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Priorities for enhancing the *ex situ* conservation and use of Australian crop wild relatives

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Abstract. Crop wild relatives - the wild cousins of cultivated plants - are increasingly recognized for their potential to contribute to the productivity, nutritional quality and sustainability of agricultural crops. However, the use of these genetic resources is dependent upon their conservation in genebanks and consequent availability to plant breeders, the status of which has not been comprehensively analyzed in Australia. Such conservation assessments are given urgency by reports of increasing threats to natural populations due to habitat destruction, climate change, and invasive species, among other causes. Here we document Australian wild plants related to important food crops, and outline their priorities for *ex situ* conservation. Given that no major domesticated food plants originated in the country, Australia's native flora of crop wild relatives is surprisingly rich, including potentially valuable cousins of banana, eggplant, melon, mung bean, pigeonpea, rice, sorghum, sweetpotato, soybean, and yam. Species richness of the wild relatives of major food crops is concentrated in the northern and northeastern tropical regions, in the Northern Territory, Western Australia, and Queensland. Geographic priorities for collecting of these taxa for *ex situ* conservation, due to the limited representation of their populations in genebanks, largely align with areas of high species richness. Proposed dam building and agricultural expansion in northern Australia make conservation action for these species more urgent. We outline key steps needed for enhancing the *ex situ* conservation of Australia's heritage of major food crop wild relatives, and discuss the critical activities required to increase their use.

Additional keywords: biodiversity, climate change adaptation, food security, genetic resources, plant breeding.

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Introduction

Crop wild relatives - wild plants closely related to domesticated species - have proved useful as genetic resources in breeding more productive, nutritious, and resilient crop cultivars (Tankley and McCouch 1997, Zhu *et al.* 2000, Hajjar and Hodgkin 2007, Dempewolf *et al.* 2017). The use of traits derived from these species is expected to increase with better information on the taxa (Wiersema *et al.* 2012), improved breeding technologies (Ford-Lloyd *et al.* 2011, McCouch *et al.* 2013), and the greater need for exotic germplasm in plant breeding to overcome compounding agricultural production challenges (Guarino and Lobell 2011, McCouch *et al.* 2013, Dempewolf *et al.* 2017).

Unfortunately the potential for use of crop wild relatives may well be constrained by their limited representation in genebanks and the ongoing loss of natural populations due to habitat modification, invasive species, pollution, over-collecting, climate change and other impacts (Castañeda-Álvarez *et al.* 2016). This is why our most important global agreements on agriculture, development and conservation, such as the Sustainable Development Goals (Target 2.5) (United Nations Sustainable Development Platform 2016), Aichi Biodiversity Targets (Target 13) (Convention on Biological Diversity 2016), and the International Treaty on Plant Genetic Resources for Food and Agriculture (Article 5) (FAO 2002) explicitly prioritize the comprehensive conservation of crop wild relative diversity.

The introgression of useful traits from wild relatives into productive cultivars, and the elimination of linkage drag of non-useful traits, requires years of effort and frequently necessitates the employment of advanced breeding tools. Agronomically valuable traits are often masked in the wild species, which generally exhibit weedy characteristics. Perhaps for these reasons, the wild species have historically been given relatively low priority by agricultural research, biodiversity conservation, and natural resource management organizations, slipping between the cracks in institutional conservation mandates even while their use in crop breeding has gained momentum and while threats to natural populations have compounded.

The generation of greater information on these species, including their identities, distributions, use potential, and conservation status, as well as the sharing of such information across organizations, are foundational steps in beginning to fill in these cracks. Here we document the wild relatives of major food crops occurring in Australia, estimating their potential distributions and quantifying their degree of representation in publicly available genebanks. We outline key steps needed for enhancing the *ex situ* conservation of Australia's heritage of major food crop wild relatives, and discuss the critical activities required to increase their use.

Crop wild relatives of Australia

As the development of agricultural practices on the island continent during the early Holocene was quite limited, Australia's historical contribution as the birthplace of internationally significant cultivated food crop species is negligible (Khoury *et al.* 2016), with the exception of macadamia nuts (*Macadamia integrifolia* Maiden & Betche and *Macadamia tetraphylla* L.A.S. Johnson, and hybrids), which were domesticated much more recently (Peace *et al.* 2008). Thus Australia's heritage of crop wild relatives would at first glance be predicted to be relatively sparse.

However, northern Australia's ecogeographic affinities with Southeast Asia, South Asia, and the tropical Pacific region have provided appropriate conditions for the persistence of the southernmost distributed populations of the wild relatives of a range of important agricultural crops originating in those or other regions, including banana, eggplant, melon, mung bean, pigeonpea, rice, sorghum, sweetpotato, soybean and yam. Our survey of wild relatives listed in taxonomic and genetic resource information systems and associated literature revealed over 150 native and naturalized taxa, closely or distantly related to ca. 30 agricultural crops, as occurring in Australia (Table 1, see also Table S1 available as supplementary material to this paper). Of these, the relatives of rice, pigeonpea, sorghum, and soybean have received the greatest research attention as genetic resources, including for pest and disease resistance, abiotic stress tolerance, breeding utility traits, yield, and quality (Wiersema *et al.* 2012, Vincent *et al.* 2013, Khoury *et al.* 2015a, The Harlan and de Wet Crop Wild Relative Inventory 2017, USDA NPGS Genetic Resources Information Network 2017).

Table 1. Number of crop wild relative taxa native to or naturalized in Australia, closely or distantly related to major and minor food crops. See Table S1, available as Supplementary Material to this paper, for full details for all taxa. Crop importance categorisation follows Castañeda-Álvarez *et al.* (2016)

Associated crop	Associated crop scientific name	Associated crop importance	Number of wild relatives - occurrence type	Number of wild relatives - use type
Alfalfa	<i>Medicago sativa</i> L.	Major	Naturalized (1)	Distant (1)
Asparagus	<i>Asparagus officinalis</i> L.	Major	Naturalized (3)	Close / high potential (1), Distant (2)
Banana	<i>Musa acuminata</i> Colla	Major	Native (2)	Close / high potential (1), Distant (1)
Brassica crops (mustard, rapeseed, turnip, cabbage, wall-rocket, rocket, radish)	<i>Brassica carinata</i> A. Braun, <i>Brassica juncea</i> (L.) Czern., <i>Brassica napus</i> L., <i>Brassica nigra</i> (L.) W. D. J. Koch, <i>Brassica oleracea</i> L., <i>Brassica rapa</i> L., <i>Diplotaxis tenuifolia</i> (L.) DC., <i>Eruca vesicaria</i> (L.), <i>Raphanus sativus</i> L.	Major	Naturalized (4)	Close / high potential (3), Distant (1)
Coconut	<i>Cocos nucifera</i> L.	Major	Native (1)	Close / high potential (1)

