birds from this population and measured their migratory activity (restlessness, Zugunruhe) as in earlier experiments[7]. 77% of these birds proved to be migratory-active, and 23% migratory-inactive (table). From these 2 groups of birds, we formed in 1977 and 1981 a total of 10 breeding pairs of migrants and 11 pairs of nonmigrants which were kept in outdoor aviaries. We successfully raised 39 birds of the F_1-generation (table) and investigated their migratory activity in the same way as described for the parental birds. These data supported 2 of the 3 predictions listed above: 1. the offspring of the nonmigrants showed a significant (30%) increase in the number of nonmigrants compared to the parental population, 2. the offspring of the nonmigrants showed an opposite and significantly different ratio of nonmigrants to migrants in comparison with the offspring of migrants. Moreover, although not statistically significant, there was also some evidence in favor of the 3rd prediction: the number of migrants in the offspring of pairing of migrants was 8% higher than in the parental population. Further, we found that the migratory-active offspring from migrants produced about 40% more migratory activity than that from nonmigrants. This is in accordance with our earlier findings[4] that the amount of migratory activity is also genetically controlled.

The results of this study demonstrate that in the investigated partially migratory blackcap population, the characters 'migratory' and 'nonmigratory' are inheritable and thus establish polymorphism as a controlling system of partial migration in birds. It is probable that polymorphism also controls migration in other blackcap populations and in other bird species[3,8,9]. Whether this migratory behavior described in the present report is exclusively genetically determined needs further investigation, which is in progress. Since inbreeding the 2 morphs 'migrants' and 'nonmigrants' resulted in a considerable change of their ratio from one generation to the next, the observed dimorphism appears to be highly adaptive to changing environmental conditions. The rate of this adaptation is presently under investigation.

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Unusual distribution of constitutive heterochromatin (C-bands) in the somatic chromosomes of a passerine bird *Erithacus svecicus*

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Summary. The distribution of constitutive heterochromatin (C-bands) has been studied in a passerine bird, *Erithacus svecicus* (Linnaeus) (Turdidae, Passeriformes, Aves) (2n = 76 ±). In 7 out of 9 pairs of macrochromosomes pericentromeric heterochromatin has been observed. The smaller 2 pairs of macrochromosomes are entirely heterochromatic.

The phylogenetic implications of constitutive heterochromatin have been repeatedly discussed[2-4]. In birds, where generally uniformity is observed in chromosome number[5], morphology[6], and also in G-bands[7-8], the C-banding analysis seems to be a possible clue for detecting taxonomic variations. The present paper describes an unusual karyotype in the bluethroat, *Erithacus svecicus* (also known as *Luscinia* or *Cyanosylvia svecica*).

Four male birds collected from Athagarh, Orissa were studied. The species was identified by the Zoological Survey of India (Indian Museum, Calcutta, India). The stuffed specimens are deposited with the authors at the Department of Zoology, Utkal University. Chromosome preparations were obtained from bone marrow cells following the usual air-drying technique of Ford and Hamerton[9], and stained with Giemsa. The nomenclature of chromosomes is in accordance with that proposed by Levan et al.[10]. The C-banding analysis of Sumner[11] has been employed with slight modifications[12] for the demonstration of constitutive heterochromatin.

A good number of metaphase spreads studied showed the diploid chromosome number to be 76 ± (table 1). The karyotype comprises 18 macro and 58 microchromosomes. The macrochromosomes are arranged in 4 groups depending upon centromeric indices and relative lengths (fig. 1). Groups I and II comprise a single pair of m- and sm-chromosomes respectively. Group III comprises 4 pairs of st-chromosomes and group IV comprises 3 pairs of t-chromosomes. As only male birds were available the gonosome could not be identified. The microchromosomes are either acrocentric or dot-shaped in nature. Table 2 summarizes the morphometric data of the macrochromosomes. The karyotype of a congeneric species *Luscinia calliope* (2n=80)[13] has been described. Comparison with this and other confamilial species reveals the karyotype of *Phoenicurus phoenicurus*[14] to be more close to *E. svecicus* (table 3).

Table 1. Frequency distribution of 2n of *E. svecicus* in 80 metaphases

	Chromosome No.												
	68	69	70	71	72	73	74	75	76	77	78	79	80
Frequency	-	-	2	-	1	2	5	2	57	1	7	1	2

Table 2. Morphometric data for macrochromosomes of *E. svecicus*

Pair No.	1	2	3	4	5	6	7	8	9
Relative lenght	5.1	11.2	8.1	7.3	6.0	5.1	5.0	3.4	3.4
Centrometric index	41.6	33.3	21.0	17.6	14.2	16.6	-	-	-

