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Low microsatellites used to investigate leopard genetic structure severely restricts the results by Ropiquet et al. (2015) to infer population structure for managers

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ABSTRACT

Low microsatellites used to investigate leopard genetic structure severely restricts the results by Ropiquet et al. (2015) to infer population structure for managers.

The statistical power of microsatellites is reduced as fewer loci are used and the use of insufficient data when analysing for population structure can have severely misleading results [1–3]. The use of only eight microsatellite markers to report on the contemporary genetic structure strongly limits the statistical accuracy and validity of the results by Ropiquet et al. (2015) and therefore restricts firm conclusion from results [3]. This is a sever caveat to this study, yet the authors did not report on why so few microsatellites were used, nor is there a note on the likely inaccuracy of their findings as a result.

The use of so few microsatellites is likely the compounding factor explaining the large discrepancy in population estimates (K) from GENELAND ($K = 8$ to 20), while STRUCTURE software was as low as $K = 2$. This implies poor statistical power, yet the researchers firmly conclude “Both GENELAND and the multivariate analysis suggested the dataset comprises a single gene pool” [4]. In addition, Ropiquet et al.’s [4] own Principle Contribution Analyses (PCA) results suggest moderate substructuring resulting in what appears to be five groups, rejecting their firm conclusion that leopards in southern Africa “comprise a single gene pool” [4]. Furthermore, nowhere in text is the polymorphic content of the markers or allele frequencies reported nor is there any explanation as to why this was not reported on. These are central to describing genetic structure [5] and without these data the statement of one gene pool cannot be supported. The divergences of population structure and PCA results at very least require some discussion regarding how this impairs the use of their results and that these results should rather be used to point out the importance of further research as opposed to inform rigid conservation management.

Notably, considering the very low quantity of peer-reviewed studies available on the genetic structure of leopard in southern Africa using either mtDNA [6] or nuclear DNA [7], no research comparisons were made to existing research. This is concerning as accurate, objective, responsible and useful research should consider available support, or alternative findings require discussions regarding why there may be departures from other studies findings. This is important in order to improve science.

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In summary, the use of only eight microsatellites, and the large differences between population estimates does not support Ropiquet et al. [4] claims for one genepool for leopards in Southern Africa. When such low statistical power is used and large variations in results occur, it is not possible to make a convincing case to infer population structure. The variation obtained from just eight markers is most likely a confounding factor, and no reliable statistical deductions should be made from data obtained from such a small set of short tandem repeat (STR) markers. Managers should therefore refrain from relying on the findings from this paper that the leopard population is a single genepool, as the results are not able to support such claims. It is deeply concerning that poor data is adopted with such ridged claims within peer-reviewed science.

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