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Abstract W427

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A status update on rhino reference genome assemblies

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Generating complete genome sequences from all rhinoceros species is a prerequisite for exploring the comparative genomics and evolutionary relationships within the Rhinocerotidae. In addition, providing access to reference genome assemblies will enable future projects aimed at developing markers for genetic monitoring, assessing population genomic structure and local adaptations, as well as to quantify the extent to which recent demographic declines have affected genome-wide diversity, inbreeding and genetic load within each species. The aim of this presentation is to provide a status update on ongoing collaborative projects aimed at assembling genome sequences from several species, both in Africa and Asia. I will also outline some ongoing species-specific projects currently underway in Stockholm that aim to examine micro-evolutionary changes using a population genomic approach.