Cotton	<i>Gossypium arboreum</i> L., <i>Gossypium barbadense</i> L., <i>Gossypium herbaceum</i> L., <i>Gossypium hirsutum</i> L.	Major	Native (18)	Distant (18)
Eggplant	<i>Solanum melongena</i> L.	Major	Native (2)	Close / high potential (1), distant (1)
Lettuce	<i>Lactuca sativa</i> L.	Major	Naturalized (3)	Close / high potential (3)
Melon	<i>Cucumis melo</i> L.	Major	Native (1), naturalized (1)	Close / high potential (1), distant (1)
Melon, cucumber	<i>Cucumis melo</i> L., <i>Cucumis sativus</i> L.	Major	Naturalized (1)	Distant (1)
Mung bean	<i>Vigna radiata</i> (L.) R. Wilczek	Major	Native (1)	Close / high potential (1)
Olive	<i>Olea europaea</i> L.	Major	Native (1)	Distant (1)
Pigeonpea	<i>Cajanus cajan</i> (L.) Huth	Major	Native (8)	Close / high potential (7), distant (1)
Prunus crops (plum, almond, peach, cherry)	<i>Prunus cerasifera</i> Ehrh., <i>Prunus dulcis</i> (Mill.) D. A. Webb, <i>Prunus persica</i> (L.) Batsch, <i>Prunus salicina</i> Lindl.	Major	Naturalized (1)	Close / high potential (1)
Rice	<i>Oryza sativa</i> L., <i>Oryza glaberrima</i> Steud.	Major	Native (3)	Close / high potential (3)
Safflower	<i>Carthamus tinctorius</i> L.	Major	Naturalized (1)	Close / high potential (1)
Solanum crops (potato, tomato, eggplant)	<i>Solanum tuberosum</i> L., <i>Solanum lycopersicum</i> L., <i>Solanum melongena</i> L.	Major	Native (2)	Distant (2)
Sorghum	<i>Sorghum bicolor</i> (L.) Moench	Major	Native (16)	Close / high potential (16)
Soybean	<i>Glycine max</i> (L.) Merr.	Major	Native (25)	Close / high potential (10), distant (15)
Sugar beet	<i>Beta vulgaris</i> L.	Major	Naturalized (1)	Close / high potential (1)
Sugarcane	<i>Saccharum officinarum</i> L.	Major	Native (1)	Distant (1)
Sweetpotato	<i>Ipomoea batatas</i> (L.) Lam.	Major	Native (1), naturalized (1)	Close / high potential (2)
Water yam	<i>Dioscorea alata</i> L.	Major	Native (1)	Close / high potential (1)
Watermelon	<i>Citrullus lanatus</i> (Thunb.) Matsum. & Nakai	Major	Naturalized (1)	Close / high potential (1)

Abaca	<i>Musa textilis</i> Nee	Minor	Native (1)	Close / high potential (1)
Air yam, bitter yam	<i>Dioscorea bulbifera</i> L., <i>Dioscorea dumetorum</i> (Kunth) Pax	Minor	Native (1)	Close / high potential (1)
Fonio millet	<i>Digitaria exilis</i> (Kippist) Stapf	Minor	Native (30)	Close / high potential (1), distant (29)
Japanese millet	<i>Echinochloa frumentacea</i> Link	Minor	Native (7), naturalized (1)	Distant (8)
Land cress	<i>Barbarea verna</i> (Mill.) Asch.	Minor	Native (2)	Distant (2)
Macadamia nut	<i>Macadamia integrifolia</i> Maiden & Betche, <i>Macadamia tetraphylla</i> L. A. S. Johnson	Minor	Native (4)	Close / high potential (4)
Yellowcress	<i>Rorippa indica</i> (L.) Hiern	Minor	Native (5)	Distant (5)

Conservation status and *ex situ* conservation gaps for crop wild relatives of Australia

Australian native plants congeneric with important food crop species and represented in the Environment Protection and Biodiversity Conservation Act (EPBC Act 1999) List of Threatened Flora include *Musa fitzalanii* F. Muell. (Extinct); *Cajanus mareebensis* (S. T. Reynolds & Pedley) Maesen (Endangered); *Macadamia integrifolia* (Vulnerable), *M. jansenii* C. L. Gross & P. H. Weston (Endangered), *M. ternifolia* F. Muell. (Vulnerable), and *M. tetraphylla* (Vulnerable); *Glycine latrobeana* (Meisn.) Benth. (Vulnerable); and *Solanum dunalianum* Gaudich. (Vulnerable) and *S. karsense* Symon (Vulnerable) (Commonwealth of Australia 2016). The main reported threats to these species include changed fire regimes, weed invasion, disease, feral pigs, illegal collection, timber harvesting, land clearing, habitat destruction, agricultural expansion, urbanization, road works, grazing, salinity, river flow regulation, alienation of floodplains, and (in the case of *Macadamia* taxa) loss of genetic diversity through hybridization with commercial varieties. Of listed taxa, the *Macadamia* species have received the most significant conservation planning attention, including though protecting remaining populations by controlling invasive weeds, improving habitat and implementing fire management plans and establishing insurance populations both in surrounding areas of natural populations as well as in botanic gardens.

We performed a detailed *ex situ* conservation gap analysis on the 58 native or naturalized Australian taxa that are either close relatives of major food crops (defined as being members of the primary or secondary genepools of such crops), or have been explicitly listed in publications describing confirmed or specific potential uses in plant breeding of these crops, indicating their relatively high potential value as genetic resources (Supplementary Table 1) (Wiersema *et al.* 2012, Vincent *et al.* 2013, Khoury *et al.* 2015a, 2015b, Castañeda-Álvarez *et al.* 2016, The Harlan and de Wet Crop Wild Relative Inventory 2017, USDA NPGS Genetic Resources Information Network 2017). These include Australian native relatives of banana, eggplant,

melon, mung bean, pigeonpea, rice, sorghum, soybean, sweetpotato and yam; and naturalized relatives of asparagus, *Brassica* crops, lettuce, plum, safflower, sugar beet, sweetpotato and watermelon. We also assessed the four native *Macadamia* taxa due to their iconic importance for Australia.

Mapping these species' potential distributions using the Maxent algorithm (Phillips *et al.* 2006), based upon reference specimens held in herbaria and genebanks, in combination with climatic information, potential ranges of Australian wild relatives of high potential value for crop breeding were found in all continental States and Territories, with increasing richness in the northern and northeastern (tropical) regions of the Northern Territory, Western Australia and Queensland (Figure 1, Supplementary Figures 1-5).

