CHROMOSOME POLYMORPHISM AND TRENDS IN SPECIATION IN THE NATRIX STOLATA AND XENOCHROPHIS PISCATOR
Chromosome polymorphism and trends in speciation in the
Natrix stolata and Xenochrophis piscator.

The two populations of Natrix stolata and
Xenochrophis piscator, separated by long distances,
revealed variations in chromosome number, form and
behaviour during mitosis and meiosis. The chromosomal
polymorphism and structural repatterning in the two
populations seem to be of great significance in speciation.

Natrix stolata:

The genus Natrix comprises a taxonomically
complex group consisting of a large number of species
of very wide distribution. On the morphological grounds
the populations from Chandigarh and Agra have been
labelled as Natrix stolata whereas their caryotypes
reveal a number of differences. The diploid number of
chromosomes in the Chandigarh population of this species
is 34, and these can be arbitrarily classified into 12Vs,
2 rods and 20 dots. In the population from Utter Pradesh
the somatic number of 36 chromosomes can be distinguished
as 10Vs, 6 rods and 20 dots. Thus, in the latter popu­
lation a pair of V chromosomes is missing, and there are
6 acrocentrics unlike two in the animals from Chandigarh.
The caryotype uniformity at intraspecific level is a
fairly consistent feature in reptiles so that the present
findings are rather unusual. Evidently this brings in the question, whether these two populations represent different cytological races of morphologically uniform species or two sub-species.

There are a large number of reports on a similar cytological differentiation within a species in the animal kingdom. Probably, the two populations of *Natrix stolata* also constitute different cytological races occupying far distant ecological niches. However, Chandigarh and Utter Pradesh come in the same geographical range, i.e. the Shivaliks, and the two populations can only exist as two ecological races of the species. Presumably the chromosomal differences, being of adaptive significance, have become stabilized without phenotypic differentiation. This variation can also be regarded as chromosomal polymorphism similar to that in the lizard, *Gerrohonestes scincicauda* (Matthey, 1949).

Since both the complements carry the same number of arms, the two caryotypes can be easily derived from one another through centric fusions, similar to that established in mammals, and many other animal species (Robertson, 1916, Sharman, 1956, Ford et al. 1957, Matthey and Maylan, 1961, Nadler, 1964). The centric fusions also seem to have played a major role in the evolution of caryotypes in the family Agamidae (Matthey, 1951).
The two caryotypes could arise in the following manner through centromere fusion in 4 rods giving rise to 2Vs or by misdivision of centromeres in 2 Vs, resulting into 4 rods.

\[2n = 36\]

10Vs - 6 rods - 20 dots

(10Vs - 4 rods - 2 rods - 20 dots)

(10Vs - 2 Vs - 2 rods - 20 dots)

12Vs - 2 rods - 20 dots

\[2n = 34\]

However, it seems probable that such a transformation involves the centric fusion rather than fission, since the latter process requires donors which could provide centromeres to the acrocentrics arising as a result of fission. Considering the centric fusions as the evolutionary mechanism of caryotype, the Chandigarh population seems to be more advanced owing to its lower number of chromosomes as a whole. Thus, the caryotypes are suggestive of a step towards species differentiation. In most instances, the chromosome polymorphism has been known within a single population, whereas in the present case it involves the two different populations.

**Xenochrophis piscator:**

The animal populations separated by long distances, and other ecological and geographical barriers often
reveal caryotype variability, although morphologically such populations look alike in the taxonomic details. Malnate and Minton (1965) suggested the presence of variants and interpopulation differences within this species. There are innumerable chromosomal differences between the two populations of *Xenochrophis piscator* (table LXI).

### Table LXI

**Chromosomal differences between the two populations of *Xenochrophis piscator***

<table>
<thead>
<tr>
<th>I. Characteristics</th>
<th>Quilon population</th>
<th>Agra population</th>
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<tbody>
<tr>
<td>1. Caryotype</td>
<td>10V's-6 rods-20 rods</td>
<td>8V's-2 rods-23 dots</td>
</tr>
<tr>
<td>2. Diploid number (2n)</td>
<td>36</td>
<td>38</td>
</tr>
<tr>
<td>3. Number of metacentrics</td>
<td>10 metacentrics and submetacentrics</td>
<td>8 metacentrics</td>
</tr>
<tr>
<td>4. Number of acrocentrics</td>
<td>6</td>
<td>2</td>
</tr>
<tr>
<td>5. Number of micro-chromosomes</td>
<td>20</td>
<td>28</td>
</tr>
<tr>
<td>6. Differentiation of microchromosomes</td>
<td>the micro-chromosomes are of almost same size.</td>
<td>micro-chromosomes are divided into two categories of 8 slightly bigger and 20 smaller chromosomes.</td>
</tr>
<tr>
<td>7. Fundamental number of arms</td>
<td>46</td>
<td>46</td>
</tr>
<tr>
<td>8. Length of the whole caryotype</td>
<td>60.6 microns</td>
<td>65.8 micron</td>
</tr>
</tbody>
</table>
9. Ratio of the largest pair to the caryotype

0.200
0.150

10. Ratio of the smallest pair to the caryotype

0.017
0.020

11. Total macro complement percentage

75
56

12. Total micro-complement percentage

25
44

II. The metacentric and submetacentric chromosomes differ markedly. The differences are in the position of the centromere.

