W920: Genetic Analysis and Marker Development in the Sumatran Rhinoceros (*Dicerorhinus sumatrensis*)

Wednesday, January 15, 2020 10:30 AM - 10:50 AM ♥ Royal Palm Salon 5-6

The Sumatran rhinoceros is critically endangered, with fewer than 100 individuals surviving across its current range. Accurate census estimates of the remaining populations are essential for development and implementation of conservation plans. In order to enable molecular censusing, we developed microsatellite markers with amplicon sizes of short length, appropriate for non-invasive fecal sampling. A bioinformatics routine identified Illumina MiSeq genomic reads with short tandem repeats, and screened for loci that were polymorphic within the dataset. Twenty-nine novel polymorphic microsatellite markers were characterized (A = 2.4; HO = 0.30). These were sufficient to distinguish among individuals (PID < 0.0001), and to distinguish among siblings (PID(sib) < 0.0001). Markers were tested using samples in Indonesia, including fecal samples collected from wild rhinoceros in Sumatra. A subset of markers was established as polymorphic and effective for genotyping DNA from fecal samples of wild rhinoceros

To aid in conservation planning, we sequenced 218 bp of control region mitochondrial (mt) DNA, identifying 17 distinct mitochondrial haplotypes across modern (N = 13) and museum (N = 26) samples. Museum specimens from Laos and Myanmar had divergent mtDNA, consistent with the placement of western mainland rhinos into the distinct subspecies D. s. lasiotis (presumed extinct). Haplotypes from Bornean rhinos were highly diverse, but dissimilar from those of other regions, supporting the distinctiveness of the subspecies D. s. harrissoni. Rhinos from Sumatra and Peninsular Malaysia shared mtDNA haplotypes, consistent with their traditional placement into a single subspecies D. s sumatrensis. Modern samples of D. s. sumatrensis were genotyped at 18 microsatellite loci. Rhinos within Sumatra formed 2 sub-populations, likely separated by the Barisan Mountains, though with only modest genetic differentiation between them. There are so few remaining Sumatran rhinoceros that separate management strategies for subspecies or subpopulations may not be viable, while each surviving rhino pedigree is likely to retain unique alleles. Because rapid genetic erosion is inevitable, along with the potential for fixation of harmful genetic variants, we underscore two overriding priorities for the species: 1) translocation of wild rhinos to ex situ facilities, and 2) collection and storage of gametes and cell lines from every surviving captive and wild individual. (Additional co-authors will be listed in the talk or poster.)

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