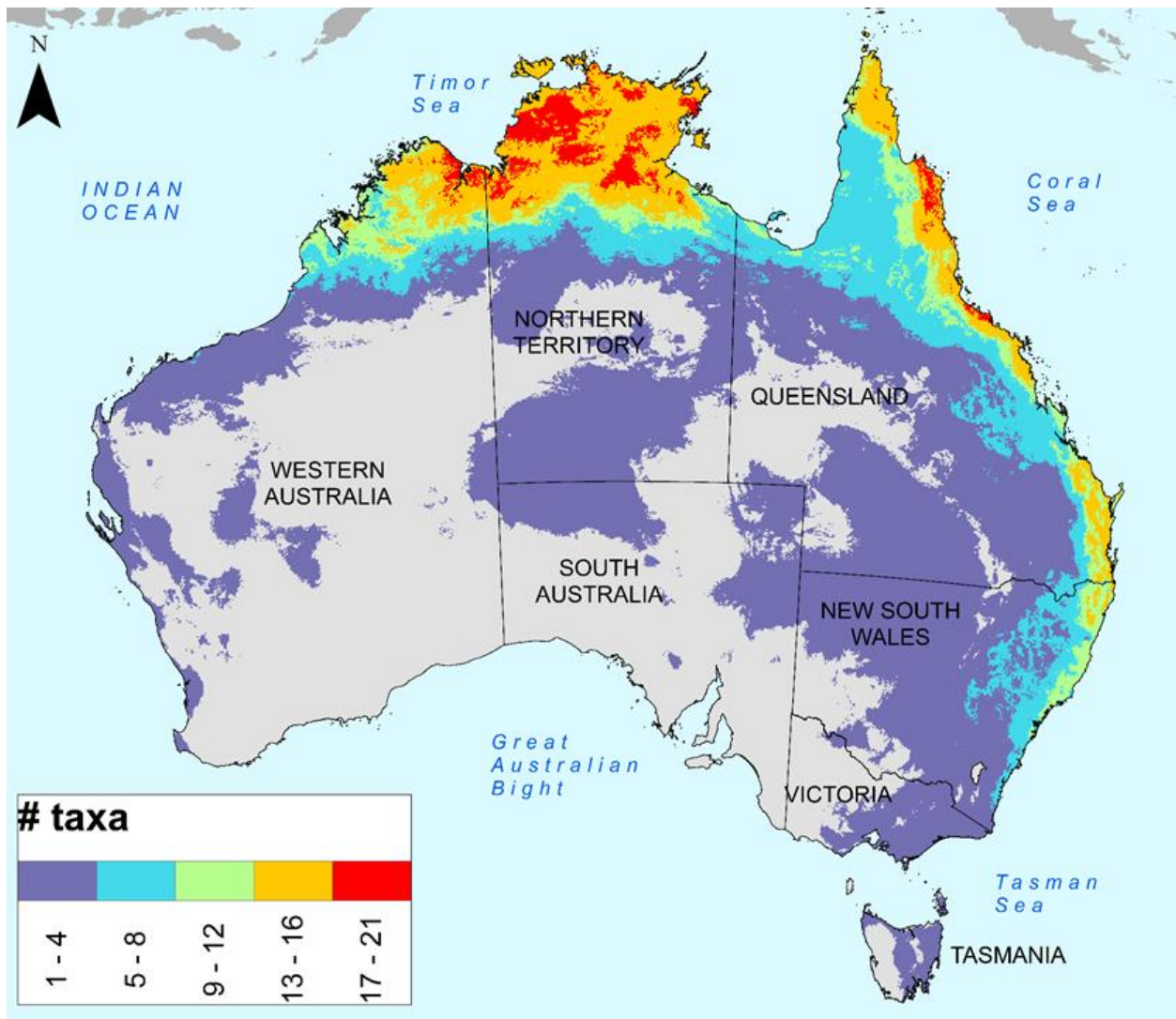


Fig. 1. Potential species distribution richness of crop wild relatives in Australia. The map displays overlapping potential distribution models for 45 assessed native crop wild relatives of major food crops. Warmer colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 21 taxa potentially occurring within the same ca. 5 km² grid.

Comparing the potential distribution models with the locations where these species were previously collected and are now conserved in publicly available agricultural research genebank collections (including the Australian Grains Genebank, the international genebank collections of the CGIAR, the USDA National Plant Germplasm System and the European genebanks listed in EURISCO), we found that the country's wild relatives are generally under-represented in these *ex situ* conservation systems with regard to the geographic extent of their distributions as well as the diversity of habitats they occupy. Thirty-one (67.4%) of the 46 potentially highly valuable native wild relative species (and 40 [69%] out of 58 total assessed relatives) were assigned a high priority for further collecting due to their particularly severe under-representation *ex situ* (Table 2, Supplementary Table 1). Of the four major crop genebanks with a range of wild relatives distributed in Australia, pigeonpea and sorghum relatives were found to be particularly underrepresented in genebanks, whereas soybean and rice relatives were comparatively better conserved.

Table 2. Australian native crop wild relatives, closely related to or determined as of high potential use value for the improvement of major food crops, and determined as high priority for further collecting in order to increase their representation in *ex situ* conservation. Number of distinct populations in genebanks was estimated by counting the number of germplasm accessions with unique localities described in passport data. The final priority score (FPS) assigned in the gap analysis was categorised as follows: high priority for further collecting for taxa where $FPS \geq 7.5$ (i.e., very little or no current representation in genebanks); medium priority where $5 \leq FPS < 7.5$; low priority where $2.5 \leq FPS < 5$; and sufficiently represented for taxa whose $FPS < 2.5$. See Table S1 (available as supplementary material to this paper) for results for all assessed taxa

Crop wild relative taxon	Associated crop	Distinct populations in genebanks	Final priority score
<i>Cajanus acutifolius</i> (F.Muell.) Maesen	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	7	8.5
<i>Cajanus cinereus</i> (F.Muell.) F.Muell.	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	0	9.9
<i>Cajanus confertiflorus</i> F. Muell.	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	1	8.9
<i>Cajanus lanceolatus</i> (W.Fitzg.) Maesen	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	2	9.3
<i>Cajanus latisepalus</i> Maesen	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	0	9.9
<i>Cajanus reticulatus</i> (Dryand.) F.Muell.	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	0	9.9

<i>Cajanus scarabaeoides</i> (L.) Thouars	Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	57	8.0
<i>Cucumis melo</i> subsp. <i>agrestis</i> L.	Melon (<i>Cucumis melo</i> L.)	0	10.0
<i>Dioscorea transversa</i> R. Br.	Water yam (<i>Dioscorea alata</i> L.)	0	10.0
<i>Ipomoea littoralis</i> Blume	Sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.)	2	10.0
<i>Macadamia integrifolia</i> Maiden & Betche	Macadamia nut (<i>Macadamia integrifolia</i> Maiden & Betche and <i>Macadamia tetraphylla</i> L. A. S. Johnson)	1	9.2
<i>Macadamia janseni</i> C. L. Gross & P. H. Weston	Macadamia nut (<i>Macadamia integrifolia</i> Maiden & Betche and <i>Macadamia tetraphylla</i> L. A. S. Johnson)	0	10.0
<i>Macadamia ternifolia</i> F. Muell.	Macadamia nut (<i>Macadamia integrifolia</i> Maiden & Betche and <i>Macadamia tetraphylla</i> L. A. S. Johnson)	0	10.0
<i>Macadamia tetraphylla</i> L. A. S. Johnson	Macadamia nut (<i>Macadamia integrifolia</i> Maiden & Betche and <i>Macadamia tetraphylla</i> L. A. S. Johnson)	0	10.0
<i>Musa acuminata</i> subsp. <i>banksii</i> Colla	Banana (<i>Musa acuminata</i> Colla)	2	9.5
<i>Oryza meridionalis</i> Ng	Rice (<i>Oryza sativa</i> L.)	1	9.5
<i>Solanum melanospermum</i> F. Muell.	Eggplant (<i>Solanum melongena</i> L.)	1	9.0
<i>Sorghum amplum</i> Lazarides	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	8.8
<i>Sorghum angustum</i> S. T. Blake	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.5
<i>Sorghum brachypodium</i> Lazarides	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	2	7.7
<i>Sorghum ecarinatum</i> Lazarides	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	8.9
<i>Sorghum exstans</i> Lazarides	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.8

