2	2	1	1	2	2	2	1	1	1	1	1	2	2	2	40
187.C1467	4	2	3	2	3	3	2	1	1	1	2	2	3	2	1	1	1	3	2	1	1	41
188.C1478	3	1	1	2	3	3	1	2	1	1	2	2	2	2	1	2	1	2	2	1	2	37
189.C1585	4	2	1	1	2	3	1	1	1	1	2	1	2	1	1	1	2	2	2	1	2	34
190.C1517	4	2	2	3	2	3	2	2	1	1	2	2	2	1	1	2	2	2	2	2	2	42
191.C1561	3	1	3	2	4	3	1	2	2	1	2	1	2	2	1	1	2	2	2	2	2	41

Group 14: DERIVED DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
192. C225	1	1	1	1	2	3	1	2	1	2	1	2	1	1	1	1	1	2	2	1	1	29
193. C231	3	2	2	1	2	2	1	2	1	1	2	1	3	1	1	1	1	1	2	1	1	32
194. C289	3	2	1	1	2	3	1	1	1	1	2	2	3	1	1	1	1	2	1	1	2	33
195. C296	4	2	2	1	3	3	1	2	1	2	2	3	3	1	1	2	1	3	2	2	2	43
196. C309	2	2	1	2	3	2	1	2	1	1	2	2	3	1	1	1	2	2	2	2	1	36
197. C320	3	1	1	2	2	3	2	1	1	1	2	2	3	1	1	1	1	2	2	1	1	34
198. C321	4	2	3	2	2	3	1	1	1	1	2	1	2	1	2	1	2	2	2	1	1	37
199. C325	2	2	2	2	2	4	1	1	1	1	2	2	2	2	1	1	1	3	1	2	1	36
200. C336	3	2	3	1	2	4	1	2	1	1	2	2	3	2	1	1	2	3	2	1	1	40
201. C337	2	2	2	2	2	3	1	1	1	1	2	2	2	1	1	1	1	2	2	1	2	34
202. C343	3	2	3	1	2	3	1	1	1	1	2	2	2	2	1	2	1	3	1	1	2	37
203. C347	3	2	1	2	2	4	2	1	1	1	2	2	3	1	1	2	1	2	2	1	2	38
204. C348	2	2	1	1	3	5	1	1	1	1	2	3	3	2	1	2	1	2	2	1	2	39
205. C359	3	2	1	1	2	1	1	2	1	1	2	2	3	1	1	1	1	2	2	1	2	33
206. C362	2	1	1	1	2	2	1	1	1	1	2	2	2	1	1	2	1	2	2	1	2	31
207. C365	2	2	1	1	2	3	1	1	1	1	2	2	3	1	1	1	2	1	2	1	2	33
208. C717	2	2	3	2	2	4	1	2	1	1	2	1	3	1	1	1	1	1	2	2	1	36

Table 4. continued

Group 15: SOUTHERN US TYPE DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
209. C222	3	2	3	2	3	2	1	1	1	1	2	2	3	2	1	1	1	1	2	1	1	36
210. C232	3	2	1	2	4	4	1	1	1	1	1	1	2	1	1	1	2	2	1	2	2	36
211. C245	4	1	1	2	2	3	1	2	1	1	2	2	2	1	1	1	1	2	2	1	1	34
212. C252	3	2	2	1	3	2	1	1	1	1	2	1	1	1	1	1	1	2	1	1	1	30
213. C262	2	1	2	1	2	3	2	1	1	2	2	2	1	1	1	1	1	1	2	1	2	32
214. C266	3	2	2	1	2	2	1	1	1	1	2	2	3	2	1	1	2	2	2	2	2	37
215. C914	2	2	1	1	3	3	2	1	1	1	2	2	3	1	1	1	2	1	2	2	2	36
216.C1480	3	2	1	2	4	4	2	2	1	1	2	2	2	1	1	1	2	2	2	2	2	41
217.C1488	3	1	2	2	3	4	2	1	1	1	2	1	2	1	1	1	1	2	2	1	2	36
218.C1492	4	2	3	2	3	5	1	2	1	1	2	3	2	2	1	1	1	3	2	2	2	45
219.C1509	3	2	1	2	2	7	2	2	1	1	2	2	3	1	1	2	2	1	2	1	1	41
220.C1516	3	2	3	2	3	5	2	2	1	1	2	2	3	2	1	2	2	2	2	2	2	46
221.C1565	3	2	2	1	3	3	2	1	1	1	2	2	3	1	1	2	2	2	2	1	2	39
222.C1588	4	2	3	2	2	4	1	2	1	1	2	2	3	2	1	1	1	3	2	1	2	42

Group 16: SERBIAN DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
223. C210	2	2	1	2	2	2	1	1	1	1	1	2	3	1	1	1	1	2	1	1	2	31
224. C228	2	2	2	1	2	3	1	2	1	1	2	1	1	2	1	1	2	1	1	1	1	31
225. C280	2	2	1	1	2	2	1	1	1	1	2	1	2	1	1	1	1	1	2	1	1	28
226. C317	3	1	1	2	2	2	1	1	1	1	2	3	4	1	1	1	1	2	2	1	1	34
227. C327	2	2	1	2	2	3	1	1	1	1	2	1	1	1	1	1	1	1	2	1	2	30
228. C611	2	2	1	1	2	5	1	2	1	1	2	2	2	1	1	2	2	1	2	1	2	36
229. C672	2	2	3	1	2	3	1	1	1	1	2	2	2	1	1	1	1	1	2	2	1	33
230. C680	1	1	3	1	2	3	1	2	1	1	2	1	2	1	1	1	1	2	2	1	2	32
231. C683	2	1	3	2	2	5	1	2	1	1	2	2	1	2	1	1	1	2	2	1	2	37
232. C721	2	2	1	1	2	3	1	1	1	1	2	1	2	1	1	1	1	2	2	1	1	30
233. C827	2	2	3	1	2	3	1	2	1	1	2	2	3	1	1	1	1	1	2	1	2	35
234. C828	2	2	4	2	2	3	2	2	1	1	2	2	2	2	1	1	1	2	2	1	2	39
235. C864	1	2	3	2	2	2	1	1	1	1	2	2	2	2	1	1	1	2	2	1	1	33
236. C865	2	1	2	1	2	4	1	1	1	1	2	2	2	1	1	1	1	2	1	1	1	31

Table 4. continued

Group 17: HARD DENTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
237. C22	2	2	2	1	2	3	2	1	1	1	2	2	2	2	1	1	1	1	2	1	2	34
238. C31	2	3	3	3	3	3	1	2	1	1	2	2	2	2	1	1	3	2	2	1	1	41
239. C55	2	2	2	1	4	3	2	2	1	1	2	2	3	2	1	1	2	2	2	1	2	40
240. C60	2	2	2	3	2	1	2	1	1	1	1	2	2	1	2	1	2	3	2	2	2	37
241. C76	2	2	3	1	2	3	2	1	1	1	2	2	3	1	1	1	1	2	2	1	1	33
242. C110	2	1	1	2	2	3	1	1	1	1	2	3	2	1	1	1	1	1	1	1	1	30
243. C133	2	1	1	1	2	3	1	1	1	1	2	1	1	1	1	1	1	1	2	1	2	28
244. C214	2	2	1	2	2	3	1	1	1	1	2	2	2	1	1	1	1	1	2	1	1	31
245. C244	2	2	3	1	2	6	1	2	1	1	2	3	3	1	1	1	2	2	2	2	1	39
246. C282	2	2	3	1	2	3	1	1	1	1	2	2	3	1	1	1	1	1	2	1	2	34
247. C369	2	2	2	1	2	4	1	1	1	1	2	2	3	2	1	1	3	3	1	1	2	38
248. C380	2	2	2	2	2	3	1	1	1	1	2	2	2	1	1	2	1	2	2	2	1	35
249. C382	2	1	2	1	2	2	1	1	1	1	2	2	2	1	1	1	1	2	2	1	2	31
250. C432	2	2	3	1	2	3	1	1	1	1	2	1	3	1	1	1	1	1	2	1	1	32
251. C433	2	3	1	1	2	3	1	2	1	1	2	1	3	1	1	1	1	1	2	1	2	33
252. C569	2	2	1	1	2	1	1	1	1	1	2	2	2	1	1	1	2	1	1	1	1	28
253. C616	2	2	2	2	2	3	1	1	1	1	2	2	3	1	1	1	1	2	2	1	2	35
254. C632	2	2	2	1	2	4	1	1	1	1	2	2	3	1	1	1	2	1	2	1	1	34
255. C659	2	2	2	2	2	3	1	1	1	1	2	2	3	1	1	1	1	1	2	1	2	34
256. C829	2	2	2	1	2	1	1	1	1	1	2	1	2	1	1	1	1	1	2	1	1	28

Group 18: SOFT FLINTS

	Acp1	Adh1	Cat3	Enp1	Est8	Glu1	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Pgm1	Pgm2	Pgd1	Pgd2	Phi1	Total
257. C74	3	2	2	1	2	4	1	1	1	3	2	2	2	1	1	1	1	2	2	2	1	34
258. C114	1	1	3	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	26
259. C124	2	1	1	2	2	3	1	1	1	1	1	2	1	1	1	2	1	1	2	1	1	29
260. C127	2	1	1	2	2	1	1	3	1	1	2	1	2	1	1	1	2	2	1	1	2	31
261. C139	3	2	3	2	2	3	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	33
262. C211	2	1	1	1	2	4	1	1	1	1	2	1	3	1	1	1	2	1	2	1	2	32
263. C235	2	2	2	1	3	3	2	1	1	1	2	1	3	1	1	1	1	3	2	1	1	35
264. C326	2	2	3	1	3	3	1	1	1	1	2	1	3	1	1	1	1	2	2	1	2	35
265. C330	1	2	3	2	2	4	1	1	1	1	2	2	1	1	1	1	1	1	2	2	1	33
266. C356	2	2	2	1	3	2	2	1	1	1	2	1	3	1	1	1	1	1	2	1	1	32
267. C360	2	1	2	2	2	4	1	1	1	1	2	1	3	1	1	1	2	3	2	1	1	35
268. C387	2	1	2	2	2	2	1	2	1	1	2	1	3	1	1	1	1	1	2	1	1	31
269. C393	2	2	3	1	3	3	1	1	1	1	2	2	3	1	2	1	1	3	2	1	1	37
270. C398	2	1	3	2	2	5	1	1	1	1	1	1	3	1	1	1	1	1	2	1	1	33
271. C454	2	1	3	2	2	4	1	1	1	1	2	1	3	1	1	2	1	2	2	1	2	36
272. C533	2	2	4	1	2	2	2	1	1	1	2	2	3	1	1	1	1	1	2	1	2	35
273. C575	2	2	2	2	2	3	1	1	1	1	2	2	2	1	1	1	1	1	2	1	1	32
274. C612	2	2	3	2	4	4	1	1	1	1	2	2	2	1	1	1	1	1	2	2	2	38
275. C620	2	1	4	1	3	5	1	1	1	1	2	1	1	1	1	1	2	1	2	1	1	34
276. C647	2	2	4	2	2	6	1	2	1	1	2	2	2	1	1	2	1	1	2	1	2	40

Table 5. Polymorphism of loci in analyzed groups (number of alleles per locus)

	Loci																					
Group	Acp 1	Adh 1	Cat 3	Enp 1	Est 8	Glu 1	Got 1	Got 2	Got 3	Idh 1	Idh 2	Mdh 1	Mdh 2	Mdh 3	Mdh 4	Mdh 5	Pgm 1	Pgm 2	Pgd 1	Pgd 2	Phi 1	Total
1.	4	2	3	2	4	6	2	3	1	2	2	3	3	2	2	2	1	3	2	2	2	53
2.	5	2	3	2	4	7	3	2	1	3	3	3	4	4	1	2	2	3	2	4	2	62
3.	4	2	4	3	5	7	2	2	1	1	2	4	3	2	2	2	2	3	3	3	2	59
4.	3	2	3	3	2	6	2	2	1	3	2	5	3	2	2	2	2	2	2	2	3	54
5.	5	2	3	3	4	6	2	2	1	1	2	4	4	2	1	2	2	3	2	2	2	55
6.	5	2	4	2	4	6	3	2	1	1	2	3	5	3	2	2	2	2	3	4	2	60
7.	4	2	3	3	3	6	3	2	1	1	2	4	3	2	2	2	2	3	2	2	2	54
8.	5	2	3	3	3	7	2	2	1	1	2	3	3	3	1	2	2	3	2	1	2	53
9.	5	2	3	3	4	8	2	2	1	1	2	3	3	2	1	2	2	2	2	2	3	55
10.	4	2	3	2	3	8	2	2	1	1	2	3	3	2	1	2	2	2	2	2	3	52
11.	5	3	3	3	4	6	2	3	1	2	2	3	3	2	1	2	2	3	2	2	2	56
12.	4	2	3	2	3	7	2	3	1	2	2	2	4	2	1	2	2	2	2	2	2	52
13.	5	2	4	4	4	6	2	3	2	1	2	4	3	3	1	2	2	3	2	3	3	61
14.	5	2	4	2	3	6	3	2	1	2	2	3	3	3	2	2	2	3	4	3	2	56
15.	5	2	3	2	4	7	2	2	1	2	2	3	3	2	1	2	2	3	2	3	2	55
16.	4	2	4	3	2	6	2	2	1	1	2	3	4	2	1	2	2	2	2	2	2	51
17.	3	3	4	3	4	6	2	2	1	1	2	4	4	2	2	2	3	4	2	2	3	59
18.	4	2	4	2	4	6	2	3	1	3	2	3	3	1	2	2	2	3	2	2	2	55

Table 6. Frequencies of detected alleles in populations of Montenegrin flints (group 1)

Locus	Number of populations															Average
Allele	34	1184	1194	1229	1239	1259	1263	1265	1266	1268	1286	1287	1291	1302	1304	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.03	0.00	0.00	0.01
2	0.70	0.13	0.30	0.20	0.23	0.48	0.33	0.25	0.39	0.39	0.14	0.33	0.39	0.25	0.47	0.33
3	0.03	0.40	0.27	0.20	0.40	0.19	0.03	0.00	0.00	0.00	0.67	0.58	0.14	0.11	0.00	0.20
4	0.27	0.47	0.43	0.60	0.37	0.33	0.64	0.75	0.61	0.61	0.19	0.03	0.44	0.64	0.53	0.46
Adh1-4	1.00	1.00	0.90	0.73	0.93	0.85	1.00	0.61	0.75	0.94	0.75	0.56	0.97	0.91	1.00	0.86
6	0.00	0.00	0.10	0.27	0.07	0.15	0.00	0.39	0.25	0.06	0.25	0.44	0.03	0.09	0.00	0.14
Cat3-7	0.10	0.20	0.05	0.10	0.10	0.11	0.00	0.18	0.17	0.11	0.00	0.00	0.12	0.17	0.11	0.10
9	0.85	0.80	0.80	0.75	0.70	0.85	0.97	0.59	0.69	0.83	1.00	1.00	0.82	0.58	0.44	0.78
12	0.05	0.00	0.15	0.15	0.20	0.04	0.03	0.23	0.14	0.06	0.00	0.00	0.06	0.25	0.45	0.12
Enp1-6	1.00	1.00	0.73	0.13	1.00	0.53	0.42	0.25	0.47	0.44	1.00	0.97	0.71	0.44	0.64	0.65
8	0.00	0.00	0.27	0.87	0.00	0.47	0.58	0.75	0.53	0.56	0.00	0.03	0.29	0.56	0.36	0.35
Est8-4	1.00	0.60	1.00	1.00	1.00	0.69	1.00	0.47	0.56	0.69	0.67	0.81	0.78	0.53	0.69	0.77
4.5	0.00	0.40	0.00	0.00	0.00	0.28	0.00	0.53	0.44	0.31	0.28	0.19	0.17	0.47	0.31	0.22
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.05	0.00	0.00	0.01
6	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Glui-1	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.40	0.25	0.00	0.03	0.00	0.05
2	0.54	0.20	0.93	0.73	0.50	0.53	0.31	0.40	0.33	0.20	0.07	0.00	0.25	0.50	0.57	0.40
3	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.05	0.09	0.23	0.00	0.00	0.00	0.00	0.00	0.04
6	0.08	0.23	0.04	0.10	0.11	0.03	0.03	0.15	0.00	0.07	0.00	0.00	0.03	0.17	0.08	0.07
7	0.38	0.47	0.03	0.07	0.39	0.30	0.41	0.35	0.29	0.50	0.40	0.75	0.67	0.30	0.20	0.37
N	0.00	0.00	0.00	0.00	0.00	0.11	0.25	0.05	0.29	0.00	0.13	0.00	0.05	0.00	0.15	0.07
Got1-4	1.00	1.00	1.00	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
6	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Got2-2	0.00	0.00	0.00	0.07	0.00	0.14	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.02
4	1.00	1.00	1.00	0.86	1.00	0.86	1.00	0.94	1.00	1.00	1.00	1.00	1.00	1.00	0.97	0.98
10	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.67	0.89	1.00	1.00	1.00	0.97
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.11	0.00	0.00	0.00	0.03
Idh2-4	1.00	1.00	1.00	0.62	0.93	0.75	0.69	0.69	0.67	0.94	1.00	1.00	0.81	0.94	0.94	0.87
6	0.00	0.00	0.00	0.38	0.07	0.25	0.31	0.31	0.33	0.06	0.00	0.00	0.19	0.06	0.06	0.13

Table 6. continued

Locus	Number of population															Average
Allele	34	1184	1194	1229	1239	1259	1263	1265	1266	1268	1286	1287	1291	1303	1304	
Mdh1-1	0.03	0.03	0.07	0.00	0.03	0.13	0.11	0.07	0.06	0.13	0.00	0.00	0.15	0.23	0.25	0.09
6	0.97	0.97	0.93	1.00	0.97	0.79	0.81	0.93	0.94	0.87	1.00	1.00	0.85	0.67	0.75	0.90
10.5	0.00	0.00	0.00	0.00	0.00	0.08	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mdh2-3	0.33	0.32	0.20	0.03	0.40	0.37	0.31	0.08	0.14	0.25	0.44	0.33	0.20	0.22	0.27	0.26
3.5	0.07	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.03	0.03	0.00	0.01
6	0.60	0.64	0.80	0.97	0.60	0.63	0.69	0.92	0.86	0.75	0.56	0.65	0.77	0.75	0.73	0.73
Mdh3-16	1.00	1.00	1.00	1.00	1.00	0.92	0.97	1.00	0.94	1.00	1.00	1.00	1.00	0.97	0.92	0.98
18	0.00	0.00	0.00	0.00	0.00	0.08	0.03	0.00	0.06	0.00	0.00	0.00	0.00	0.03	0.08	0.02
Mdh4-8	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.01
12	1.00	1.00	1.00	1.00	1.00	1.00	0.86	1.00	1.00	0.97	1.00	1.00	1.00	1.00	1.00	0.99
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.80	0.97	0.87	0.93	0.97
15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.03	0.13	0.07	0.03
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.17	0.00	0.00	0.01
3	0.00	0.00	0.07	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.03	0.02
4	1.00	1.00	0.93	1.00	1.00	0.86	1.00	1.00	1.00	1.00	0.94	0.97	0.83	1.00	0.97	0.97
Pgd1-2	0.79	0.63	0.97	0.93	0.27	0.72	0.69	0.14	0.44	0.92	0.97	1.00	0.72	0.92	0.44	0.70
3.8	0.21	0.37	0.03	0.07	0.73	0.28	0.31	0.86	0.56	0.08	0.03	0.00	0.28	0.08	0.56	0.30
Pgd2-5	1.00	1.00	1.00	1.00	1.00	0.92	0.97	1.00	1.00	1.00	1.00	1.00	0.81	0.83	0.61	0.94
18	0.00	0.00	0.00	0.00	0.00	0.08	0.03	0.00	0.00	0.00	0.00	0.00	0.19	0.17	0.39	0.06
Phi1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97	1.00	1.00	1.00
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00

Table 7. Frequencies of detected alleles in populations of Bosnian early dents (group 2)

Locus	Number of populations															Average
Allele	162	444	462	480	488	490	771	847	858	877	1365	1373	1375	1377	1380	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
2	0.45	0.53	0.63	1.00	0.00	1.00	1.00	0.10	0.25	0.35	0.18	0.05	0.67	0.32	0.39	0.46
3	0.08	0.10	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.13	0.03	0.13	0.03	0.05
4	0.47	0.37	0.20	0.00	1.00	0.00	0.00	0.90	0.75	0.65	0.67	0.82	0.27	0.55	0.58	0.49
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
Adh1-4	0.00	0.50	0.53	0.47	0.82	0.58	0.44	0.67	0.48	0.50	0.83	0.73	0.75	0.79	0.83	0.59
6	1.00	0.50	0.47	0.53	0.18	0.42	0.56	0.33	0.52	0.50	0.17	0.27	0.25	0.21	0.17	0.41
Cat3-7	0.00	0.03	0.23	0.00	0.00	0.00	0.34	0.00	0.00	0.38	0.48	0.18	0.10	0.03	0.08	0.12
9	1.00	0.52	0.65	1.00	0.87	1.00	0.66	0.88	0.25	0.62	0.52	0.77	0.67	0.82	0.68	0.72
12	0.00	0.45	0.12	0.00	0.13	0.00	0.00	0.12	0.75	0.00	0.00	0.05	0.23	0.15	0.32	0.16
Enp1-6	0.00	0.41	0.40	1.00	0.25	0.00	0.67	0.81	1.00	0.92	0.67	0.64	0.80	1.00	0.54	0.61
8	1.00	0.59	0.60	0.00	0.75	1.00	0.33	0.19	0.00	0.08	0.33	0.36	0.20	0.00	0.46	0.39
Est8-4	0.48	0.48	0.48	0.62	0.42	0.50	0.50	0.50	0.50	0.40	0.62	0.70	0.44	0.50	0.50	0.51
4.5	0.52	0.52	0.52	0.38	0.58	0.50	0.50	0.50	0.50	0.42	0.33	0.20	0.56	0.50	0.50	0.47
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.05	0.10	0.00	0.00	0.00	0.02
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00
Glu1-1	0.03	0.00	0.08	0.00	0.00	0.00	0.38	0.00	0.00	0.02	0.00	0.05	0.08	0.03	0.13	0.05
2	0.02	0.05	0.00	0.00	0.08	0.21	0.22	0.25	0.10	0.46	0.20	0.15	0.00	0.28	0.32	0.16
3	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.10	0.05	0.02	0.02	0.02	0.02
6	0.00	0.00	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.08	0.25	0.05	0.08	0.05
7	0.00	0.90	0.66	0.00	0.55	0.71	0.40	0.63	0.90	0.44	0.55	0.60	0.55	0.37	0.30	0.50
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
N	0.95	0.05	0.00	1.00	0.30	0.10	0.00	0.12	0.00	0.08	0.05	0.05	0.10	0.25	0.15	0.22
Got1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.01
4	1.00	0.80	1.00	0.83	1.00	1.00	1.00	1.00	0.87	1.00	1.00	1.00	1.00	1.00	1.00	0.97
6	0.00	0.20	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Got2-2	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.08	0.15	0.05	0.24	0.05	0.13	0.08	0.12
4	1.00	1.00	1.00	1.00	1.00	1.00	0.00	1.00	0.92	0.85	0.95	0.76	0.95	0.87	0.92	0.88
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	0.87	0.95	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	0.98
6	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
N	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.01
Idh2-4	0.50	0.37	0.65	0.79	0.47	0.04	0.62	0.88	0.35	0.71	0.70	0.68	0.20	0.55	0.34	0.52
6	0.50	0.63	0.33	0.21	0.53	0.96	0.38	0.12	0.65	0.29	0.30	0.32	0.80	0.45	0.66	0.48
8	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 7. continued

Locus	Number of populations															Average
Allele	162	444	462	480	488	490	771	847	858	877	1365	1373	1375	1337	1380	
Mdh1-1	0.48	0.30	0.03	0.00	0.10	1.00	0.00	0.08	0.00	0.27	0.15	0.18	0.18	0.08	0.18	0.20
6	0.52	0.70	0.95	1.00	0.90	0.00	1.00	0.92	1.00	0.69	0.85	0.82	0.75	0.92	0.80	0.79
10.5	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.07	0.00	0.02	0.01
Mdh2-3	0.00	0.28	0.25	0.20	0.63	0.79	0.62	0.00	0.00	0.63	0.05	0.10	0.13	0.05	0.17	0.26
3.5	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.17	0.23	0.03	0.05
6	1.00	0.72	0.75	0.80	0.30	0.21	0.38	1.00	1.00	0.37	0.90	0.70	0.70	0.72	0.80	0.69
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
Mdh3-16	1.00	1.00	1.00	1.00	0.30	1.00	0.54	1.00	1.00	0.50	0.90	0.98	1.00	1.00	0.93	0.88
16.9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.03
18	0.00	0.00	0.00	0.00	0.70	0.00	0.46	0.00	0.00	0.00	0.05	0.02	0.00	0.00	0.07	0.09
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00	1.00	1.00	0.88	0.93	0.93	0.98	0.88	0.97
15	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.12	0.07	0.07	0.02	0.12	0.03
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	0.79	1.00	1.00	1.00	1.00	1.00	0.95	0.98
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.21	0.00	0.00	0.00	0.00	0.00	0.05	0.02
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00
3	0.38	0.18	0.50	0.35	0.30	0.00	0.00	0.00	0.31	0.00	0.10	0.21	0.18	0.18	0.13	0.19
4	0.62	0.82	0.50	0.65	0.70	1.00	1.00	1.00	0.69	1.00	0.90	0.79	0.82	0.82	0.84	0.81
Pgd1-2	0.00	0.37	0.23	0.58	0.78	0.00	0.18	0.40	0.88	0.29	0.30	0.53	0.15	0.13	0.11	0.33
3.8	1.00	0.63	0.77	0.42	0.22	1.00	0.82	0.60	0.12	0.71	0.70	0.47	0.85	0.87	0.89	0.67
Pgd2-2.8	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.56	0.00	0.00	0.00	0.00	0.00	0.03	0.04
5	1.00	1.00	0.97	1.00	1.00	1.00	1.00	0.98	0.44	1.00	1.00	1.00	1.00	1.00	0.97	0.95
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Phi1-4	1.00	1.00	0.98	0.65	1.00	1.00	1.00	1.00	1.00	1.00	0.95	0.92	0.98	1.00	0.97	0.96
5	0.00	0.00	0.02	0.35	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.08	0.02	0.00	0.03	0.04

Table 8. Frequencies of detected alleles in populations of semi-flints from Kosmet (group 3)

Locus	Number of populations															Average
Allele	33	48	389	394	401	419	570	576	1789	1791	1794	1796	1803	1811	1815	
Acp1-2	0.08	0.00	0.41	0.48	0.00	0.56	0.26	0.03	0.33	0.28	0.30	0.28	0.70	0.26	0.48	0.30
3	0.26	0.00	0.00	0.02	0.00	0.00	0.00	0.05	0.07	0.15	0.27	0.27	0.00	0.18	0.07	0.09
4	0.66	1.00	0.59	0.50	1.00	0.44	0.74	0.92	0.60	0.52	0.43	0.45	0.30	0.56	0.45	0.61
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00
Adh1-4	0.59	0.67	0.48	0.55	0.29	0.35	0.70	0.94	0.61	0.78	0.61	0.59	0.78	0.65	0.83	0.63
6	0.41	0.34	0.52	0.45	0.71	0.65	0.30	0.06	0.39	0.22	0.39	0.41	0.22	0.35	0.17	0.37
Cat3-7	0.00	0.40	0.07	0.08	0.21	0.00	0.35	0.00	0.25	0.25	0.25	0.18	0.30	0.03	0.03	0.16
9	0.03	0.52	0.39	0.21	0.79	0.85	0.61	0.61	0.63	0.43	0.60	0.62	0.68	0.89	0.75	0.57
12	0.57	0.08	0.45	0.45	0.00	0.15	0.00	0.39	0.07	0.27	0.15	0.20	0.02	0.08	0.22	0.21
N	0.40	0.00	0.09	0.26	0.00	0.00	0.04	0.00	0.05	0.05	0.00	0.00	0.00	0.00	0.00	0.06
Enp1-6	0.68	0.83	1.00	1.00	0.81	1.00	0.65	0.66	0.95	0.96	0.95	0.75	1.00	0.90	0.97	0.87
7	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.03	0.00	0.00	0.00	0.02
8	0.32	0.00	0.00	0.00	0.19	0.00	0.35	0.34	0.05	0.04	0.00	0.22	0.00	0.10	0.03	0.11
Est8-4	0.60	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.45	0.50	0.45	0.45	0.48	0.38	0.43	0.48
4.5	0.40	0.50	0.50	0.45	0.50	0.50	0.50	0.50	0.55	0.50	0.30	0.55	0.30	0.62	0.57	0.49
5	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.12	0.00	0.00	0.02
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.01
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
2	0.34	0.38	0.17	0.50	0.00	0.40	0.39	0.60	0.45	0.25	0.33	0.42	0.25	0.20	0.35	0.34
3	0.00	0.00	0.04	0.00	0.54	0.00	0.00	0.00	0.02	0.00	0.03	0.00	0.00	0.00	0.00	0.05
6	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.05	0.02	0.03	0.15	0.00	0.08	0.03
7	0.42	0.37	0.09	0.05	0.00	0.52	0.56	0.30	0.25	0.25	0.57	0.50	0.50	0.57	0.32	0.35
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00
N	0.21	0.25	0.70	0.45	0.46	0.08	0.04	0.10	0.20	0.45	0.05	0.05	0.05	0.18	0.25	0.23
Got1-4	1.00	1.00	0.98	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.83	0.99
6	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.01
Got2-2	0.00	0.25	0.00	0.15	0.50	0.35	0.30	0.08	0.00	0.00	0.08	0.15	0.00	0.10	0.05	0.13
4	1.00	0.75	1.00	0.85	0.50	0.65	0.70	0.92	1.00	1.00	0.92	0.85	1.00	0.90	0.95	0.87
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.47	0.25	0.56	0.38	0.38	0.90	0.26	0.33	0.40	0.50	0.55	0.60	0.58	0.47	0.43	0.47
6	0.53	0.75	0.44	0.62	0.62	0.10	0.74	0.67	0.60	0.50	0.45	0.40	0.42	0.53	0.57	0.53

Table 8. continued

Locus	Number of populations															Average
Allele	33	48	389	394	401	419	570	576	1789	1791	1794	1796	1803	1811	1815	
Mdh1-1	0.03	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.29	0.05	0.08	0.23	0.10	0.18	0.13	0.08
6	0.97	1.00	1.00	0.95	0.73	1.00	1.00	1.00	0.71	0.95	0.92	0.77	0.85	0.82	0.82	0.88
9	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
10.5	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.05	0.02
Mdh2-3	0.42	0.21	0.42	0.43	0.21	0.38	0.00	0.00	0.53	0.08	0.30	0.23	0.68	0.20	0.33	0.29
3.5	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.02	0.17	0.13	0.02	0.00	0.08	0.05	0.04
6	0.58	0.79	0.58	0.57	0.79	0.48	1.00	1.00	0.45	0.75	0.57	0.75	0.32	0.72	0.62	0.67
Mdh3-16	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	0.98	1.00	0.93	1.00	0.95	0.95	0.95
18	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.02	0.00	0.07	0.00	0.05	0.05	0.05
Mdh4-8	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.01
12	0.89	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	1.00	1.00	0.99
Mdh5-12	1.00	0.92	1.00	0.53	0.98	1.00	1.00	0.90	0.98	0.95	0.98	0.85	0.95	1.00	0.75	0.92
15	0.00	0.08	0.00	0.47	0.02	0.00	0.00	0.10	0.02	0.05	0.02	0.15	0.05	0.00	0.25	0.08
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.88	0.93	0.98	1.00	0.90	1.00	0.95	0.95	0.97
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.07	0.02	0.00	0.10	0.00	0.05	0.05	0.03
Pgm2-2	0.10	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.05	0.00	0.00	0.00	0.02
3	0.32	0.12	0.00	0.20	0.02	0.00	0.28	0.30	0.15	0.08	0.13	0.13	0.23	0.11	0.15	0.15
4	0.58	0.88	0.93	0.80	0.98	1.00	0.72	0.70	0.85	0.92	0.82	0.82	0.77	0.89	0.85	0.83
Pgd1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.03	0.79	0.00	0.00	0.25	0.06	0.41	0.00	0.22	0.23	0.20	0.28	0.18	0.08	0.50	0.22
3.8	0.97	0.21	1.00	1.00	0.75	0.94	0.59	1.00	0.75	0.77	0.80	0.72	0.82	0.92	0.50	0.78
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00
5	0.55	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	0.97
10	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
Phi1-4	1.00	0.98	1.00	1.00	1.00	0.79	1.00	0.73	1.00	0.85	0.98	1.00	0.80	0.97	0.85	0.93
4	0.00	0.02	0.00	0.00	0.00	0.21	0.00	0.27	0.00	0.15	0.02	0.00	0.20	0.03	0.15	0.07