1. Largest pair

Perfect metacentric

With an off median centromere.

2. Second largest pair

Metacentric

Submetacentric

3. Third largest pair

Metacentric

Metacentric

4. Fourth largest pair

Metacentric

Acrocentric

Quilon population Nil
has six additional acrocentrics.

III. Differences in mitosis and meiosis.

1. Microchromosomes

More refractile and susceptible to clumping.

There is very little clumping.

2. Belated appearance of microchromosomes

Very much pronounced

Not well marked

3. Chiasmata

Largest bivalent may carry six chiasmata

Largest bivalent may carry as many as 9 chiasmata.
4. Pre-cocious condensation and separation at metaphase I

- Not pronounced
- Very much pronounced

5. Chiasma frequency per cell

<p>| | |</p>
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<tr>
<td>23.64</td>
<td>20.08</td>
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</table>

The quantitative and qualitative differences between the two populations of *Xenochrophis piscator*, separated by long distance and ecological barriers, pose the question whether these are of intraspecific or interspecific nature. It is more likely that the present variants represent chromosomal polymorphism. Although such polymorphism seems to be rare in the reptiles except for the analogous case of the lizard, *Gerrohonotous* (Matthey, 1931a, b and 1933), reports of its presence in mammals have accumulated in recent years (shrew, Ford et al. 1957; *Rattus norvegicus*, Yosida et al. 1965, Toshide et al. 1965; *Acomys minous*, Matthey, 1963 and *Spermophilus*, Nadler, 1964). Besides mammals, the chromosomal polymorphism has also been reported in the grasshoppers (White, 1954), mantids (Wahrman, 1954), molluscs (Staiger, 1954) and many other animal species. In these various species the polymorphism involves the number of chromosomes; polymorphism with respect to morphology, the number of chromosomes remaining the same, has been reported in *Rattus norvegicus* (Hungerford et al. 1955) and deer mouse (*Ochsmo*
et al. 1966$. Chromosomal polymorphism seems to be widely prevalent in the fresh water snakes as the same has been recognised in two populations of *Matrix stolata* in the present study. It seems that the scanty reports of polymorphism in reptiles can be ascribed to inadequate technique and the limited number of investigations, which could reliably bring out caryotypic differences between populations, if any.

Possible mechanism of changes in caryotypes in *Xenochrophis*:

Chromosomal polymorphism seems to result from structural changes in the original pattern and in all such cases, the two caryotypes can be derived from each other, by postulating a few translocations or a few centromeric fusions or fissions. In *Xenochrophis piscator*, it is not easy to envisage a mechanism by which such a changed caryotype could have come to exist as a result of simple fusion or fission, although both caryotypes have the same fundamental number of arms. It seems that Robertsonian forces are not the only ones acting on the caryotype of *Xenochrophis piscator* so that the suggested mechanism for their origin can be as follows:

The caryotypes in Agra and Quilon populations are 8Vs - 2 rods - 28 dots and 10Vs - 6 rods - 20 dots respectively. The origin of such a caryotype can be attributed to certain changed morphologies within the
original caryotype followed by fusions. But the fact remains that any chromosomal rearrangement has to undergo fixation in a population or a species, otherwise it will exist in heterozygous condition only for one or more generations. Phylogenetic relationship suggested below is largely speculative. If we start with the assumption that both the centric fusions and structural changes have been in force, the hypothetical mechanism for the conversion of the Agra caryotype into the Quilon caryotype can be as follows:

It has been consistently recognised that 8 microchromosomes in Agra population, are of larger size. Now if these 8 chromosomes were to increase in size as a result of cumulative effect in countless generations or these microchromosomes were to duplicate as a result of certain advantageous mutations, the intermediate caryotype comprising of 8Vs, 10 rods and 20 dots would be formed. Now apparent reduction of chromosome number in the Quilon population can result from the centromeric fusions in 4 pairs of acrocentrics, two by two, into two pairs of V-shaped multiples. The evolution of Quilon caryotype from the Agra caryotype through an intermediate theoretical caryotype can be as follows:

\[
\text{8Vs - 2 rods - 28 dots (Agra)}
\]

8 bigger sized 20 smaller in size
Duplication or accumulative effect
Theoretical intermediate caryotype

8Vs - 10 rods - 20 dots.

