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Different scales of adaptive diversity in *Austrodanthonia*—a case against domestication

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Key words : domestication, *Austrodanthonia*, genetic diversity

Introduction Scales of intraspecific variation have implications for the restoration of native plant communities as different populations may exhibit differences in adaptation. *Austrodanthonia* is a widespread genus of C₃ native grasses of southern Australia. These grasses are putatively self-pollinating and a ploidy series has been reported for some species. Two species, *A. bipartita* and *A. fulva*, have been the focus of domestication programs, and the most widespread species, *A. caespitosa*, has been released as a composite of wild ecotypes. Wildland stands of *A. caespitosa*, as well as *A. setacea* and *A. eriantha*, are routinely harvested as local seed sources. Domestication and selection programs have generally focused on comparison of limited numbers of genotypes, usually from higher rainfall and higher fertility areas rather than populations from diverse environments. Despite the importance of this group of plants to the pastoral industry the genetic structure of wild populations and its relationship with environment is largely unknown.

Materials and methods Genetic variation among and within 33 wild populations of the above five commonly occurring species was examined within a 75,000 km² area in central western New South Wales. This variation was related to environmental data associated with locality in which the populations were growing and site characteristics specific to the environment of individual plants. Differences in flowering traits, (using common garden experiments), and chromosome number, (flow cytometry) were related to environmental variables. Molecular markers (ALFP) were also used to examine the genetic structure between and among 13 populations of *A. caespitosa*.

Results Most populations comprised at least four *Austrodanthonia* species and coexistent cytotypes. For most species, tetraploids were the most prevalent cytotype, but no common ecological factors (climate, edaphic or micro-site) clearly distinguished cytotypes, suggesting they may readily hybridise. The occurrence of low frequencies of intermediate cytotypes and overlap in flowering times for all species provides a possible mechanism and additional evidence for inter- or intraspecific hybridisation. Most of the variation in flowering traits occurred amongst populations for all species, suggesting ecotypic variation. The partitioning of variation in flowering traits for *A. caespitosa* is given in Table 1. Flowering traits of *A. caespitosa* were related to a suite of environmental characteristics reflecting the adaptive nature of this variation. For example, northern and western populations growing in more varied and summer-dominant rainfall environments had a-seasonal flowering patterns (flowering when it rains) and a greater reproductive effort than southern populations growing in winter-dominant rainfall areas. Autumn is a season more favourable for establishment and seedling survival, and was associated with a more synchronous and short flowering period than spring flowering for all populations and all species. Molecular markers revealed low levels of differentiation between populations of *A. caespitosa*, suggesting considerable levels of geneflow between populations (Table 2).

Table 1 Variance components (%) and (df) for flowering characteristics of *A. caespitosa*.

Source of Variation	Days to first flower		Number of flowers	
	Spring	Autumn	Spring	Autumn
Ploidy	3.18(3)***	6.51(3) ns	<0.01(3) ns	0.34(3) ns
Populations	24.73(23)***	7.57(22)***	33.07(23)***	22.33(23)***
Population × ploidy	38.47(18)***	3.21(17) ns	14.74(18)**	19.99(18)**
Error	33.61	82.71	52.18	57.33

Table 2 Estimated value (se) for total genetic diversity (H_t), within population (H_w), among population (H_B) diversity, the total genetic diversity that occurs among populations (F_{st}) and number of immigrants (N_m) for 13 populations of *Austrodanthonia caespitosa* generated from AFLP markers using 586 loci.

H_t	H_w	H_B	F_{st}	N_m
0.2181	0.1824 (0.00080)	0.0357 (0.012551)	0.1656 (0.098580)	1.259

Conclusions These results suggest the current evolutionary architecture of *A. caespitosa* and closely related species is complex, and is the result of interacting effects of broad-scale and probably ongoing geneflow between populations and, importantly, between ploidy levels (via triploid bridges). This could create significant genetic variation for ecologically important traits such as flowering behaviour, which is subsequently acted on by directional selection in diverse environments across these species range. Thus, selecting for high seed yield or high synchrony of flowering in domestication programs may result in less fit cultivars, thus leaving re-established native pastures vulnerable to contemporary and future environmental extremes.