Table 9 Frequencies of detected alleles in populations of Macedonian flints (group 4)

Locus	Number of populations															Average
Allele	103	150	592	593	594	597	600	666	892	893	895	1802	1816	1821	1823	
Acp1-2	0.38	0.23	0.38	0.10	0.10	0.25	0.00	0.15	0.29	0.56	0.00	0.57	0.18	0.40	0.53	0.27
3	0.05	0.10	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.07	0.15	0.03	0.07	0.03
4	0.57	0.67	0.62	0.90	0.90	0.70	1.00	0.85	0.71	0.44	1.00	0.36	0.67	0.57	0.40	0.70
Adh1-4	0.98	0.66	0.72	0.41	0.19	0.40	0.27	0.65	0.96	0.21	0.88	0.92	0.94	0.93	0.67	0.65
6	0.02	0.34	0.28	0.59	0.81	0.60	0.73	0.35	0.04	0.79	0.12	0.08	0.06	0.07	0.33	0.35
Cat3-7	0.00	0.28	0.08	0.38	0.40	0.00	0.00	0.35	0.19	0.12	0.02	0.33	0.03	0.20	0.13	0.17
9	0.85	0.72	0.72	0.62	0.50	0.75	0.71	0.65	0.67	0.63	0.70	0.52	0.82	0.73	0.67	0.69
12	0.15	0.00	0.20	0.00	0.10	0.25	0.29	0.00	0.14	0.25	0.28	0.15	0.15	0.07	0.20	0.14
Enp1-6	0.45	0.33	0.72	0.75	1.00	0.95	1.00	0.21	0.69	0.25	0.27	0.36	0.53	0.64	0.73	0.59
7	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	0.55	0.67	0.28	0.25	0.00	0.00	0.00	0.79	0.31	0.75	0.73	0.64	0.47	0.36	0.27	0.41
Est8-4	0.38	0.43	0.50	0.48	0.43	0.62	0.50	0.50	0.50	0.50	0.50	0.60	0.50	0.33	0.53	0.49
4.5	0.62	0.57	0.50	0.52	0.57	0.38	0.50	0.50	0.50	0.50	0.50	0.40	0.50	0.67	0.47	0.51
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.07	0.00	0.03	0.01
2	0.00	0.00	0.15	0.18	0.18	0.05	0.88	0.69	0.52	0.98	0.90	0.19	0.08	0.13	0.45	0.36
3	0.00	0.75	0.00	0.05	0.10	0.33	0.00	0.00	0.00	0.00	0.00	0.09	0.15	0.05	0.00	0.10
6	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.17	0.03
7	0.65	0.25	0.85	0.42	0.32	0.57	0.12	0.15	0.40	0.02	0.00	0.67	0.40	0.42	0.30	0.37
N	0.10	0.00	0.00	0.35	0.40	0.05	0.00	0.16	0.00	0.00	0.10	0.05	0.25	0.40	0.05	0.13
Got1-4	0.60	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.85	1.00	1.00	0.95	1.00	1.00	0.96
6	0.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00	0.05	0.00	0.00	0.04
Got2-2	0.35	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.00	0.20	0.28	0.08	0.09
4	0.65	1.00	1.00	0.82	1.00	1.00	1.00	1.00	1.00	0.90	0.90	1.00	0.80	0.72	0.92	0.91
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	0.70	1.00	1.00	1.00	1.00	1.00	1.00	0.52	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
N	0.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Idh2-4	0.92	0.75	0.48	0.87	1.00	0.90	0.00	0.52	1.00	1.00	0.76	0.95	0.48	0.42	0.60	0.74
6	0.08	0.25	0.52	0.13	0.00	0.10	1.00	0.48	0.00	0.00	0.24	0.05	0.52	0.58	0.40	0.26

Table 9. continued

Locus	Number of populations															Average
Allele	103	150	592	593	594	597	600	666	892	893	895	1802	1816	1821	1823	
Mdh1-0.5	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1	0.00	0.27	0.15	0.05	0.38	0.30	0.23	0.15	0.02	0.00	0.00	0.07	0.33	0.05	0.00	0.13
6	1.00	0.73	0.85	0.88	0.62	0.70	0.77	0.66	0.98	0.92	0.56	0.86	0.67	0.92	0.87	0.81
9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00
10.5	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.19	0.00	0.08	0.44	0.07	0.00	0.03	0.10	0.06
Mdh2-3	0.50	0.20	0.00	0.08	0.00	0.30	0.77	0.08	0.06	0.00	0.00	0.17	0.40	0.15	0.10	0.19
3.5	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.03	0.01
6	0.50	0.80	1.00	0.92	0.95	0.70	0.23	0.92	0.94	1.00	1.00	0.83	0.57	0.82	0.87	0.80
Mdh3-16	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.88	1.00	1.00	0.99
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.01
Mdh4-8	0.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.44	0.10	0.00	0.13	0.28	0.09
12	0.65	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	0.56	0.90	1.00	0.87	0.72	0.91
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.77	1.00	0.92	1.00	1.00	1.00	1.00	0.95	0.98
15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.08	0.00	0.00	0.00	0.00	0.05	0.02
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.88	0.93	0.95	0.98
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.07	0.05	0.02
Pgm2-3	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.05	0.00	0.03
4	1.00	1.00	0.75	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.92	0.95	1.00	0.97
Pgd1-2	0.45	0.28	0.50	0.68	0.47	0.00	0.42	0.92	0.92	0.15	0.91	0.73	0.08	0.26	0.59	0.49
3.8	0.55	0.72	0.50	0.32	0.53	1.00	0.58	0.08	0.08	0.85	0.09	0.27	0.92	0.74	0.41	0.51
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00
Phi1-3	0.00	0.10	0.00	0.00	0.00	0.00	0.42	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
4	1.00	0.90	1.00	1.00	1.00	1.00	0.58	0.94	1.00	1.00	0.96	1.00	0.90	0.95	1.00	0.96
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.10	0.05	0.00	0.03

Table 10. Frequencies of detected alleles in populations of northeastern US 8-row types (group 5)

Locus	Number of populations															
Allele	62	64	72	83	118	125	132	170	177	184	527	1545	1550	1559	1751	Average
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
2	0.54	0.00	0.40	1.00	0.18	0.00	0.85	0.63	0.78	0.15	0.00	0.60	0.37	0.28	0.15	0.37
3	0.00	0.00	0.00	0.00	0.60	0.00	0.00	0.12	0.12	0.03	0.00	0.10	0.15	0.00	0.25	0.09
4	0.46	1.00	0.60	0.00	0.22	1.00	0.35	0.25	0.10	0.75	1.00	0.30	0.45	0.50	0.60	0.52
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.22	0.00	0.02
Adh1-4	1.00	0.61	0.98	0.73	0.50	1.00	0.83	0.94	0.08	0.50	0.73	0.60	0.53	0.35	0.75	0.68
6	0.00	0.39	0.02	0.27	0.50	0.00	0.17	0.06	0.92	0.50	0.27	0.40	0.47	0.65	0.25	0.32
Cat3-7	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	0.00	0.13	0.10	0.00	0.23	0.03	0.05
9	0.54	0.83	0.48	1.00	1.00	0.00	0.95	0.70	1.00	1.00	0.68	0.60	0.75	0.65	0.65	0.72
12	0.44	0.17	0.52	0.00	0.00	1.00	0.05	0.02	0.00	0.00	0.27	0.30	0.25	0.12	0.32	0.23
Enp1-6	0.46	0.89	0.40	1.00	0.55	0.85	1.00	0.63	1.00	0.43	0.79	0.80	0.48	0.65	0.35	0.68
7	0.08	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
8	0.46	0.11	0.46	0.00	0.45	0.15	0.00	0.37	0.00	0.57	0.21	0.20	0.52	0.35	0.65	0.30
Est8-4	0.50	0.50	0.46	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.21	0.43	0.48	0.48	0.50	0.47
4.5	0.50	0.50	0.00	0.50	0.50	0.50	0.50	0.50	0.03	0.50	0.23	0.37	0.52	0.52	0.47	0.41
5	0.00	0.00	0.54	0.00	0.00	0.00	0.00	0.00	0.47	0.00	0.31	0.20	0.00	0.00	0.00	0.10
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.03	0.02
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.85	0.00	0.00	0.00	0.03	0.00	0.15	0.38	0.09
2	0.00	1.00	0.00	0.00	0.15	0.35	0.43	0.00	0.23	0.00	0.00	0.27	0.18	0.05	0.17	0.19
3	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.05	0.12	0.00	0.00	0.05	0.00	0.00	0.00	0.02
6	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.03	0.08	0.00	0.00	0.00	0.00	0.00	0.08	0.02
7	1.00	0.00	1.00	0.96	0.45	0.22	0.52	0.07	0.57	0.95	0.67	0.65	0.62	0.45	0.32	0.56
N	0.00	0.00	0.00	0.04	0.40	0.40	0.00	0.00	0.00	0.05	0.33	0.00	0.20	0.35	0.05	0.12
Got1-4	1.00	1.00	1.00	1.00	0.38	1.00	0.43	1.00	1.00	0.93	1.00	1.00	1.00	1.00	0.78	0.90
6	0.00	0.00	0.00	0.00	0.62	0.00	0.57	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.22	0.10
Got2-2	0.00	0.00	0.00	0.75	0.00	0.30	0.00	0.00	0.23	0.08	0.00	0.00	0.05	0.33	0.03	0.11
4	1.00	1.00	1.00	0.25	1.00	0.70	1.00	1.00	0.77	0.92	1.00	1.00	0.95	0.67	0.97	0.89
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.06	0.02	0.54	0.00	0.53	0.78	0.10	0.63	0.00	0.45	0.06	0.48	0.50	0.35	0.18	0.31
6	0.94	0.98	0.46	1.00	0.47	0.22	0.90	0.37	1.00	0.55	0.94	0.52	0.50	0.65	0.82	0.69

Table 10. continued

Locus	Number of populations															Average
Allele	62	64	72	83	118	125	132	170	177	184	527	1545	1550	1559	1751	
Mdh1-1	0.00	0.00	0.46	0.00	0.00	0.00	0.03	0.00	0.83	0.00	0.10	0.33	0.00	0.20	0.38	0.21
6	1.00	1.00	0.54	1.00	0.85	0.20	0.97	1.00	0.07	1.00	0.90	0.67	0.97	0.80	0.62	0.77
10.5	0.00	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.01
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mdh2-3	0.63	0.02	0.06	0.44	0.05	0.68	0.30	0.00	0.05	0.00	0.06	0.10	0.13	0.15	0.08	0.18
3.5	0.06	0.00	0.86	0.00	0.15	0.22	0.00	0.00	0.00	0.00	0.00	0.20	0.05	0.05	0.00	0.11
5.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.83	0.00	0.00	0.00	0.00	0.00	0.00	0.06
6	0.31	0.98	0.08	0.56	0.80	0.10	0.70	1.00	0.12	1.00	0.94	0.70	0.82	0.80	0.92	0.65
Mdh3-16	0.81	1.00	0.65	1.00	1.00	1.00	1.00	1.00	1.00	0.78	1.00	1.00	1.00	0.93	1.00	0.94
18	0.19	0.00	0.35	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.07	0.00	0.06
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	0.65	1.00	1.00	0.83	1.00	1.00	1.00	1.00	0.93	1.00	1.00	0.96
15	0.00	0.00	0.00	0.00	0.35	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.04
Pgm1-9	1.00	1.00	1.00	1.00	1.00	0.98	1.00	0.85	1.00	1.00	1.00	0.95	1.00	1.00	1.00	0.98
16	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.15	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.02
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
3	0.33	0.00	0.29	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.19	0.05	0.10	0.23	0.20	0.10
4	0.67	1.00	0.71	1.00	1.00	1.00	0.95	1.00	1.00	1.00	0.81	0.95	0.87	0.77	0.80	0.90
Pgd1-2	0.22	0.98	0.21	0.00	0.00	0.15	0.66	0.35	0.03	0.79	0.37	0.25	0.18	0.10	0.28	0.30
3.8	0.78	0.02	0.79	1.00	1.00	0.85	0.34	0.65	0.97	0.21	0.63	0.75	0.82	0.90	0.72	0.70
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.03	0.02
5	1.00	1.00	1.00	1.00	1.00	1.00	0.89	1.00	1.00	1.00	0.85	1.00	1.00	1.00	0.97	0.98
Phi1-4	0.91	1.00	0.88	1.00	0.53	1.00	1.00	1.00	1.00	1.00	1.00	0.98	0.90	0.78	0.95	0.93
5	0.09	0.00	0.12	0.00	0.47	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.10	0.22	0.05	0.07

Table 11. Frequencies of detected alleles in populations of derived flints (group 6)

Locus	Number of population														Average
Allele	182	391	492	494	528	532	897	899	1330	1471	1472	1520	1521	1523	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
2	0.75	0.65	0.75	0.88	0.58	0.65	0.52	0.55	0.55	0.63	0.58	0.25	0.38	0.13	0.56
3	0.10	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.07	0.00	0.23	0.17	0.15	0.05
4	0.15	0.35	0.25	0.12	0.42	0.06	0.22	0.45	0.45	0.30	0.42	0.52	0.45	0.72	0.35
6	0.00	0.00	0.00	0.00	0.00	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Adh1-4	0.81	0.85	0.65	0.77	0.96	0.75	0.25	0.35	0.95	0.50	0.69	0.81	0.50	0.90	0.70
6	0.19	0.15	0.35	0.23	0.04	0.25	0.75	0.65	0.05	0.50	0.31	0.19	0.50	0.10	0.30
Cat3-7	0.03	0.33	0.10	0.00	0.39	0.02	0.35	0.00	0.33	0.00	0.05	0.03	0.25	0.03	0.14
9	0.55	0.67	0.38	0.44	0.50	0.23	0.55	0.34	0.60	0.82	0.90	0.87	0.60	0.47	0.56
12	0.22	0.00	0.52	0.31	0.11	0.75	0.10	0.61	0.07	0.10	0.05	0.10	0.15	0.50	0.26
N	0.20	0.00	0.00	0.25	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.04
Enp1-6	0.58	0.58	0.56	1.00	0.33	0.96	0.88	0.87	0.80	0.85	0.88	0.90	0.58	0.78	0.75
8	0.42	0.42	0.44	0.00	0.67	0.04	0.12	0.13	0.20	0.15	0.12	0.10	0.42	0.22	0.25
Est8-4	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.45	0.50	0.45	0.50	0.49
4.5	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.55	0.50	0.08	0.50	0.47
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.02
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.02
Glu1-1	0.25	0.25	0.25	0.23	0.00	0.00	0.00	0.00	0.00	0.20	0.05	0.00	0.00	0.08	0.10
2	0.18	0.19	0.00	0.40	0.17	0.25	0.05	0.00	0.40	0.10	0.25	0.55	0.38	0.30	0.23
3	0.00	0.29	0.19	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.03
6	0.00	0.00	0.35	0.00	0.17	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
7	0.57	0.27	0.21	0.33	0.60	0.33	0.90	0.60	0.35	0.37	0.70	0.42	0.62	0.57	0.50
N	0.00	0.00	0.00	0.04	0.04	0.42	0.00	0.40	0.25	0.25	0.00	0.00	0.00	0.05	0.10
Got1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	1.00	0.95	1.00	1.00	1.00	0.93	0.98
5.8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.01
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.07	0.01
Got2-2	0.28	0.00	0.17	0.00	0.15	0.38	0.13	0.00	0.00	0.00	0.05	0.21	0.00	0.33	0.12
4	0.72	1.00	0.83	1.00	0.85	0.62	0.87	1.00	1.00	1.00	0.95	0.79	1.00	0.67	0.88
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.65	0.38	0.29	0.90	0.33	0.69	0.38	0.00	0.95	0.38	0.40	0.43	0.65	0.00	0.47
6	0.35	0.62	0.71	0.10	0.67	0.31	0.62	0.92	0.05	0.62	0.60	0.57	0.35	1.00	0.53

Table 11. continued

Locus	Number of populations														Average
Allele	182	391	492	494	528	532	897	899	1330	1471	1472	1520	1521	1523	
Mdh1-1	0.25	0.00	0.00	0.13	0.02	0.00	0.25	0.00	0.03	0.15	0.05	0.00	0.33	0.03	0.09
6	0.75	1.00	1.00	0.87	0.94	1.00	0.75	0.82	0.79	0.85	0.95	0.88	0.67	0.90	0.87
10.5	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.18	0.18	0.00	0.00	0.12	0.00	0.07	0.04
Mdh2-3	0.15	0.35	0.00	0.00	0.15	0.48	0.00	0.00	0.05	0.28	0.10	0.53	0.05	0.15	0.16
3.5	0.00	0.48	0.00	0.00	0.02	0.00	0.00	0.13	0.03	0.12	0.12	0.02	0.00	0.25	0.08
4	0.00	0.00	0.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
5.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.01
6	0.85	0.17	0.67	1.00	0.83	0.52	1.00	0.87	0.92	0.60	0.67	0.45	0.95	0.60	0.73
Mdh3-16	1.00	1.00	1.00	1.00	0.96	1.00	1.00	1.00	1.00	0.90	0.90	1.00	1.00	0.95	0.99
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.02	0.00	0.00	0.05	0.01
N	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mdh4-8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	0.98	1.00	0.83	0.83	1.00	0.95	0.88	1.00	0.95	0.96
15	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.17	0.17	0.00	0.05	0.12	0.00	0.05	0.04
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.93	1.00	1.00	0.90	0.99
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.10	0.01
Pgm2-3	0.00	0.00	0.15	0.00	0.21	0.00	0.50	0.11	0.00	0.10	0.15	0.00	0.00	0.00	0.09
4	1.00	1.00	0.85	1.00	0.79	1.00	0.50	0.89	1.00	0.90	0.85	1.00	1.00	1.00	0.91
Pgd1-2	0.32	0.54	0.17	0.08	0.02	0.00	0.08	0.19	0.67	0.20	0.10	0.00	0.30	0.30	0.21
3.8	0.68	0.46	0.83	0.88	0.98	1.00	0.92	0.81	0.33	0.80	0.90	1.00	0.70	0.70	0.79
7	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Pgd2-2.8	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
5	0.36	1.00	1.00	0.77	1.00	1.00	1.00	1.00	0.70	1.00	1.00	1.00	1.00	0.98	0.91
6	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
10	0.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.00	0.00	0.00	0.00	0.00	0.07
Phi1-4	1.00	1.00	0.85	1.00	1.00	1.00	1.00	1.00	0.85	0.90	0.88	1.00	1.00	1.00	0.97
5	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.15	0.10	0.12	0.00	0.00	0.00	0.03

Table 12. Frequencies of detected alleles in populations of Mediterranean flints (group 7)

Locus	Number of populations														Average
Allele	167	189	191	518	848	851	901	920	926	934	1218	1223	1308	1309	1337	
Acp1-2	0.02	0.23	0.44	0.75	0.48	0.71	0.00	0.18	1.00	0.95	0.80	0.08	0.13	0.80	0.43	0.46
3	0.00	0.00	0.00	0.00	0.30	0.00	0.10	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
4	0.98	0.77	0.56	0.25	0.22	0.29	0.90	0.65	0.00	0.05	0.20	0.92	0.87	0.20	0.50	0.49
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.01
Adh1-4	1.00	0.67	0.82	0.63	0.81	0.65	0.65	0.58	0.21	1.00	0.58	0.90	0.41	1.00	1.00	0.73
6	0.00	0.33	0.18	0.37	0.19	0.35	0.35	0.42	0.79	0.00	0.42	0.10	0.59	0.00	0.00	0.27
Cat3-7	0.50	0.27	0.06	0.00	0.33	0.29	0.10	0.00	0.30	0.18	0.48	0.30	0.43	0.43	0.27	0.26
9	0.50	0.73	0.58	1.00	0.67	0.71	0.30	0.00	0.43	0.82	0.52	0.53	0.57	0.57	0.63	0.57
12	0.00	0.00	0.36	0.00	0.00	0.00	0.60	1.00	0.27	0.00	0.00	0.17	0.00	0.00	0.10	0.17
Enp1-6	1.00	0.17	0.60	0.96	0.55	0.44	0.10	0.00	0.00	0.28	0.58	0.72	0.35	0.65	0.15	0.44
7	0.00	0.00	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
8	0.00	0.83	0.19	0.04	0.45	0.56	0.90	1.00	1.00	0.72	0.42	0.28	0.65	0.27	0.85	0.54
Est8-4	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.40	0.50	0.50	0.50	0.50	0.50	0.49
4.5	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.58	0.50	0.50	0.50	0.50	0.50	0.51
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.03	0.00
2	1.00	0.00	0.00	0.23	0.22	0.79	0.50	0.15	0.28	0.10	0.23	0.18	0.30	0.23	0.30	0.30
3	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.05	0.05	0.03
7	0.00	0.77	0.87	0.10	0.70	0.17	0.45	0.85	0.47	0.85	0.72	0.80	0.60	0.57	0.27	0.55
N	0.00	0.21	0.13	0.67	0.00	0.04	0.05	0.00	0.00	0.05	0.05	0.00	0.10	0.15	0.35	0.12
Got1-4	1.00	1.00	1.00	1.00	0.93	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.83	1.00	0.98
6	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.01
Got2-2	0.00	0.13	0.00	0.06	0.03	0.21	0.00	0.00	0.08	0.00	0.10	0.00	0.03	0.15	0.00	0.05
4	1.00	0.87	1.00	0.94	0.97	0.79	1.00	1.00	0.92	1.00	0.90	1.00	0.97	0.85	1.00	0.95
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	1.00	0.23	0.19	0.27	1.00	0.73	0.33	0.93	0.95	0.10	0.50	0.87	0.73	0.70	0.55	0.61
6	0.00	0.77	0.81	0.73	0.00	0.27	0.67	0.07	0.05	0.90	0.50	0.13	0.27	0.30	0.45	0.39

Table 12. continued

Locus	Number of populations															Average
Allele	167	189	191	510	848	851	901	920	926	934	1218	1223	1308	1309	1337	
Mdh1-1	0.00	0.04	0.00	0.00	0.15	0.00	0.00	0.10	0.00	0.05	0.00	0.33	0.25	0.18	0.05	0.08
6	1.00	0.77	0.92	1.00	0.78	1.00	0.97	0.85	0.93	0.95	1.00	0.67	0.75	0.77	0.92	0.88
9	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10.5	0.00	0.19	0.08	0.00	0.07	0.00	0.00	0.05	0.07	0.00	0.00	0.00	0.00	0.05	0.03	0.04
Mdh2-3	0.00	0.13	0.19	0.29	0.38	0.00	0.00	0.20	0.30	0.00	0.25	0.03	0.13	0.15	0.05	0.14
3.5	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.05	0.02
6	1.00	0.85	0.81	0.71	0.62	1.00	1.00	0.80	0.70	1.00	0.75	0.97	0.87	0.63	0.90	0.84
Mdh3-16	1.00	0.98	1.00	0.85	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	0.80	0.97
18	0.00	0.02	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.20	0.03
Mdh4-8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.10	0.00	0.00	0.02
12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.87	1.00	1.00	1.00	0.90	1.00	1.00	0.98
Mdh5-12	1.00	0.79	0.96	1.00	0.92	1.00	0.90	0.90	0.95	1.00	0.98	1.00	0.98	0.93	1.00	0.95
15	0.00	0.21	0.04	0.00	0.08	0.00	0.10	0.10	0.05	0.00	0.02	0.00	0.02	0.07	0.00	0.05
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
Pgm2-2	0.00	0.04	0.04	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
3	0.00	0.27	0.00	0.13	0.00	0.21	0.00	0.33	0.00	0.03	0.00	0.10	0.00	0.05	0.13	0.09
4	1.00	0.69	0.96	0.87	1.00	0.77	1.00	0.67	1.00	0.97	0.92	0.90	1.00	0.95	0.87	0.90
Pgd1-2	1.00	0.21	0.04	0.50	0.55	0.52	0.25	0.85	0.13	0.85	0.18	0.83	0.48	0.25	0.40	0.47
3.8	0.00	0.79	0.96	0.50	0.45	0.48	0.75	0.15	0.87	0.15	0.82	0.17	0.52	0.75	0.60	0.53
Pgd2-5	1.00	0.90	0.96	1.00	1.00	0.98	1.00	1.00	1.00	1.00	0.83	1.00	1.00	0.73	0.93	0.96
10	0.00	0.10	0.04	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.27	0.07	0.04
Phi1-4	1.00	0.81	0.73	1.00	1.00	1.00	1.00	1.00	1.00	0.35	1.00	1.00	1.00	1.00	0.93	0.92
5	0.00	0.19	0.27	0.00	0.00	0.00	0.00	0.00	0.00	0.65	0.00	0.00	0.00	0.00	0.07	0.08

Table 13 . Frequencies of detected alleles in populations of small-grain flints (group 8)

Locus	Number of populations										
Allele	159	161	163	166	558	900	935	1475	1497	1822	Average
Acp1-1	0.00	0.00	0.40	0.13	0.00	0.00	0.00	0.05	0.00	0.00	0.02
2	0.88	0.78	1.00	0.87	0.98	0.38	0.75	0.10	0.15	0.43	0.63
3	0.00	0.22	0.00	0.00	0.00	0.05	0.00	0.13	0.00	0.07	0.05
4	0.12	0.00	0.00	0.00	0.02	0.57	0.25	0.60	0.85	0.48	0.29
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.02	0.01
Adh1-4	0.95	0.68	0.70	1.00	0.98	0.74	0.53	0.69	1.00	0.59	0.79
6	0.05	0.32	0.30	0.00	0.02	0.26	0.47	0.31	0.00	0.41	0.21
Cat3-7	0.38	0.23	0.00	0.15	0.23	0.48	0.50	0.18	0.28	0.28	0.27
9	0.47	0.77	1.00	0.83	0.75	0.50	0.50	0.82	0.57	0.67	0.69
12	0.15	0.00	0.00	0.02	0.02	0.02	0.00	0.00	0.15	0.05	0.04
Enp1-6	0.98	0.08	0.38	0.20	0.13	0.30	0.50	0.70	0.88	1.00	0.51
7	0.00	0.00	0.00	0.05	0.00	0.00	0.05	0.00	0.00	0.00	0.01
8	0.02	0.92	0.62	0.75	0.87	0.70	0.45	0.30	0.12	0.00	0.48
Est8-4	0.50	0.50	0.40	0.50	0.50	0.40	0.50	0.50	0.50	0.50	0.48
4.5	0.50	0.50	0.40	0.50	0.50	0.60	0.50	0.50	0.50	0.50	0.50
5	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.03	0.01
2	0.00	0.00	0.65	0.00	0.73	0.13	0.15	0.25	0.15	0.35	0.24
3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.02	0.02
6	0.00	0.00	0.00	0.30	0.00	0.00	0.00	0.13	0.00	0.15	0.06
7	1.00	1.00	0.00	0.70	0.27	0.42	0.80	0.42	0.60	0.23	0.54
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.02
N	0.00	0.00	0.35	0.00	0.00	0.40	0.05	0.00	0.25	0.00	0.11
Got1-4	1.00	1.00	1.00	1.00	1.00	0.75	1.00	1.00	1.00	1.00	0.97
6	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.03
Got2-2	0.00	0.00	0.00	0.45	0.45	0.00	0.00	0.00	0.33	0.08	0.13
4	1.00	1.00	1.00	0.55	0.55	1.00	1.00	1.00	0.67	0.92	0.87
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.60	0.00	0.80	0.28	0.25	0.00	1.00	0.30	0.43	0.48	0.41
6	0.40	1.00	0.20	0.72	0.75	1.00	0.00	0.70	0.57	0.52	0.59

Table 13. continued

Locus	Number of populations										Average
Allele	159	161	163	166	558	900	935	1475	1497	1822	
Mdh1-1	0.00	0.45	0.18	0.00	0.25	0.20	0.35	0.23	0.18	0.15	0.20
6	0.87	0.55	0.82	1.00	0.75	0.80	0.65	0.77	0.82	0.85	0.79
10.5	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mdh2-3	0.00	0.00	0.00	0.00	0.33	0.20	0.00	0.28	0.05	0.15	0.10
3.5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.05	0.15	0.04
6	1.00	1.00	1.00	1.00	0.67	0.80	1.00	0.55	0.90	0.70	0.86
Mdh3-16	1.00	1.00	1.00	1.00	1.00	0.60	1.00	0.68	0.98	0.65	0.89
16.3	0.00	0.00	0.00	0.00	0.00	0.40	0.00	0.00	0.00	0.00	0.04
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.32	0.02	0.35	0.07
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	0.50	0.90	0.88	1.00	1.00	1.00	0.93
15	0.00	0.00	0.00	0.00	0.50	0.10	0.12	0.00	0.00	0.00	0.07
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	0.70	0.95	1.00	1.00	0.95
16	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.05	0.00	0.00	0.05
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00
3	0.00	0.38	0.00	0.00	0.00	0.18	0.00	0.10	0.13	0.00	0.08
4	1.00	0.62	1.00	1.00	1.00	0.82	1.00	0.90	0.87	0.97	0.92
Pgd1-2	0.20	0.32	0.13	0.87	0.95	0.28	0.70	0.38	0.98	0.39	0.52
3.8	0.80	0.68	0.87	0.13	0.05	0.72	0.30	0.62	0.02	0.61	0.48
Pgd2-5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Phi1-4	1.00	0.40	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94
5	0.00	0.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06

Table 14. Frequencies of detected alleles in populations of 8-row soft dents (group 9)

Locus	Number of populations															Average
Allele	69	582	602	737	762	796	1481	1489	1496	1506	1507	1524	1537	1583	1804	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.11	0.00	0.01
2	0.33	0.58	0.00	0.13	0.39	0.00	0.37	0.00	0.42	0.22	0.45	0.08	0.39	0.50	0.22	0.27
3	0.31	0.12	0.77	0.38	0.36	1.00	0.23	0.39	0.14	0.11	0.00	0.06	0.08	0.08	0.45	0.30
4	0.36	0.05	0.23	0.57	0.25	0.00	0.40	0.61	0.36	0.67	0.55	0.83	0.53	0.31	0.33	0.40
6	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Adh1-4	0.31	0.75	0.93	1.00	0.33	1.00	0.43	0.83	0.72	0.78	0.94	0.89	0.94	0.92	0.86	0.78
6	0.69	0.25	0.07	0.00	0.67	0.00	0.57	0.17	0.28	0.22	0.06	0.11	0.06	0.08	0.14	0.22
Cat3-7	0.00	0.03	0.00	0.00	0.00	0.00	0.05	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
9	0.97	0.75	0.80	0.75	0.78	0.85	0.85	0.82	1.00	0.42	0.67	0.86	0.86	0.97	0.78	0.81
12	0.03	0.22	0.20	0.25	0.22	0.15	0.10	0.15	0.00	0.58	0.25	0.14	0.14	0.03	0.22	0.18
Enp1-4	0.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
6	0.28	0.31	0.53	1.00	1.00	0.20	0.67	0.40	1.00	0.31	0.61	0.86	0.47	0.92	0.97	0.64
8	0.53	0.69	0.47	0.00	0.00	0.80	0.33	0.60	0.00	0.69	0.39	0.14	0.53	0.08	0.03	0.35
Est8-4	0.28	0.25	1.00	1.00	0.47	1.00	0.67	1.00	0.50	0.31	0.72	0.53	0.86	0.53	0.50	0.59
4.5	0.72	0.69	0.00	0.00	0.53	0.00	0.33	0.00	0.50	0.69	0.17	0.42	0.94	0.47	0.50	0.40
5	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.05	0.00	0.00	0.00	0.01
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
Glu1-1	0.00	0.00	0.13	0.20	0.00	0.00	0.13	0.00	0.03	0.00	0.00	0.00	0.08	0.00	0.06	0.04
2	0.00	0.08	0.17	0.67	0.14	0.00	0.00	0.08	0.11	0.08	0.08	0.08	0.14	0.28	0.29	0.15
3	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.03	0.02
6	0.27	0.28	0.04	0.07	0.00	0.47	0.00	0.23	0.03	0.00	0.00	0.25	0.06	0.00	0.00	0.11
7	0.73	0.64	0.62	0.07	0.64	0.53	0.87	0.27	0.78	0.64	0.53	0.39	0.47	0.67	0.50	0.56
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
N	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.05	0.17	0.39	0.22	0.17	0.05	0.12	0.09
Got1-4	1.00	1.00	0.90	1.00	1.00	1.00	1.00	1.00	0.97	1.00	1.00	0.97	0.86	0.97	1.00	0.98
6	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.03	0.14	0.03	0.00	0.02
Got2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.06	0.19	0.08	0.06	0.04
4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.86	1.00	0.94	0.81	0.92	0.94	0.96
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.64	1.00	0.37	0.00	0.36	0.70	0.93	0.83	0.78	0.33	0.64	0.22	0.28	0.83	0.18	0.54
6	0.36	0.00	0.63	1.00	0.64	0.30	0.07	0.17	0.22	0.67	0.36	0.78	0.72	0.17	0.82	0.46