<i>Sorghum interjectum</i> Lazarides	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.5
<i>Sorghum intrans</i> F. Muell. ex Benth.	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.6
<i>Sorghum laxiflorum</i> F. M. Bailey	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	2	8.8
<i>Sorghum macrospermum</i> E. D. Garber	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.7
<i>Sorghum matarankense</i> E. D. Garber & Snyder	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	1	9.4
<i>Sorghum nitidum</i> (Vahl) Pers.	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	2	9.6
<i>Sorghum stipoideum</i> (Ewart & Jean White) Gardner & Hubb.	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	3	7.9
<i>Sorghum timorense</i> (Kunth) Buse	Sorghum (<i>Sorghum bicolor</i> (L.) Moench)	2	9.1
<i>Vigna radiata</i> var. <i>sublobata</i> (L.) Wilczek	Mung bean (<i>Vigna radiata</i> (L.) R. Wilczek)	8	7.8

The geographic concentration of wild populations prioritized for collecting for *ex situ* conservation largely parallel species richness patterns (Figure 2, Supplementary Figures 1-5). As these areas overlap considerably with proposed dam building and lands identified as suitable for agricultural expansion (Petheram *et al.* 2014), urgent collecting of these populations is prudent.

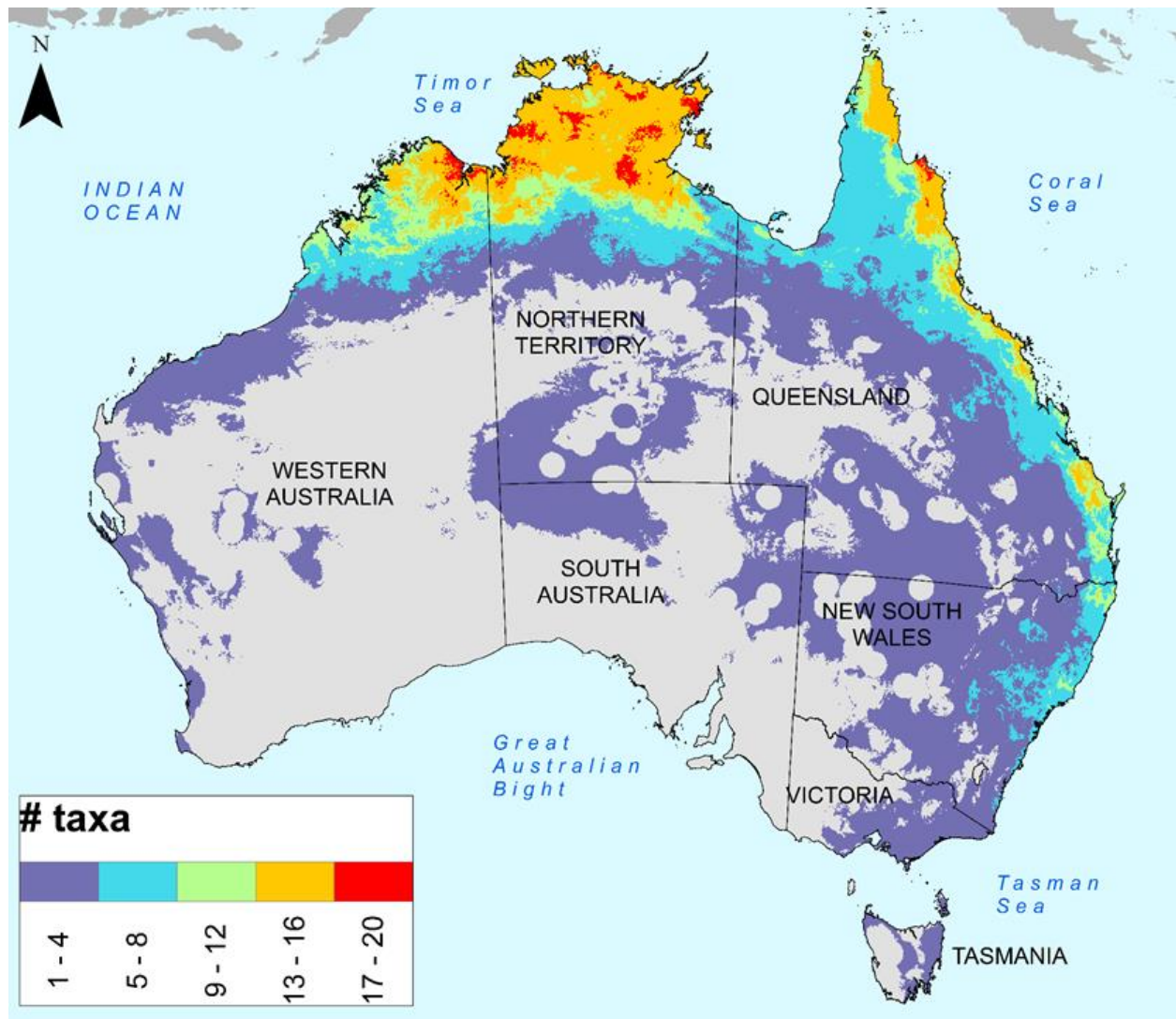


Fig. 2. Priority areas for further collecting of Australian crop wild relatives. The map displays geographic regions where crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Warmer colours indicate greater overlap of potential distributions of under-represented taxa. Blank circular areas (in comparison to Figure 1) represent regions where germplasm has already been collected, with accessions from these areas currently conserved in genebanks.

Conservation and use priorities for Australian crop wild relatives

Significantly improving the safeguarding and use of Australia's crop wild relatives will require a series of research and conservation actions and collaborations:

Conservation. Current efforts to collect crop wild relatives in Australia are spearheaded by the Australian Grains Genebank and the Australian Seed Bank Partnership (ASPB) in collaboration with State and Territory conservation and land management authorities, the Australian Federal Government and local communities, with public *ex situ* conservation managed by the Australian Grains Genebank (Horsham, Victoria) and PlantBank (Sydney, NSW). Other institutions

conserving significant germplasm collections of Australian wild relatives include the international collections of the CGIAR (particularly for relatives of pigeonpea, sorghum and rice), the USDA National Plant Germplasm System and the European genebanks listed in EURISCO. Public lands likely to possess the greatest numbers of populations of crop wild relatives include those managed by the States and Territories of Australia and Indigenous Land Councils from around the country. The capacity and the interest of these institutions and organizations in effectively conserving Australia's crop wild relatives will be important to the success of efforts to improve their protection.

Given the relatively low level of representation of Australia's crop wild relatives in agricultural research genebank collections and the considerable potential threats to populations in their natural habitats, both the collection for *ex situ* conservation and the active management of taxa in conservation areas need to be enhanced considerably to fulfil the country's conservation commitments. *Ex situ* and *in situ* conservation systems need greater long-term support in order to sustainably manage the costs of conservation. At the least, information on the distributions of vulnerable crop wild relatives should inform further development planning in the northernmost regions of Australia, with the aim of avoiding or mitigating impacts to the wild plant populations that could play an important role in Australian and global food security.

