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MOLECULAR SEXING OF CONURES- COMPARATIVE EVALUATION OF THE EFFICACY OF THREE DIFFERENT PRIMER PAIRS

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ABSTRACT

Sexing in birds is important for scientific management, behavioral and ecological studies and also to improve breeding programme in captivity. Sexing by examining external morphology is difficult in more than 50% of the world's bird species. Since maintenance of ideal sex ratio is important for any successful breeding programme pet breeders encounter difficulties with breeding of monomorphic birds. In the present study, DNA was isolated from feathers and polymerase chain reaction was done using three different sets of primers to identify the sex of a popular pet bird, *Pyrrhura molinae* (Green-cheeked conure), which is monomorphic in nature. The primer sets were designed to amplify intron 9 and 16 of *CHDI*gene and intron 16 of NIPBL gene. Both *CHD1* (encoding chromo helicase- DNA-binding protein 1) and NIPBL (Nipped B homolog) is located in both the sex chromosomes, Z and W of birds.Intron 9 of *CHDI* gene was amplified by PCR technique in DNA isolated from the feather. As female birds are heterogametic (ZW) PCR amplification generated fragments of two different sizes- 1100 bp and 600 bp, whereas in male birds (ZZ), only a single fragment of 1100 bp was observed. Two different pattern generated on electrophoresis of amplicons, in male and female birds, helps to identify the sex accurately. The other two primer sets did not consistently yield different patterns in all male and female birds raising doubts in their efficacy in being used for sex identification of conures

KEYWORDS: CHD 1, Conure, NIPBL, *Pyrrhura molinae*, Sexing