Table 14. continued

Locus	Number of populations															Average
Allele	69	582	602	737	762	796	1481	1489	1496	1506	1507	1524	1537	1583	1804	
Mdh1-1	0.00	0.06	0.27	0.00	0.00	0.00	0.04	0.00	0.11	0.11	0.22	0.08	0.28	0.28	0.11	0.11
6	1.00	0.94	0.73	1.00	0.97	1.00	0.96	0.83	0.89	0.89	0.78	0.92	0.72	0.72	0.89	0.88
10.5	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mdh2-3	0.36	0.06	0.13	0.10	0.06	0.70	0.36	0.53	0.42	0.22	0.11	0.17	0.39	0.31	0.17	0.27
3.5	0.20	0.00	0.00	0.00	0.08	0.20	0.00	0.00	0.00	0.03	0.08	0.00	0.00	0.00	0.00	0.04
6	0.44	0.94	0.87	0.90	0.86	0.10	0.64	0.47	0.58	0.75	0.81	0.83	0.61	0.69	0.83	0.69
Mdh3-16	1.00	0.78	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.89	0.94	0.97	0.86	1.00	1.00	0.96
18	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.06	0.03	0.14	0.00	0.00	0.04
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	0.78	1.00	1.00	1.00	1.00	1.00	1.00	0.92	1.00	0.94	0.89	0.86	1.00	0.89	0.95
15	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.06	0.11	0.14	0.00	0.11	0.05
Pgm1-9	1.00	1.00	1.00	0.90	1.00	1.00	1.00	0.83	0.94	1.00	1.00	1.00	0.89	1.00	0.92	0.97
16	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.17	0.06	0.00	0.00	0.00	0.11	0.00	0.08	0.03
Pgm2-3	0.50	0.00	0.07	0.00	0.31	0.20	0.10	0.00	0.11	0.28	0.00	0.11	0.11	0.19	0.31	0.16
4	0.50	1.00	0.93	1.00	0.69	0.80	0.90	1.00	0.89	0.72	1.00	0.89	0.83	0.81	0.69	0.84
Pgd1-2	0.22	0.19	0.87	0.33	0.03	0.75	0.00	0.39	0.39	0.19	0.69	0.14	0.17	0.17	0.19	0.32
3.8	0.78	0.81	0.13	0.67	0.97	0.25	1.00	0.61	0.61	0.81	0.31	0.86	0.83	0.83	0.81	0.68
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.11	0.00	0.06	0.00	0.03	0.00	0.14	0.04
5	1.00	1.00	1.00	1.00	1.00	0.86	1.00	1.00	0.89	1.00	0.94	1.00	0.97	0.92	0.86	0.96
Phi1-3	0.28	0.00	0.00	0.00	0.30	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.42	0.25	0.36	0.11
4	0.47	1.00	0.30	0.87	0.35	0.83	0.83	0.93	1.00	0.95	0.91	1.00	0.53	0.64	0.53	0.74
5	0.25	0.00	0.70	0.13	0.35	0.17	0.17	0.07	0.00	0.00	0.09	0.00	0.05	0.11	0.11	0.15

Table 15. Frequencies of detected alleles in populations of Roumanian flints (group 10)

Locus	Number of populations									Average
Allele	676	690	692	700	1528	1530	1549	1552	1592	
Acp1-2	0.20	0.05	0.13	0.23	0.15	0.05	0.23	0.30	0.10	0.16
3	0.00	0.00	0.00	0.02	0.00	0.05	0.12	0.05	0.50	0.09
4	0.72	0.95	0.47	0.75	0.83	0.73	0.65	0.65	0.40	0.69
6	0.00	0.00	0.40	0.00	0.02	0.17	0.00	0.00	0.00	0.06
Adh1-4	0.22	0.77	0.58	0.76	0.50	0.62	0.90	0.71	0.83	0.65
6	0.78	0.23	0.42	0.24	0.50	0.38	0.10	0.29	0.17	0.35
Cat3-7	0.00	0.00	0.00	0.13	0.00	0.03	0.00	0.05	0.03	0.04
9	0.65	0.40	0.78	0.67	0.65	0.35	0.80	0.62	0.72	0.63
12	0.35	0.60	0.22	0.20	0.27	0.62	0.12	0.33	0.25	0.33
Enp1-6	0.40	0.70	0.48	0.35	0.72	0.58	0.55	0.45	0.85	0.56
8	0.60	0.30	0.52	0.65	0.28	0.42	0.45	0.55	0.15	0.44
Est8-4	0.50	0.50	0.50	0.50	0.50	0.50	0.40	0.50	0.50	0.49
4.5	0.50	0.50	0.50	0.50	0.50	0.50	0.53	0.50	0.50	0.50
5	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.01
Glu1-1	0.00	0.00	0.00	0.00	0.03	0.00	0.13	0.05	0.00	0.03
2	0.05	0.03	0.00	0.00	0.12	0.03	0.07	0.15	0.12	0.06
3	0.00	0.25	0.00	0.00	0.30	0.15	0.00	0.05	0.00	0.08
6	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.13	0.10	0.03
7	0.75	0.37	0.85	0.95	0.48	0.52	0.70	0.52	0.65	0.65
8	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.01
10	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
N	0.20	0.35	0.15	0.00	0.00	0.30	0.10	0.10	0.05	0.14
Got1-4	1.00	0.93	0.63	1.00	1.00	1.00	0.88	0.98	1.00	0.94
6	0.00	0.07	0.37	0.00	0.00	0.00	0.12	0.02	0.00	0.06
Got2-2	0.00	0.20	0.00	0.23	0.20	0.05	0.03	0.08	0.18	0.11
4	1.00	0.80	1.00	0.77	0.80	0.95	0.97	0.92	0.82	0.89
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.23	0.55	0.95	0.38	0.23	0.28	0.43	0.63	0.33	0.45
6	0.77	0.45	0.05	0.62	0.77	0.72	0.57	0.37	0.67	0.55

Table 15. continued

Locus	Number of populations									Average
Allele	676	690	692	700	1528	1530	1549	1552	1592	
Mdh1-1	0.03	0.20	0.00	0.08	0.05	0.23	0.10	0.15	0.08	0.10
6	0.97	0.80	1.00	0.92	0.95	0.65	0.90	0.85	0.90	0.88
10.5	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.02	0.02
Mdh2-3	0.00	0.18	0.43	0.45	0.05	0.15	0.13	0.23	0.18	0.20
3.5	0.00	0.00	0.00	0.00	0.03	0.10	0.35	0.10	0.12	0.08
6	1.00	0.82	0.57	0.55	0.92	0.75	0.52	0.67	0.70	0.72
Mdh3-16	0.97	1.00	1.00	1.00	0.95	0.98	1.00	0.98	0.95	0.98
18	0.03	0.00	0.00	0.00	0.05	0.02	0.00	0.02	0.05	0.02
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	0.73	1.00	1.00	1.00	0.97
15	0.00	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.00	0.03
Pgm1-9	1.00	1.00	0.83	1.00	1.00	1.00	0.90	0.98	1.00	0.97
16	0.00	0.00	0.17	0.00	0.00	0.00	0.10	0.02	0.00	0.03
Pgm2-3	0.03	0.08	0.00	0.00	0.13	0.15	0.03	0.18	0.30	0.10
4	0.97	0.92	1.00	1.00	0.87	0.85	0.97	0.82	0.70	0.90
Pgd1-2	0.03	0.00	0.29	0.05	0.28	0.25	0.33	0.18	0.50	0.21
3.8	0.97	1.00	0.71	0.95	0.72	0.75	0.67	0.82	0.50	0.79
Pgd2-2.8	0.00	0.05	0.00	0.20	0.00	0.00	0.25	0.16	0.08	0.08
5	1.00	0.95	1.00	0.80	1.00	1.00	0.75	0.84	0.92	0.92
Phi1-3	0.00	0.00	0.00	0.00	0.00	0.33	0.00	0.00	0.00	0.04
4	1.00	1.00	1.00	0.93	1.00	0.67	0.83	0.95	1.00	0.93
5	0.00	0.00	0.00	0.07	0.00	0.00	0.17	0.05	0.00	0.03

Table 16. Frequencies of detected alleles in populations of large-eared flints (group 11)

Locus	Number of populations														Average
Allele	138	141	715	832	838	918	922	984	1544	1577	1717	1729	1744	1833	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
2	0.58	0.61	0.17	0.57	0.31	0.42	0.31	0.00	0.03	0.17	0.28	0.14	0.28	0.42	0.31
3	0.06	0.00	0.28	0.00	0.16	0.25	0.38	0.07	0.00	0.17	0.11	0.22	0.05	0.19	0.14
4	0.28	0.39	0.55	0.43	0.47	0.33	0.28	0.93	0.97	0.58	0.47	0.58	0.50	0.39	0.50
6	0.00	0.00	0.00	0.00	0.06	0.00	0.03	0.00	0.00	0.08	0.14	0.06	0.17	0.00	0.04
Adh1-2	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	0.72	1.00	0.75	0.17	0.23	0.78	0.50	0.40	0.33	0.69	0.61	0.61	0.47	0.78	0.58
6	0.28	0.00	0.19	0.83	0.77	0.22	0.50	0.60	0.67	0.31	0.39	0.39	0.53	0.22	0.42
Cat3-7	0.08	0.08	0.00	0.00	0.14	0.17	0.00	0.13	0.00	0.06	0.03	0.06	0.11	0.03	0.06
9	0.81	0.89	0.83	1.00	0.39	0.69	0.78	0.87	0.50	0.44	0.50	0.83	0.67	0.69	0.71
12	0.11	0.03	0.17	0.00	0.47	0.14	0.22	0.00	0.50	0.50	0.47	0.11	0.22	0.28	0.23
Enp1-6	0.94	0.53	0.58	0.37	0.41	0.22	0.69	1.00	0.23	0.92	0.39	0.53	0.86	0.78	0.60
8	0.06	0.47	0.42	0.37	0.59	0.78	0.31	0.00	0.77	0.08	0.61	0.47	0.14	0.22	0.38
10	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Est8-4	0.25	0.14	0.47	1.00	0.56	0.47	0.33	1.00	1.00	0.39	0.28	0.58	0.69	0.28	0.53
4.5	0.69	0.72	0.53	0.00	0.44	0.47	0.50	0.00	0.00	0.56	0.64	0.36	0.22	0.33	0.39
5	0.03	0.08	0.00	0.00	0.00	0.06	0.17	0.00	0.00	0.05	0.03	0.06	0.03	0.39	0.07
6	0.03	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.06	0.00	0.01
Glu1-1	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.00	0.00	0.03	0.01
2	0.45	0.00	0.17	0.00	0.00	0.33	0.03	0.00	0.03	0.00	0.08	0.39	0.08	0.11	0.12
3	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.38	0.00	0.06	0.06	0.00	0.00	0.03
6	0.08	0.00	0.00	0.90	0.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.14
7	0.47	1.00	0.69	0.00	0.00	0.61	0.75	1.00	0.53	0.64	0.83	0.44	0.64	0.86	0.61
N	0.00	0.00	0.11	0.00	0.20	0.06	0.22	0.00	0.14	0.33	0.00	0.11	0.11	0.00	0.09
Got1-4	0.97	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	0.99
6	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.01
Got2-2	0.00	0.00	0.03	0.00	0.00	0.67	0.03	0.03	0.38	0.31	0.00	0.17	0.00	0.00	0.11
4	1.00	1.00	0.97	1.00	1.00	0.33	0.97	0.97	0.67	0.69	1.00	0.83	1.00	1.00	0.89
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.78	1.00	1.00	1.00	1.00	0.98
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.00	0.02
Idh2-4	0.17	0.00	0.58	0.59	0.09	0.11	0.56	0.17	0.43	0.08	0.33	0.25	0.33	0.17	0.28
6	0.83	1.00	0.42	0.41	0.91	0.89	0.44	0.83	0.57	0.92	0.67	0.75	0.67	0.83	0.72

Table 16. continued

Locus	Number of populations														Average
Allele	138	141	715	832	838	918	922	984	1544	1577	1717	1729	1744	1833	
Mdh1-1	0.00	0.00	0.24	0.00	0.00	0.44	0.03	0.32	0.21	0.22	0.25	0.08	0.03	0.14	0.14
6	1.00	1.00	0.76	1.00	1.00	0.53	0.97	0.68	0.79	0.78	0.75	0.92	0.97	0.86	0.86
10.5	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mdh2-3	0.00	0.22	0.06	0.00	0.00	0.28	0.06	0.00	0.00	0.44	0.42	0.28	0.25	0.14	0.15
3.5	0.00	0.06	0.00	0.50	0.23	0.05	0.00	0.00	0.07	0.00	0.00	0.00	0.06	0.22	0.09
6	1.00	0.72	0.94	0.50	0.77	0.67	0.94	1.00	0.93	0.56	0.58	0.72	0.69	0.64	0.76
Mdh3-16	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	0.92	0.86	0.98
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.08	0.14	0.02
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	0.94	0.88	1.00	1.00	0.94	0.69	1.00	0.93	0.83	0.94	0.86	1.00	0.86	0.92
15	0.00	0.06	0.12	0.00	0.00	0.06	0.31	0.00	0.07	0.17	0.06	0.14	0.00	0.14	0.08
Pgm1-9	0.64	0.47	1.00	1.00	1.00	0.92	1.00	0.70	0.97	1.00	1.00	0.97	0.97	0.89	0.89
16	0.36	0.53	0.00	0.00	0.00	0.08	0.00	0.30	0.03	0.00	0.00	0.03	0.03	0.11	0.11
Pgm2-2	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.02
3	0.33	0.06	0.31	0.37	0.03	0.03	0.06	0.03	0.00	0.08	0.19	0.19	0.28	0.06	0.14
4	0.67	0.72	0.69	0.63	0.97	0.97	0.94	0.97	1.00	0.92	0.81	0.81	0.69	0.94	0.84
Pgd1-2	0.17	0.00	0.00	0.57	0.10	0.64	0.14	0.23	0.33	0.19	0.00	0.28	0.22	0.17	0.22
3.8	0.83	1.00	1.00	0.43	0.90	0.36	0.86	0.77	0.67	0.81	1.00	0.72	0.78	0.83	0.78
Pgd2-2.8	0.00	0.00	0.00	0.00	0.20	0.00	0.06	0.00	0.03	0.00	0.00	0.00	0.08	0.00	0.03
5	1.00	1.00	1.00	1.00	0.80	1.00	0.94	1.00	0.97	1.00	1.00	1.00	0.92	1.00	0.97
Phi1-4	1.00	1.00	0.89	1.00	1.00	0.97	0.92	1.00	1.00	0.92	1.00	0.97	0.92	0.89	0.96
5	0.00	0.00	0.11	0.00	0.00	0.03	0.08	0.00	0.00	0.08	0.00	0.03	0.08	0.11	0.04

Table 17. Frequencies of detected alleles in populations of white semi-dents 'Moravac' (group 12)

Locus	Number of populations														Average
Allele	58	90	198	385	435	539	654	669	724	799	802	804	870	882	887	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.33	0.55	0.48	0.35	0.00	0.73	0.03	0.83	0.75	0.10	0.38	0.54	0.10	0.04	0.35	0.36
3	0.07	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.10	0.00	0.00	0.00	0.00	0.15	0.03
4	0.60	0.42	0.52	0.65	1.00	0.27	0.97	0.17	0.20	0.80	0.62	0.46	0.90	0.96	0.50	0.61
Adh1-4	0.63	0.71	0.48	0.53	0.72	0.96	1.00	0.75	0.71	0.87	1.00	1.00	0.97	1.00	0.53	0.79
6	0.37	0.29	0.52	0.47	0.28	0.04	0.00	0.25	0.29	0.13	0.00	0.00	0.03	0.00	0.47	0.21
Cat3-7	0.15	0.10	0.00	0.00	0.00	0.15	0.10	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.05
9	0.85	0.60	1.00	0.79	0.43	0.85	0.45	1.00	0.50	0.65	0.43	1.00	1.00	1.00	0.98	0.77
12	0.00	0.30	0.00	0.21	0.57	0.00	0.45	0.00	0.50	0.27	0.42	0.00	0.00	0.00	0.02	0.18
Enp1-6	1.00	0.63	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98
8	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Est8-4	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.46	0.50	0.50	0.50	0.50
4.5	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.42	0.50	0.50	0.50	0.49
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.01
Glu1-1	0.10	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.03
2	0.03	0.28	0.00	0.06	0.03	0.18	0.58	0.42	0.00	0.63	0.00	0.15	0.00	0.17	0.15	0.18
3	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.01
6	0.02	0.00	0.17	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.04
7	0.53	0.47	0.83	0.44	0.47	0.57	0.27	0.00	0.70	0.32	0.90	0.52	1.00	0.52	0.20	0.52
10	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
N	0.20	0.25	0.00	0.13	0.50	0.15	0.00	0.58	0.15	0.05	0.10	0.16	0.00	0.29	0.65	0.21
Got1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.77	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Got2-2	0.11	0.00	0.13	0.00	0.00	0.00	0.35	0.02	0.00	0.53	0.00	0.00	0.00	0.10	0.20	0.10
4	0.89	1.00	0.87	1.00	1.00	1.00	0.65	0.98	1.00	0.47	0.95	1.00	1.00	0.90	0.80	0.90
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.33	0.96
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.67	0.04
Idh2-4	0.73	0.43	0.46	0.54	0.30	0.98	0.15	0.33	0.10	0.33	0.13	0.79	0.43	0.81	0.00	0.43
6	0.27	0.57	0.54	0.46	0.70	0.02	0.85	0.67	0.90	0.67	0.87	0.21	0.57	0.19	1.00	0.57

Table 17. continued

Locus	Number of populations															Average
Allele	58	90	198	385	435	539	654	669	724	799	862	884	870	882	887	
Mdh1-1	0.20	0.00	0.27	0.19	0.15	0.00	0.00	0.00	0.13	0.25	0.00	0.02	0.00	0.15	0.00	0.09
6	0.80	1.00	0.73	0.81	0.85	1.00	1.00	1.00	0.87	0.75	1.00	0.98	1.00	0.85	1.00	0.91
Mdh2-3	0.18	0.00	0.04	0.44	0.03	0.03	0.13	0.42	0.33	0.03	0.20	0.19	0.34	0.35	0.38	0.26
3.5	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
4.5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
6	0.82	1.00	0.96	0.56	0.95	0.17	0.87	0.58	0.67	0.97	0.80	0.79	0.63	0.65	0.62	0.74
Mdh3-16	1.00	1.00	1.00	0.98	0.83	1.00	1.00	0.94	1.00	1.00	1.00	0.98	1.00	1.00	1.00	0.98
18	0.00	0.00	0.00	0.02	0.17	0.00	0.00	0.06	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.02
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	0.85	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.83	1.00	1.00	1.00	1.00	0.98
15	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.02
Pgm1-9	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.79	0.65	0.83	0.85	1.00	1.00	0.79	1.00	0.93
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.35	0.17	0.15	0.00	0.00	0.21	0.00	0.07
Pgm2-3	0.13	0.00	0.04	1.00	0.35	0.28	0.00	0.35	0.00	0.06	0.23	0.46	0.10	0.21	0.00	0.21
4	0.87	1.00	0.96	0.00	0.65	0.72	1.00	0.65	1.00	0.94	0.77	0.54	0.90	0.79	1.00	0.79
Pgd1-2	0.13	0.33	0.00	0.42	0.83	0.08	0.00	0.17	0.00	0.32	0.53	0.17	0.00	0.79	0.25	0.27
3.8	0.87	0.67	1.00	0.58	0.17	0.92	1.00	0.83	1.00	0.68	0.47	0.83	1.00	0.21	0.75	0.73
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.13	0.00	0.00	0.00	0.00	0.58	0.05
5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	0.87	1.00	1.00	1.00	1.00	0.42	0.95
Phi1-4	1.00	0.83	0.71	1.00	0.65	1.00	0.58	0.73	1.00	0.95	0.73	1.00	0.80	0.73	1.00	0.85
5	0.00	0.17	0.29	0.00	0.35	0.00	0.42	0.27	0.00	0.05	0.27	0.00	0.20	0.27	0.00	0.15

Table 18. Frequencies of detected alleles in populations of USA corn type belts (group 13)

Locus	Number of populations																									Average
Allele	196	216	233	236	243	258	273	278	284	384	426	482	559	566	577	638	645	694	761	1444	1467	1478	1505	1517	1561	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
2	0.14	0.94	0.06	0.00	0.25	0.44	0.16	0.00	0.00	0.38	0.12	0.22	1.00	0.56	0.78	0.08	0.38	0.62	0.94	0.31	0.44	0.64	0.39	0.14	0.50	0.39
3	0.00	0.00	0.86	0.40	0.47	0.00	0.00	0.00	1.00	0.04	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.06	0.09	0.14	0.17	0.11	0.17	0.12
4	0.86	0.06	0.08	0.60	0.28	0.56	0.84	1.00	0.00	0.58	0.69	0.76	0.00	0.44	0.22	0.92	0.62	0.38	0.03	0.58	0.44	0.22	0.41	0.72	0.33	0.47
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.03	0.00	0.03	0.00	0.00	0.02
Adh1-4	0.96	0.39	0.25	0.75	0.89	0.17	0.38	0.70	0.13	1.00	0.98	0.92	1.00	0.65	0.90	0.93	0.76	0.94	0.97	0.78	0.84	1.00	0.69	0.42	1.00	0.76
6	0.04	0.61	0.75	0.25	0.11	0.83	0.62	0.30	0.87	0.00	0.02	0.08	0.00	0.35	0.10	0.07	0.24	0.06	0.03	0.22	0.16	0.00	0.31	0.58	0.00	0.24
Cat3-7	0.08	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.02	0.22	0.00	0.00	0.00	0.08	0.08	0.00	0.00	0.00	0.39	0.05
9	0.78	0.44	0.94	0.70	0.69	1.00	0.91	0.87	1.00	0.12	0.14	0.62	0.58	0.54	0.26	0.72	0.62	0.90	1.00	0.67	0.53	1.00	1.00	0.67	0.55	0.69
12	0.14	0.56	0.06	0.30	0.31	0.00	0.00	0.13	0.00	0.88	0.86	0.16	0.38	0.46	0.28	0.06	0.38	0.10	0.00	0.25	0.39	0.00	0.00	0.33	0.06	0.24
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Enp1-4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.00	0.00
6	1.00	1.00	1.00	0.84	1.00	1.00	1.00	0.87	0.00	1.00	1.00	0.80	0.94	1.00	1.00	1.00	0.96	0.88	1.00	0.64	0.67	0.86	1.00	0.78	0.61	0.89
7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
8	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.13	1.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.36	0.33	0.14	0.00	0.00	0.39	0.11
Est8-4	0.50	0.14	0.22	0.41	0.36	0.47	0.69	0.53	0.80	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.20	1.00	0.53	0.47	0.67	0.50	0.44	0.33	0.49
4,5	0.50	0.64	0.78	0.59	0.56	0.45	0.31	0.47	0.20	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.60	0.00	0.47	0.50	0.30	0.50	0.56	0.39	0.48
5	0.00	0.22	0.00	0.00	0.08	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.00	0.03	0.03	0.00	0.00	0.17	0.03
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00

Locus	Number of populations																										Average
Allele	196	216	233	236	243	258	273	278	284	384	426	482	559	566	577	638	645	694	761	1444	1467	1478	1505	1517	1561		
Glu1-1	0.00	0.00	0.00	0.06	0.22	0.00	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.03	0.09	0.00	0.00	0.00	0.00	0.00		0.04
2	0.00	0.25	0.00	0.37	0.03	0.00	0.12	0.42	0.00	0.00	0.14	0.44	0.84	0.02	0.10	0.26	0.48	0.00	0.00	0.36	0.17	0.00	0.00	0.03	0.11		0.20
3	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.00
6	0.00	0.00	0.00	0.07	0.00	0.00	0.20	0.24	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.44	0.00	0.00	0.00	0.17	0.00	0.00	0.00		0.05
7	0.52	0.64	0.83	0.27	0.68	1.00	0.23	0.34	0.05	0.69	0.76	0.24	0.08	0.44	0.22	0.58	0.18	0.28	0.72	0.33	0.67	0.67	0.75	0.75	0.83		0.51
N	0.48	0.11	0.17	0.20	0.07	0.00	0.00	0.00	0.00	0.31	0.08	0.32	0.08	0.52	0.60	0.16	0.32	0.28	0.25	0.22	0.16	0.16	0.17	0.22	0.06		0.20
Got1-4	1.00	1.00	1.00	0.66	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.78	1.00	1.00	0.98	1.00	1.00	0.97	0.94	1.00	1.00	0.97	1.00		0.97
6	0.00	0.00	0.00	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.02	0.00	0.00	0.03	0.06	0.00	0.00	0.03	0.00		0.03
Got2-2	0.00	0.00	0.00	0.16	0.17	0.00	0.13	0.00	0.00	0.00	0.35	0.20	0.00	0.00	0.00	0.04	0.26	0.00	0.13	0.25	0.00	0.36	0.00	0.08	0.08		0.09
4	1.00	1.00	1.00	0.84	0.83	1.00	0.87	1.00	1.00	1.00	0.65	0.80	1.00	1.00	1.00	0.80	0.74	1.00	0.87	0.75	1.00	0.64	1.00	0.92	0.92		0.90
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.01
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.67		0.99
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.33		0.01
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		1.00
Idh2-4	0.82	0.28	0.53	0.87	0.19	0.72	0.91	0.97	0.70	0.16	0.28	0.76	0.18	0.48	0.50	0.20	0.70	0.18	0.44	0.39	0.31	0.44	0.53	0.31	0.56		0.48
6	0.18	0.72	0.47	0.13	0.81	0.28	0.09	0.03	0.30	0.84	0.72	0.24	0.82	0.52	0.50	0.80	0.30	0.82	0.56	0.61	0.69	0.56	0.47	0.69	0.44		0.52

continued

Table 18 continued

Locus	Number of populations																									Average
Allele	196	216	233	236	243	258	273	278	284	384	426	482	559	566	577	638	645	694	761	1444	1467	1478	1505	1517	1561	
Mdh1-1	0.00	0.08	0.00	0.13	0.08	0.00	0.10	0.00	0.20	0.14	0.34	0.50	0.16	0.02	0.14	0.00	0.22	0.36	0.17	0.11	0.17	0.11	0.00	0.47	0.00	0.15
6	0.94	0.92	1.00	0.87	0.92	1.00	0.90	1.00	0.80	0.86	0.62	0.46	0.84	0.98	0.86	1.00	0.78	0.64	0.83	0.89	0.83	0.89	1.00	0.53	1.00	0.85
9	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10.5	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mdh2-3	0.12	0.00	0.53	0.20	0.22	0.44	0.00	0.03	0.18	0.98	0.14	0.34	0.00	0.82	0.00	0.42	0.26	0.00	0.70	0.00	0.39	0.31	0.56	0.58	0.28	0.29
3.5	0.00	0.00	0.00	0.00	0.00	0.06	0.48	0.97	0.00	0.02	0.22	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.10	0.17	0.14	0.00	0.00	0.00	0.00	0.10
6	0.88	1.00	0.47	0.80	0.78	0.50	0.52	0.00	0.82	0.00	0.64	0.66	0.92	0.14	1.00	0.50	0.74	1.00	0.20	0.83	0.47	0.69	0.44	0.42	0.72	0.61
Mdh3-16	1.00	1.00	0.22	1.00	0.73	0.97	1.00	1.00	1.00	0.69	0.96	1.00	1.00	1.00	0.98	0.32	1.00	0.66	1.00	1.00	0.94	0.69	1.00	1.00	0.69	0.87
16.9	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	0.00	0.00	0.78	0.00	0.15	0.03	0.00	0.00	0.00	0.31	0.04	0.00	0.00	0.00	0.02	0.68	0.00	0.34	0.00	0.00	0.06	0.31	0.00	0.00	0.31	0.13
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	0.89	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00	0.97	1.00	0.99
15	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.03	0.00	0.01

Locus	Number of populations																									Average
Allele	196	216	233	236	243	258	273	278	284	384	426	482	559	566	577	638	645	694	761	1444	1467	1478	1505	1517	1561	
Pgm1-9	1.00	0.97	0.53	0.90	1.00	0.61	1.00	0.73	1.00	0.98	0.98	1.00	1.00	0.98	1.00	1.00	1.00	1.00	0.90	1.00	1.00	1.00	0.97	0.92	0.94	0.95
16	0.00	0.03	0.47	0.10	0.00	0.39	0.00	0.27	0.00	0.02	0.02	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.03	0.08	0.06	0.05
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.06	0.00	0.00	0.00	0.10	0.00	0.00	0.03	0.14	0.00	0.00	0.00	0.02
3	0.00	0.22	0.00	0.13	0.00	0.22	0.00	0.37	0.00	0.00	0.06	0.14	0.38	0.40	0.04	0.06	0.00	0.29	0.00	0.00	0.05	0.00	0.33	0.06	0.14	0.12
4	1.00	0.78	1.00	0.87	1.00	0.78	1.00	0.63	1.00	1.00	0.94	0.86	0.60	0.54	0.96	0.94	1.00	0.61	1.00	1.00	0.92	0.86	0.67	0.94	0.86	0.86
Pgd1-2	0.06	0.64	0.36	0.63	0.31	0.00	0.63	0.76	0.00	0.06	0.72	0.02	0.10	0.22	0.00	0.72	0.00	0.00	0.50	0.35	0.58	0.47	0.53	0.25	0.77	0.32
3.8	0.94	0.36	0.64	0.37	0.69	1.00	0.37	0.24	1.00	0.94	0.28	0.98	0.90	0.78	1.00	0.28	1.00	1.00	0.50	0.65	0.42	0.53	0.47	0.75	0.23	0.68
Pgd2-2.8	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.05
5	1.00	1.00	1.00	0.97	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00	1.00	1.00	0.87	1.00	1.00	1.00	0.94	1.00	1.00	1.00	0.97	0.88	0.94
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.12	0.01
Phi1-4	0.80	1.00	1.00	1.00	0.94	1.00	1.00	1.00	0.87	1.00	0.94	1.00	1.00	0.48	1.00	0.94	0.98	1.00	0.78	0.97	1.00	0.89	0.69	0.64	0.75	0.91
5	0.20	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.13	0.00	0.06	0.00	0.00	0.52	0.00	0.06	0.02	0.00	0.22	0.03	0.00	0.11	0.31	0.36	0.25	0.09

Table 19. Frequencies of detected alleles in populations of derived dents (group 14)

