



Digest: Why are there no ring species?*

Nagarjun Vijay^{1,2}

¹University of Michigan, Ann Arbor, Michigan 48109

²E-mail: nagarju@umich.edu

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Geographical barriers are known to act as a scaffold around which a series of interbreeding populations can form a ring. When the terminal forms that reunite after encircling the barrier are reproductively isolated, the entire collection of populations is called a ring species. However, even popular examples of ring species do not measure up to the textbook definition (Wake 1997; Highton 1998; Alcaide et al. 2014). The paucity of examples is further exacerbated by the eventual break up of ring species into multiple species (Martins et al. 2013).

Ring species are considered rare novelties, yet they have been studied in the hopes of understanding the processes that are important to speciation (Irwin et al. 2001). The idea is that the series of populations around the ring provide snapshots of different stages of spatial and temporal separation prior to reproductive isolation. While continuous gene-flow between the populations along the ring is the ideal scenario, periods of allopatry in different parts of the ring have been noted in most well-studied examples. Genetic studies of species complexes that had once been considered ring species have shown they do not adhere to the traditional definition of a ring species, but have generated a wealth of data on the importance of gene-flow as well as geographic separation.

Species distribution is dictated by barriers that give shape to a species' range (exogenous barriers) and barriers that cause population structuring within the species' range (endogenous barriers). Understanding the relative importance of these two types of barriers is an important question in speciation research.

In this issue, Martins and de Aguiar (2016) simulate the evolution of ring species and evaluate the importance of exogenous versus endogenous barriers, compare different spatial distributions, and highlight the conditions that will favor the emergence of ring species. Interestingly, the simulations show that exogenous

barriers are more important than endogenous barriers when both types of barriers are incorporated in the same model.

By calculating partial rank correlation coefficients, Martins and de Aguiar are able to rank the importance of the parameters being explored in their model. The width of the corridor along the ring and carrying capacity show up as the most important model parameters. Although the models explored in this study do not allow for heterogeneity in mutation rate or efficacy of selection among loci, they highlight the importance of number of loci as well as the mutation rate.

Using different combinations of these two parameters—mating area and corridor width—the researchers are able to show how well each parameter combination favors the formation of a single species, multiple species, and ring species. Formation of single species is favored when corridors are wide and mating areas are large. Formation of multiple species is favored under opposite conditions. The combination of very narrow corridors and less spatial structuring in the direction of range expansion favors the formation of ring species. Such narrow corridors are vulnerable to breaks in gene flow due to local perturbations. This is consistent with the pattern of allopatry seen at different points along the range of ring species and could explain why perfect examples of ring species are not found in nature.

The recent availability of whole-genome sequencing data has led to the study of genome-wide patterns of nucleotide sequence differentiation in a multitude of species (Seehausen et al. 2014). Future work could incorporate insights from these data, such as genome-wide heterogeneity in differentiation as well as genetics of reproductive isolation in simulations, as in Flaxman (2014) and Roesti et al. (2014), to provide further insight into the role of barriers to gene flow in speciation.

LITERATURE CITED

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