Because many of Australia's native crop wild relatives cross national borders and the genetic resources of such species are valuable well beyond the country's own agricultural production systems, conservation efforts are best aligned with neighboring national activities and with regional and global initiatives to conserve crop wild relative diversity (e.g., Crop Wild Relative Project 2017). Furthermore, as the wild relatives of the most important agricultural crops produced by Australia are largely native to distant regions outside its national borders (Khoury *et al.* 2016), the country should continue to actively support the expansion of international conservation and well as facilitated genetic resource exchange policy efforts (i.e., FAO 2002) in order to enhance its present and future access to these increasingly critical sources of genetic variation.

One particularly challenging research priority is the development of better *ex situ* conservation protocols for crop wild relatives, including species-specific testing for appropriate moisture and temperature conditions for long-term storage as well as robust methods for assessing viability. For some taxa, orthodox (-18° C) storage may not be appropriate, necessitating the development of *in vitro* or cryopreservation, field collections, or in extreme cases, full dependence upon coordinated efforts toward management *in situ*. In these research areas, the genetic resources community has much to learn from, and would benefit greatly from, collaborations with Australian as well as international organizations immersed in wild plant conservation and restoration research (e.g. PlantBank, the Kew Millennium Seed Bank Partnership and the USDA Forest Service and USDA Agricultural Research Service collaboration (2014)).

Documentation, characterization and evaluation. Crop wild relative accessions conserved *ex situ* in Australian genebanks, and in most cases also within the international and other national genebank institutions previously mentioned, have been documented with regard to specific collection locality information (i.e. “passport data”), as well as general morphological characterization to international crop or other descriptors standards. The wild relatives of mung bean, pigeonpea, rice, sorghum and soybean have been distributed from the Australian Grains Genebank to researchers nationally and internationally, with relatives of mung bean, rice and sorghum the most highly requested. These accessions are known informally to have been evaluated for a range of agronomic and quality traits, but the results are only partly available in publically accessible articles and repositories. Characterization and evaluation of the wild relatives of mung bean, rice, sorghum and soybean have been the most extensively published, including with regard to biology; phylogenetic relationships; biotic, abiotic and quality traits; and, less frequently, for cross compatibility with their associated crops (Price *et al.* 2005, Rebetzke and Lawn 2006, Dillon *et al.* 2007, Kamala *et al.* 2009, Krishnan *et al.* 2014, Lawn *et al.* 2016, Nguyen *et al.* 2016, Brozynska *et al.* 2017).

Although progress is being made via eco-geographic modeling advances, new high-throughput characterization and evaluation technologies, and increasingly powerful and inexpensive genotypic tools, the general lack of access to genetic and evaluation data for agronomically and nutritionally beneficial traits remains a significant constraint to enhanced use of most crop wild relatives (Gur and Zamir 2004, Dempewolf *et al.* 2017). Substantial further research and partnerships among organizations interested in the generation, maintenance, and open provision of these data would provide powerful novel resources for plant breeders and for conservationists, as well as researchers focused on domestication, evolution and other fields (Volk and Richards 2011, McCouch *et al.* 2013).

While this article contributes to the literature on wild plants of Australia with the potential to contribute genetic resources for breeding major food crops, broader surveys of the nation’s plants and more extensive gap analyses are needed to identify and outline enhancement priorities for species that may be candidates for domestication as new crops, or contribute to the improvement of minor food, and well as industrial, fiber, medicinal, ornamental and other non-food crops of economic value.

Pre-breeding. The ability of crop breeders to continue to offer new cultivars that are productive under increasingly rapid climatic change as well as water, phosphorus and other natural resource limitations, is a serious concern (Lobell *et al.* 2008, Cordell *et al.* 2009), especially as new varieties commonly require numerous years of development (McCouch *et al.* 2013). Such timeframes are generally elongated further when employing genetic variation derived from wild plants.

Timeframes needed to make use of crop wild relatives can be shortened through pro-active pre-breeding, the process of crossing wild genetic resources with standard cultivars in order to

generate materials that contain novel useful diversity which can be incorporated more easily into advanced plant breeding programs (Prohens *et al.* 2017). These efforts have traditionally been performed by the public sector, whose activities have been curtailed in recent decades due to decreasing funding (Morris *et al.* 2006). Renewed support is thus very much needed for public and public-private partnership programs that tackle the initial challenge of introducing genes of interest from wild relatives into domesticated materials and making these materials available to the agricultural research community.

The full extent of previous utilization of Australia's native wild relatives in crop breeding efforts is not readily determinable, as historical use by the private sector is generally proprietary information and as use even by the public sector is rarely reported in full. An information system under development by the pertinent international policy mechanism on exchange of crop genetic resources (FAO 2002) should help to provide more thorough documentation of the use of Australia's native wild relatives in the future.

From the available information on breeding efforts, native species related to rice, pigeonpea, sorghum and soybean stand out with regard to the extent of documentation of their uses as genetic resources, including for pest and disease resistance, abiotic stress and metal tolerance, breeding utility traits, yield and quality, with Australian native cousins of pigeonpea in particular having contributed significantly to international crop breeding efforts (Khoury *et al.* 2015a, USDA NPGS Genetic Resources Information Network 2017). Published research on native distant relatives of sorghum resulted in inter-specific hybrids, however, genetic incompatibilities and linkage drag have limited the utilisation of these wide crosses in pre-breeding programs (Hodnett *et al.* 2005, Price *et al.* 2005).

The time is ripe for fuller discovery, exploration and celebration of Australia's wealth of crop wild relatives. Concerted efforts are needed to conserve, characterize and make more easily available the valuable traits within these genetic resources, so that these plants can persist into the future, and so that their contributions to agricultural productivity, food and nutrition security and environmental sustainability will be more fully realised.

Conflicts of Interest

The authors declare no conflicts of interest.