Locus	Number of populations																	Average
Allele	225	231	289	296	309	320	321	325	336	337	343	347	348	359	362	365	717	
Acp1-1	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
2	0.00	0.25	0.23	0.27	0.60	0.68	0.45	0.70	0.67	0.71	0.33	0.48	0.44	0.08	0.81	0.58	0.79	0.48
3	0.00	0.20	0.12	0.15	0.00	0.07	0.03	0.00	0.00	0.00	0.60	0.08	0.00	0.02	0.00	0.00	0.00	0.07
4	1.00	0.55	0.65	0.45	0.40	0.25	0.32	0.30	0.29	0.29	0.07	0.52	0.56	0.90	0.19	0.42	0.21	0.43
6	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Adh1-4	1.00	0.53	0.97	0.73	0.60	1.00	0.29	0.85	0.52	0.33	0.97	0.65	0.29	0.58	1.00	0.54	0.69	0.68
6	0.00	0.47	0.03	0.27	0.40	0.00	0.71	0.15	0.48	0.67	0.03	0.35	0.71	0.42	0.00	0.46	0.31	0.32
Cat3-7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.02
9	1.00	0.95	1.00	0.75	1.00	1.00	0.87	0.90	0.27	0.56	0.77	1.00	1.00	1.00	1.00	1.00	0.90	0.88
12	0.00	0.05	0.00	0.25	0.00	0.00	0.00	0.00	0.27	0.44	0.15	0.00	0.00	0.00	0.00	0.00	0.04	0.07
N	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
Enp1-6	1.00	1.00	1.00	1.00	0.80	0.43	0.80	0.45	1.00	0.92	1.00	0.98	1.00	1.00	1.00	1.00	0.83	0.89
8	0.00	0.00	0.00	0.00	0.20	0.57	0.20	0.55	0.00	0.08	0.00	0.02	0.00	0.00	0.00	0.00	0.17	0.11
Est8-4	0.50	0.50	0.50	0.35	0.38	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.39	0.50	0.50	0.50	0.50	0.48
4.5	0.50	0.50	0.50	0.48	0.42	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.44	0.50	0.50	0.50	0.50	0.49
5	0.00	0.00	0.00	0.17	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.03
Glu1-1	0.00	0.35	0.20	0.00	0.00	0.05	0.00	0.03	0.00	0.00	0.10	0.08	0.27	0.00	0.00	0.00	0.09	0.07
2	0.20	0.00	0.00	0.03	0.03	0.10	0.08	0.05	0.27	0.00	0.03	0.20	0.06	0.00	0.00	0.46	0.04	0.09
3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.17	0.25	0.00	0.00	0.00	0.00	0.03
6	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.01
7	0.55	0.65	0.75	0.95	0.97	0.85	0.77	0.67	0.61	0.50	0.87	0.55	0.38	1.00	0.83	0.21	0.76	0.78
N	0.25	0.00	0.05	0.00	0.00	0.00	0.15	0.25	0.08	0.46	0.00	0.00	0.04	0.00	0.17	0.33	0.00	0.10
Got1-4	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	1.00	0.78	1.00	1.00	1.00	1.00	1.00	0.99
6	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.01
Got2-2	0.53	0.08	0.00	0.08	0.18	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.04	0.06
4	0.47	0.92	1.00	0.92	0.82	1.00	1.00	1.00	0.94	1.00	1.00	1.00	1.00	0.97	1.00	1.00	0.96	0.94
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	0.95	1.00	1.00	0.85	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
6	0.05	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Idh2-4	0.00	0.30	0.18	0.25	0.03	0.30	0.50	0.55	0.77	0.27	0.08	0.25	0.33	0.03	0.85	0.25	0.79	0.34
6	1.00	0.70	0.82	0.75	0.97	0.70	0.50	0.45	0.23	0.73	0.92	0.75	0.67	0.97	0.15	0.75	0.21	0.66

Table 19. continued

Locus	Number of populations																	Average
Allele	225	231	289	296	309	320	321	325	336	337	343	347	348	359	362	365	717	
Mdh1-1	0.45	0.00	0.13	0.30	0.05	0.03	0.00	0.05	0.04	0.02	0.33	0.28	0.25	0.28	0.00	0.04	0.00	0.13
6	0.55	1.00	0.87	0.67	0.95	0.97	1.00	0.95	0.96	0.98	0.67	0.72	0.58	0.72	0.79	0.96	1.00	0.85
10.5	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.21	0.00	0.00	0.02
Mdh2-3	0.00	0.20	0.00	0.30	0.03	0.38	0.00	0.55	0.12	0.21	0.00	0.33	0.31	0.00	0.63	0.44	0.50	0.24
3.5	0.00	0.43	0.35	0.35	0.07	0.10	0.33	0.00	0.17	0.00	0.10	0.15	0.02	0.32	0.00	0.42	0.06	0.17
6	1.00	0.37	0.57	0.35	0.90	0.52	0.67	0.45	0.71	0.79	0.90	0.52	0.67	0.60	0.37	0.14	0.44	0.59
Mdh3-16	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97	0.83	1.00	0.90	1.00	0.96	1.00	1.00	1.00	1.00	0.98
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.17	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.02
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00
Mdh4-8	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
12	1.00	1.00	1.00	1.00	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
Mdh5-12	1.00	1.00	1.00	0.78	1.00	1.00	1.00	1.00	1.00	1.00	0.88	0.98	0.85	1.00	0.79	1.00	1.00	0.96
15	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.02	0.15	0.00	0.21	0.00	0.00	0.04
Pgm1-9	1.00	1.00	1.00	1.00	0.85	1.00	0.90	1.00	0.96	1.00	1.00	1.00	1.00	1.00	1.00	0.92	1.00	0.98
16	0.00	0.00	0.00	0.00	0.15	0.00	0.10	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.02
Pgm2-2	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.03	0.02	0.00	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.03
3	0.34	0.00	0.27	0.07	0.33	0.40	0.08	0.27	0.25	0.08	0.03	0.35	0.35	0.28	0.19	0.00	0.00	0.19
4	0.66	1.00	0.73	0.90	0.67	0.60	0.92	0.70	0.73	0.92	0.58	0.65	0.65	0.72	0.81	1.00	1.00	0.78
Pgd1-2	0.77	0.10	0.00	0.47	0.00	0.03	0.12	0.00	0.00	0.27	0.00	0.40	0.46	0.48	0.21	0.12	0.42	0.23
3.8	0.23	0.90	1.00	0.53	0.70	0.97	0.88	1.00	0.83	0.73	1.00	0.60	0.54	0.52	0.79	0.88	0.58	0.74
7	0.00	0.00	0.00	0.00	0.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Pgd2-2.8	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.02
5	1.00	1.00	1.00	0.89	0.75	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	0.97
6	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Phi1-4	1.00	1.00	0.65	0.98	1.00	1.00	1.00	1.00	1.00	0.79	0.75	0.73	0.69	0.68	0.91	0.67	1.00	0.87
5	0.00	0.00	0.35	0.02	0.00	0.00	0.00	0.00	0.00	0.21	0.25	0.27	0.31	0.32	0.09	0.33	0.00	0.13

Table 20. Frequencies of detected alleles in populations of southern USA type dents (group 15)

Locus	Number of populations														Average
Allele	222	232	245	252	262	266	914	1480	1488	1492	1589	1516	1565	1588	
Acp1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00
2	0.39	0.05	0.08	0.28	0.44	0.11	0.22	0.41	0.25	0.17	0.34	0.28	0.25	0.42	0.26
3	0.08	0.53	0.08	0.44	0.00	0.36	0.00	0.12	0.28	0.14	0.16	0.28	0.19	0.08	0.19
4	0.53	0.42	0.81	0.28	0.56	0.53	0.78	0.47	0.47	0.64	0.50	0.52	0.56	0.47	0.54
6	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.01
Adh1-4	0.53	0.64	1.00	0.97	1.00	0.67	0.30	0.63	1.00	0.50	0.81	0.64	0.75	0.86	0.74
6	0.47	0.36	0.00	0.03	0.00	0.33	0.70	0.37	0.00	0.50	0.19	0.36	0.25	0.14	0.26
Cat3-7	0.33	0.00	0.00	0.19	0.00	0.25	0.00	0.00	0.00	0.03	0.00	0.06	0.00	0.03	0.06
9	0.64	1.00	1.00	0.81	0.58	0.75	1.00	1.00	0.84	0.64	1.00	0.75	0.92	0.69	0.83
12	0.03	0.00	0.00	0.00	0.42	0.00	0.00	0.00	0.16	0.33	0.00	0.19	0.08	0.28	0.11
Enp1-6	0.83	0.31	0.72	1.00	1.00	1.00	1.00	0.77	0.80	0.92	0.63	0.86	1.00	0.86	0.84
8	0.17	0.69	0.28	0.00	0.00	0.00	0.00	0.23	0.20	0.08	0.37	0.14	0.00	0.14	0.16
Est8-4	0.25	0.39	0.14	0.39	0.14	0.56	0.47	0.43	0.50	0.39	0.31	0.14	0.53	0.36	0.36
4.5	0.42	0.41	0.86	0.58	0.86	0.44	0.43	0.37	0.46	0.56	0.69	0.83	0.36	0.64	0.57
5	0.33	0.17	0.00	0.03	0.00	0.00	0.10	0.10	0.00	0.05	0.00	0.03	0.11	0.00	0.06
6	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.10	0.04	0.00	0.00	0.00	0.00	0.00	0.01
Glu1-1	0.17	0.03	0.00	0.00	0.50	0.00	0.00	0.34	0.12	0.14	0.28	0.06	0.00	0.03	0.12
2	0.00	0.00	0.08	0.00	0.00	0.00	0.34	0.13	0.09	0.11	0.03	0.11	0.08	0.06	0.07
3	0.00	0.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.03	0.03	0.00	0.00	0.03
6	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.03	0.00	0.00	0.03	0.00	0.00	0.00	0.02
7	0.83	0.67	0.75	0.39	0.22	0.83	0.50	0.50	0.66	0.50	0.22	0.08	0.59	0.58	0.52
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
N	0.00	0.11	0.17	0.61	0.28	0.17	0.00	0.00	0.13	0.11	0.38	0.72	0.33	0.33	0.24
Got1-4	1.00	1.00	1.00	1.00	0.94	1.00	0.80	0.87	0.97	1.00	0.94	0.94	0.75	1.00	0.94
6	0.00	0.00	0.00	0.00	0.06	0.00	0.20	0.13	0.03	0.00	0.06	0.06	0.25	0.00	0.06
Got2-2	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.17	0.00	0.03	0.09	0.11	0.00	0.06	0.04
4	1.00	1.00	0.94	1.00	1.00	1.00	1.00	0.83	1.00	0.97	0.91	0.89	1.00	0.94	0.96
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
6	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Idh2-4	0.56	0.00	0.53	0.64	0.75	0.78	0.59	0.41	0.34	0.50	0.69	0.47	0.58	0.47	0.52
6	0.44	1.00	0.47	0.36	0.25	0.22	0.41	0.59	0.66	0.50	0.31	0.53	0.42	0.53	0.48

Table 20. continued

Locus	Number of populations														Average
Allele	222	232	245	252	262	266	914	1480	1488	1492	1509	1516	1565	1588	
Mdh1-1	0.28	0.00	0.36	0.00	0.03	0.08	0.37	0.41	0.00	0.03	0.15	0.11	0.33	0.17	0.17
6	0.72	1.00	0.64	1.00	0.97	0.92	0.63	0.59	1.00	0.92	0.85	0.89	0.67	0.83	0.83
10.5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
Mdh2-3	0.03	0.28	0.42	0.00	0.00	0.61	0.28	0.59	0.13	0.28	0.21	0.14	0.11	0.14	0.23
3.5	0.03	0.00	0.00	0.00	0.00	0.14	0.06	0.00	0.00	0.00	0.03	0.19	0.08	0.31	0.06
6	0.94	0.72	0.58	1.00	1.00	0.25	0.66	0.41	0.87	0.72	0.76	0.67	0.81	0.55	0.71
Mdh3-16	0.50	1.00	1.00	1.00	1.00	0.58	1.00	1.00	1.00	0.97	1.00	0.86	1.00	0.75	0.90
18	0.50	0.00	0.00	0.00	0.00	0.42	0.00	0.00	0.00	0.03	0.00	0.14	0.00	0.25	0.10
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97	0.97	0.92	1.00	0.99
15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.08	0.00	0.01
Pgm1-9	1.00	0.94	1.00	1.00	1.00	0.89	0.87	0.97	1.00	1.00	0.87	0.94	0.86	1.00	0.95
16	0.00	0.06	0.00	0.00	0.00	0.11	0.13	0.03	0.00	0.00	0.13	0.06	0.14	0.00	0.05
Pgm2-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.06	0.01
3	0.00	0.14	0.39	0.11	0.00	0.06	0.00	0.31	0.22	0.03	0.00	0.25	0.39	0.00	0.14
4	1.00	0.86	0.61	0.89	1.00	0.94	1.00	0.69	0.78	0.92	1.00	0.75	0.61	0.86	0.85
Pgd1-2	0.39	0.00	0.53	0.00	0.25	0.17	0.50	0.25	0.09	0.08	0.71	0.19	0.08	0.31	0.25
3.8	0.61	1.00	0.47	1.00	0.75	0.83	0.50	0.75	0.91	0.92	0.29	0.81	0.92	0.69	0.75
Pgd2-2.8	0.00	0.06	0.00	0.00	0.00	0.08	0.00	0.13	0.00	0.06	0.00	0.00	0.00	0.00	0.03
5	1.00	0.94	1.00	1.00	1.00	0.92	0.87	0.87	1.00	0.94	1.00	0.92	1,00	1.00	0.96
10	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Phi1-4	1.00	0.83	1.00	1.00	0.67	0.83	0.78	0.81	0.84	0.89	1.00	0.75	0.72	0.92	0.86
5	0.00	0.17	0.00	0.00	0.33	0.17	0.22	0.19	0.16	0.11	0.00	0.25	0.28	0.08	0.14

Table 21. Frequencies of detected alleles in populations of Serbian dents (group 16)

Locus	Number of populations														Average
Allele	210	228	280	317	327	611	672	680	683	721	827	828	864	865	
Acp1-1	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.96	0.23	0.33	0.67	0.79	0.48	0.00	1.00	0.23	0.88	0.10	0.44	1.00	0.92	0.57
4	0.04	0.77	0.67	0.00	0.21	0.52	0.33	0.00	0.77	0.12	0.90	0.56	0.00	0.08	0.36
6	0.00	0.00	0.00	0.29	0.00	0.00	0.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07
Adh1-4	0.46	0.23	0.42	1.00	0.79	0.98	0.69	1.00	1.00	0.71	0.96	0.61	0.83	1.00	0.76
6	0.54	0.73	0.58	0.00	0.21	0.02	0.31	0.00	0.00	0.29	0.04	0.39	0.17	0.00	0.24
Cat3-7	0.00	0.04	0.00	0.00	0.00	0.00	0.02	0.10	0.14	0.00	0.04	0.06	0.12	0.00	0.04
9	1.00	0.96	1.00	1.00	1.00	1.00	0.25	0.77	0.44	1.00	0.50	0.46	0.71	0.15	0.73
12	0.00	0.00	0.00	0.00	0.00	0.00	0.73	0.00	0.42	0.00	0.46	0.44	0.00	0.85	0.21
N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.04	0.17	0.00	0.02
Enp1-6	0.98	1.00	1.00	0.90	0.71	1.00	1.00	1.00	0.50	1.00	1.00	0.77	0.79	1.00	0.90
7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.21	0.00	0.05
8	0.02	0.00	0.00	0.10	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.05
Est8-4	0.50	0.50	0.50	0.50	0.50	0.46	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50
4.5	0.50	0.50	0.50	0.50	0.50	0.54	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50
Glu1-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.01
2	0.00	0.00	0.00	0.69	0.29	0.15	0.33	0.27	0.08	0.21	0.15	0.19	0.00	0.38	0.20
3	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.31	0.00	0.00	0.00	0.00	0.00	0.03
6	0.00	0.04	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.08	0.04
7	0.50	0.83	0.79	0.31	0.33	0.48	0.21	0.35	0.27	0.75	0.52	0.19	0.75	0.50	0.48
N	0.50	0.13	0.21	0.00	0.38	0.17	0.46	0.38	0.17	0.04	0.33	0.62	0.00	0.04	0.24
Got1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00	1.00
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
Got2-2	0.00	0.06	0.00	0.00	0.00	0.33	0.00	0.10	0.06	0.00	0.10	0.15	0.00	0.00	0.06
4	1.00	0.94	1.00	1.00	1.00	0.67	1.00	0.90	0.94	1.00	0.90	0.85	1.00	1.00	0.94
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	1.00	0.27	0.44	0.72	0.60	0.50	0.12	0.83	0.50	0.31	0.63	0.19	0.12	0.63	0.49
6	0.00	0.73	0.56	0.28	0.40	0.50	0.88	0.17	0.50	0.69	0.37	0.81	0.88	0.37	0.51

Table 21. continued

Locus	Number of populations														Average
Allele	210	228	280	317	327	611	672	680	683	721	827	828	864	865	
Mdh1-1	0.31	0.00	0.00	0.19	0.00	0.10	0.48	0.00	0.38	0.00	0.48	0.10	0.15	0.46	0.19
6	0.69	1.00	1.00	0.75	1.00	0.90	0.52	1.00	0.62	1.00	0.52	0.90	0.85	0.54	0.81
10.5	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mdh2-3	0.44	0.00	0.00	0.54	0.00	0.19	0.73	0.00	1.00	0.46	0.40	0.29	0.13	0.50	0.33
3.5	0.50	0.00	0.35	0.21	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.09
6	0.06	1.00	0.65	0.21	1.00	0.81	0.27	0.83	0.00	0.54	0.56	0.71	0.87	0.50	0.57
N	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.01
Mdh3-16	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00	0.60	0.54	1.00	0.93
18	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.40	0.46	0.00	0.07
Mdh4-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	0.77	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98
15	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Pgm1-9	1.00	0.81	1.00	1.00	1.00	0.77	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97
16	0.00	0.19	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
Pgm2-3	0.17	0.00	0.00	0.09	0.00	0.00	0.00	0.17	0.17	0.04	0.00	0.17	0.12	0.02	0.07
4	0.83	1.00	1.00	0.91	1.00	1.00	1.00	0.83	0.83	0.96	1.00	0.83	0.88	0.98	0.93
Pgd1-2	0.00	0.00	0.02	0.11	0.21	0.50	0.04	0.02	0.21	0.54	0.04	0.19	0.19	1.00	0.22
3.8	1.00	1.00	0.98	0.89	0.79	0.50	0.96	0.98	0.79	0.46	0.96	0.81	0.81	0.00	0.78
Pgd2-2.8	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
5	1.00	1.00	1.00	1.00	1.00	1.00	0.75	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98
Phi1-4	0.63	1.00	1.00	1.00	0.90	0.96	1.00	0.63	0.56	1.00	0.77	0.71	1.00	1.00	0.87
5	0.37	0.00	0.00	0.00	0.10	0.04	0.00	0.37	0.44	0.00	0.23	0.29	0.00	0.00	0.13

Table 22. Frequencies of detected alleles in populations of hard dents (group 17)

Locus	Number of populations																			Average
Allele	22	31	55	60	76	110	133	214	244	282	369	380	382	432	433	569	616	632	659	829	
Acp 2	0.68	0.38	0.48	0.48	0.58	0.90	0.16	0.20	0.86	0.02	0.92	0.63	0.86	0.13	0.34	0.62	0.26	0.86	0.04	0.00	0.47
4	0.32	0.62	0.52	0.52	0.42	0.10	0.84	0.80	0.14	0.98	0.08	0.37	0.14	0.87	0.66	0.38	0.74	0.14	0.96	0.80	0.52
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.01
Adh1-4	0.92	0.84	0.98	0.89	0.11	1.00	1.00	0.48	0.82	0.90	0.83	0.52	1.00	0.80	0.80	0.88	0.37	0.94	0.92	0.62	0.77
6	0.00	0.08	0.02	0.11	0.89	0.00	0.00	0.52	0.18	0.10	0.17	0.48	0.00	0.20	0.08	0.12	0.63	0.06	0.08	0.38	0.21
N	0.08	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.02
Cat3-7	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.27	0.00	0.00	0.00	0.32	0.00	0.00	0.00	0.10	0.00	0.00	0.04
9	0.86	0.82	0.56	0.66	0.73	1.00	1.00	1.00	0.73	0.58	0.36	0.98	0.30	0.62	1.00	1.00	0.32	0.86	0.36	0.20	0.70
12	0.14	0.12	0.44	0.34	0.23	0.00	0.00	0.00	0.23	0.15	0.64	0.02	0.70	0.06	0.00	0.00	0.68	0.00	0.64	0.80	0.26
N	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
Enp1-6	1.00	0.20	1.00	0.84	1.00	0.94	1.00	0.90	1.00	1.00	1.00	0.81	1.00	1.00	1.00	1.00	0.66	1.00	0.52	1.00	0.89
7	0.00	0.08	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
8	0.00	0.72	0.00	0.06	0.00	0.06	0.00	0.10	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.00	0.34	0.00	0.48	0.00	0.10
Est 4	0.50	0.60	0.46	0.50	0.50	0.50	0.50	0.50	0.50	0.42	0.50	0.50	0.24	0.50	0.50	0.50	0.50	0.50	0.34	0.80	0.51
5	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4.5	0.50	0.32	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.58	0.50	0.50	0.76	0.50	0.50	0.50	0.50	0.50	0.66	0.12	0.49
Glut-1	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
2	0.52	0.04	0.56	0.00	0.14	0.00	0.44	0.20	0.00	0.50	0.30	0.19	0.00	0.52	0.50	0.00	0.06	0.18	0.02	0.00	0.22
3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.02
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	0.28	0.76	0.28	1.00	0.70	0.58	0.36	0.64	0.32	0.38	0.38	0.69	0.80	0.35	0.14	0.00	0.58	0.28	0.78	1.00	0.51
N	0.20	0.20	0.16	0.00	0.16	0.21	0.20	0.08	0.52	0.12	0.16	0.12	0.20	0.13	0.36	1.00	0.36	0.32	0.20	0.00	0.24
Got1-4	0.80	1.00	0.98	0.82	0.78	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96
6	0.20	0.00	0.02	0.18	0.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.04
Got2-2	0.00	0.06	0.66	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.35	0.00	0.00	0.00	0.00	0.00	0.06
4	1.00	0.94	0.34	1.00	1.00	1.00	1.00	1.00	0.86	1.00	1.00	1.00	1.00	1.00	0.65	1.00	1.00	1.00	1.00	1.00	0.94
Got3-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh2-4	0.27	0.92	0.96	1.00	0.42	0.21	0.72	0.62	0.84	0.80	0.26	0.44	0.18	0.87	0.52	0.46	0.06	0.46	0.14	0.96	0.56
6	0.73	0.08	0.04	0.00	0.58	0.79	0.28	0.38	0.16	0.20	0.74	0.56	0.82	0.13	0.48	0.54	0.94	0.54	0.86	0.04	0.44

Table 22. continued

Locus	Number of population																			Average
Allele	22	31	55	60	76	110	133	214	244	282	369	380	382	432	433	569	616	632	659	829	
Mdh1-1	0.38	0.38	0.18	0.18	0.86	0.02	0.00	0.26	0.06	0.32	0.17	0.31	0.26	0.00	0.00	0.16	0.13	0.22	0.23	0.00	0.21
6	0.62	0.62	0.82	0.82	0.00	0.38	1.00	0.72	0.86	0.68	0.83	0.69	0.74	1.00	1.00	0.84	0.87	0.78	0.77	1.00	0.74
10.5	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
N	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
Mdh2-3	0.46	0.10	0.12	0.82	0.50	0.88	0.00	0.10	0.58	0.08	0.19	0.33	0.16	0.26	0.54	0.68	0.06	0.34	0.27	0.72	0.35
3.5	0.00	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.14	0.20	0.34	0.00	0.00	0.04	0.02	0.00	0.23	0.12	0.23	0.00	0.06
6	0.54	0.90	0.76	0.18	0.28	0.12	1.00	0.90	0.28	0.72	0.77	0.67	0.84	0.70	0.44	0.32	0.71	0.54	0.50	0.28	0.58
N	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mdh3-16	0.52	0.86	0.90	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96
18	0.48	0.14	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
Mdh4-8	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	1.00	1.00	1.00	0.96	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.85	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Pgm1-9	1.00	0.88	0.66	0.79	1.00	1.00	1.00	1.00	0.70	1.00	0.70	1.00	1.00	1.00	1.00	0.84	1.00	0.98	1.00	1.00	0.93
16	0.00	0.08	0.34	0.21	0.00	0.00	0.00	0.00	0.30	0.00	0.26	0.00	0.00	0.00	0.00	0.16	0.00	0.02	0.00	0.00	0.07
N	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Pgm2-2	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	0.00	0.28	0.46	0.37	0.20	0.00	0.00	0.00	0.28	0.00	0.28	0.04	0.44	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.11
4	1.00	0.72	0.54	0.57	0.80	1.00	1.00	1.00	0.92	1.00	0.54	0.96	0.56	1.00	1.00	1.00	0.88	1.00	1.00	1.00	0.88
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Pgd1-2	0.92	0.58	0.18	0.09	0.40	0.00	0.42	0.46	0.28	0.96	0.00	0.04	0.50	0.73	0.40	0.00	0.16	0.14	0.48	0.34	0.36
3.8	0.06	0.42	0.82	0.91	0.60	1.00	0.58	0.54	0.72	0.04	1.00	0.96	0.50	0.27	0.60	1.00	0.84	0.86	0.52	0.66	0.64
Pgd2-2.8	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.34	0.00	0.26	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
5	1.00	1.00	1.00	0.87	1.00	1.00	1.00	1.00	0.66	1.00	1.00	0.90	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97
Phi1-3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	0.82	1.00	0.64	0.88	1.00	1.00	0.96	1.00	1.00	0.50	0.96	1.00	0.08	1.00	0.92	1.00	0.80	1.00	0.98	1.00	0.88
5	0.18	0.00	0.36	0.12	0.00	0.00	0.04	0.00	0.02	0.50	0.04	0.00	0.92	0.00	0.08	0.00	0.20	0.00	0.02	0.00	0.12

Table 23. Frequencies of detected alleles in populations of soft flints (group 18)

Locus		Number of populations																			Average
	Allele	74	114	124	127	139	211	235	326	330	356	360	387	393	398	454	533	575	612	620	647	
Acp	2	0.20	0.00	0.00	0.40	0.12	0.84	0.92	0.00	0.00	0.21	0.79	0.60	0.34	0.90	0.92	0.50	0.16	0.85	0.62	0.50	0.45
	3	0.12	0.00	0.00	0.00	0.12	0.00	0.00	0.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	4	0.68	1.00	0.24	0.60	0.76	0.16	0.08	0.62	1.00	0.79	0.21	0.40	0.66	0.10	0.08	0.50	0.84	0.15	0.38	0.42	0.48
	6	0.00	0.00	0.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
Adh1-4		0.50	1.00	1.00	1.00	0.89	1.00	0.26	0.52	0.79	0.12	1.00	1.00	0.46	1.00	1.00	0.73	0.90	0.46	1.00	0.63	0.77
	6	0.50	0.00	0.00	0.00	0.11	0.00	0.74	0.48	0.21	0.88	0.00	0.00	0.54	0.00	0.00	0.27	0.10	0.54	0.00	0.37	0.23
Cat3-7		0.00	0.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.26	0.00	0.00	0.06	0.00	0.36	0.12	0.02	0.06
	9	0.90	0.48	1.00	0.00	0.94	1.00	0.64	0.84	0.50	0.82	0.96	0.96	0.38	0.72	0.80	0.60	0.70	0.52	0.54	0.80	0.72
	12	0.10	0.20	0.00	1.00	0.02	0.00	0.36	0.12	0.24	0.18	0.00	0.00	0.36	0.24	0.12	0.26	0.30	0.12	0.30	0.06	0.18
	N	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.04	0.26	0.00	0.04	0.00	0.00	0.04	0.08	0.08	0.00	0.00	0.04	0.12	0.04
Enp1-6		1.00	0.96	0.82	0.92	0.96	1.00	1.00	1.00	0.16	1.00	0.46	0.44	1.00	0.58	0.32	1.00	0.68	0.90	1.00	0.90	0.81
	8	0.00	0.04	0.18	0.08	0.04	0.00	0.00	0.00	0.84	0.00	0.54	0.56	0.00	0.42	0.68	0.00	0.32	0.10	0.00	0.10	0.19
Est	4	0.50	0.50	0.50	0.50	0.50	0.50	0.24	0.40	0.50	0.52	0.50	0.50	0.48	0.50	0.50	0.50	0.50	0.24	0.46	0.50	0.47
	5	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.12	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.18	0.16	0.00	0.03
	4.5	0.50	0.50	0.50	0.50	0.50	0.50	0.56	0.48	0.50	0.48	0.50	0.50	0.48	0.50	0.50	0.50	0.50	0.54	0.38	0.50	0.50
	N	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
Glu1-1		0.18	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.02	0.58	0.00	0.02	0.00	0.00	0.04	0.05
	2	0.26	0.00	0.74	0.00	0.10	0.16	0.42	0.08	0.24	0.04	0.12	0.00	0.42	0.05	0.22	0.00	0.28	0.37	0.28	0.12	0.20
	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.40	0.02	0.03
	6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.15	0.02	0.06	0.01
	7	0.44	0.44	0.14	1.00	0.86	0.26	0.06	0.64	0.26	0.96	0.18	0.00	0.30	0.11	0.18	0.76	0.70	0.27	0.22	0.68	0.46
	N	0.12	0.56	0.12	0.00	0.04	0.56	0.52	0.28	0.44	0.00	0.64	0.20	0.28	0.73	0.00	0.24	0.00	0.21	0.00	0.06	0.25
Got1-4		1.00	1.00	1.00	1.00	1.00	1.00	0.52	1.00	1.00	0.56	1.00	1.00	1.00	1.00	1.00	0.80	1.00	1.00	1.00	1.00	0.94
	6	0.00	0.00	0.00	0.00	0.00	0.00	0.48	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.06
Got2-2		0.00	0.00	0.00	0.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.09
	4	1.00	1.00	1.00	0.08	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.24	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.88	0.91
	6	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Got3-4		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Idh1-4		0.40	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97
	6	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
	N	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Idh2-4		0.68	0.00	0.00	0.22	0.38	0.56	0.20	0.46	0.34	0.32	0.55	0.85	0.58	1.00	0.59	0.40	0.48	0.26	0.22	0.64	0.44
	6	0.32	1.00	1.00	0.78	0.62	0.44	0.80	0.54	0.66	0.68	0.45	0.15	0.42	0.00	0.41	0.60	0.52	0.74	0.78	0.36	0.56

Table 23. continued

Locus	Number of populations																				Average
Alleles	74	114	124	127	139	211	235	326	330	356	360	387	393	398	454	553	575	612	620	647	
Mdh1-1	0.16	0.00	0.48	0.02	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.27	0.00	0.00	0.30	0.00	0.00	0.00	0.42	0.09
6	0.82	1.00	0.52	1.00	0.96	1.00	1.00	1.00	0.94	1.00	1.00	1.00	0.73	1.00	1.00	0.70	0.92	0.98	1.00	0.58	0.91
10.5	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
Mdh2-3	0.54	0.00	0.00	0.92	0.25	0.68	0.44	0.17	0.00	0.08	0.76	0.44	0.11	0.34	0.12	0.42	0.36	0.67	0.00	0.14	0.32
3.5	0.00	0.00	0.00	0.00	0.00	0.16	0.34	0.12	0.00	0.33	0.03	0.42	0.31	0.64	0.16	0.02	0.00	0.00	0.00	0.00	0.13
6	0.46	1.00	1.00	0.08	0.75	0.16	0.22	0.71	1.00	0.59	0.21	0.14	0.58	0.02	0.72	0.56	0.64	0.33	1.00	0.86	0.55
Mdh3-16	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh4-8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Mdh5-12	1.00	1.00	0.76	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00	1.00	1.00	1.00	0.82	0.98
15	0.00	0.00	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.18	0.02
Pgm1-9	1.00	1.00	1.00	0.98	1.00	0.96	1.00	1.00	1.00	1.00	0.73	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.76	1.00	0.97
16	0.00	0.00	0.00	0.02	0.00	0.04	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.00	0.03
Pgm2-2	0.00	0.00	0.30	0.00	0.00	0.00	0.30	0.10	0.00	0.00	0.07	0.00	0.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
3	0.04	0.00	0.00	0.36	0.00	0.00	0.16	0.00	0.00	0.00	0.20	0.00	0.04	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.05
4	0.96	1.00	1.00	0.64	1.00	1.00	0.54	0.90	1.00	1.00	0.73	1.00	0.56	1.00	0.90	1.00	1.00	1.00	1.00	1.00	0.91
Pgd1-2	0.16	0.00	0.74	0.00	0.00	0.50	0.22	0.42	0.06	0.22	0.16	0.76	0.36	0.98	0.13	0.26	0.30	0.25	0.44	0.46	0.32
3.8	0.84	1.00	0.26	1.00	1.00	0.50	0.78	0.58	0.94	0.78	0.84	0.24	0.62	0.02	0.87	0.74	0.70	0.75	0.56	0.54	0.68
Pgd2-2.8	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.01
5	0.96	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.83	1.00	1.00	0.99
Phi1-4	1.00	1.00	1.00	0.76	1.00	0.64	1.00	0.66	1.00	1.00	1.00	1.00	1.00	1.00	0.86	0.80	1.00	0.33	1.00	0.68	0.90
5	0.00	0.00	0.00	0.22	0.00	0.36	0.00	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.20	0.00	0.67	0.00	0.12	0.10

