

Centres of origin: do they exist, can we identify them, does it matter?

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Introduction

This workshop assessed the importance and feasibility of identifying "centres of origin" as a guide to selecting areas for survey for classical biocontrol agents for invasive weeds. After an introduction to the issues (McClay), presentations were made on biogeographical methods and problems associated with the centre-of-origin concept (Crisp) and the role of molecular genetic methods in identifying areas of origin (Hufbauer). Two case histories were presented, on the identification of the geographical origin of a wax scale insect (Qin) and of the invasive shrub *Ligustrum robustum* (Evans, Shaw). These presentations were followed by a general discussion (recorder Tim Heard).

Terms and concepts

It is important to distinguish some of the concepts used in relation to "centres of origin" and as guides to selecting areas to survey for biological control agents. The "native range" is the area where a species occurs without having been introduced, deliberately or accidentally, by humans. The "centre of origin" of a species (or higher taxon) is the range that the taxon occupied when it first separated from its sister group. This may or may not be a smaller area than its present native range. The "source of introduction" or "provenance" is the location within the native range from which a founding population was introduced into the exotic range. A "centre of diversification" is an area containing a high diversity of native species closely related to the target weed; this may or may not be an indication of the area in which the target species itself

originated, depending on the phylogenetic relationship between the target weed and the other species involved.

Biogeographic methods are available for inferring centres of origin. However, it should be noted that the vicariance school rejects the very notion of a "centre" of origin (Craw et al. 1999, Nelson & Ladiges 2001). Speciation theory suggests that some species evolve from widely occurring meta-populations, rather than from a localized site or "centre". It is difficult to distinguish these alternatives retrospectively, as indicated by the controversy over whether *Homo sapiens* originated over a broad front or in an African centre. Moreover, species' ranges expand and contract with time, and present distribution is not a reliable indicator of that in the distant past (Losos & Glor 2003). The Progression Rule (Brundin 1988, Hennig 1966), a long-standing approach that is still in use, makes the fallacious assumption that a species-poor ("basal") sister taxon occupies the centre of origin from which migration proceeded to the area occupied by its species-rich ("derived") sister taxon (Platnick 1981). Other methods for inferring ancestral areas using a phylogeny have been proposed by Bremer (1992), Page (1994), and Ronquist (1997). The last two attempt to trade off vicariance against jump dispersal and involve difficult decisions about the relative weight (probability) of different events, such as vicariance, dispersal, speciation and extinction. Although some data sets will give unambiguous answers to the area of origin using these methods, in many cases the area of origin cannot be resolved. It was suggested that weed biologists should ask whether it is important to find the (perhaps mythical) centre of origin of the host taxon, or whether they should sample the native range as widely as possible in a direct search for novel biocontrol agents. If the purpose is to identify the native range of a weed, this is better addressed by the methods of population genetics than by biogeographic methods.

The modes of speciation discussed above (see also Levin 2000) will influence patterns of molecular variation used to detect potential areas of origin of species. Speciation via vicariance is likely to lead to greater genetic variation than speciation via dispersal or sympatric speciation. The ability to detect the geographic location in which an organism speciated will depend upon the mode of speciation, the subse-

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quent geographic range and history of the species, the samples obtained for analysis, and the markers used. It is critical to obtain samples of the species of interest from across the native range.

Phylogeography is the field of study concerned with mapping of lineages of populations and closely related species through time and geographical space (Avice 2000). In reconstructing phylogeographic relationships, the most useful markers are ordered markers such as sequence data. By knowing the location of samples of the species of interest, plus the location of closely related species, it is possible to infer a common geographic region at the base of the lineage. Because gene trees may not always represent the history of a species, it is key to obtain sequences from more than a single gene to determine if there is concordance between them.

Qin et al. (1994) used cladistic and biogeographic analyses to identify the geographic origin of an insect pest, the wax scale *Ceroplastes sinensis*. Similar analyses may be useful for some cosmopolitan weeds. Shaw and Evans used molecular methods to identify Sri Lanka as the provenance of the invasive privet *Ligustrum robustum* ssp. *walkeri* in La Réunion, but this area had a limited range of host-specific agents. It was felt that surveys in the area of origin, if this could be identified, might increase the pool of candidate agents.

Conclusion

The discussion covered a variety of topics including the geographic origins of alligatorweed, water hyacinth, parkinsonia, parthenium, melaleuca, and climbing fern. Practitioners appeared to feel that the attempt to determine the centre of origin was worthwhile as a way of prioritizing areas for survey, despite some of the biogeographic problems surrounding the concept. In some cases it may be more appropriate to say that the goal is to identify the native range, rather than the centre of origin. It is clear that these issues need to be further

explored in order to provide practical guidance in the selection of survey areas, and the participants in the workshop hope to do so in a future paper.

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