Background: *Medemia argun* is a rare wild palm tree species. Its global existence is assumed to include the main population of about 1000 trees in the Nubian Desert of Sudan and some scattered individuals in southern Egypt. The species had previously been assumed to be extinct, but then reported to be extant about 20 years ago.

Aims: To assess genetic variation and explore population genetic structure of *M*. *argun*, through development and analysis of microsatellite markers.

Methods: The genome sequence mining approach was applied in order to identify microsatellites in the chloroplast genome of *Bismarckia nobilis*, a species closely related of *M. argun*. A set of 49 markers were designed, and their characteristics are now provided. Seven chloroplast DNA markers were developed for use in the genetic characterisation of this threatened species.

Results: Five markers were found polymorphic in *M. argun*, which enabled the assessment of the genetic diversity of the species. Significant genetic differentiation was observed among generations and collection sites, accompanied by low genetic variation. The seven markers developed were polymorphic among the wild relatives *Hyphaene thebaica* and *Borassus aethiopum*.

Conclusions: This is the first study to report molecular markers for *M. argun*. Our results suggest that the genetic consequences of population fragmentation in *M. argun* are beginning to be evident.