Table 24. Average frequencies for some alleles

Group	Locus Acp1		Locus Adh1		Locus Glu1		Locus Got1		Locus Idh2		Locus Mdh2		Locus Pgm1		Locus Pgd1	
	Acp1-2	Acp1-4	Adh1-4	Adh1-6	Glu1-2	Glu1-N	Got1-4	Got1-6	Idh2-4	Idh2-6	Mdh2-3	Mdh2-3.5	Pgm1-9	Pgm1-16	Pgd1-2	Pgd1-3.8
1	0.33	0.46	0.86	0.14	0.40	0.07	0.99	0.01	0.87	0.13	0.26	0.01	1.00	0.00	0.70	0.30
2	0.46	0.49	0.59	0.41	0.16	0.22	0.97	0.02	0.52	0.48	0.26	0.05	0.98	0.02	0.33	0.67
3	0.30	0.61	0.63	0.37	0.34	0.23	0.99	0.01	0.47	0.53	0.29	0.04	0.97	0.03	0.22	0.78
4	0.27	0.70	0.65	0.33	0.36	0.13	0.96	0.04	0.74	0.26	0.19	0.01	0.98	0.02	0.49	0.51
5	0.37	0.52	0.68	0.32	0.19	0.12	0.90	0.10	0.31	0.69	0.18	0.11	0.98	0.02	0.30	0.70
6	0.56	0.35	0.70	0.30	0.23	0.10	0.98	0.02	0.47	0.53	0.16	0.08	0.99	0.01	0.21	0.79
7	0.46	0.49	0.73	0.27	0.30	0.12	0.98	0.01	0.61	0.39	0.14	0.02	1.00	0.00	0.47	0.53
8	0.63	0.29	0.79	0.21	0.24	0.11	0.97	0.03	0.41	0.59	0.10	0.04	0.95	0.05	0.52	0.48
9	0.27	0.40	0.78	0.22	0.15	0.09	0.98	0.02	0.54	0.46	0.27	0.04	0.97	0.03	0.32	0.68
10	0.16	0.69	0.65	0.35	0.06	0.14	0.94	0.06	0.45	0.55	0.20	0.08	0.97	0.03	0.21	0.79
11	0.31	0.50	0.58	0.42	0.12	0.09	0.99	0.01	0.28	0.72	0.15	0.09	0.89	0.11	0.22	0.78
12	0.36	0.61	0.79	0.21	0.18	0.21	0.98	0.02	0.43	0.57	0.26	0.00	0.93	0.07	0.27	0.73
13	0.39	0.47	0.76	0.24	0.20	0.20	0.99	0.01	0.48	0.52	0.29	0.10	0.95	0.05	0.32	0.68
14	0.48	0.43	0.68	0.32	0.09	0.10	0.99	0.00	0.34	0.66	0.24	0.17	0.98	0.02	0.23	0.74
15	0.26	0.54	0.74	0.26	0.07	0.24	0.94	0.06	0.52	0.48	0.23	0.06	0.95	0.05	0.25	0.74
16	0.57	0.36	0.76	0.24	0.20	0.24	1.00	0.00	0.49	0.51	0.33	0.09	0.97	0.03	0.22	0.78
17	0.47	0.52	0.77	0.21	0.22	0.24	0.96	0.04	0.56	0.44	0.35	0.06	0.93	0.07	0.36	0.64
18	0.45	0.48	0.77	0.23	0.20	0.25	0.94	0.06	0.44	0.56	0.32	0.13	0.97	0.03	0.32	0.68

Table 25. Polymorphism of loci and heterozygosity

Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)	Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)
Group 1: MONTENEGRIN FLINTS			Group 2: BOSNIAN EARLY DENTS		
1. C34	29	0.096	1. C162	29	0.125
2.C1184	33	0.108	2. C444	62	0.255
3.C1194	43	0.099	3. C462	67	0.238
4.C1229	43	0.120	4. C480	38	0.157
5.C1239	38	0.121	5. C488	52	0.208
6.C1259	71	0.248	6. C490	24	0.088
7.C1263	52	0.174	7. C771	48	0.208
8.C1265	52	0.192	8. C847	52	0.157
9.C1266	52	0.210	9. C858	57	0.189
10.C1268	52	0.159	10. C877	57	0.252
11.C1286	32	0.148	11.C1365	71	0.239
12.C1287	43	0.134	12.C1373	71	0.258
13.C1291	67	0.195	13.C1375	67	0.180
14.C1302	62	0.215	14.C1377	57	0.203
15.C1304	67	0.229	15.C1380	86	0.259
Group 3: SEMI-FLINTS FROM KOSMET			Group 4: MACEDONIAN FLINTS		
1. C33	62	0.256	1. C103	62	0.250
2. C48	57	0.202	2. C150	52	0.208
3. C389	43	0.178	3. C592	48	0.195
4. C394	52	0.234	4. C593	52	0.188
5. C401	57	0.200	5. C594	38	0.158
6. C419	57	0.212	6. C597	43	0.167
7. C570	48	0.214	7. C600	38	0.153
8. C576	57	0.195	8. C666	62	0.224
9.C1789	62	0.241	9. C892	43	0.132
10.C1791	71	0.230	10. C893	57	0.163
11.C1794	67	0.242	11. C895	52	0.143
12.C1796	76	0.284	12.C1802	52	0.188
13.C1803	62	0.236	13.C1816	76	0.260
14.C1811	71	0.213	14.C1821	76	0.232
15.C1815	81	0.276	15.C1823	67	0.245
Group 5: NORTHEAST US 8-ROW TYPES			Group 6: DERIVED FLINTS		
1. C62	48	0.188	1. C182	57	0.251
2. C64	33	0.075	2. C391	43	0.213
3. C72	57	0.228	3. C492	57	0.241
4. C83	24	0.088	4. C494	43	0.161
5. C118	52	0.247	5. C528	62	0.201
6. C125	43	0.114	6. C532	48	0.186
7. C132	57	0.179	7. C897	52	0.200
8. C170	48	0.180	8. C899	62	0.193
9. C177	38	0.126	9.C1330	67	0.208
10. C184	48	0.177	10.C1471	67	0.240
11. C527	52	0.186	11.C1472	76	0.200
12.C1545	62	0.243	12.C1520	52	0.196
13.C1550	67	0.231	13.C1521	48	0.225
14.C1559	67	0.278	14.C1523	71	0.232
15.C1751	71	0.260			

Table 25. continued

Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)	Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)
Group 7: MEDITERRANEAN FLINTS			Group 8: SMALL-GRAIN FLINTS		
1. C167	14	0.049	1. C159	38	0.119
2. C189	76	0.247	2. C161	43	0.174
3. C191	67	0.194	3. C163	33	0.143
4. C510	52	0.181	4. C166	38	0.148
5. C848	57	0.219	5. C558	57	0.185
6. C851	52	0.202	6. C900	62	0.254
7. C901	48	0.170	7. C935	48	0.203
8. C920	48	0.160	8.C1475	62	0.267
9. C926	52	0.164	9.C1497	57	0.189
10. C934	48	0.123	10.C1822	57	0.244
11.C1218	62	0.217			
12.C1223	52	0.159			
13.C1308	67	0.222			
14.C1309	71	0.253			
15.C1337	62	0.225			
Group 9: 8-ROW SOFT DENTS			Group 10: ROMANIAN FLINTS		
1. C69	52	0.238	1. C676	52	0.150
2. C582	52	0.200	2. C690	62	0.210
3. C602	57	0.179	3. C692	52	0.214
4. C737	33	0.106	4. C700	62	0.208
5. C762	52	0.209	5.C1528	62	0.233
6. C796	43	0.132	6.C1530	71	0.288
7.C1481	52	0.169	7.C1549	76	0.262
8.C1489	52	0.193	8.C1552	81	0.266
9.C1496	62	0.199	9.C1592	67	0.234
10.C1506	67	0.246			
11.C1507	67	0.220			
12.C1524	71	0.184			
13.C1537	86	0.263			
14.C1583	71	0.205			
15.C1804	76	0.253			
Group 11: LARGE EARED FLINTS			Group 12: WHITE SEMI-DENTS "MORAVAC"		
1. C138	52	0.193	1. C58	52	0.192
2. C141	38	0.157	2. C90	48	0.220
3. C715	62	0.217	3. C198	48	0.169
4. C832	38	0.168	4. C385	48	0.203
5. C838	52	0.191	5. C435	52	0.214
6. C918	71	0.255	6. C539	43	0.129
7. C922	71	0.274	7. C654	38	0.149
8. C984	43	0.117	8. C669	62	0.220
9.C1544	62	0.195	9. C724	48	0.174
10.C1577	71	0.257	10. C799	67	0.219
11.C1717	52	0.232	11. C802	57	0.199
12.C1729	76	0.257	12. C804	43	0.156
13.C1744	71	0.258	13. C870	33	0.119
14.C1833	76	0.242	14. C882	52	0.180
			15. C887	48	0.203

Table 25. continued

Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)	Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)
Group 13: US CORN BELT-TYPE DENTS			Group 14: DERIVED DENTS		
1. C196	48	0.136	1. C225	33	0.147
2. C216	52	0.177	2. C231	43	0.175
3. C233	48	0.174	3. C289	43	0.160
4. C236	71	0.247	4. C296	71	0.295
5. C243	57	0.207	5. C309	62	0.194
6. C258	38	0.151	6. C320	48	0.115
7. C273	48	0.169	7. C321	57	0.196
8. C278	48	0.167	8. C325	57	0.194
9. C284	33	0.102	9. C336	62	0.224
10. C384	48	0.133	10. C337	57	0.199
11. C426	67	0.207	11. C343	57	0.177
12. C482	62	0.219	12. C347	62	0.252
13. C559	43	0.133	13. C348	57	0.258
14. C566	67	0.246	14. C359	48	0.176
15. C577	43	0.148	15. C362	48	0.156
16. C638	62	0.204	16. C365	48	0.190
17. C645	57	0.197	17. C717	52	0.178
18. C694	48	0.187			
19. C761	48	0.146			
20.C1444	67	0.241			
21.C1467	62	0.242			
22.C1478	62	0.227			
23.C1505	48	0.209			
24.C1517	81	0.259			
25.C1561	71	0.278			
Group 15: SOUTHERN US TYPE DENTS			Group 16: SERBIAN DENTS		
1. C222	52	0.222	1. C210	43	0.159
2. C232	48	0.189	2. C228	43	0.121
3. C245	48	0.199	3. C280	33	0.131
4. C252	33	0.126	4. C317	43	0.160
5. C262	48	0.163	5. C327	38	0.154
6. C266	67	0.227	6. C611	52	0.195
7. C914	57	0.247	7. C672	52	0.206
8.C1480	71	0.287	8. C680	43	0.146
9.C1488	52	0.181	9. C683	57	0.236
10.C1492	71	0.202	10. C721	38	0.143
11.C1509	62	0.221	11. C827	48	0.190
12.C1516	86	0.261	12. C828	71	0.268
13.C1565	67	0.252	13. C864	52	0.174
14.C1588	67	0.247	14. C865	38	0.143

Table 25. continued

Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)	Number of population	Mean proportion of polymor. locy (in %)	Heterozygos. expected (He)
Group 17: HARD DENTS			Group 18: SOFT FLINTS		
1. C22	57	0.217	1. C74	57	0.219
2. C31	67	0.223	2. C114	19	0.081
3. C55	71	0.252	3. C124	33	0.135
4. C60	67	0.208	4. C127	43	0.131
5. C76	52	0.221	5. C139	43	0.125
6. C110	33	0.112	6. C211	38	0.147
7. C133	28	0.113	7. C235	48	0.216
8. C214	43	0.169	8. C326	48	0.210
9. C244	62	0.229	9. C330	43	0.148
10. C282	48	0.173	10. C356	43	0.154
11. C369	57	0.210	11. C360	48	0.185
12. C380	62	0.202	12. C387	43	0.165
13. C382	48	0.164	13. C393	52	0.256
14. C432	38	0.153	14. C398	33	0.121
15. C433	43	0.190	15. C454	52	0.176
16. C569	33	0.126	16. C533	52	0.216
17. C616	57	0.193	17. C575	48	0.179
18. C632	48	0.168	18. C612	57	0.229
19. C659	52	0.197	19. C620	33	0.171
20. C829	33	0.107	20. C647	62	0.233

Table 26. Gene differentiation among populations within groups

Group	H_T	H_S	D_{ST}	G_{ST}
1.	0.200	0.163	0.037	0.185
2.	0.284	0.201	0.083	0.292
3.	0.268	0.228	0.040	0.149
4.	0.253	0.194	0.059	0.233
5.	0.276	0.187	0.089	0.322
6.	0.258	0.211	0.047	0.182
7.	0.254	0.187	0.067	0.264
8.	0.262	0.193	0.069	0.263
9.	0.268	0.200	0.068	0.254
10.	0.256	0.229	0.027	0.105
11.	0.268	0.215	0.053	0.198
12.	0.287	0.183	0.104	0.362
13.	0.270	0.192	0.078	0.286
14.	0.242	0.193	0.049	0.202
15.	0.258	0.216	0.042	0.163
16.	0.244	0.182	0.062	0.254
17.	0.259	0.182	0.077	0.297
18.	0.255	0.175	0.080	0.314

Table 27. Average alleles per loci detected in different corn germplasm

A. Exotic germplasm		
Races from Bolivia	5.2	(Goodman & Stuber,1983)
US southwestern populations	4.3	(Doebley et al.,1983)
US northern flints	4.0	(Doebley et al.,1986)
US southern dents	4.0	(Doebley et al.,1986)
B. Open-pollinated populations		
US corn belt dents	2.7	(Smith, 1986)
YU corn collection	4.0	
YU corn belt dents	2.7	
YU southern dents	2.6	
YU northeastern flint	2.6	
YU montenegrin flints	2.5	
C. Inbred lines and hybrids		
US historically important lines	3.5	(Stuber & Goodman,1983)
US widely used lines	2.2	(Stuber & Goodman,1983)
US hybrids	2.3	(Smith, 1984)
YU hybrids	1.8	

Table 28. Average frequencies for some alleles in different corn germplasm

	Designation of germplasm *													
Allele	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Acp1 - 2	0.65	0.22	0.03	0.25	0.37	0.37	0.39	0.26	0.37	0.33	0.32	0.33	0.52	0.55
4	0.23	0.42	0.64	0.43	0.50	0.50	0.47	0.54	0.52	0.46	0.53	0.56	0.43	0.45
Adh1 - 4	0.97	0.97	0.46	0.93	0.82	0.70	0.76	0.74	0.68	0.86	0.86	0.97	0.98	0.95
6	0.02	0.03	0.54	0.07	0.18	0.30	0.24	0.26	0.32	0.14	0.13	0.03	0.02	0.05
Cat3 - 9	0.74	0.74	0.56	0.87	0.88	0.72	0.69	0.83	0.72	0.78	0.88	0.92	1.00	1.00
12	0.01	0.02	0.30	0.12	0.12	0.17	0.24	0.11	0.23	0.12	0.08	0.08	0.00	0.00
Got1 - 4	0.31	0.70	-	-	0.98	0.97	0.99	0.94	0.90	0.99	0.92	0.92	0.95	0.97
6	0.68	0.28	-	-	0.02	0.03	0.01	0.06	0.10	0.01	0.08	0.08	0.05	0.03
Idh2 - 4	0.93	0.44	0.14	0.66	0.51	0.50	0.48	0.52	0.31	0.87	0.48	0.23	0.50	0.70
6	0.07	0.56	0.86	0.34	0.49	0.50	0.52	0.48	0.69	0.13	0.52	0.77	0.50	0.30
Mdh2 - 3	0.60	0.13	0.09	0.42	0.33	0.21	0.29	0.23	0.18	0.26	0.26	0.23	0.00	0.13
3.5	0.01	0.11	0.01	0.14	0.25	0.06	0.10	0.06	0.11	0.01	0.23	0.10	0.37	0.18
Pgd1 - 2	0.43	0.33	0.06	0.35	0.31	0.35	0.32	0.25	0.30	0.70	0.30	0.38	0.28	0.13
3.8	0.54	0.68	0.94	0.63	0.69	0.65	0.68	0.75	0.70	0.30	0.68	0.59	0.72	0.87
Pgm1 - 9	0.98	0.86	0.99	0.85	0.94	0.96	0.95	0.95	0.98	1.00	0.98	1.00	1.00	0.75
16	0.00	0.11	0.01	0.14	0.06	0.04	0.05	0.05	0.02	0.00	0.02	0.00	0.00	0.25

*) 1- Races from Bolivia (Goodman and Stuber, 1983); 2- Southwestern pop. (Doebley et al. 1983); 3- Northern flints (Doebley et al. 1986); 4- Southern dents (Doebley et al. in prep.); 5- US corn belt dents (Smith, 1986); 6- Yu corn collection; 7- Yu corn belt dents; 8- Yu southern dents; 9- Yu northeastern flints; 10- Yu Montenegrin flints ; 11- US Histor. important inbred lines (Stuber and Goodman, 1983); 12- US widely used inbred lines (Stuber and Goodman, 1983); 13- US SC hybrids (Smith, 1984); 14- YU SC hybrids (Gerić et al. unpub.)

FIGURES 1-36

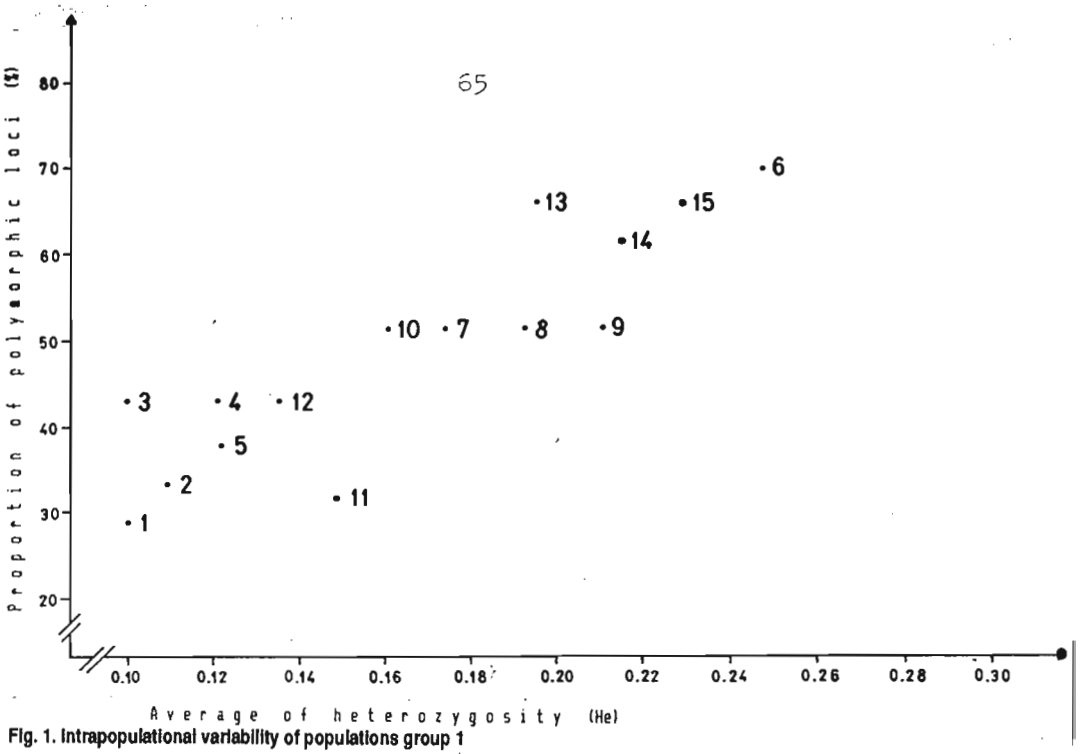

Fig. 1. Intrapopulational variability of populations group 1
1-C34, 2-C1184, 3-C1194, 4-C1229, 5-C1239, 6C1259, 7-C1263, 8-C1265
9-C1266, 10-C1268, 11-C1286, 12-C1287, 13-C1291, 14-C1302, 15-C1304

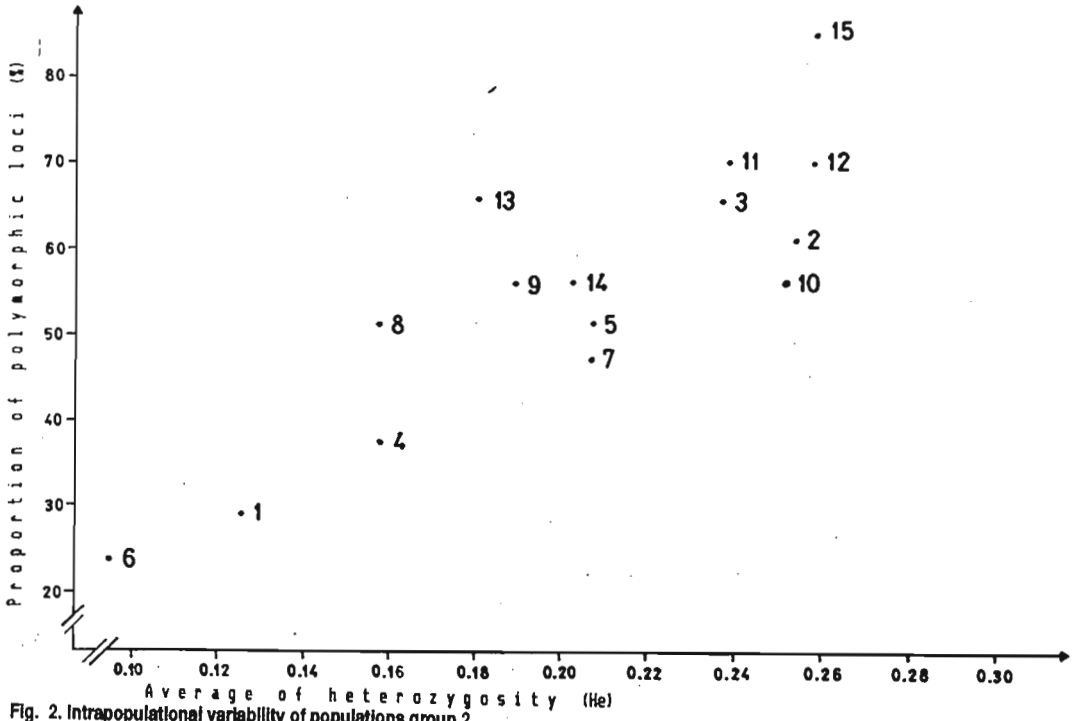

Fig. 2. Intrapopulational variability of populations group 2
1-C162, 2-C444, 3-C462, 4-C488, 5-C488, 6-C498, 7-C771, 8-C847,
9-C858, 10-C877, 11-C1365, 12-C1373, 13-C1375, 14-C1377, 15-C1388

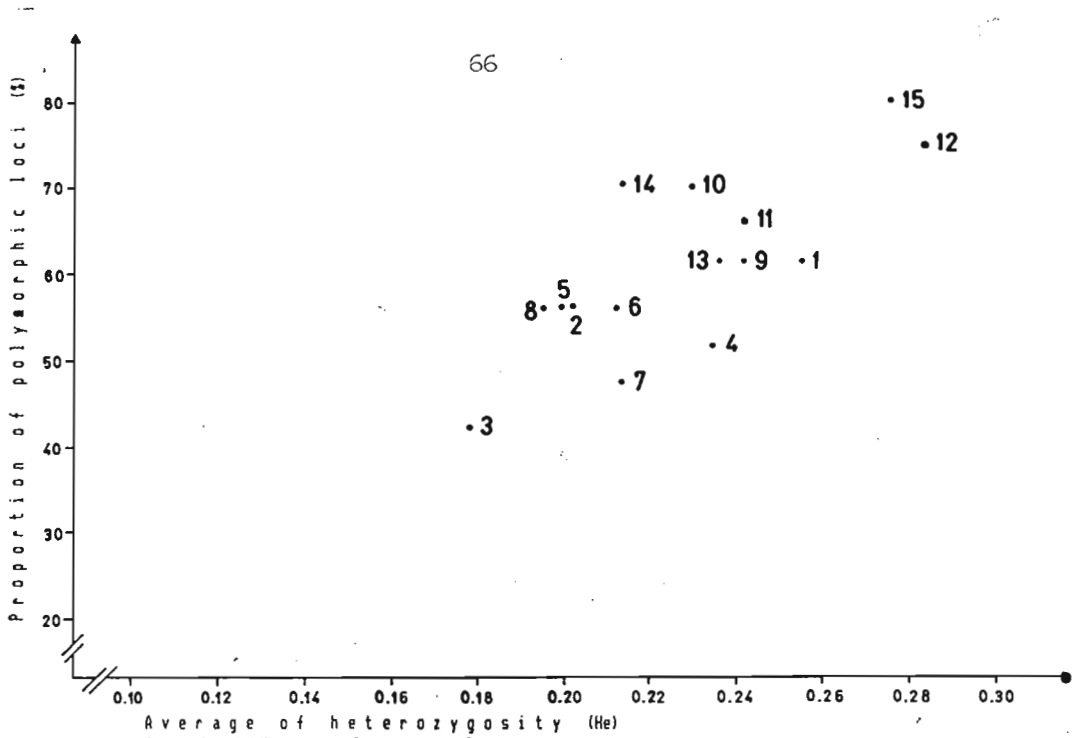

Fig. 3. Intrapopulational variability of populations group 3
1-C33, 2-C48, 3-C389, 4-C394, 5-C401, 6-C419, 7-C570, 8-C576,
9-C1789, 10-C1791, 11-C1794, 12-C1796, 13-C1803, 14-C1811, 15-C1815

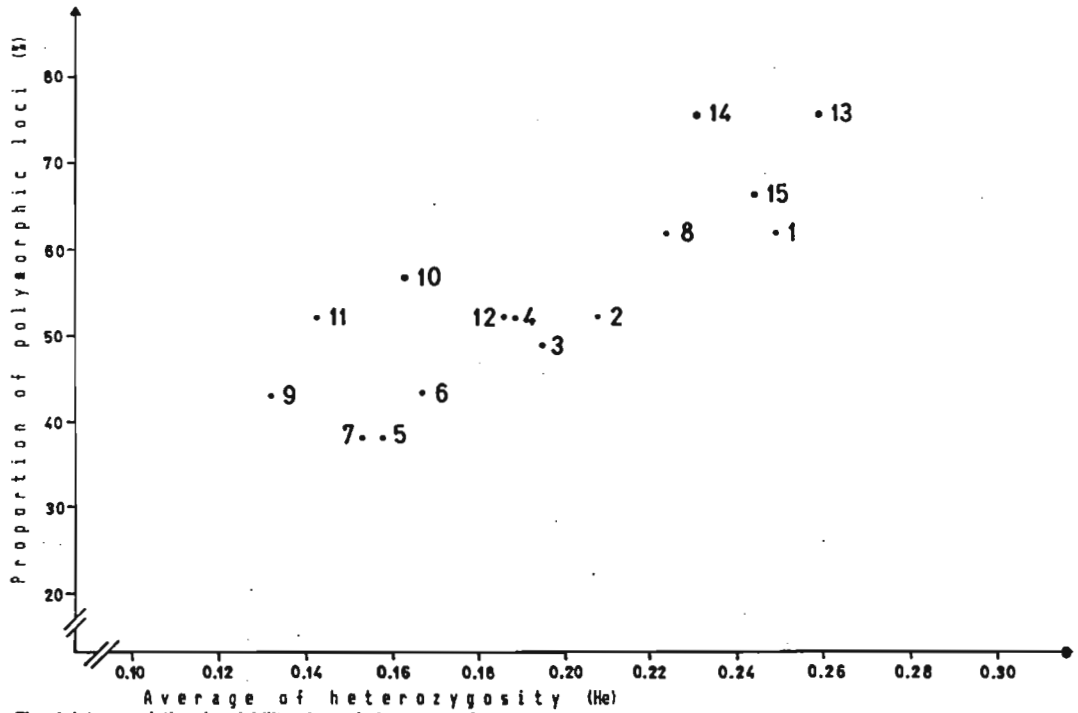

Fig. 4. Intrapopulational variability of populations group 4
1-C103, 2-C150, 3-C592, 4-C593, 5-C594, 6-C597, 7-C666, 8-C666,
9-C892, 10-C893, 11-C895, 12-C1802, 13-C1816, 14-C1821, 15-C1823

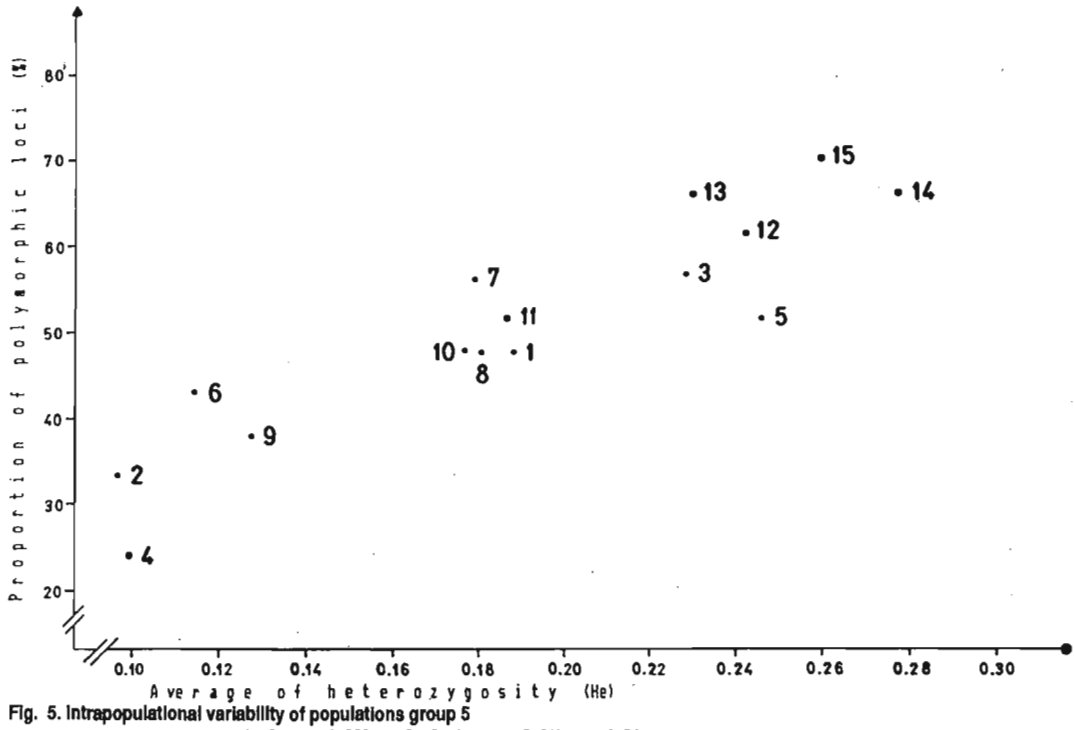

Fig. 5. Intrapopulational variability of populations group 5
1-C62, 2-C64, 3-C72, 4-C83, 5-C118, 6-C125, 7-C132, 8-C170,
9-C177, 10-C184, 11-C527, 12-C1545, 13-C1550, 14-C1559, 15-C1751

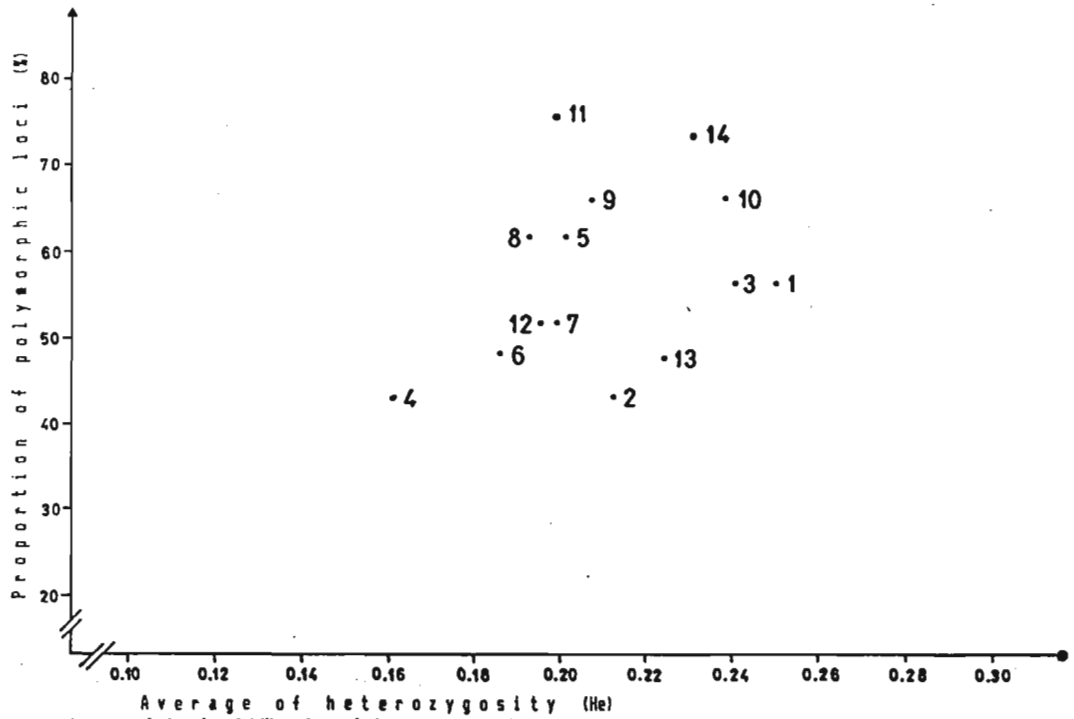

Fig. 6. Intrapopulational variability of populations group 6
1-C182, 2-C391, 3-C492, 4-C494, 5-C528, 6-C532, 7-C897, 8-C899,
9-C1359, 10-C1471, 11-C1472, 12-C1520, 13-C1521, 14-C1523

