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Abstract W426

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W426

Developing genetic tools for conservation management of Asian rhinos

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**Alfred L. Roca** , University of Illinois at Urbana-Champaign, urbana, IL

The Javan rhinoceros (*Rhinoceros sondaicus*) and the Sumatran rhinoceros (*Dicerorhinus sumatrensis*) are both restricted in the wild to small populations in Indonesia. To permit censusing of these species non-invasively, we developed microsatellite markers for use with faecal DNA. We developed a bioinformatics pipeline that requires DNA from only one or two individuals to determine whether next generation sequencing (NGS) reads contain microsatellites and whether loci are polymorphic. This precluded the need for large-scale laboratory screening of markers to identify those that were polymorphic.

Since modern samples of Javan rhinoceros were not available, we relied on DNA from a museum specimen to identify 915 potentially polymorphic STR loci using the bioinformatics pipeline. Lack of access to Javan rhino faecal samples means that primers are being evaluated for DNA amplification using Indian rhinoceros (*R. unicornis*) faecal DNA. They are subsequently being tested for polymorphisms using DNA from fecal samples of wild Javan rhinoceros.

For Sumatran rhinoceros, 861 potentially polymorphic STR loci were identified after bioinformatics analysis of NGS reads using DNA from blood samples of 2 rhinos housed in USA zoos. We tested primer pairs that successfully amplified 29 polymorphic loci in the zoo rhinos. These primers will be used on non-invasively collected faecal samples from wild rhinos. For both species, development of genetic markers can aid in conservation and management through assessment of genetic diversity and relatedness, identification of conservation units, and census estimates.

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