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References

- Brozynska M, Copetti D, Furtado A, Wing RA, Crayn D, Fox G, Ishikawa R, Henry RJ (2017) Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. *Plant Biotechnol Journal* **15**(6), 765-774.
- Castañeda-Álvarez NP, Khoury CK, Achicanoy H, Bernau V, Dempewolf H, Eastwood RJ, Guarino L, Harker RH, Jarvis A, Maxted N, Mueller JV, Ramírez-Villegas J, Sosa CC, Struik PC, Vincent H, Toll J (2016) Global conservation priorities for crop wild relatives. *Nature Plants* **2**(4), 16022.
- Commonwealth of Australia (2016) 'Environment Protection and Biodiversity Conservation Act (EPBC Act 1999).' Available at http://www.environment.gov.au/cgi-bin/sprat/public/publicthreatenedlist.pl?wanted=flora#flora_critically_endangered. [Verified 17 November 2016]
- Convention on Biological Diversity (2016) 'Aichi Biodiversity Targets.' Available at: <https://www.cbd.int/sp/targets/default.shtml> [Verified 10 October 2017]
- Cordell D, Drangert J-O, White S (2009) The story of phosphorus: global food security and food for thought. *Global Env. Change* **19**, 292-305.
- Crop Wild Relative Project (2017) Available at: <http://www.cwrdiversity.org/> [Verified 10 October 2017]
- Dempewolf H, Baute G, Anderson J, Kilian B, Smith C, Guarino L (2017) Past and Future Use of Wild Relatives in Crop Breeding. *Crop Science* **57**(3), 1070-1082.
- Dillon SL, Lawrence PK, Henry RJ, Price HJ (2007) Sorghum resolved as a distinct genus based on combined ITS1, ndhF and Adh1 analyses. *Plant Systematics and Evolution* **268**, 29-43.
- FAO (2002) *The International Treaty on Plant Genetic Resources for Food and Agriculture* (Food and Agriculture Organization of the United Nations: Rome)
- Ford-Lloyd B, Schmidt M, Armstrong SJ, Barazani O, Engels J, Hadas R, Hammer K, Kell SP, Kang D, Khoshbakht K, Li Y, Long C, Lu B-R, Ma K, Nguyen VT, Qiu L, Ge S, Wei W, Zhang Z, Maxted N (2011) Crop wild relatives - undervalued, underutilized and under threat? *BioScience* **61**, 559-565.
- Guarino L, Lobell DB (2011) A walk on the wild side. *Nat. Clim. Change* **1**(8), 374-375.

- Gur A, Zamir D (2004) Unused natural variation can lift yield barriers in plant breeding. *PLoS Biology* **2**, e245.
- Hajjar R, Hodgkin T (2007) The use of wild relatives for crop improvement: a survey of developments over the past 20 years. *Euphytica* **156**, 1-13.
- Hodnett GL, Burson BL, Rooney WL, Dillon SL, Price HJ (2005) Pollen–Pistil Interactions Result in Reproductive Isolation between *Sorghum bicolor* and Divergent *Sorghum* Species. *Crop Science* **45**, 1403-1409.
- Kamala V, Sharma HC, Manohar Rao D, Varaprasad KS, Bramel PJ (2009) Wild relatives of sorghum as sources of resistance to sorghum shoot fly, *Atherigona soccata*. *Plant Breeding* **128**, 137–142.
- Khoury CK, Achicanoy HA, Bjorkman AD, Navarro-Racines C, Guarino L, Flores-Palacios X, Engels JMM, Wiersema JH, Dempewolf H, Sotelo S, Ramírez-Villegas J, Castañeda-Álvarez NP, Fowler C, Jarvis A, Rieseberg LH, and Struik PC (2016) Origins of food crops connect countries worldwide. *Proc. R. Soc. B* **283**(1832), 20160792.
- Khoury CK, Castañeda-Álvarez NP, Achicanoy HA, Sosa CC, Bernau V, Kassa MT, Norton SL, van der Maesen LJG, Upadhyaya HD, Ramírez-Villegas J, Jarvis A, and Struik PC (2015a) Crop wild relatives of pigeonpea [*Cajanus cajan* (L.) Millsp.]: distributions, *ex situ* conservation status, and potential genetic resources for abiotic stress tolerance. *Biological Conservation* **184**, 259-270.
- Khoury CK, Heider B, Castañeda-Álvarez NP, Achicanoy HA, Sosa CC, Miller RE, Scotland RW, Wood JRI, Rossel G, Eserman LA, Jarret RL, Yencho GC, Bernau V, Juarez H, Sotelo S, de Haan S, and Struik PC (2015b). Distributions, *ex situ* conservation priorities, and genetic resource potential of crop wild relatives of sweetpotato [*Ipomoea batatas* (L.) Lam., *I. series Batatas*]. *Frontiers in Plant Science* **6**, 251.
- Krishnan S, Waters D, Henry RJ (2014) Australian Wild Rice Reveals Pre-Domestication Origin of Polymorphism Deserts in Rice Genome. *PLOS ONE* **9**(6), e98843.
- Lawn RJ, Vu Hang TT, Bielig LM, Kilian A (2016) Genetic compatibility among morphotypes of *Vigna lanceolata* and implications for breeding improved cultivars. *Crop and Pasture Science* **67**(7), 739-750.
- Lobell DB, Burke MB, Tebaldi C, Mastrandrea MD, Falcon WP, Naylor RL (2008) Prioritizing climate change adaptation needs for food security in 2030. *Science* **319**, 607-610.
- McCouch S, Baute GJ, Bradeen J, Bramel P, Bretting PK, Buckler E, *et al.* (2013) Agriculture: feeding the future. *Nature* **499** (7456), 23-24.

- Morris M, Edmeades G, Pehu E (2006) The global need for plant breeding capacity: what roles for the Public and Private Sectors? *HortScience* **41**(1), 30-39.
- Nguyen TD, Vu Hang TT, Bielig LM, Lawn RJ (2016) Expression and heritability of late flowering and other quantitative traits in cultivated × Australian wild mungbean hybrids. *Crop & Pasture Science* **67**(12), 1235-1251.
- Peace C, Ming R, Schmidt A, Manners J, Vithanage V (2008) Genomics of Macadamia, a recently domesticated tree nut crop. In Moore PH, Ming R, eds., *Genomics of Tropical Crop Plants*. Springer New York, New York, NY, 313–32.
- Petheram C, Gallant J, Wilson P, Stone P, Eades G, Roger L, Read A, Tickell S, Commander P, Moon A, McFarlane D, Marvanek S (2014) *Northern rivers and dams: a preliminary assessment of surface water storage potential for northern Australia*. CSIRO Land and Water Flagship Technical Report (CSIRO, Australia).
- Phillips SJ, Anderson RP, Schapire RE (2006) Maximum entropy modeling of species geographic distributions. *Ecological Modelling* **190**(3-4), 231–259.
- Price HJ, Hodnett GL, Burson BL, Dillon SL, Rooney WL (2005) A *Sorghum bicolor* x *S. macrospermum* hybrid recovered by embryo rescue and culture. *Australian Journal of Botany* **53**, 579-582.
- Prohens J, Gramazio P, Plazas M, Dempewolf H, Kilian B, Díez MJ, Fita A, Herraiz FJ, Rodriguez-Burruezo A, Solar S, Knapp S, Vilanova, S (2017) Introgressiomics: a new approach for using crop wild relatives in breeding for adaptation to climate change. *Euphytica*, **213**(7), 158.
- Rebetzke G, Lawn R (2006) Root and shoot attributes of indigenous perennial accessions of the wild mungbean (*Vigna radiata* ssp. *sublobata*). *Australian Journal of Agricultural Research* **57** (7), 791-799.
- Tanksley SD, McCouch SR (1997) Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* **277** (5329), 1063-1066.
- The Harlan and de Wet Crop Wild Relative Inventory (2017). Available at <http://www.cwrdiversity.org/checklist/> [Verified 19 September 2017]
- United Nations Sustainable Development Platform (2016) ‘Goal 2.’ Available at <https://sustainabledevelopment.un.org/sdg2> [Verified 10 October 2017]
- USDA Forest Service and USDA Agricultural Research Service (2014) *Joint Strategic Framework on the Conservation and Use of Native Crop Wild Relatives in the United States*. Available online at:

<https://www.fs.fed.us/wildflowers/ethnobotany/documents/cwr/FrameworkNativeCropWildRelativesOct2014.pdf> [Verified 10 October 2017]

USDA NPGS Genetic Resources Information Network (2017) 'GRIN taxonomy.' Available at <https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearchcwr.aspx> [Verified 19 September 2017]

Vincent H, Wiersema J, Kell S, Fielder H, Dobbie S, Castañeda-Álvarez N, Guarino L, Eastwood R, Leon B, Maxted N (2013) A prioritized crop wild relative inventory to help underpin global food security. *Biological Conservation* **167**: 265–275.