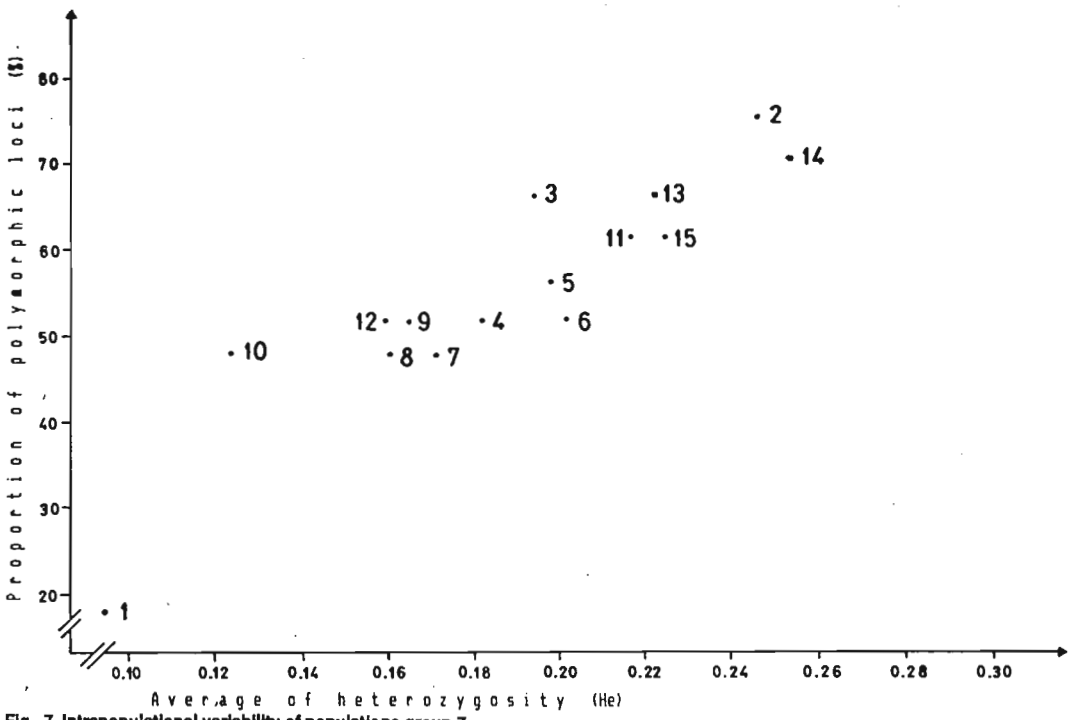

Fig. 7. Intrapopulational variability of populations group 7
1-C167, 2-C189, 3-C191, 4-C510, 5-C848, 6-C851, 7-C901, 8-C920, 9-C926, 10-C934, 11-C1218, 12-C1223, 13-C1308, 14-C1309, 15-C1337

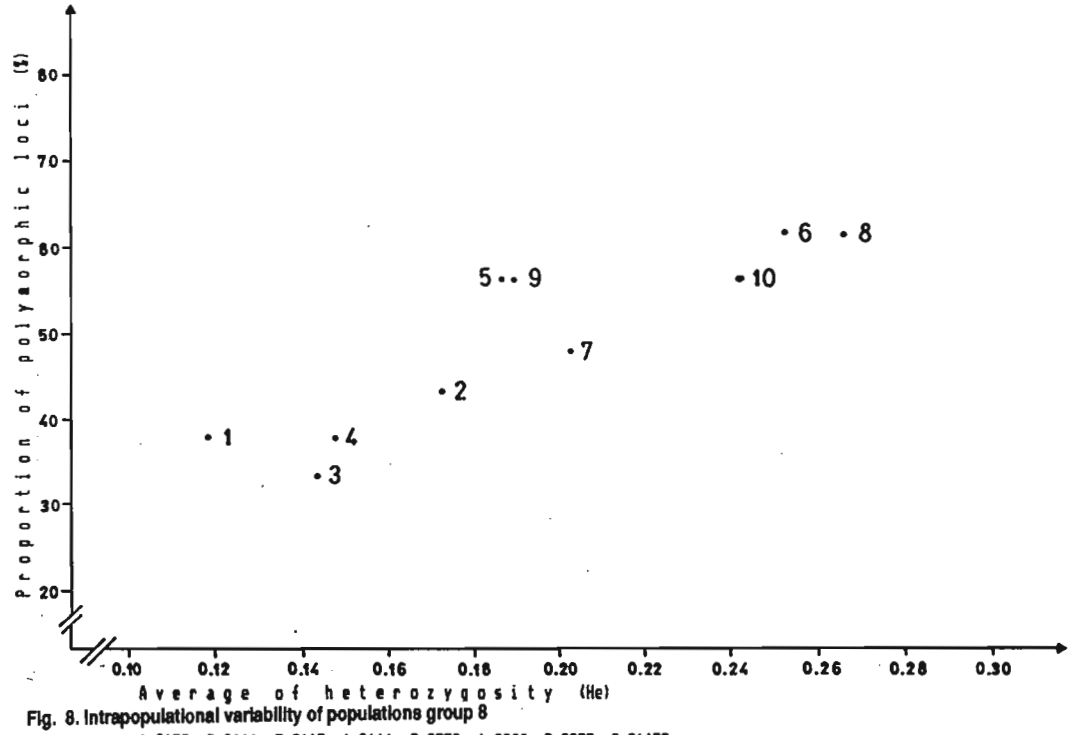

Fig. 8. Intrapopulational variability of populations group 8
1-C159, 2-C161, 3-C163, 4-C166, 5-C558, 6-C900, 7-C935, 8-C1475, 9-C1497, 10-C1822

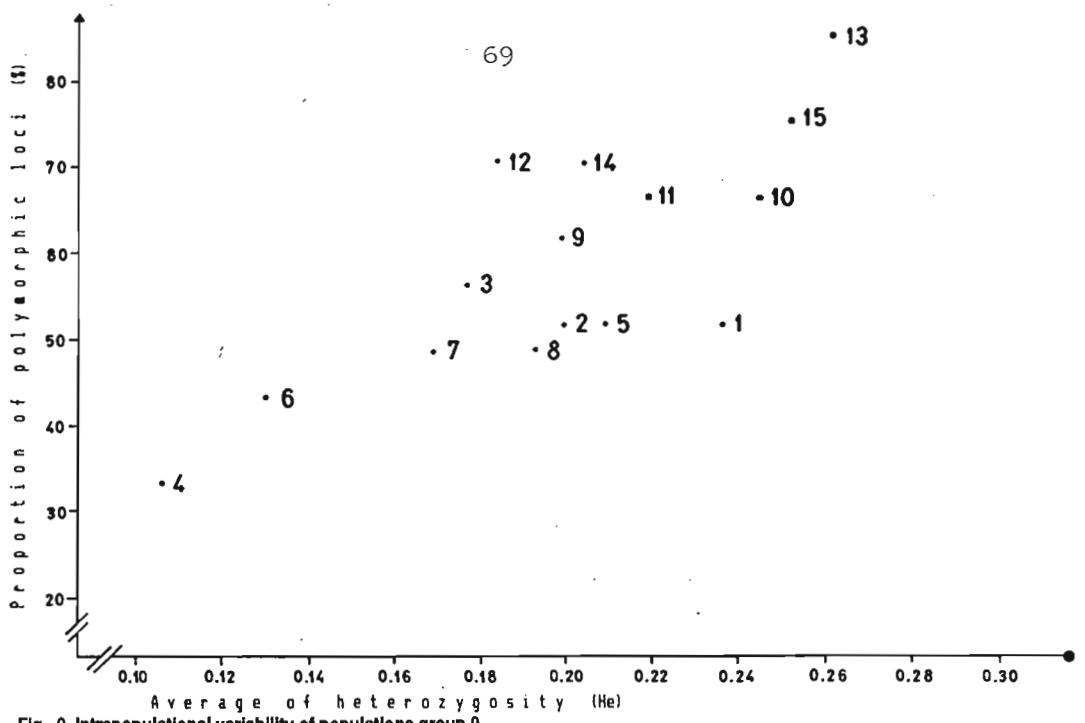

Fig. 9. Intrapopulational variability of populations group 9
1-C69, 2-C582, 3-C602, 4-C737, 5-C762, 6-C796, 7-C1481, 8-C1489, 9-C1496, 10-C1506, 11-C1507, 12-C1524, 13-C1537, 14-C1583, 15-C1804

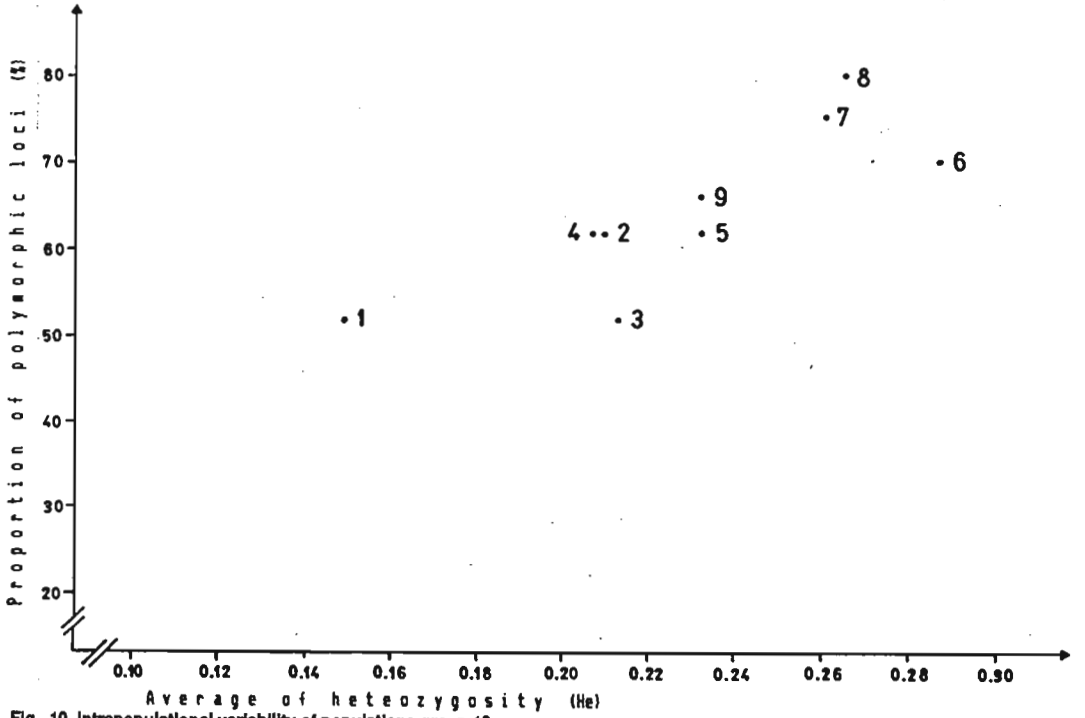

Fig. 10. Intrapopulational variability of populations group 10
1-C676, 2-C698, 3-C692, 4-C706, 5-C1528, 6-C1536, 7-C1549, 8-C1552, 9-C1592

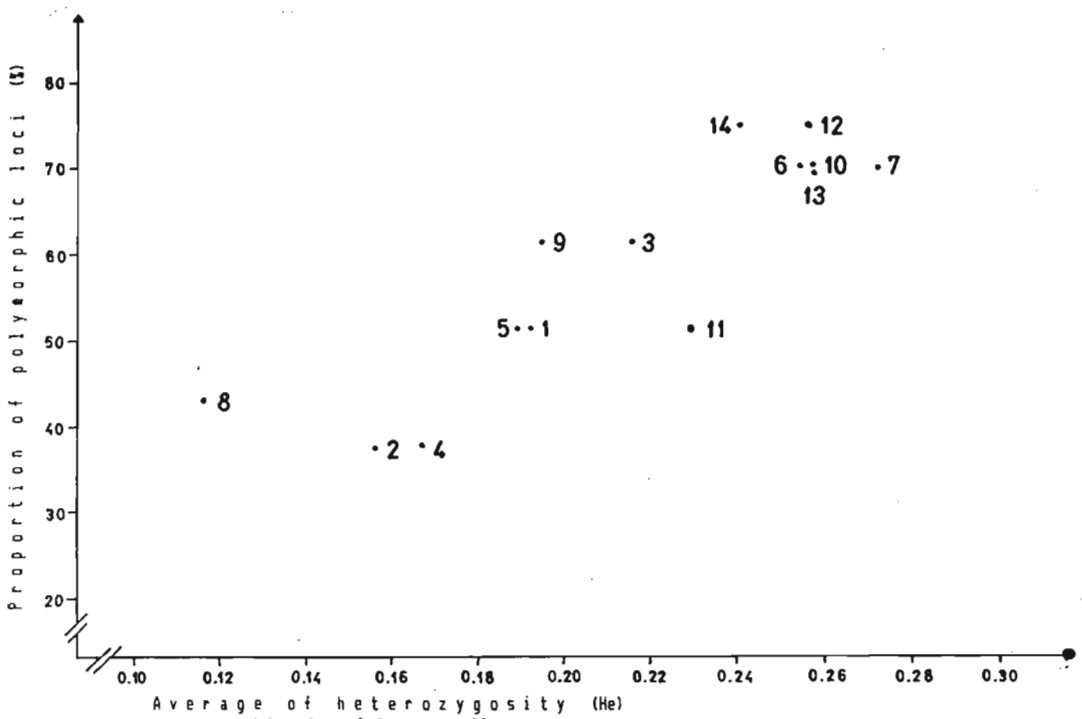

Fig. 11. Intrapopulational variability of populations group 11
1-C138, 2-C141, 3-C715, 4-C832, 5-C838, 6-C918, 7-C922, 8-C984, 9-C1544, 10-C1577, 11-C1717, 12-C1729, 13-C1744, 14-C1833

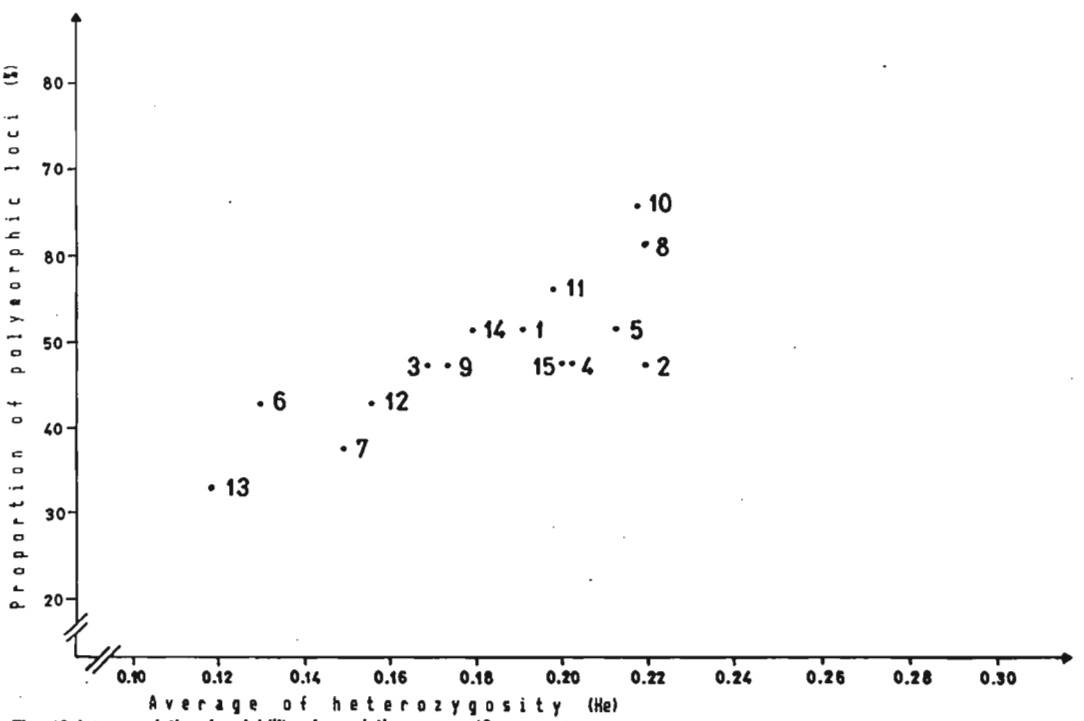

Fig. 12. Intrapopulational variability of populations group 12
1-C58, 2-C98, 3-C198, 4-C385, 5-C435, 6-C539, 7-C654, 8-C669, 9-C724, 10-C799, 11-C862, 12-C884, 13-C878, 14-C882, 15-C887

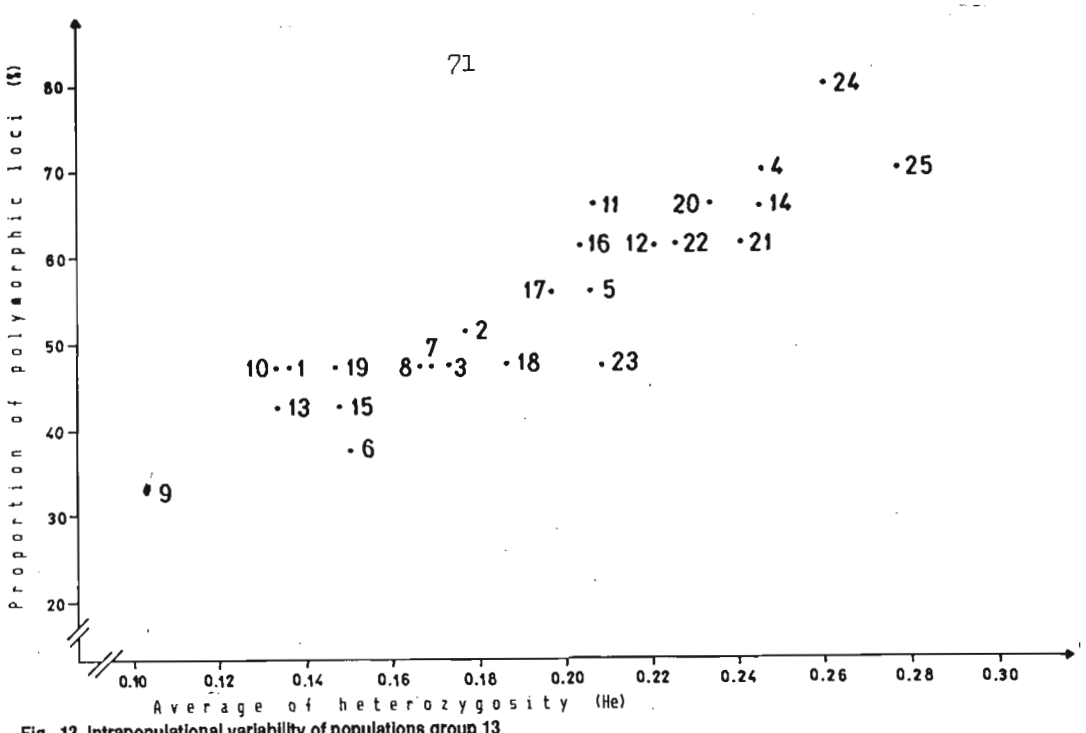

Fig. 13. Intrapopulational variability of populations group 13
1-C196, 2-C216, 3-C233, 4-C236, 5-C243, 6-C258, 7-C273, 8-C278, 9-C284, 10-C384, 11-C426, 12-C482, 13-C559, 14-C566, 15-C577, 16-C638, 17-C645, 18-C694, 19-C761, 20-C1444, 21-C1467, 22-C1478, 23-C1505, 24-C1517, 25-C1

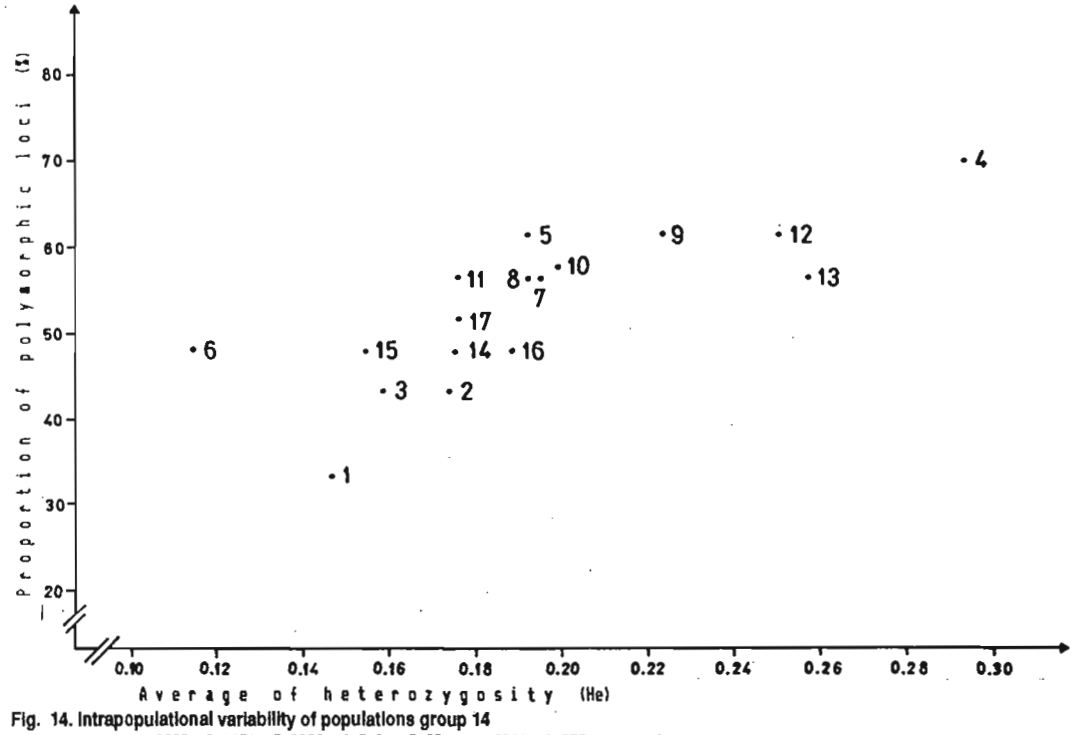

Fig. 14. Intrapopulational variability of populations group 14
1-C225, 2-C231, 3-C289, 4-C296, 5-C309, 6-C320, 7-C321, 8-C325, 9-C336, 10-C337, 11-C343, 12-C347, 13-C348, 14-C359, 15-C362, 16-C365, 17-C717

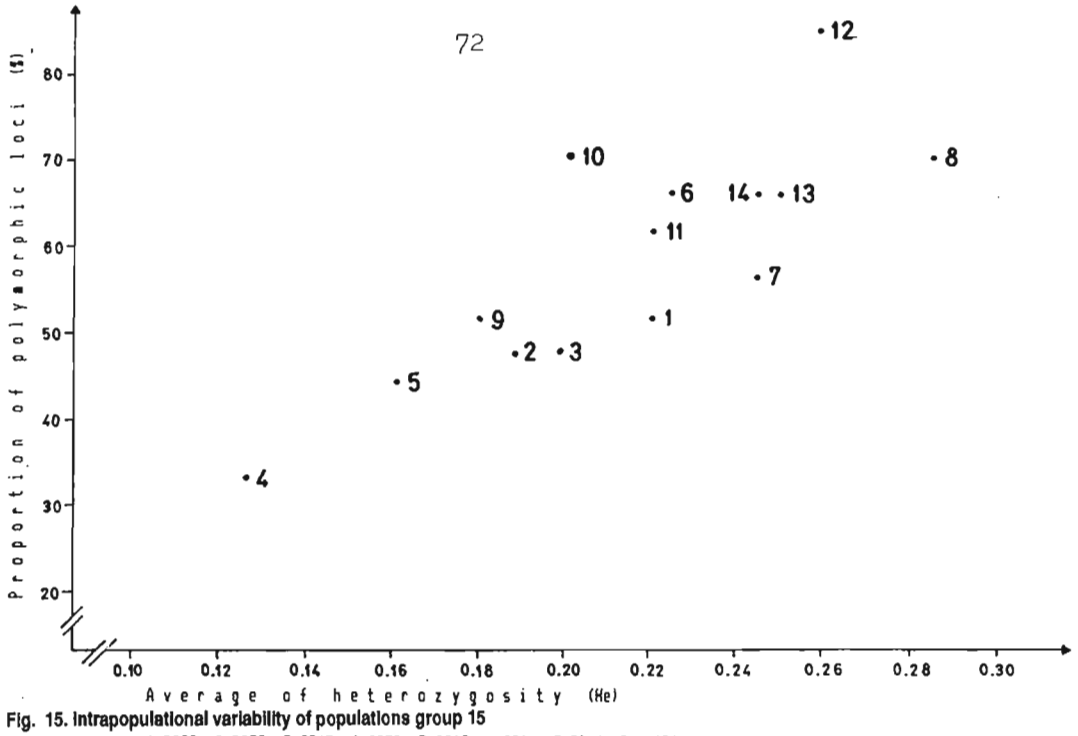

Fig. 15. Intrapopulational variability of populations group 15
1-C222, 2-C232, 3-C245, 4-C252, 5-C262, 6-C266, 7-C914, 8-C1480
9-C1488, 10-C1492, 11-C1509, 12-C1516, 13-C1565, 14-C1588

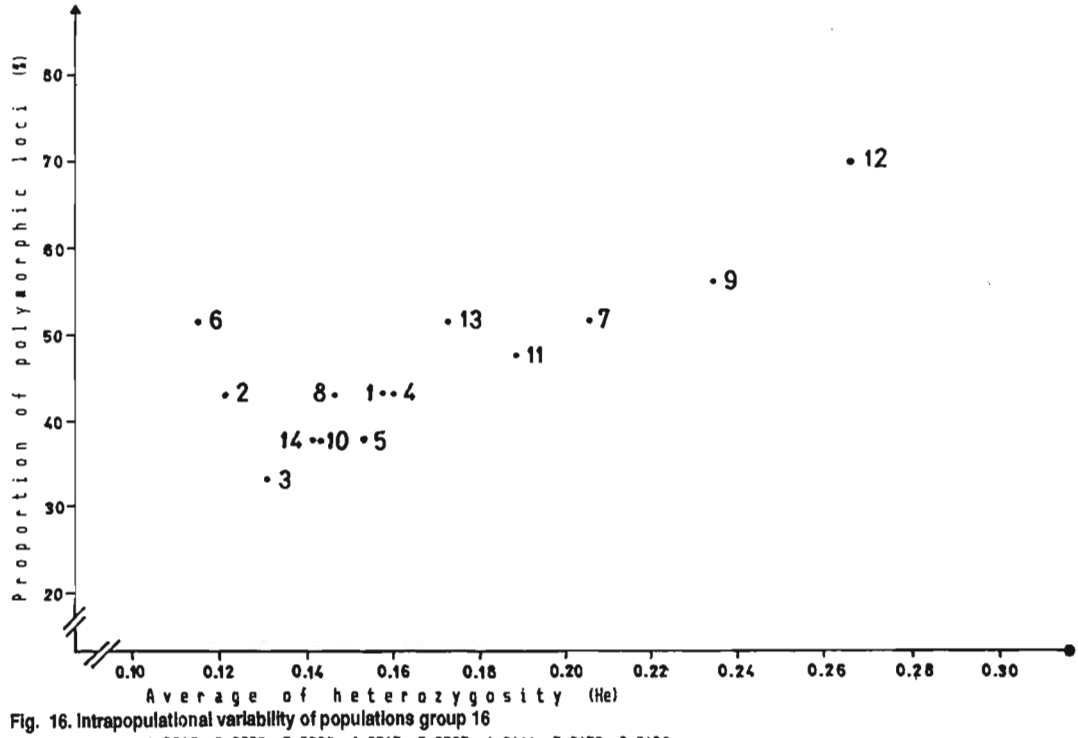

Fig. 16. Intrapopulational variability of populations group 16
1-C218, 2-C228, 3-C280, 4-C317, 5-C327, 6-C611, 7-C672, 8-C680,
9-C683, 10-C721, 11-C827, 12-C828, 13-C864, 14-C865

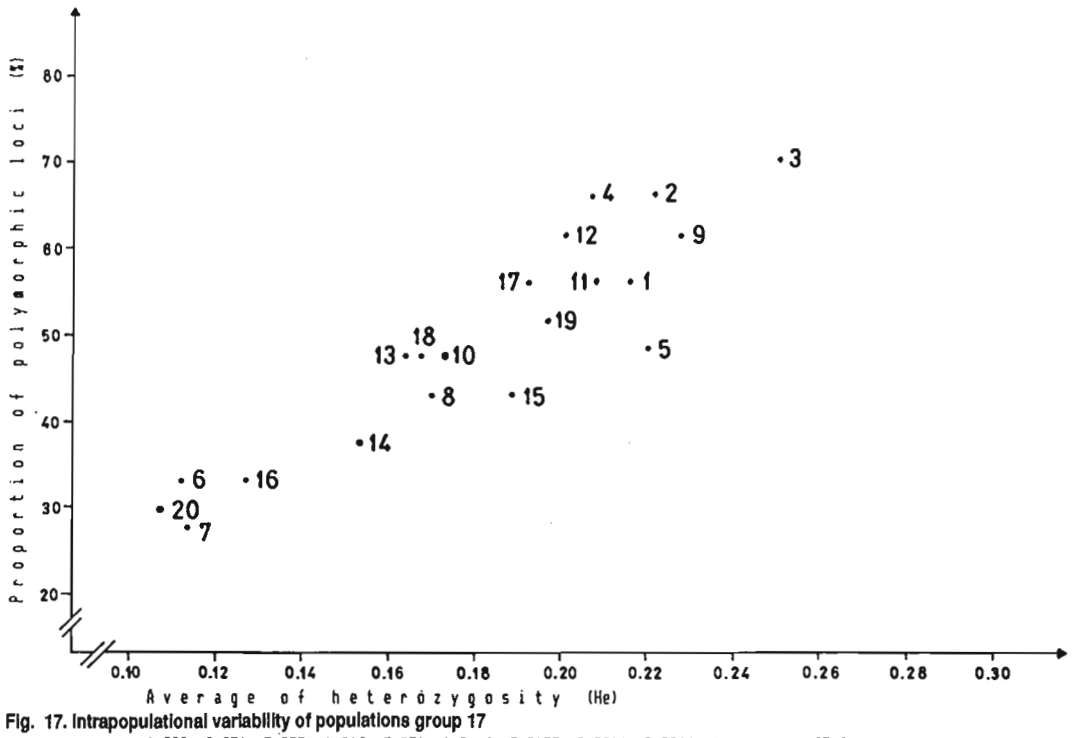

Fig. 17. Intrapopulational variability of populations group 17
1-C22, 2-C31, 3-C55, 4-C60, 5-C76, 6-C110, 7-C133, 8-C214, 9-C244, 10-C282, 11-C369, 12-C380, 13-C382, 14-C432, 15-C433, 16-C569, 17-C616, 18-C632, 19-C659, 20-C829

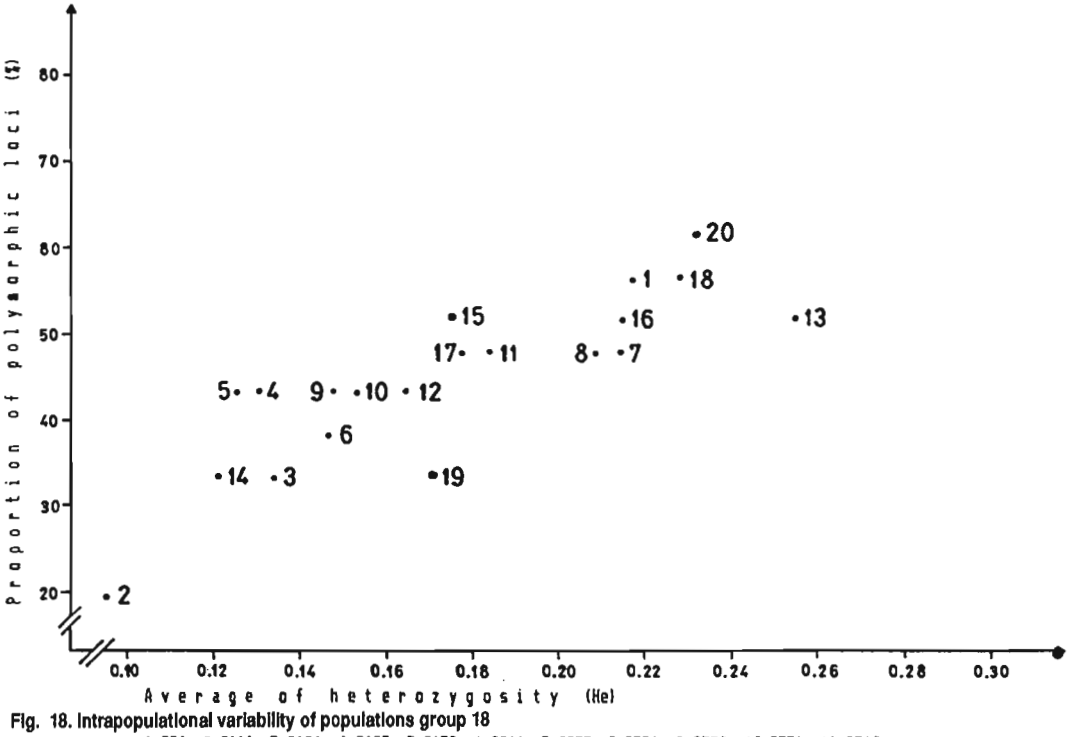

Fig. 18. Intrapopulational variability of populations group 18
1-C74, 2-C114, 3-C124, 4-C127, 5-C139, 6-C211, 7-C235, 8-C326, 9-C330, 10-C356, 11-C360, 12-C387, 13-C393, 14-C398, 15-C454, 16-C533, 17-C575, 18-C612, 19-C620, 20-C647

