

# LOCAL DIFFERENTIATION IN SOME NATURAL POPULATIONS OF JUSTICIA SIMPLEX

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**B**OTH theoretical and experimental analyses of gene frequency distribution under several forms of population structure provide a basic method for evolutionary studies since as DOBZHANSKY (1951) has succinctly put it, "the race formation begins when the frequency of a certain gene or genes becomes slightly different in one part of a population from what it is in other parts." Such local differentiation within a population, as shown by WRIGHT (1943), is most likely to be attained in a population subdivided into partially isolated subgroups where selection and random drift together can readily bring about significant genetic differences among these isolates. An extensive study of microgeographic variation for flower color has been reported in *Linanthus parryae* (EPLING, LEWIS and BALL 1960). Several other examples met with in animal populations have been reviewed by DOBZHANSKY (1951) and SHEPPARD (1958). The present paper reports a preliminary analysis of gene frequencies at a petal color locus in the local populations of *Justicia simplex* D. Don (Acanthaceae) which showed polymorphism and a tendency for marked local differentiation.

*Justicia simplex* is a diminutive annual occurring rather abundantly on a hilly ridge having its several regions interspersed among the inhabited parts of Delhi and New Delhi and, thus, their plant populations very well represent the isolates of WRIGHT's model, each having panmixia and more or less homogeneous distribution of this species. At eight different locations the relative frequencies of plants with pink or white petals were recorded over two years (1960 and 1961) by counting *all* individuals within a predetermined area of sampling in each case. Hence, the sample size varied largely depending on the density of plant distribution.

Table 1 gives the proportions in percentages of whites (recessive homozygotes) to the dominant class, pink petal color, and the frequency of the recessive allele ( $q$ ) which was directly obtained as the square root of respective phenotypic frequencies (columns 3 and 6) the mating system being panmixia. The quantities  $N$ ,  $q_0$  and  $q_1$  are sample size, and gene frequencies in years 1960 and 1961, respectively; the variance of  $q$ , or  $\sigma_q^2$ , has been computed with the following formulae after WRIGHT (1943):

Let  $q_i$  be the observed gene frequency in  $i$ th sample. Then in a group of  $K$  samples of  $N$  individuals each ( $N$  is the harmonic mean of  $N_i$ 's), not necessarily drawn from a homogeneous population,

$$\text{mean gene frequency for entire population, } \bar{q} = \frac{\sum_i^K q_i N_i}{\sum N_i};$$

TABLE 1

*Phenotypic frequencies of whites (in percent of total) and analysis of gene frequency changes*

Location	<i>N</i>	1960 Percent whites	$\hat{q}_0$	<i>N</i>	1961 Percent whites	$\hat{q}_1$	$\frac{\Delta q}{(\hat{q}_1 - \hat{q}_0)}$	<i>s</i>
A	218	13.9	.373	118	30.5	.552	.179	.258
B	111	13.5	.368	158	35.4	.595	.227	.195
C	101	10.9	.330	153	27.0	.520	.190	.216
D	106	4.7	.217	154	20.1	.448	.231	.101
E	131	5.3	.230	147	7.5	.274	.044	.467
F	130	10.0	.316	95	7.5	.274	-.042	2.381
G	80	5.0	.224	117	4.3	.207	-.017	1.325
H	84	15.5	.394	137	16.6	.406	.012	.884
Population mean, $\bar{q}_0 = .294 \pm .044$						$\bar{q}_1 = .495 \pm .051$		
$\sigma_{q_0}^{2'} = .0048$						$\sigma_{q_1}^{2'} = .0292$		

increment in gene frequency between years,  $\Delta q = (q_1 - q_0)$ ;

interpopulation variance within a year,  $\sigma_q^2 = \frac{\sum_i^K (q_i - \bar{q})^2}{K}$ ;

mean sampling variance,  $\sigma_{\delta q}^2 = \frac{\bar{q}(1 - \bar{q}) - \sigma_q^2}{N - 1}$ ;

and hence, net interpopulation variance,  $\sigma_q^{2'} = \frac{K\sigma_q^2}{K + C - 1} - \sigma_{\delta q}^2$ , where

$$C = \frac{\sigma_q^2}{\bar{q}(1 - \bar{q})}.$$

The last-named quantity provides a measure of variance due to real differentiation of local populations.

It is seen from Table 1 that in four of the populations sampled, namely A,B, C and D, the value of  $q$  had increased significantly in year 1961 while the remaining four locations showed very little change. It should be pointed out that, spatially-speaking, locations A,B,C,D, were from one region while E,F and G,H were taken in two other mutually distant regions. The ecological habitats in these three regions seem to differ in only one notable aspect; that is A,B,C,D have many shady trees growing and a soil type with a greater waterholding capacity than do the other regions. However, a relatively high value of  $q$  at location H suggests that gene frequency differences were not consistently associated with increasing distances. Estimates of  $\sigma_q^{2'}$  in these two years clearly suggest a tendency for greater local differentiation in 1961 for this marker character.

In order to account for the observed changes in both  $q$  and  $\sigma_q^{2'}$  various factors may now be considered. The two seasons under observation differed very marked-

ly in the total rainfall and other accompanying weather conditions which could have introduced a selection differential particularly in one region or the other. Whether the adaptive differences were due to a differential germination (cf. the example of *Linanthus parryae*), seedling survival or fertility, is also uncertain at this stage. Now, taking the selective values of pink and white to be  $s$  and 1, respectively, it is easily shown that an estimate of  $s$  is given by the expression

$$q_0^2(1 - q_1)$$

$s = \frac{q_0^2(1 - q_1)}{q_0^2(1 - q_1) + \Delta q}$ . The last column of Table 1 gives these estimates for each of the populations. Apparently, such extreme values as those obtained are not quite realistic, and therefore, it would be more plausible to attribute gene frequency changes to both selection and random drift. The role of migration would only be to counteract such differentiation in a subdivided population so that even more intense selection must be invoked to account for these results. A number of reports on microgeographical race formation under such an evolutionarily optimum population structure have been interpreted to involve selection, random drift or both of these factors (CAIN and SHEPPARD 1950; EPLING, LEWIS and BALL 1960), and WRIGHT (1948) has made a comparative study of the roles of directed and random processes under various theoretical situations. For an elaborate analysis of *Justicia* populations, further work on various ecological, genetical and statistical aspects has been undertaken.

#### SUMMARY

In several natural populations of *Justicia simplex*, analysis of gene frequencies at a petal color locus revealed polymorphism and an increasing tendency for local differentiation. These partially isolated, panmictic populations typically formed the isolates of WRIGHT's model of optimum population structure that can allow random drift to play a greater role in such differentiation into microgeographical races. In the present example the observed significant changes in gene frequencies at four of the locations sampled might have involved both selection and random drift.

#### LITERATURE CITED

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