Volk GM, Richards CM (2011) Integration of georeferencing, habitat, sampling, and genetic data for documentation of wild plant genetic resources. *Hortic. Sci.* **46** (11), 1446-1449.

Wiersema JH, León B, Garvey EJ (2012) Identifying wild relatives of subtropical and temperate fruit and nut crops. *Acta Hort.* **948**, 285-288.

Zhu Y, Chen H, Fan J, Wang Y, Li Y, Chen J, *et al.* (2000) Genetic diversity and disease control in rice. *Nature* **406** (6797), 718-722.

Priorities for enhancing the *ex situ* conservation and use of Australian crop wild relatives

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Table S1. List of closely and distantly related crop wild relatives of major and minor food crops, identified as native to or naturalized in Australia (Wiersema *et al.* 2012, Vincent *et al.* 2013, Castañeda-Álvarez *et al.* 2016, The Harlan and de Wet Crop Wild Relative Inventory 2017, USDA NPGS Genetic Resources Information Network 2017), with gap analysis assessment results reported for close relatives and other species of high potential value for breeding of major food crops (Khoury *et al.* 2015a, Khoury *et al.* 2015b, Castañeda-Álvarez *et al.* 2016, and novel updated assessments following the same methodology). Potential distribution models assessment scores: ATAUC = five-fold average area under the ROC curve of test data, STAUC = standard deviation of the test AUC of the five different folds, ASD15 = proportion of the potential distribution model ensemble with standard deviation above 0.15. SRS = sampling representativeness score (scale of 0-10, with 0 indicating complete current conservation *ex situ* and thus no priority for further collecting, and 10 indicating no current *ex situ* conservation of the taxon and thus critical priority for further collecting), GRS = geographic representativeness score, and ERS = ecological, or diversity of habitats, representativeness score (ERS). The Final Priority Score (FPS) is the mean of SRS, GRS, and ERS. High priority for further collecting was assigned for taxa where $FPS \geq 7.5$ (i.e., very little or no current representation in genebanks); medium priority where $5 \leq FPS < 7.5$; low priority where $2.5 \leq FPS < 5$; and sufficiently represented for taxa whose $FPS < 2.5$.

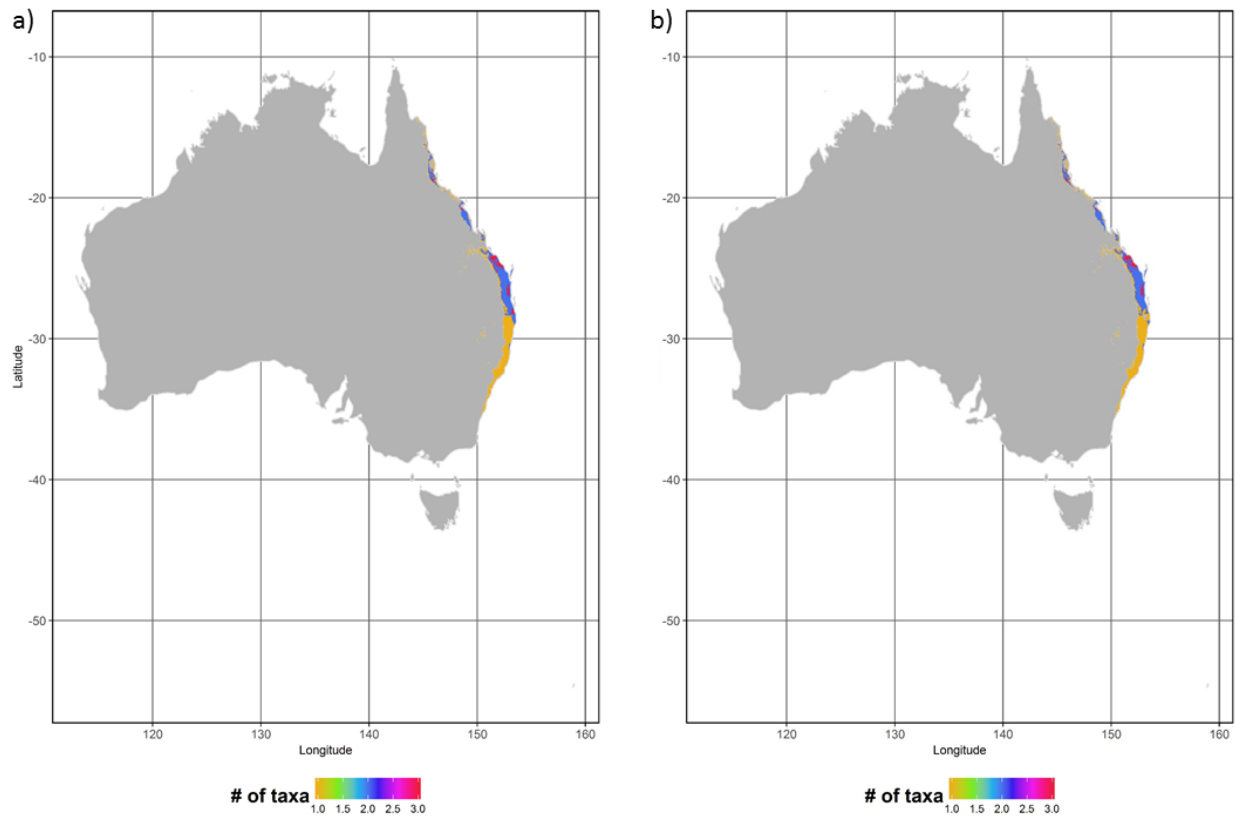


Figure S1. a) Potential species distribution richness of macadamia crop wild relatives in Australia. The map displays overlapping potential distribution models for 4 assessed macadamia crop wild relatives. Blue-purple-red colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 3 taxa potentially occurring within the same ca. 5 km² grid. b) Priority areas for further collecting of Australian macadamia crop wild relatives. The map displays geographic regions where macadamia crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Blue-purple-red colours indicate greater overlap of potential distributions of under-represented taxa.