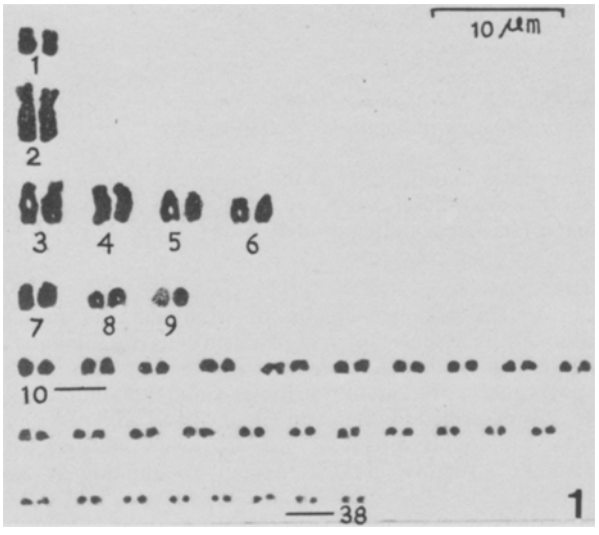

Figure 1. Normal karyotype of male *E. svecicus*.

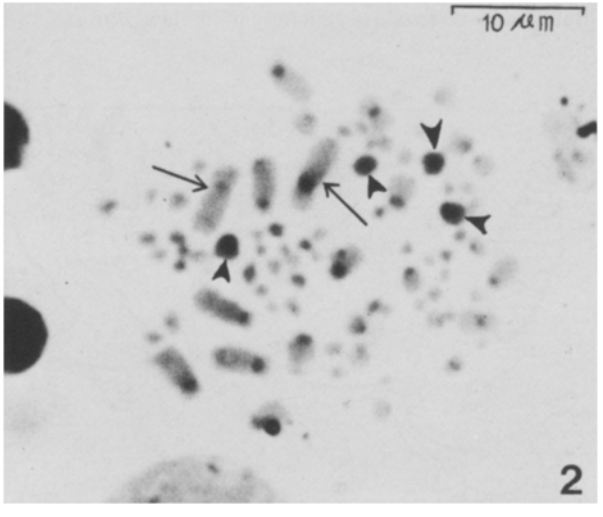

Figure 2. C-banded metaphase of *E. svecicus*. The arrows indicate C-bands of 2nd chromosome and arrowheads indicate 8th and 9th chromosome pair.

But further comment on karyological relationship is not indicated at this juncture, as more has to be learnt in this context.

The C-banding has been successfully demonstrated in only 1 out of 4 specimens. The result shows unusual distribution of heterochromatin (C-bands). All the macrochromosomes except the 8th and 9th pairs (fig. 2) possess pericentromeric heterochromatin. The latter 2 pairs are entirely heterochromatic and are very prominent in the karyotype. As far as we know, the presence of 2 pairs of entirely heterochromatic macrochromosomes is unique among bird karyotypes analyzed so far. However, similar results have been documented by Gemperl et al.[21] for some members of the Cricetinae (Mammalia), where some of the smaller chromosomes are entirely heterochromatic. These authors suggested that such heterochromatin probably brings about variations at lower taxonomic levels. But such speculations in the case of *E. svecicus* would be premature. Due to the paucity of literature on C-banding in Aves the role of heterochromatic smaller macrochromosomes remains unexplained at this stage and a widening the scope of the study would be of value.

Table 3. The 2n of 12 different species of the family Turdidae

Species	2n	Authors
Luscinia calliope	80	Udagawa[13]
Turdus chrysolaus	84	Yamashina[15]
Phoenicurus phoenicurus	76	Hammar[14]
Turdus aureus	84	van Brink[16]
Turdus sibiricus f. *davisoni*	84	van Brink[16]
Turdus celaenops	84	Udagawa[17]
Turdus migratorius	80	Jovanovic and Atkins[18]
Turdus naumanni	84	Udagawa[17]
Turdus pallidus	84	Udagawa[17]
Turdus merula	80	Hammar[19]
Oenanthe oenanthe	80	Hammar[19]
Saxicolla torquata	86	Piccini and Stella[20]
Erithacus svecicus	76	Bhunya and Sultana[1]

The C-banded karyotype also shows the microchromosomes to possess varying amounts of heterochromatin. Only 3–4 pairs of microchromosomes are entirely heterochromatic. Most of them show no staining, or a dot at the centromere. Among the macrochromosomes, No. 2 shows prominent heterozygosity in the C-bands which deserves mentioning; one of the homologues shows a dark band at the centromere and the other, a negligible amount (arrows in fig. 2). The amount of constitutive heterochromatin, although constant for individual chromosomes, has been observed to vary between homologues of chromosome pairs in some species due to a different base composition of DNA in these regions[22]. Lau et al.[22] have proposed that such heterozygosity may be due to inter-subspecific hybridization between individuals of different geographical races. It is presumed here that in the present case too the heterozygous C-bands of the 2nd chromosome could have resulted from hybridization between 2 *E. svecicus* birds of different geographical origins. More studies on C-banding patterns are needed, especially with birds of different geographical origins.

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