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USING RANDOM SEQUENCE PRIMERS IN THE POLYMERASE CHAIN REACTION TO IDENTIFY GENDER-SPECIFIC GENETIC MARKERS IN HOUSE WRENS

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Visual gender identification in birds can be difficult if not impossible in sexually monomorphic species and is complicated even in dimorphic species when the sex of juvenile birds is sought due the lack of external sex characteristics. Surgical examination is reliable but is not practical because it is invasive and may place the organism at great risk. Furthermore, surgeries are time consuming and can only be performed by experienced field technicians making large scale gender identification an impossible task. Genetic based gender verification techniques, such as karyotype analysis, have been used to locate the W sex chromosome found only in heterogametic females. However, such studies have met with limited success due to difficulties in obtaining avian chromosome spreads or due to indistinguishable sex chromosomes. A reliable gender identification method that uses genetic markers identified within the DNA would be an asset to the researcher because it would require only a minimal blood sample which could be collected in the field without harming the bird and stored easily for long periods of time. Griffiths (1993) described such a technique based on the generation of RAPD markers (Random Amplified Polymorphic DNA). The use of RAPDs involves the amplification of genomic DNA in the polymerase chain reaction (PCR) using primers of arbitrary oligonucleotide sequence to generate a range of DNA fragments that can be separated by agarose gel electrophoresis. This study employs Griffiths' method to generate a reliable sex probe for the house wren (Troglodytes aedon) using RAPDs to isolate female-specific markers from random locations on the W sex chromosome. If successful, the sex probe will be used in future studies of house wren sex ratios. Specifically, gender identification information of house wren nestlings will be used to investigate facultative manipulation of sex ratios and similar phenomena that will require large-scale, accurate, and efficient determination of gender.