



Cover image: Pictured are a tigress and cub in Ranthambore Tiger Reserve, India. Anubhab Khan et al. used whole-genome sequences from 57 Bengal tigers (*Panthera tigris tigris*) to estimate individual inbreeding and mutation loads in a small, isolated population and two large, connected populations of wild tigers in India. Individuals in the isolated population were more inbred with a higher frequency of loss-of-function mutations compared with the connected populations. However, the isolated population had relatively fewer mutations, likely due to purging of deleterious recessive mutations. The findings suggest that genome-wide analysis can enable genetic rescue strategies for alleviating the effects of inbreeding depression in small, isolated tiger populations. See the article by Khan et al., e2023018118. Image courtesy of Kaushalkumar Patel.

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