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Defining ‘ethnobotanical convergence’

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In a recent forum article published in this journal, Garnatje et al [1] propose a new term, ‘ethnobotanical convergence’, to describe “similar uses for plants included in the same node of a phylogeny”. Drawing a parallel between cultural and organismal evolution, Garnatje et al [1] suggest “some plants have similar morphological characteristics because they have close phylogenetic placement, a phenomenon termed ‘evolutionary convergence’”. Evolutionary biologists do not interpret the morphological characteristics shared by related species as convergence, but as homology. Applying phylogenetic methods to test hypotheses of homology, convergent traits are those with independent origins in unrelated species [2]. The definition of ‘ethnobotanical convergence’ Garnatje et al [1] propose is fraught with problems because it overlooks the accepted meaning of the term convergence, and also the challenges of identifying independent origin of traditional knowledge. We argue that the term ‘ethnobotanical convergence’ should be limited to cases where there is clear evidence to support a hypothesis of independent discovery.

Whether plant use is the result of independent discovery may be important when designing bioprospecting strategies. Several authors have suggested that independent discovery of plant properties by people of different cultures is strongly suggestive of plants’ bioactivity [3-5]. Plant use that is found in more than one culture could be the result of independent discovery, shared ancestry or cross-cultural transmission of knowledge (see for example, [6,7]). Evolutionary anthropologists have adopted phylogenetic methods to discriminate between these alternative explanations for cultural similarity [8]. Using a phylogenetic framework derived from linguistic data, traits are mapped onto the phylogeny. A rigorous definition of ‘ethnobotanical convergence’ would depend on these approaches to identify multiple independent origins of plant use.

Here we outline two scenarios that could result in the shared use of closely related plants, using the terms horizontal (transmission of knowledge between cultures) and vertical (from one generation to the next, and from ancestral to descendent cultures) to describe modes of transmission of knowledge. In our first scenario, closely related peoples use closely related plants. This is not in itself indicative of independent discovery, since the knowledge could be “ancestral”, the result of vertical transmission of knowledge. Shared use by closely related people is not especially informative in a bioprospecting context. In our second scenario, distantly related peoples use closely related plants. In this case shared use could be interpreted as independent discovery of the plant's use. However, it would be important to consider the spatial distribution of the people, since horizontal transmission is possible between cultures newly in proximity, perhaps following migration or trade (see [9] for an example of cross-cultural adoption of plant use following migration). So far, for bioprospecting, independent discovery of the uses of plants has been inferred or implied, without recourse to linguistic phylogeny. For example, Saslis-Lagoudakis et al [10] compared medicinal floras of linguistically unrelated and geographically separated peoples so that shared use could be attributed to independent discovery. In contrast, Garnatje et al [1] cite the use of congeneric oregano species as ethnobotanical convergence. The cultures cited by Garnatje et al [1] as using oregano species have had significant historical opportunity for knowledge transmission, making it difficult to attribute similar use to independent discovery. In such cases, linguistic relationships between the compared societies to account for cultural relatedness (Galton's problem), evidence from written records, and comparison of cognate or loaned plant names may discriminate between shared ancestral knowledge, knowledge transmission and true ethnobotanical convergence.

That closely related plants are chemically similar drives the rational use of phylogenies of plants in bioprospecting [10]. Plants included in the same clade of a phylogeny might be expected to have similar therapeutic applications across cultures because they have similar bioactivity. Lineages rich in species used medicinally, termed "hot nodes" [11], encompass the "similar uses for plants included in the same node of a phylogeny" referred to by Garnatje et al [1]. Phylogenetically-informed bioprospecting of medicinal plants depends on interdisciplinary approaches that combine plant phylogenies, cultural phylogenies and ethnobotanical data. Introducing confused terminology at the outset will hinder the interdisciplinary conversations required.

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