Molecular phylogenies and their application to biogeographic questions, as illustrated by Kondo et al. [1] in their study of *Livistona* palms in Australia, are providing unprecedented insight into speciation and the historical movement of taxa around the world [2]. While such studies often allow for the clarification of taxonomic relationships, they can also raise challenging dilemmas in regard to species management plans and the policy that underpins these strategies [3]. Although framed as a test of species range formation, the Kondo et al. [1] study generates conclusions that are particularly relevant for policy relating to the management of non-native populations. In this commentary, we highlight the broader relevance of the article by Kondo et al. [1] to concepts that define native or non-native status, and discuss the implications for conservation and management policies.

Kondo et al. [1] used nuclear microsatellite data to investigate the relationship between *Livistona mariae* F.Muell., an iconic palm endemic to central Australia, and its nearest relative, *Livistona rigida* Becc. Their study establishes that *L. mariae* and *L. rigida* diverged from a common ancestor around 15 375 years ago (90% highest posterior density interval: 6625–30875 year BP) [1]. This timeframe invalidates the hypothesis that *L. mariae* is a relictual population which has survived since before the aridification of central Australia (15 Ma) [4,5], and also the alternate explanation of dispersal via Pliocene river connections. The two taxa were found to be very closely related, in a pattern which indicates that they should be treated as a single species or subspecies rather than fully separate species; this finding strongly supports recent long-distance dispersal of a common ancestor into central Australia.

Two types of long-distance dispersal vectors are considered by Kondo et al. [1]: fruit-eating birds and bats, or humans. The former vectors are known to consume and distribute the seeds. Early human colonizers were present (at least sporadically) in central Australia during the timeframe established for genetic divergence between the two palms [6]. Moreover, the growing shoot (palm-heart) of *L. mariae* was eaten as a vegetable [7], which may have provided an incentive for humans to attempt to establish populations in new areas. As discussed by Kondo et al. [1], the vast distance between *L. rigida* and *L. mariae* (ca 1000 km) makes it highly improbable that birds or bats dispersed the seeds. Therefore, human dispersal remains the only plausible explanation for *L. mariae* in central Australia.

Given the insights of Kondo et al. [1] regarding the establishment of *Livistona* in central Australia, several questions are raised: are the *L. mariae* populations native or non-native; does progress towards speciation since arrival affect the native status; what implications does this status have on conservation management; and is existing policy adequately equipped to deal with this situation and others of a similar nature?

The native status of *Livistona* populations in central Australia can be assessed at three levels: at the international level, using the International Union for Conservation of Nature (IUCN) guidelines [8]; at the national level, under the *Environment Protection and Biodiversity Conservation Act 1999* [9] and at the territory level, under the *Territory Parks and Wildlife Conservation Act 2005* [10]. Until now, all three jurisdictions have recognized these *L. mariae* populations as native in central Australia; this has earned the taxon eligibility for conservation management.

However, as Kondo et al. [1] have excluded all previously accepted explanations for the occurrence of *L. mariae* in central Australia, and have concluded human dispersal is the most parsimonious explanation, the native status of these populations should be reassessed. At the international level, the populations would be regarded as non-native, and would be ineligible for conservation assessment [11]. At the national and territory levels, the populations would be regarded as native and retain eligibility for conservation management: at the national level, because it was present in Australia pre-AD 1400 [9]; at the territory level, because it appears to have been moved by Aboriginal people pre-AD 1788 [10]. The lack of agreement on native status creates a challenging dilemma, as management decisions are tightly linked with native or non-native status.

This inconsistency regarding status has occurred through the lack of a standard assessment process. Globally, native or non-native status is generally determined by one (or both) of two concepts: presence in an area before an arbitrary cut-off date imparts native status, and human-mediated movement of individuals results in non-native status. As demonstrated in the case of *L. mariae*, the differences between definitions can result in inconsistent assessment of status. Clearly, we were not less human before any of the arbitrary cut-off dates in use, and the territory legislation [10] is the only example we are aware of where status is explicitly influenced by the heritage of the human disperser. The study by Kondo et al. [1] is one example of an increasing
body of evidence documenting human-mediated population establishment over many millennia and across many regions [12]. This suggests that conflicts between assessment criteria will continue to arise unless we revisit our definitions.

A novel framework for assessing native or non-native status has recently been proposed [13], which provides a universally applicable definition. This framework uses the concept of a projected dispersal envelope (PDE) to define the region where populations are or could be native. Within the PDE, all new populations are regarded as native; the actual dispersal vector of a new population (whether human-mediated or not) is irrelevant. New populations established outside the PDE (implicitly by humans) have non-native status. In this way, the framework is based on where a taxon may expand its range naturally, rather than on an arbitrary date or a known (or assumed) record of human dispersal. This framework clarifies the assessment of populations where we are unable to positively identify human-mediated dispersal, but can include/exclude dispersal by natural vectors.

The dispersal envelope of the ancestral palm from which both L. mariae and L. rigida have descended can be inferred from the current distribution of L. rigida, in combination with biogeography and the life-history traits of both palms. The location of L. mariae in central Australia is, and always was, outside the dispersal envelope of the ancestral palm. Therefore, the palm populations in central Australia were initially non-native. Divergence from the ancestral taxon does not alter this status, as the native status of a population is not affected by speciation [13]. Under this new, universally applicable framework for assessing status, L. mariae is a non-native taxon with no native range.

The implications of this finding are serious, as relevant laws for conservation assessment and management of L. mariae are only applicable to native taxa [9,10]; assessment of L. mariae as non-native would render it ineligible for conservation management. However, L. mariae has significant cultural, historical and natural values [4,7,14]. In our opinion, native or non-native status provides an important premise for developing management strategies, but should not be used to automatically determine specific management goals; because these goals should also reflect any ecosystem impacts, ecological functionality and cultural heritage among other factors. Integration of these factors has been a central component of recent discussions among invasion and conservation biologists, regarding the relevance of the native/non-native dichotomy [15–17]. The current consensus is that recognizing non-native status adds value to our understanding and management of non-native populations [18,19], while also allowing for pragmatic management objectives.

Another palm, the coconut (Cocos nucifera L.), is an additional example of the need for pragmatic management, moving away from the simplistic arguments of ‘conserving natives’ and ‘controlling aliens’. The status of coconut populations in Australia is highly disputed, despite substantial evidence of native status [20]. The application of molecular phylogenies to biogeographic chronologies has recently provided further insight into the distribution history of the coconut [21], in much the same way that Kondo et al. [1] have provided insight into the distribution history of L. mariae. This insight reaffirms that coconut populations are native to coastal Australia, but should not necessarily mandate coconut conservation in situations where the recent establishment of large populations is having negative ecological impacts.

Molecular phylogenies clearly have much to offer our understanding of biogeographic processes and patterns. The presence of L. mariae in central Australia has aroused curiosity in the scientific (and broader) community ever since it was first described. The study by Kondo et al. [1] provides a valid alternative to the long-accepted relic hypothesis and has changed our understanding of this iconic palm. The study has also facilitated a broader examination of issues with existing policy, which suggests the concepts that currently define natives and non-natives are inadequate, particularly with regard to human-mediated introductions. While these concepts may be simple to define, they are fundamentally limited for guiding appropriate policy as we strive to protect biodiversity in a world of rapid global change.

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References
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