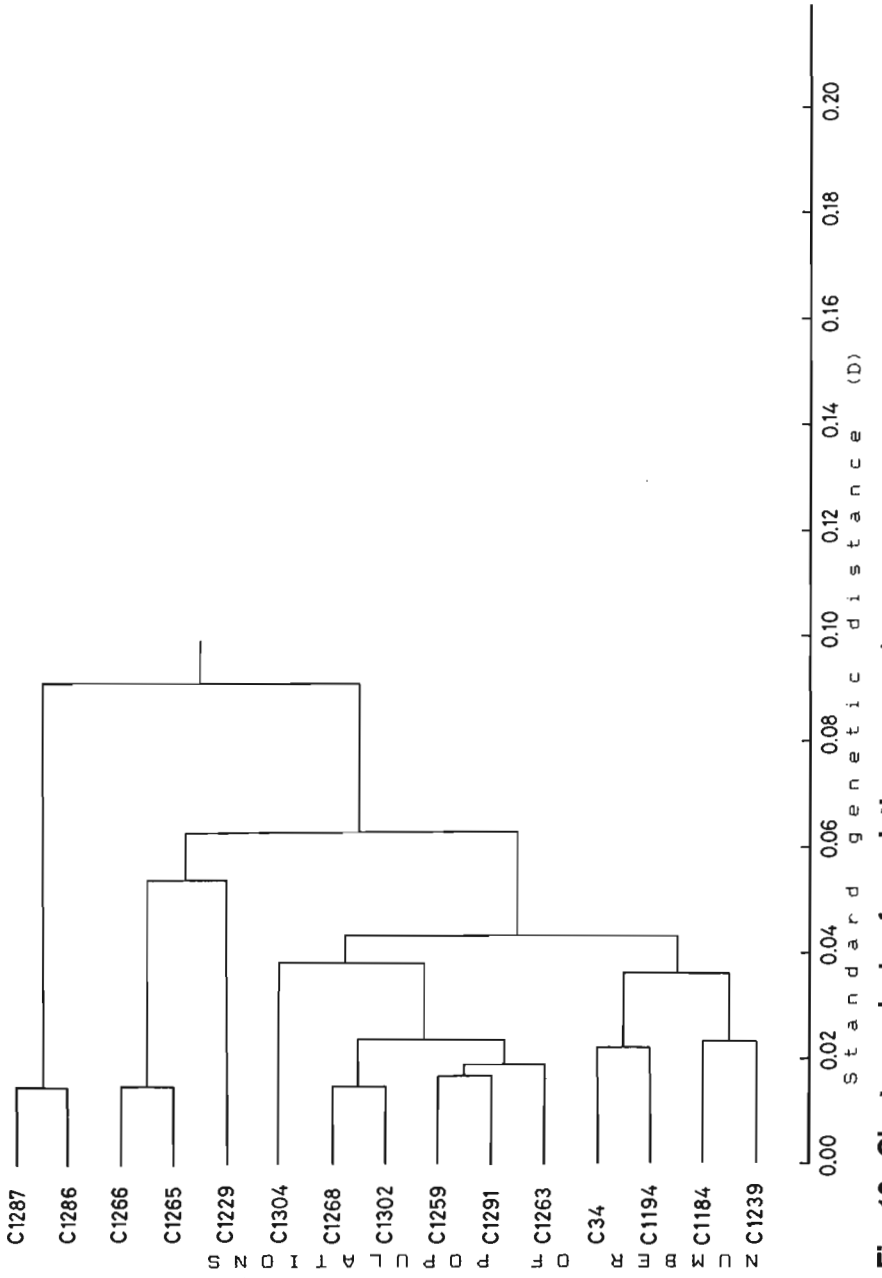

Fig. 19. Cluster analysis of populations group 1

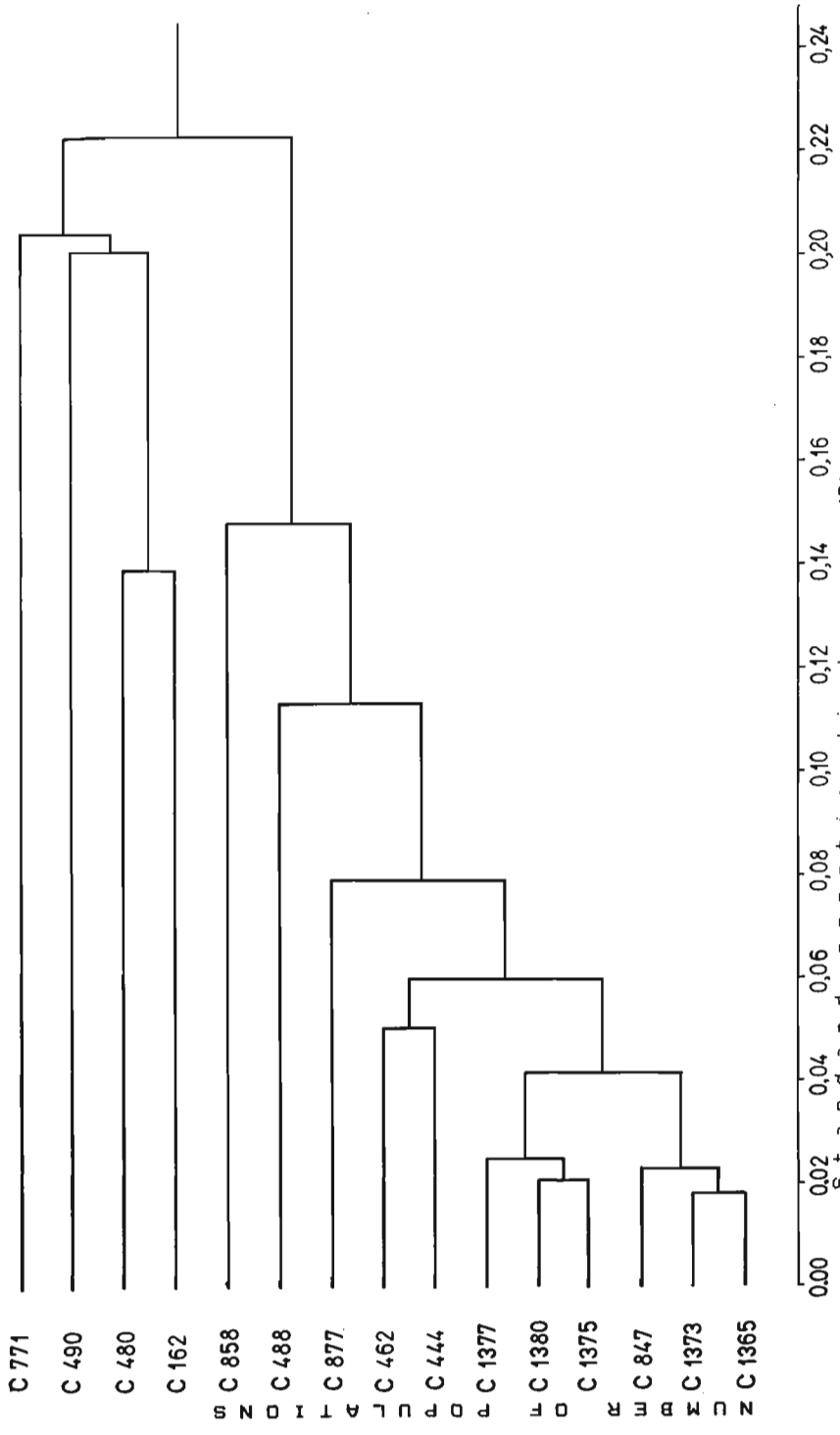

Fig. 20. Cluster analysis of populations group 2

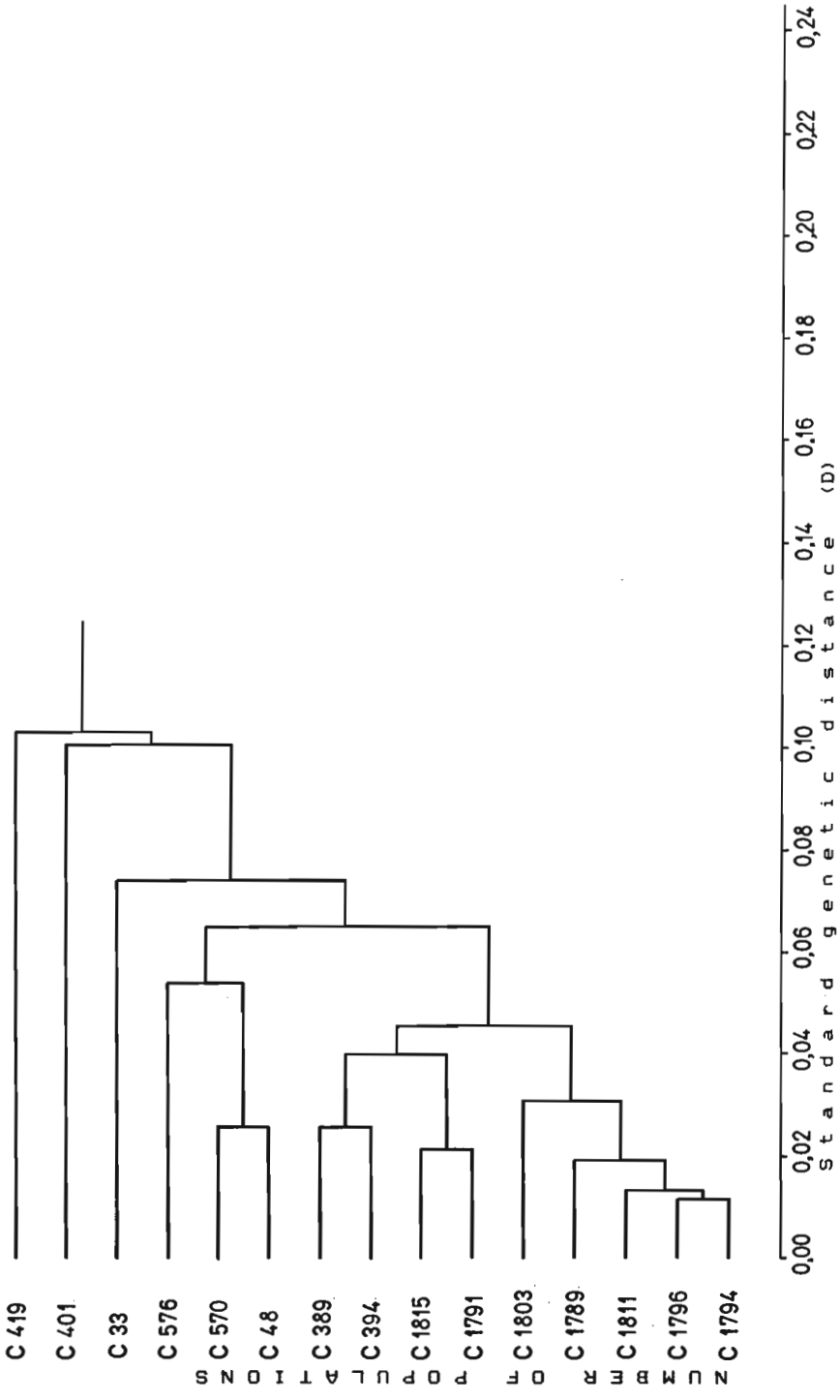

Fig. 21. Cluster analysis of populations group 3

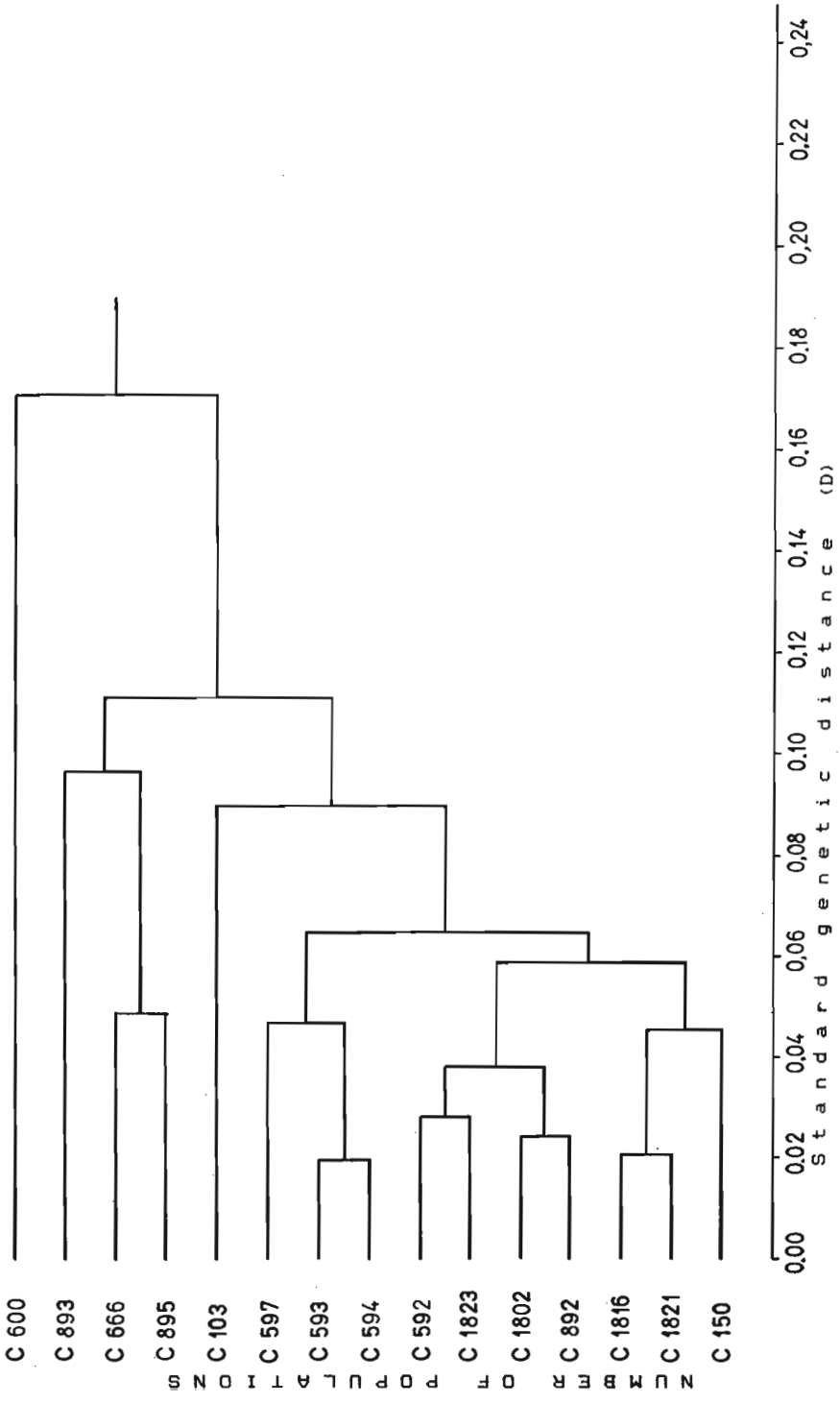

Fig. 22. Cluster analysis of populations group 4

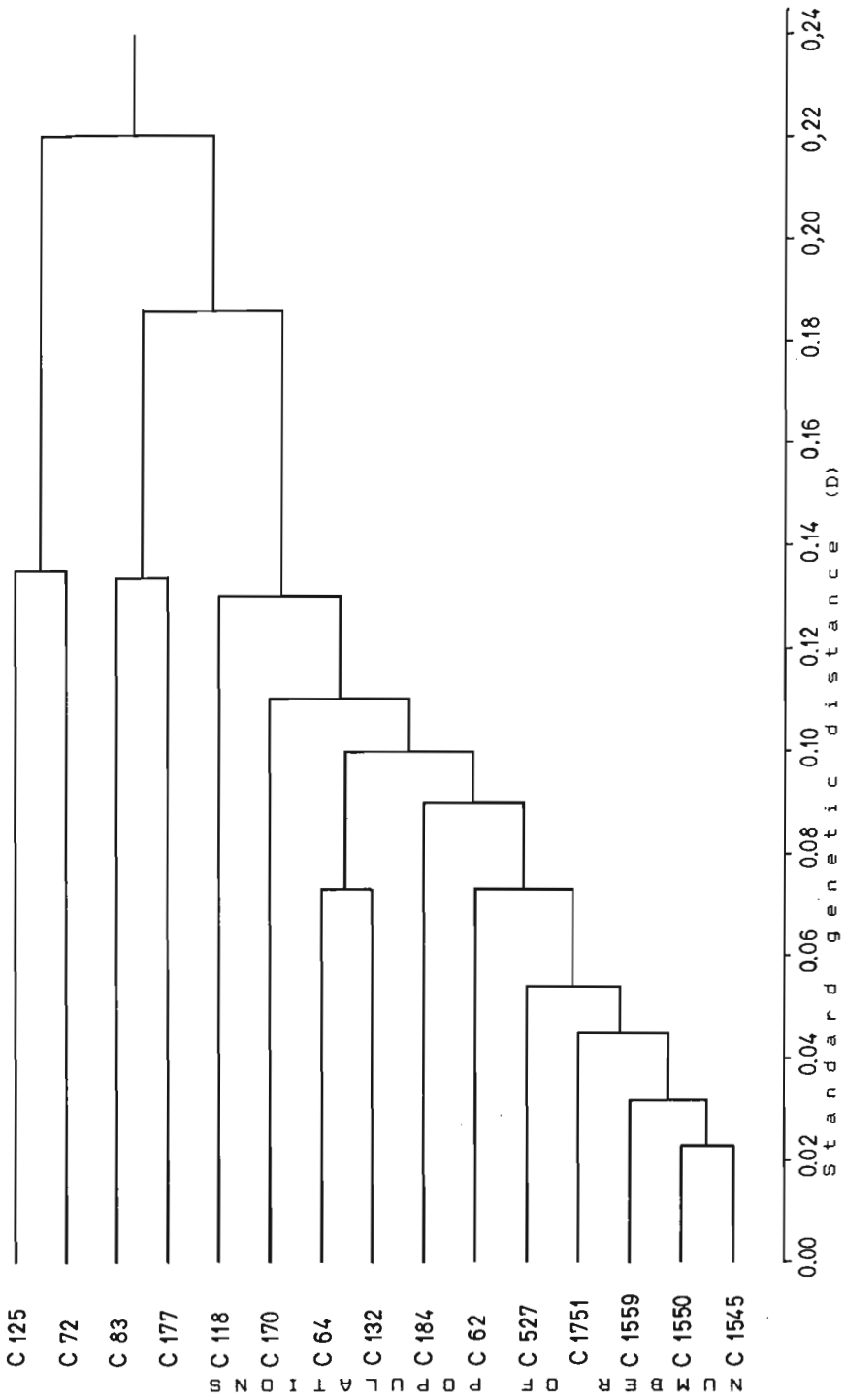

Fig. 23. Cluster analysis of populations group 5

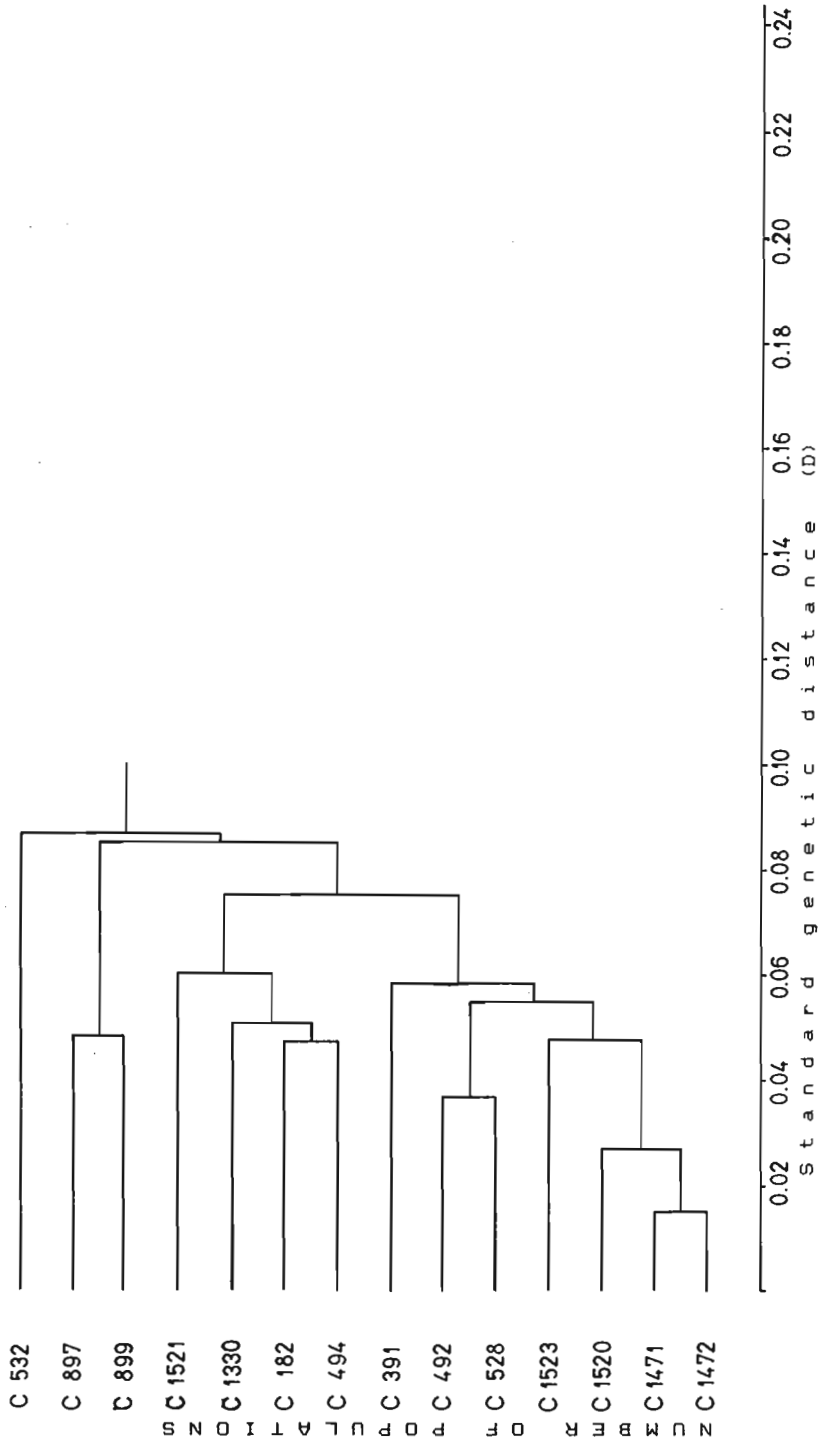

Fig. 24. Cluster analysis of populations group 6

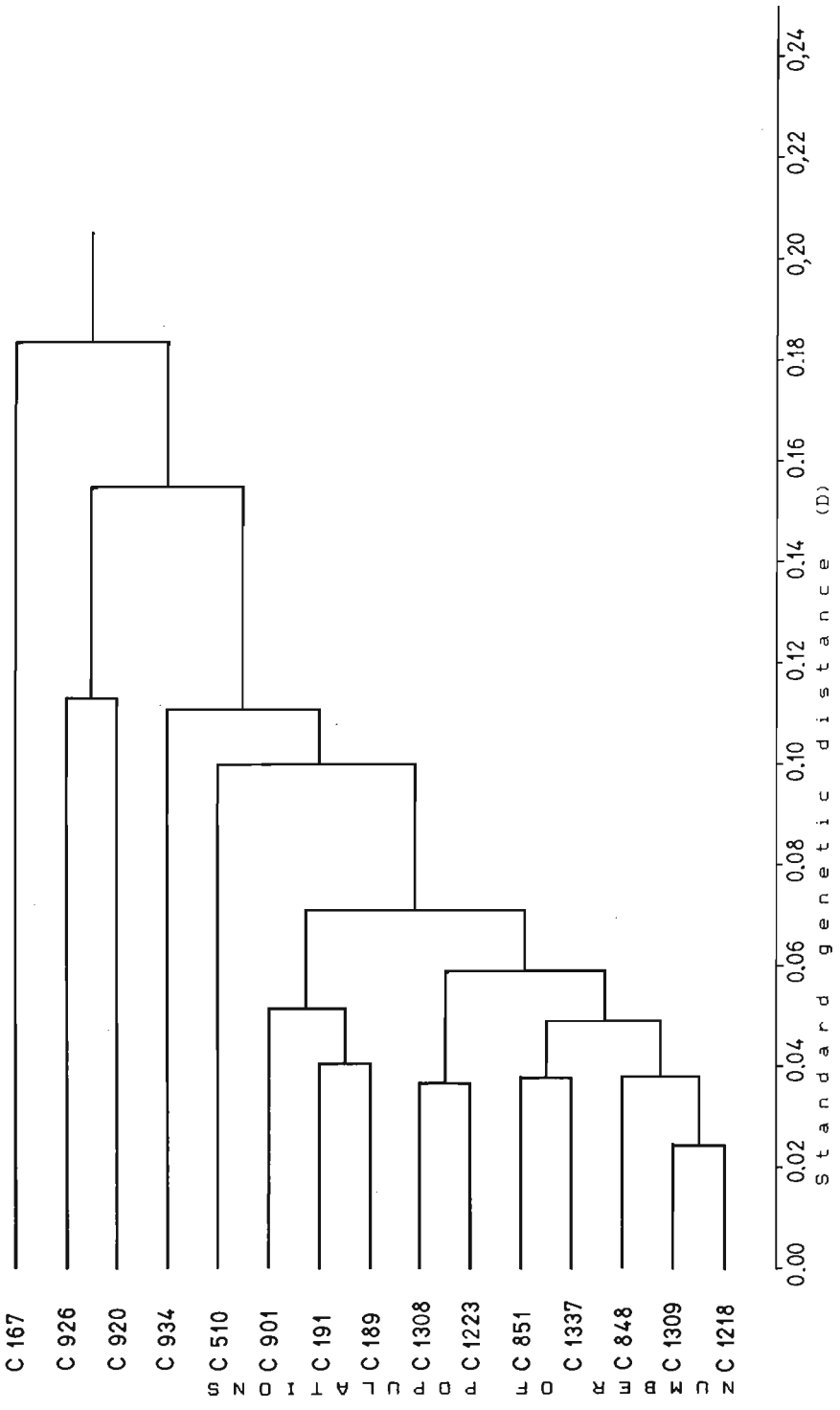

Fig. 25. Cluster analysis of populations group 7

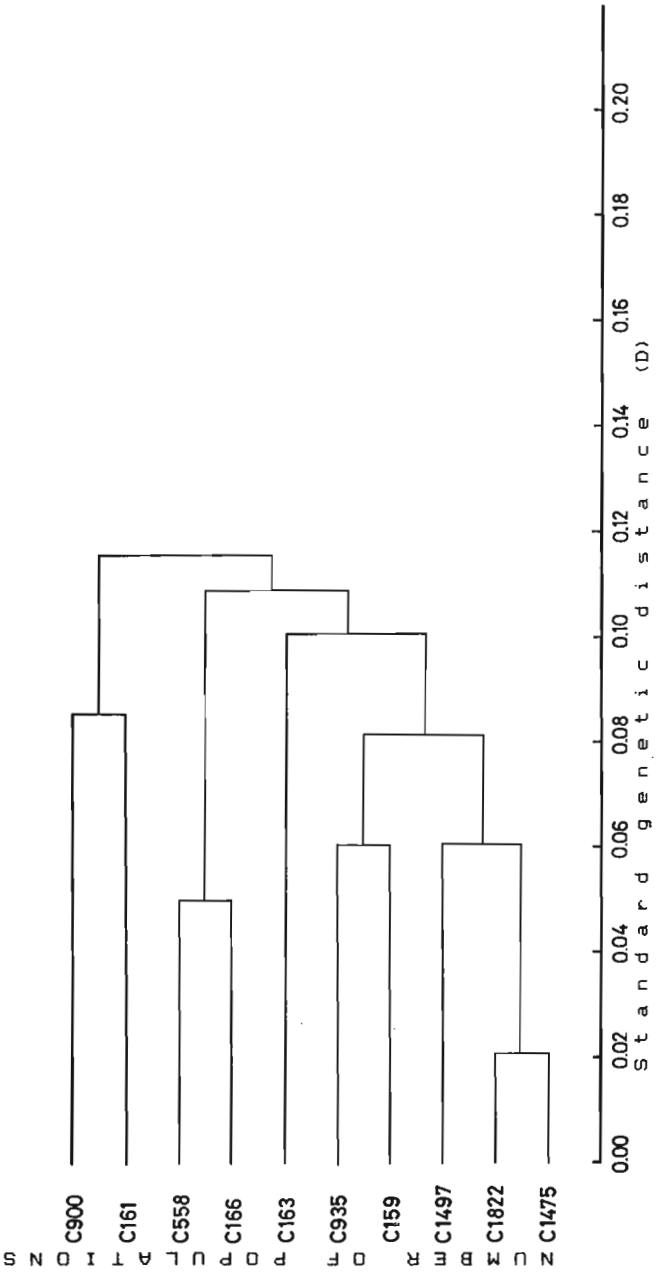

Fig. 26. Cluster analysis of populations group 8

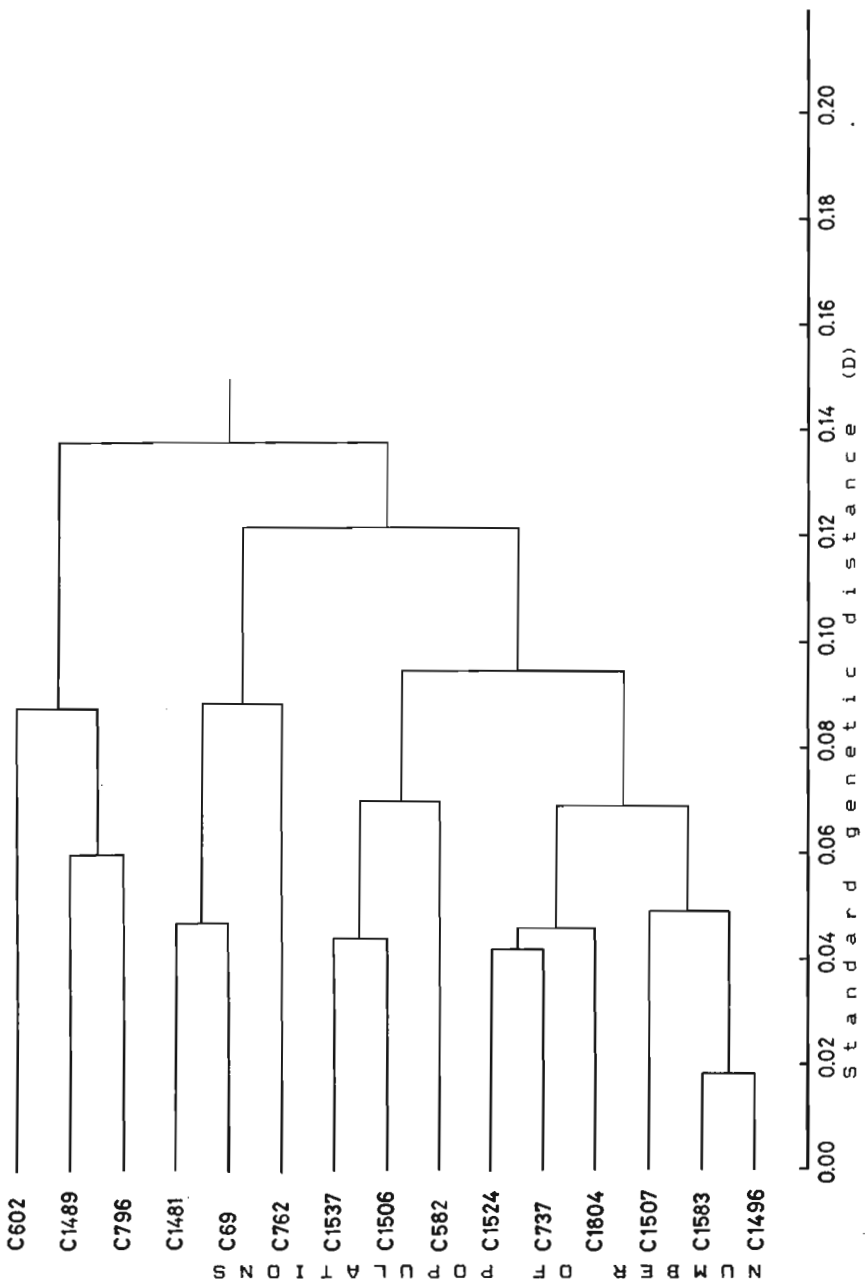

Fig. 27. Cluster analysis of populations group 9

