The use of non-invasive genetic sexing of echidnas from hair and scat samples for captive management and conservation

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The sex of an echidna cannot be easily determined by their appearance as they lack gender specific external features such as a scrotum. Non-invasive approaches to distinguish males from females have a number of applications in captive management and breeding programs as it removes the need for intensive handling and ultrasounds. Systematic sexing from hair and scats can also be used to address questions about sex ratios in the wild. Monotremes have an extraordinarily complex sex chromosome system, where the male echidna has 5X and 4Y chromosomes. Our systematic identification of X and Y specific sequences can be used to determine the sex of monotremes. Here, we have established a non-invasive PCR based technique using hair and scats to determine the sex of echidnas in wild and captive populations. Using as few as 10 echidna hair follicles or 300 mg of dried scat, genomic DNA was extracted followed by PCR amplification of two Y chromosome (male-specific) genes and one X chromosome gene; *Crspy*, *Amhy* and *Amhx,* respectively. Eight echidnas from the Perth Zoo breeding program were sexed using this technique, revealing a strong female bias, not uncommon for captive bred mammals. These results are aiding in the husbandry and continued breeding of this captive population. We have also successfully sexed a number of wild echidnas to begin exploring sex ratios in the wild. We are currently expanding the use of this technique in conservation, captive breeding and management of these iconic mammals throughout Australia.

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ABSTRACT BOOK