

Abstract

The concerning of sexes is important for wildlife population study and conservation, however many monomorphic birds are hardly to determine sex in the field. This study tried to determine sex of Stripe-throated Bulbuls, the Asiatic monomorphic passerines, by using DNA sexing technique. Thirtythree adult Stripe-throated Bulbulshad been caught from their natural habitats in Chiang Dao Wildlife Sanctuary. All the birds were caught between March 2013 and October 2013 by using mist nets. Each bird was collected five morphometric data and approximately of 0.1 ml of blood sample for further DNA analysis. The bird's genomic DNA was obtained by using proteinase K extraction kit. The primers P8 and P2 were used to amplify CHD gene by polymerase chain reactions (PCR). For most sex determination, the PCR's product was visualized for the number of allele's band; a bird with one band is male and a bird with two bands is female. To predict the sex of our study species, we combined both molecular and morphometric data together to generate the multiple logistic regression which predicted 77.8% of our population tested in this study and based on small sample size. This mathematic analysis along with DNA sexing technique will be very helpful for sex determination of Stripe-throated Bulbuls in the field. Future study needs to deal with bigger of sample size for robust predictions. Our study may be used as a model for further wildlife bird population study.