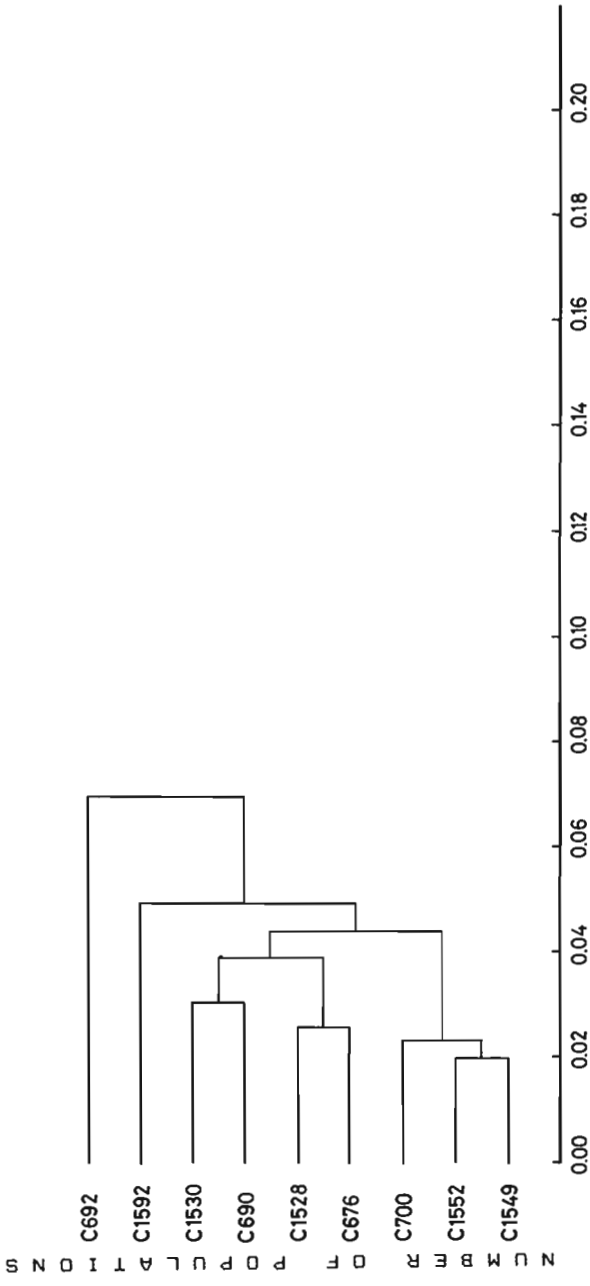

Fig. 28. Cluster analysis of populations group 10

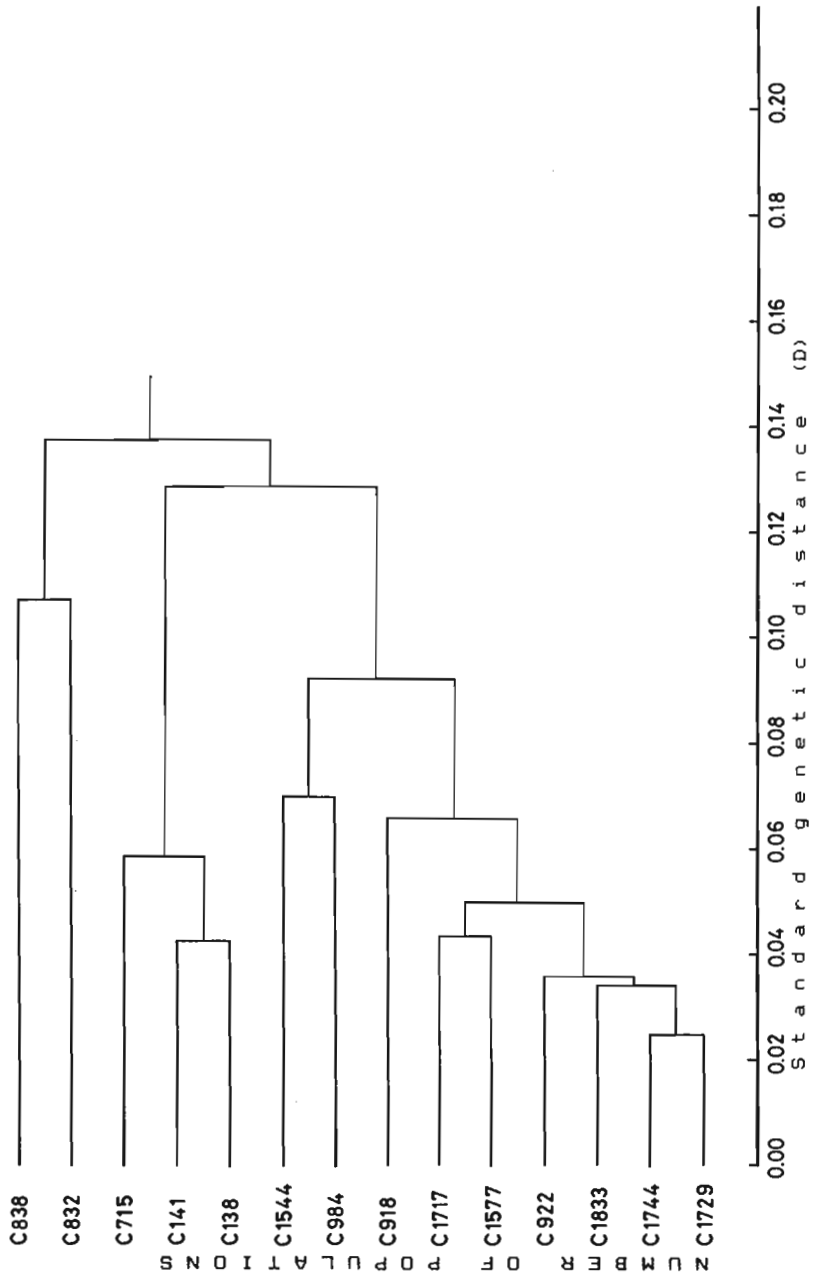

Fig. 29. Cluster analysis of populations group 11

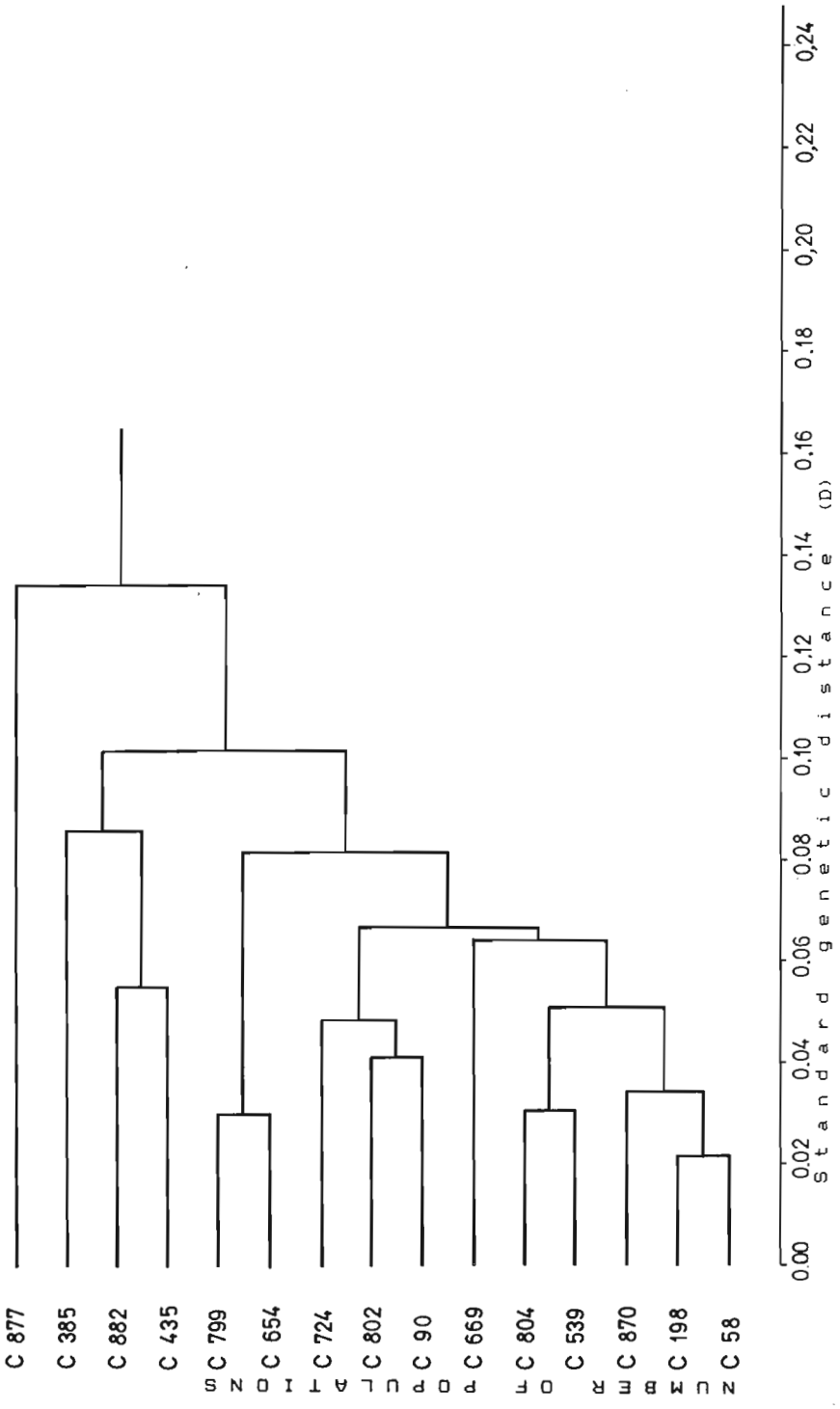

Fig. 30. Cluster analysis of populations group 12

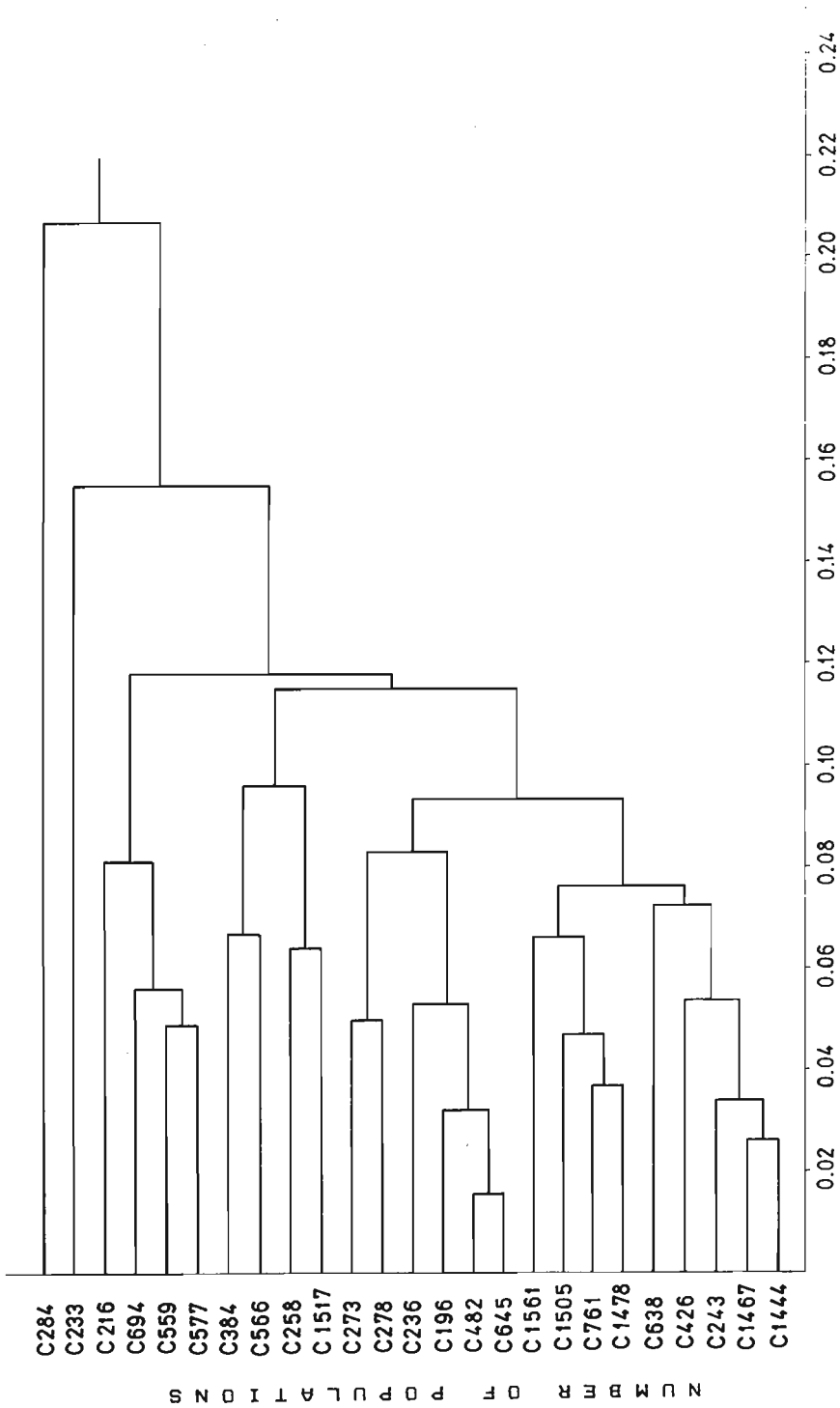

Fig. 31. Cluster analysis of populations group 13

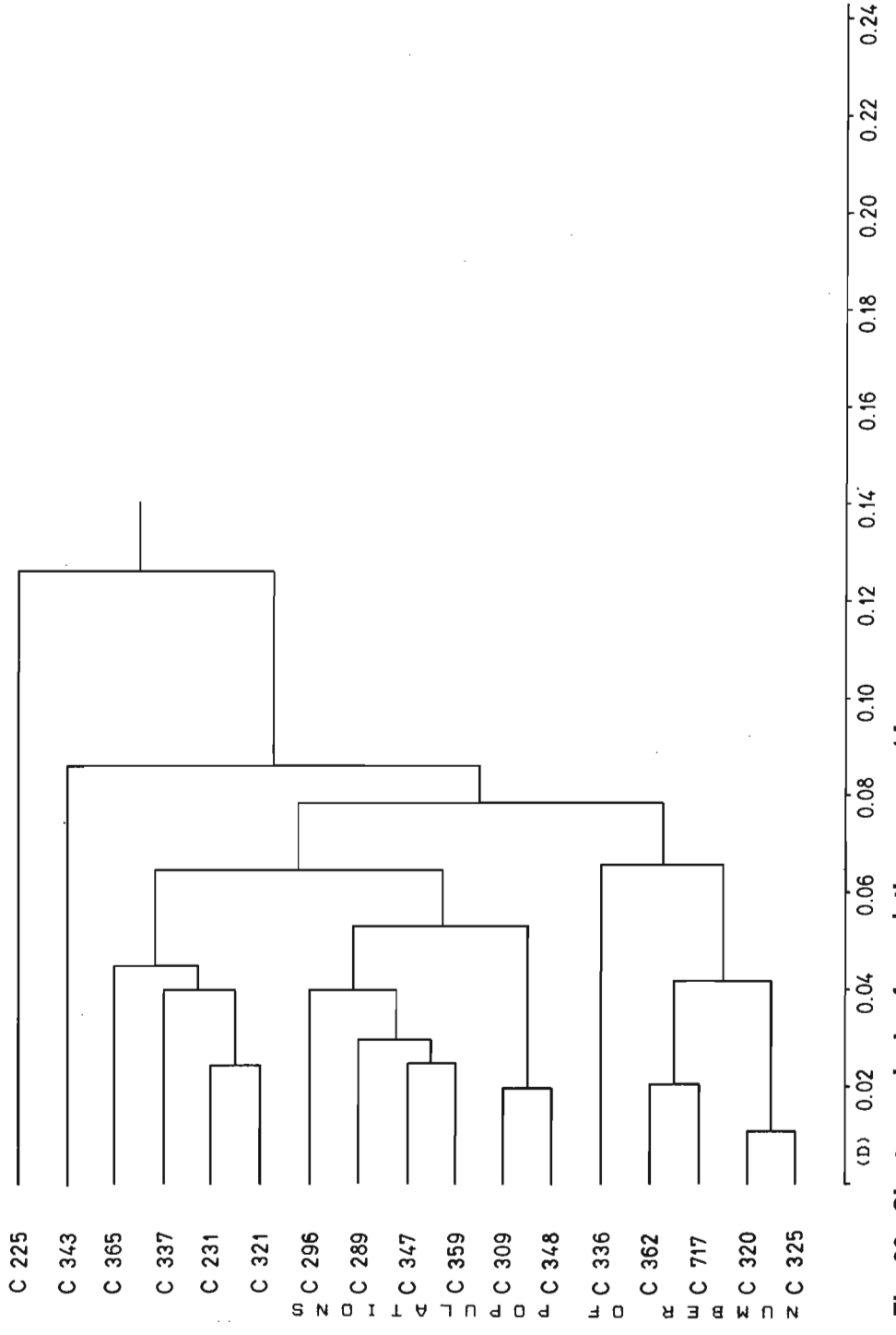

Fig. 32. Cluster analysis of populations group 14

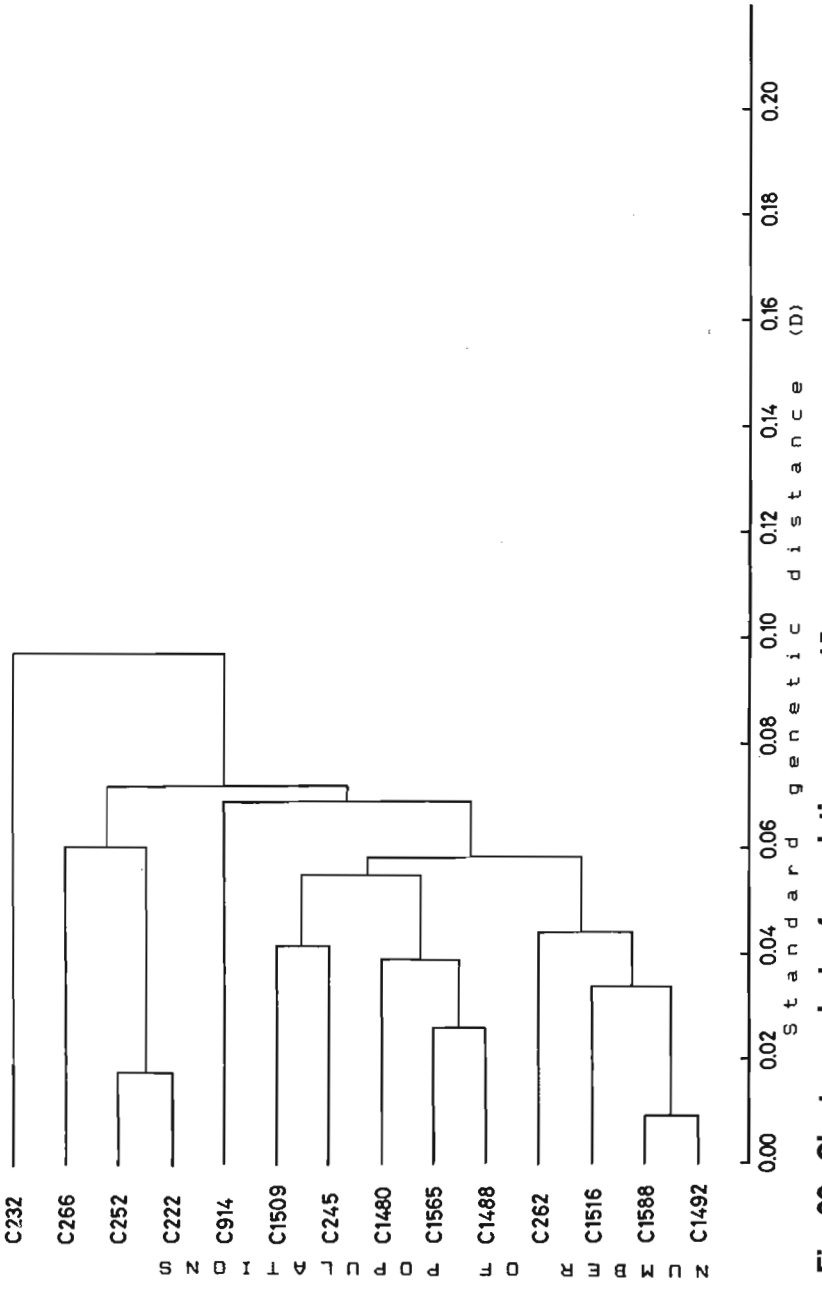

Fig. 33. Cluster analysis of populations group 15

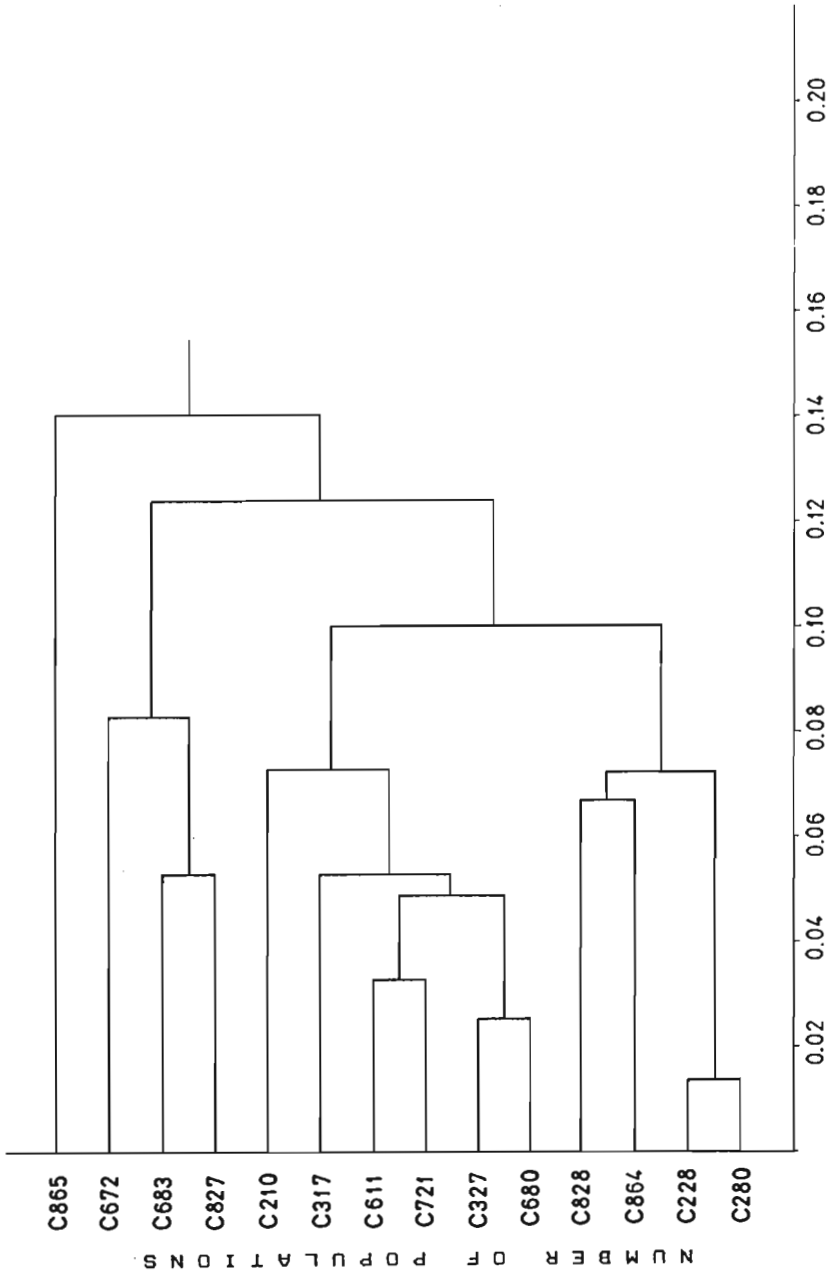

Fig. 34. Cluster analysis of populations group 16

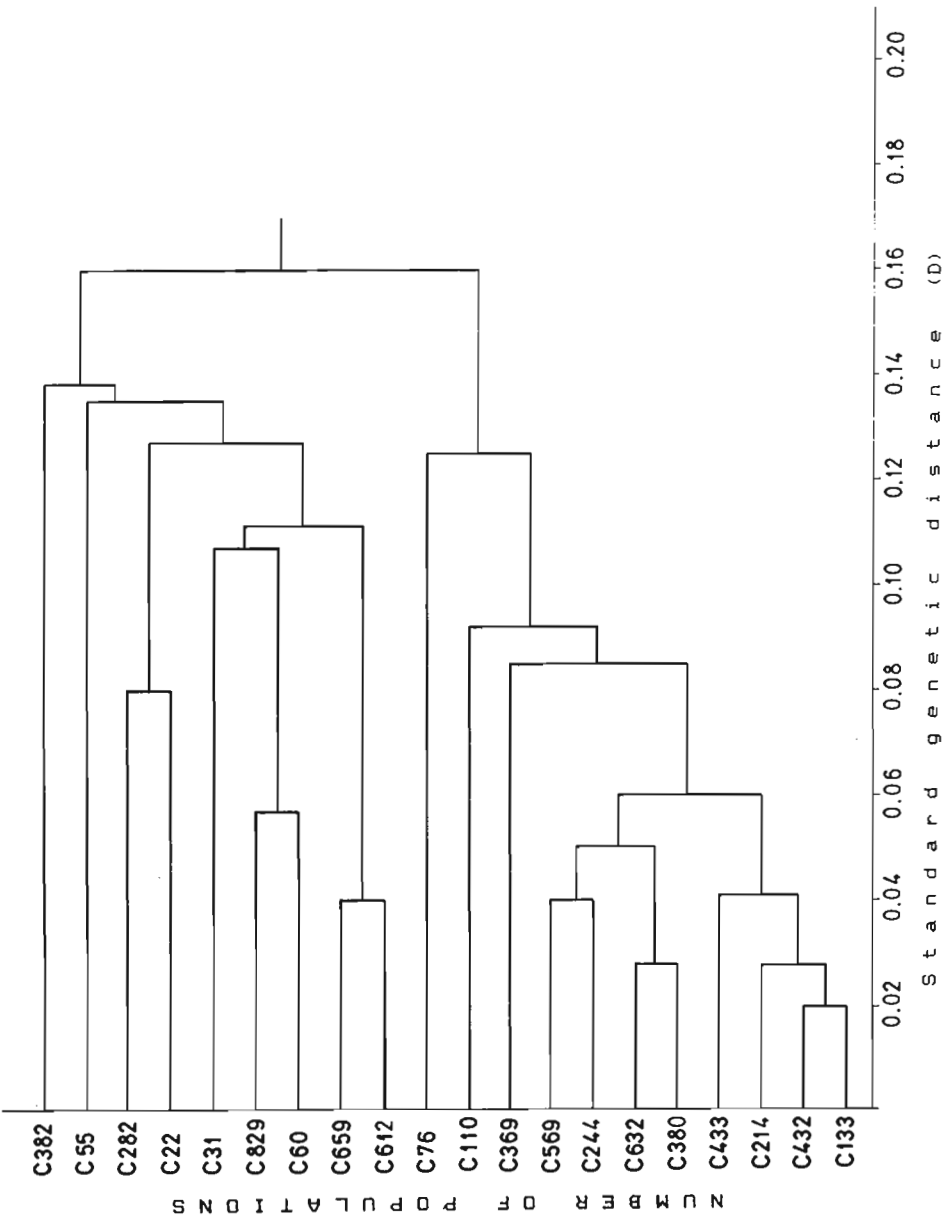

Fig. 35. Cluster analysis of populations group 17

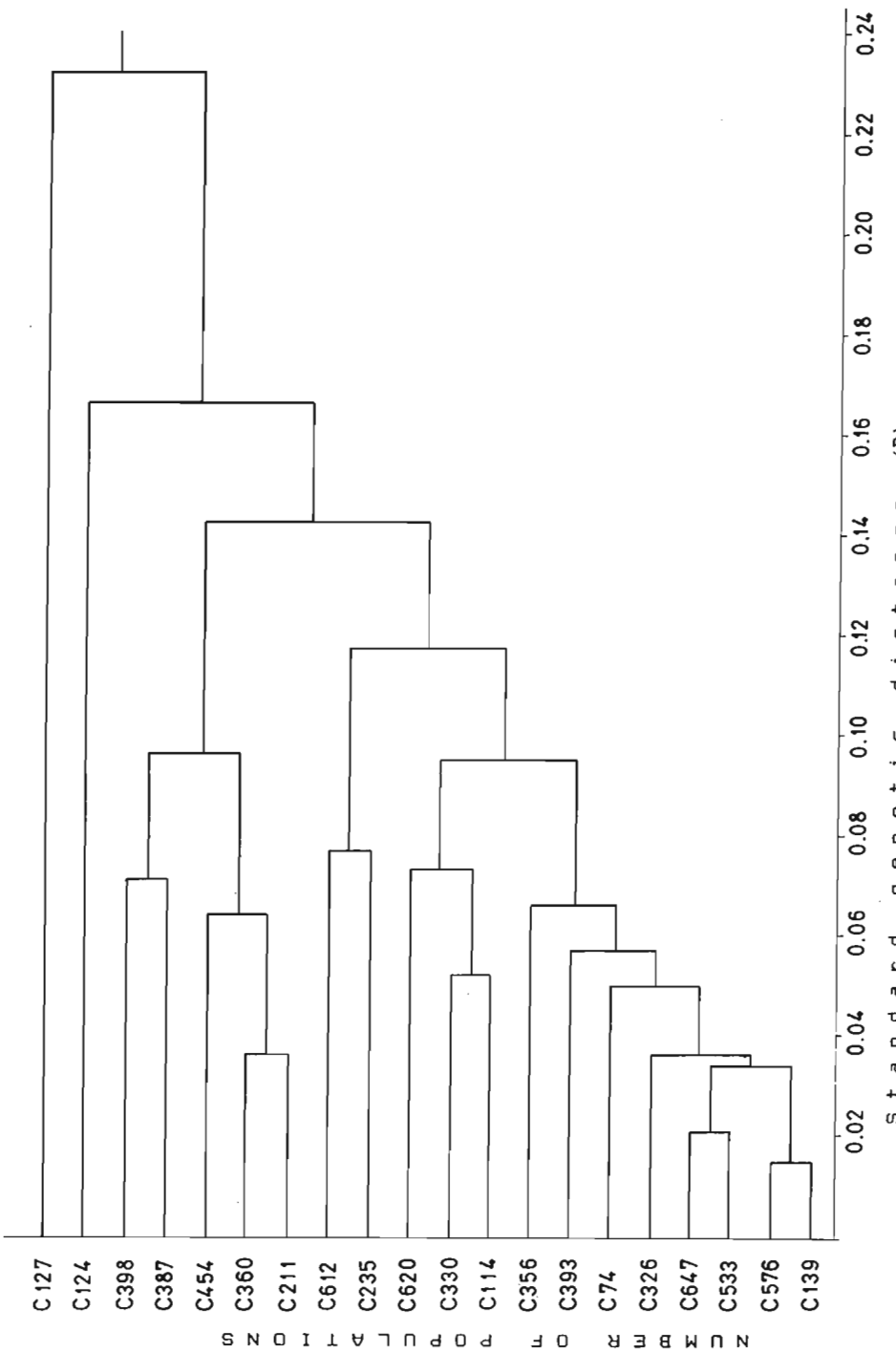

Fig. 36. Cluster analysis of populations group 18