Population genomics of the critically endangered spoon-billed sandpiper

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The nature of genetic changes contributing to species extinction and impeding population recovery remains poorly understood. To elucidate possible genetic components of drastic population decline, we studied the population genetic history of the critically endangered spoon-billed sandpiper and its sister species, the red-necked stint, which is of least concern. At present, the spoon-billed sandpiper population is estimated at 100-200 breeding pairs, making it one of the rarest vertebrates. Using several complete genome sequences of both species, we found that while the red-necked stint population was relatively constant across 500,000 years, the spoon-billed sandpiper population peaked 15,000-25,000 years ago during the last glacial maximum, when suitable breeding habitat was likely abundant, and has been declining since. The increase of the population prior to the ongoing decline led to accumulation of recessive deleterious polymorphisms, imposing an additional burden on the spoon-billed sandpiper population. Thus, complex demographic changes leading to gain of deleterious genetic diversity pose an additional risk to species survival and recovery by increasing the cost of inbreeding. Specifically, species that had greater habitat availability during the last glacial maximum may be especially prone to this effect.