Fusion of 4 rods two by two

10 Vs - 6 rods - 20 dots

The entire course of evolution might have worked in reverse direction which can be represented as follows:-

10Vs - 6 rods - 20 dots

Fission in one of the pairs

8Vs - 10 rods - 20 dots

Deletion in 8 of the rods.

8Vs - 2 rods - 28 dots (8 of bigger size).

In fact the former mechanism of transformation seems to be more logical as the second requires donors, to provide centromeres to the acrocentrics arising as a result of fission, which cannot be accounted for.

Adaptive mechanism and trends in speciation

The chromosomal variation in the two populations of *Xenochrophis piscator* leads one to assume that such a polymorphism originated in the ancestral stock. It is
possible that the original caryotype of the species could be still existing in either of the units as such or with a certain amount of variation which might have crept in. In the former case there might have been forms within the original caryotype with 8 micro-chromosomes of larger dimensions. Later on, duplications might have occurred and subsequently few adaptive changes in the chromosome structure might have led to the evolution of the caryotype as found in the Quilon population. Adaptive chromosomal polymorphism has been very commonly reported in isolated populations of *Drosophila*, where a close parallelism exists between the extent and kind of adaptive cytological polymorphism and cytotaxonomic differences. Thus, in the *Repleta* group of the genus *Drosophila*, there are relatively few chromosomal rearrangements either within or between species, whereas in the *Obscura* group there is a higher frequency of paracentric inversions, both in state of flux in natural populations, and as stable cytotaxonomic differences between the species (Wasserman, 1954 and Patterson and Stone, 1952). Furthermore, it is generally accepted that paracentric inversions in *Drosophila* populations function, as a mechanism for perpetuating adaptive genic polymorphism although there
is no complete unanimity of opinion as to just how these mechanisms operate in the natural populations (Dobzhansky, 1951, Wallace, 1953 and Cain and Sheppared, 1954). Moreover, it has been logically accepted that polymorphic species have a higher adaptive fitness in that particular niche. Thus it can be inferred that the standard caryotype of Xenochrophis piscator exhibited polymorphism and these polymorphic forms, when isolated by geographical barriers, became stable.

The adaptive character of most cytological polymorphs depends, of course, on the fact that by suppressing crossing over between certain chromosomal regions they set limits to the free recombination of genes within the population and thus permit stable combinations of genes which are co-adapted to one another. Evolutionary significance will certainly emerge in an increasing measure from the study of different geographical ranges along with the included populations. However, greater opportunity is available for peripheral populations to utilize favourable mutations, gene sequence, or chromosomal rearrangements by radiation in a new habitat (White, 1959). It, however, seems that only fusions and cryptic structural changes have been operating on the caryotype of Xenochrophis
Fusions are suggested for the origin of polymorphic caryotypes as there are no donors which could provide centromeres to the acrocentrics arising as a result of fission.

The population at Quilon seems to be more advanced than that at Agra because of its low chromosome number and low number of acrocentrics. Cross breeding experiments between populations may bring out heterozygous combinations yielding expected configurations during meiosis and may provide adequate proof for the assumptions outlined above.

There is no reason to conclude that the caryotype from Agra population is nearer to the original or this too is a polymorphic representation of another standard form unknown so far and which gave rise to the Agra and Quilon variants. When a species becomes cosmopolitan from a basically endemic group there is presumably some stabilizing genetic mechanism or the species is versatile and can adjust to any change in environment by chromosomal structural adjustments best suited to the population. This results in polymorphism at the intraspecific level.

With limitations, the available cytological data indicate that adaptive polymorphism is of a wide occurrence at intraspecific level. One is also tempted
to suggest that the polymorphic forms, when isolated, both reproductively and ecologically, can be designated as two cytological races or for that matter may even be raised to the level of sub-species. This is confirmed by the existence of varied caryotypes in widely distributed species of plant and animal groups, which subsequently lead to the origin of new species. Thus, in *Xenochrophis piscator*, there exists another polymorphic form which can be labelled as the sub-species of *Xenochrophis piscator*.

**Systematic status of the Genus Xenochrophis:**

The earlier workers grouped most of the freshwater snakes under the genus *Natrix*. Malnate and Minton (1965), made a proper distinction between the various genera and evaluated the systematic position of the genus *Natrix*. They have, thus, suggested that the intraspecies and interpopulation variations are common in the Genus *Xenochrophis*. These authors have admitted the possibility of even the existence of sub-species within *Xenochrophis piscator* whose range has not been delimited. Thus, with marked chromosomal differences between the caryotypes, it is worth while to raise them to a distinct status. In all probability the chromosomal polymorphism has been the underlying cause of such variations. Marked chromosomal differences between populations suggest that the taxonomic status of this genus needs further revision.