Low levels of allozyme differentiation between *Pyxidanthera* (pyxie-moss) taxa (*Diapensiaceae*)

MARY Jo W. GODT and J. L. HAMRICK

Received May 27, 1994; in revised version August 9, 1994

**Key words:** *Diapensiaceae, Pyxidanthera barbulata, Pyxidanthera brevifolia, pyxie-moss.* – Allozymes, conservation, genetic diversity.

**Abstract:** Two *Pyxidanthera* morphs of questionable taxonomic rank are described in the eastern United States. We analyzed leaf samples from nine *Pyxidanthera* populations (four of each morph and one with intermediate morphology) for 13 allozyme loci. Our results do not support differentiation of the two morphs at the species level. Mean genetic identity among populations was high (I = 0.97), and typical of that found for conspecific populations. The proportion of total genetic diversity found among populations was low (ĜST = 0.079). Several low frequency alleles were confined to each of the morphs, being found in some of the populations of each morph, but not all.

Nomenclatural assignments fundamentally affect our perception of the biological world, and have far-reaching consequences for the preservation of species and entities of lesser taxonomic rank (AVISE 1993). The necessity of naming species in the tropics, where vast numbers of taxonomic units have yet to be identified, is well-recognized. However, many entities of questionable taxonomic rank and taxa with obscure phylogenies still exist in temperate regions, despite the fact that these floras have been relatively intensively studied. In this paper we examine one such group.

*Pyxidanthera* (*Diapensiaceae*) is a prostrate, evergreen subshrub. Vegetatively, *Pyxidanthera*, with its small, dense, awl-shaped leaves, and creeping habit, superficially resembles a moss, giving rise to its common name, pyxie-moss. In early spring, pyxie-moss “mats” produce numerous attractive single white flowers. *Pyxidanthera* is reported to be obligately outcrossed (PRIMACK & WYATT 1975). Pyxie-moss seeds are small (0.6–0.8 mm) and produced within a capsule (RADFORD & al. 1968). The distribution of *Pyxidanthera* stretches from Long Island, New York, along the Atlantic Coastal Plain into northern South Carolina. Two taxa have been described in this region: *Pyxidanthera barbulata* Michx. and *P. brevifolia* Wells. Wells (1929) differentiated *P. brevifolia* from *P. barbulata* on the basis of its smaller, thicker leaves and more compact branching habit. *Pyxidanthera brevifolia* was described from the dry sandhills region of North Carolina, where it is found on xeric longleaf pine and turkey oak knolls and ridges. The distinct mor-
phology of *P. brevifolia* was considered to be the result of adaptation to this xeric environment (WELLS 1929). The current distribution of *P. brevifolia* is limited almost exclusively to Fort Bragg, a U. S. military base in North Carolina. *Pyxidanthera barbulata* is found in pine barrens, pocosin ecotones, and pine/wiregrass flatwoods, on soils that retain moisture to a greater degree than those of the sandhills. There is a slight tendency for *P. brevifolia* to begin blooming earlier than *P. barbulata*, probably due to temperature differences associated with soil types (A. WEAKLEY, NC Heritage Program, pers. comm.). The chromosome numbers of *P. barbulata* (RADFORD & al. 1968) and *P. brevifolia* (REYNOLDS 1968) are n = 6.

The taxonomy of the two *Pyxidanthera* morphs has been controversial. For example, RADFORD & al. (1968) indicate that the genus is monotypic but that it is represented by “two fairly well-marked varieties”, while FERNALD (1950) indicates that the genus is represented by “a single or possibly two species”. Interest in elucidating the taxonomic relationship of the two *Pyxidanthera* morphs has arisen in part because of the limited distribution of *Pyxidanthera brevifolia* and the need to determine whether it merits particular protection and conservation. The objective of this study was to assess allozyme diversity in *Pyxidanthera* in order to determine the genetic similarity of populations exhibiting the two described morphologies.

**Material and methods**

Twenty to forty samples of *Pyxidanthera* were collected from nine populations (Fig. 1; Table 1). Four populations had *P. brevifolia* morphology, four had *P. barbulata* morphology, and one was intermediate (BRUCE SORRIE, NC Nature Conservancy, pers. comm.). The population exhibiting intermediate morphology (BR 056) may have resulted from hybridization between *P. barbulata* and *P. brevifolia* (BRUCE SORRIE, pers. comm.). Voucher specimens were deposited at GA and NCU. Samples were placed on ice and transported to the University of Georgia within 48 hrs of collection. Samples were quick-frozen with liquid nitrogen and crushed using a mortar and pestle. Two crushing buffers (MITTON & al. 1979, WENDEL & PARKS 1982) were tried on a subset of samples. Preliminary experiments indicated that, in general the WENDEL & PARKS (1982) buffer produced better results. This buffer was added to the leaf material of the population samples after crushing. Enzyme extracts were adsorbed onto chromatography paper wicks that were stored at −70 °C until samples were analyzed electrophoretically. Ten enzyme systems produced consistently resolvable bands. These enzymes (and the loci scored) were amino acid transferase (Aat-1); diaphorase (Dia-1), isocitrate dehydrogenase (Idh-1 and -2); fluorescent esterase (Fe-1 and -2); malate dehydrogenase (Mdh-1); malic enzyme (Me); menadione reductase (Mnr-1); phosphoglucosomerase (Pgi-2); phosphoglucomutase (Pgm-1); and triose phosphate isomerase (Tpi-1 and -2). Stain recipes are given in SOLTIS & al. (1983), except for amino acid transferase and diaphorase, which are described in CHELIAK & PITTEL (1984). The following electrophoretic buffer systems were used to resolve the enzyme loci (numbers refer to table 1 in SOLTIS & al. 1983): System 6 (Dia-1, and Tpi-1 and -2); System 7 (Aat-1, Mnr-1); and System 11 (Idh-1 and -2, Mdh-1, Pgi-2, and Pgm-1). A modified System 8 was used to resolve Fe-1, Fe-2, and Me. Allozymes were numbered consecutively, with the fastest migrating allozyme designated one, the second fastest, two, etc. Standard measures of genetic diversity (HAMRICK & GODT 1989) including the percent polymorphic loci (P), the mean number of alleles per locus (A) and per polymorphic locus (AP), the effective number of alleles per locus (Ae), and genetic diversity or expected heterozygosity (Hₑ) were calculated for each population. Population means were calculated for each putative taxon, and across all sampled populations. Because no diagnostic differences were detected between the two described taxa, the data from all the populations...