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Genotype of *Sturnus contra* (Sturnidae - Passeriformes: Aves)

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Abstract

The present communiqué pertains to the chromosomal investigation of pied myna, *Sturnus contra* of the Family - Sturnidae : Order - Passeriformes : Class - Aves. The chromosomes were extracted from bone marrow cells of previously colchicinized grown-up individuals. The chromosome count vacillated between 78 and 85 with more than 50% of the cells depicting 2n = 82. There was an apparent distinction in size between macro- and micro- chromosomes.

Keywords : *Sturnus contra, Aves, Sturnidae.*

Introduction

The class Aves, the second major group of vertebrates, comprises almost nine thousand species of living birds distributed over 175 families and 26 orders (Garg, 1992). However, to date, merely 8% of the world's bird species have been cytogenetically studied; these comprise 802 species covering roughly a hundred of families from 25 orders with the exception of the order Colliformes (Garg & Shrivastava, 2013 a, b, c, d, e, f, g, h). The study, at hand, brings on record some grave cytogenetic information about pied myna, *Sturnus contra*.

Material & Method

Thirty six specimens of the barbet, *Megalaima zeylanica caniceps* were procured during suitable seasons. Harvesting of chromosomes was invariably done, *in vivo*, from bone-marrow cells of previously colchicinized adult individuals. The chromosomal plates were prepared after Rothfels & Siminovitch (1958) with certain modifications.

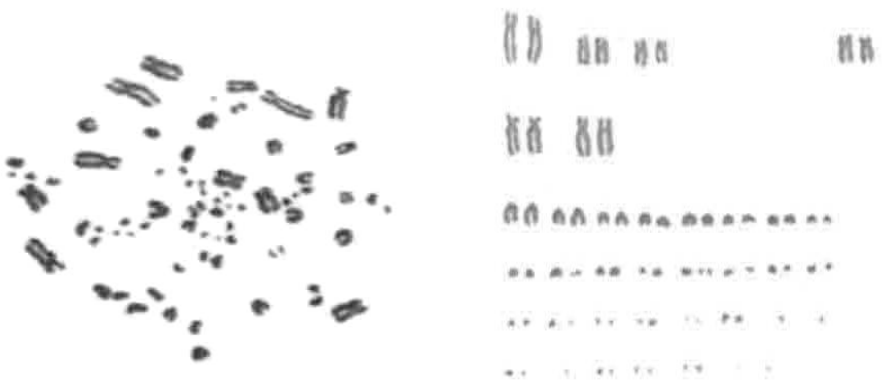
Cells were located and photographed at an initial magnification of 1500 x using an oil-immersion objective. A 35mm reflex camera, without lens, was adapted to take photo-micrographs using Kodak technical print film, Tri-X pan. A halonix tungsten lamp (12 V - 55 W) was used as the source of illumination.

The morphometric analysis, including percentage relative length (% L^R) and arm ratio (r), of the macro chromosomes was carried out from ten well spread metaphase plates of each sex. Computational program used after Elhance *et al.* (1997) provided mean and standard error. Classification of chromosomes, based on placement of centromere, was done according to Levan *et al.* (1964).

Results

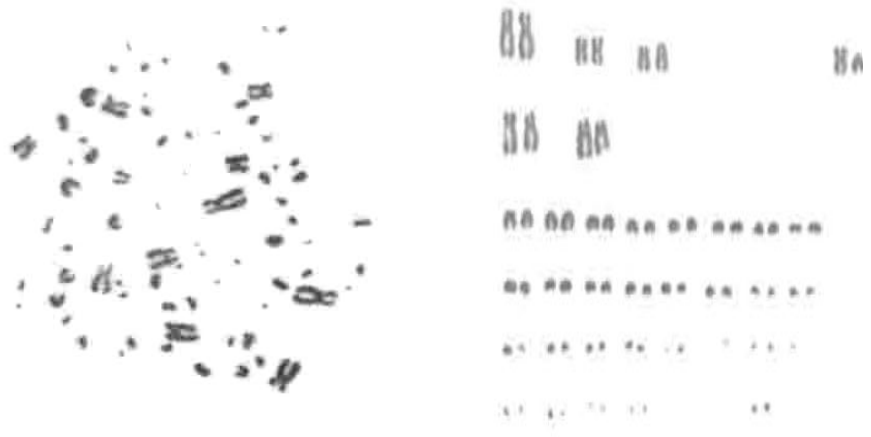
In all, one hundred well spread metaphase plates were examined. The diploid chromosome count varied from 78 to 85 with most prominent crest at 82 which has been taken as the diploid chromosome numeral of this species.

There was no morphological ambiguity between macro- and micro- chromosomes. Macrochromosomes were divisible into two groups :



Metaphase plate & karyotype of *Sturnus contra* (male).

Group I had four pairs of chromosomes comprising three autosomal pairs (Chromosome 1, 2, and 3) and a sex element (Z) - all had centromeres in their median county. Chromosome 1 is the largest element of the set being 5.04µ long, making up 25.33% of the total macrochromosomal length.



Metaphase plate & karyotype of *Sturnus contra* (female).

Chromosomes 2 and 3 were 2.96 and 2.37µ long respectively. The Z-chromosome was a little short of length than chromosomes 2 and 3 with an absolute length of 2.33µ.

Group II was made of two sub-metacentric chromosomes (chromosomes 4 and 5). Chromosome 4 is second largest chromosome of the set adding up to 20.01% of TML. Chromosome 5 was third in row, in the order of size ($_{L}^{R}$ = 16.16%).

Though W was a large chromosome as regard to its share in total macro-chromosomal length, yet it is the smallest element among macrochromosomes. It has a sub-terminal centromere and constitutes 7.81% of TML.

Morphometric data of macrochromosomes has been given hereunder:

Chromosome Number	% Relative Length	Centromeric Index	Chromosome Type
1	25.33 ± 0.39	70.86 ± 0.59	m
2	14.89 ± 0.13	39.95 ± 0.04	m
3	11.90 ± 0.36	42.01 ± 0.37	m
4	20.01 ± 0.22	30.61 ± 0.33	sm
5	16.16 ± 0.43	27.83 ± 0.78	sm
Z	11.71 ± 0.26	45.00 ± 0.50	m
W	07.81 ± 0.17	21.81 ± 0.73	st

The left over thirty five pairs of chromosome, that contributed more than half of the total chromosomal length and strewn all over the genome, were placed in the category of microchromosomes, as none of them shared ≥ 2.5% of TML on its own.

Discussion

Of 4,921 species of perching birds, 111 belong to family Sturnidae. However, merely six species viz. *Acridotheres facus* (Sharma *et al*., 1980), *A. ginginianus* (Srivastava & Misra, 1973) *A. tristis* (Patnaik & Prasad, 1980), *Sturnus malabricus* and *S. pagodarum* (Ansari & Kaul, 1977), *S. vulgaris* (Bulatova, 1981) have been chromosomally studied.

The present report hereby covers one more sturnid - *S. contra*, that exhibit karyological affinity with its other confamilial species. All the species possess six pairs of biarmed macrochromosomes. A little deviation was noticed in *S. vulgaris* by Bulatova (1981) as the third chromosome pair was telomeric. In all probability, such minor shifts in the location of centromere cropped up because of pericentric inversions involving a small chromosomal fragment. In all the sturnids reported so far, the unpaired element - W was found to be transitionally flanked by macro- and micro-chromosomes.

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