

depth the disc achenes failed to germinate whilst the ray achenes showed some germination (fig. 1). Initial growth of seedlings raised from the 2 achenes was similar but later on (after 9 days of emergence), the seedlings from the ray achenes produced significantly more dry matter (fig. 2).

**Discussion.** The relatively better germination exhibited by ray achenes, especially from a greater sowing depth, may be attributed to higher seed energy reserve which enables the seedlings to emerge out of the deeper layer of soil. The failure of emergence of seedlings from the disc achenes (which have a lower seed reserve) sown at 5 cm depth also signifies the importance of seed energy reserves in seedling emergence. The calorific difference in seeds might be due to changes in seed weight and/or proportion of storage products. Flint and Palmblad<sup>7</sup> have suggested that an increased proportion of protein and carbohydrate provides the readily available energy which results in quick germination. This appears to be true with the ray achenes in the present study. The effect of seed reserve is also reflected in dry matter yield of the seedlings. The better growth of seedlings from the ray achenes (fig. 2) appears to be the result of the higher protein, carbohydrate and energy content of the ray achenes. Seed fitness is frequently determined by the amount and nature of stored embryonic capital which influences the outcome of seedling competition occurring before plants become photosynthetically self-sufficient<sup>13</sup>. Thus, the cohort of seedling populations originating from the ray achenes may be better adapted than those from the disc achenes in competitive situations.

Further, the ability of the ray achenes to germinate from the greater sowing depth has special bearing with respect to population maintenance of this weed in Meghalaya, which experiences high rainfall during the period of seed production so that the seeds are likely to be buried under eroded material (Rai and Tripathi, unpublished data).

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# Partial migration in birds: experimental proof of polymorphism as a controlling system<sup>1</sup>

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**Summary.** When, from a partially migratory population of blackcaps, migratory-active (a) and -inactive (i) individuals were bred, the a × a pairs produced more birds of the type a than the original population and the i × i pairs, and the latter also more birds of the type i than the original population. Thus the characters 'migratory' and 'resident' in the blackcap are inherited and polymorphism is now demonstrated as a controlling system for partial migration in birds.

When hand-raised experimental groups of blackcaps (*Sylvia atricapilla*) of 4 different populations from Europe and Africa with various (exclusively and partially) migratory habits were investigated in constant experimental conditions, we found that their migratory activity was a fairly good reflection of the different migratory habits observed in the field<sup>3</sup>. Crossing blackcaps from an exclusively migratory European population with those from an almost non-migratory African population, we observed in the F<sub>1</sub>-hybrids an increase in migratory active individuals of 33% in comparison to the African parental population<sup>4</sup>. These findings demonstrated endogenous controlling factors for migration and supported the hypothesis first proposed by Lack<sup>5</sup> that partial migration in birds is based on polymorphism. According to this hypothesis, the decision as to how many and which individuals from a partially migratory population depart from or winter in the breeding area, respectively, depends on genetic factors. To test the polymorphism (in this special case dimorphism) hypothesis, inbreeding the 2 supposed morphs 'migrant' and 'nonmigrant' appears to be the most promising method. In the case of polymorphism, the offspring of the pairing migrants × migrants should show an increase in the

ratio of migrants to nonmigrants compared to the original population (prediction 1) and to the offspring of the pairing nonmigrants × nonmigrants (prediction 2). Similarly the offspring of the pairing nonmigrants × nonmigrants should show an increased amount of nonmigrants compared to the original population (prediction 3). We started such inbreeding experiments in 1977 with blackcaps from a partially migratory population from southern France<sup>3,6</sup>. From 1976<sup>3</sup>–1980, we handraised 102

	Original partially migratory population (n = 102)	F <sub>1</sub> -individuals from pairing nonmigratory × nonmigratory birds (n = 19)	F <sub>1</sub> -individuals from pairing migratory × migratory birds (n = 20)
No. of migratory active individuals	79	9	17
No. of nonmigratory individuals	23	10	3
	p < 0.01	p < 0.025 (χ <sup>2</sup> -test)	

birds from this population and measured their migratory activity (restlessness, Zugunruhe) as in earlier experiments<sup>7</sup>. 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<sub>1</sub>-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<sup>4</sup> 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<sup>3,8,9</sup>. 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<sup>2-4</sup>. In birds, where generally uniformity is observed in chromosome number<sup>5</sup>, morphology<sup>6</sup>, and also in G-bands<sup>7-8</sup>, 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<sup>9</sup>, and stained with Giemsa. The nomenclature of chromosomes is in accordance with that proposed by Levan et al.<sup>10</sup>. The C-banding analysis of Sumner<sup>11</sup> has been employed

with slight modifications<sup>12</sup> 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)<sup>13</sup> has been described. Comparison with this and other congeneric species reveals the karyotype of *Phoenicurus phoenicurus*<sup>14</sup> 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 length	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	-	-	-