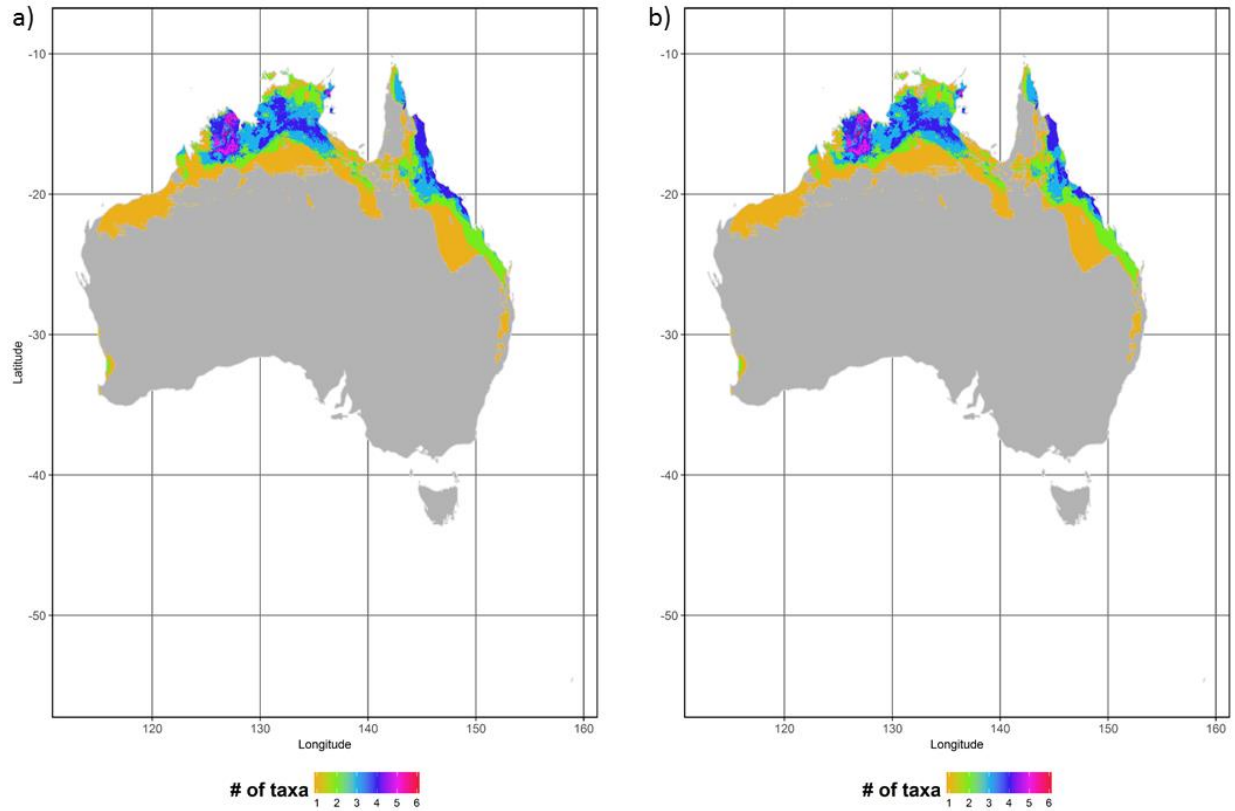


Figure S2. a) Potential species distribution richness of pigeonpea crop wild relatives in Australia. The map displays overlapping potential distribution models for 7 assessed pigeonpea crop wild relatives. Blue-purple-red colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 6 taxa potentially occurring within the same ca. 5 km² grid. b) Priority areas for further collecting of Australian pigeonpea crop wild relatives. The map displays geographic regions where pigeonpea crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Blue-purple-red colours indicate greater overlap of potential distributions of under-represented taxa.

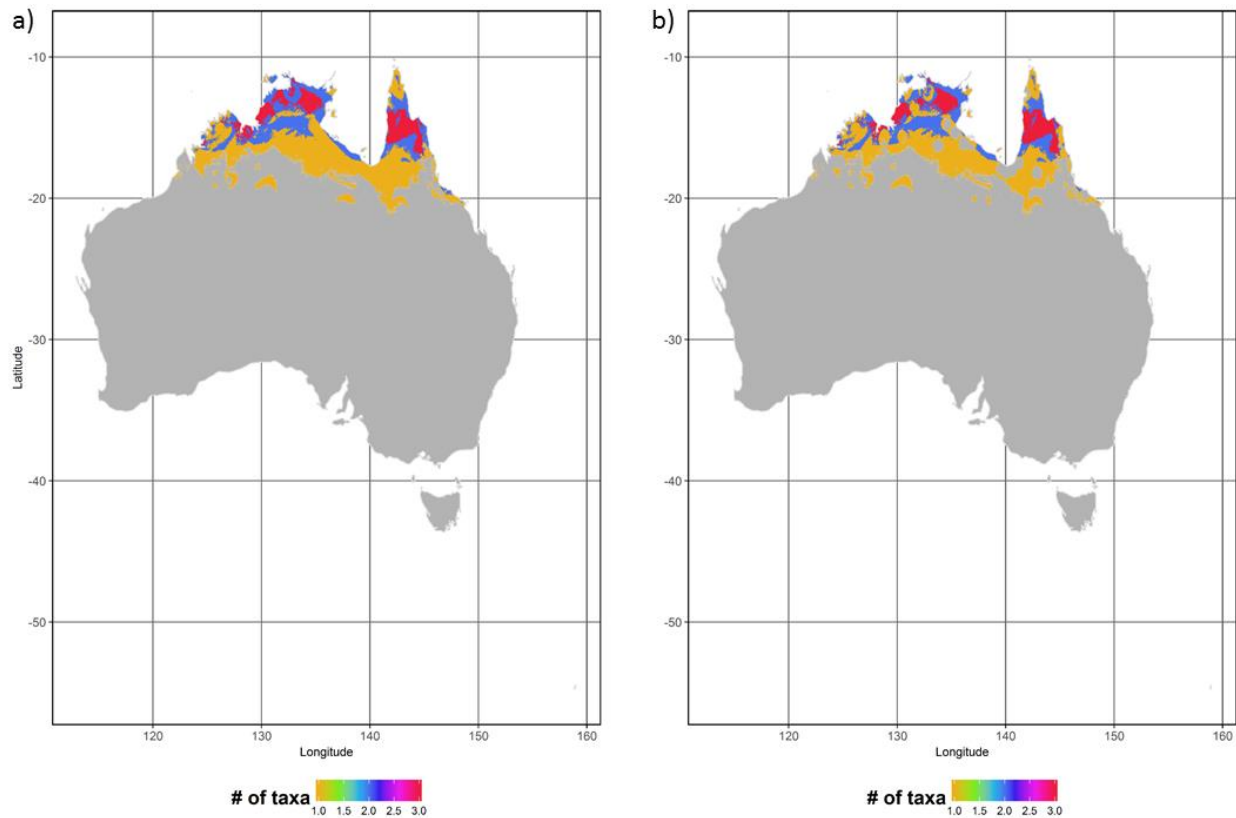


Figure S3. a) Potential species distribution richness of rice crop wild relatives in Australia. The map displays overlapping potential distribution models for 3 assessed rice crop wild relatives. Blue-purple-red colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 3 taxa potentially occurring within the same ca. 5 km² grid. b) Priority areas for further collecting of Australian rice crop wild relatives. The map displays geographic regions where rice crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Blue-purple-red colours indicate greater overlap of potential distributions of under-represented taxa. Blank circular areas (in comparison to (a)) represent regions where germplasm has already been collected, with accessions from these areas currently conserved in genebanks.

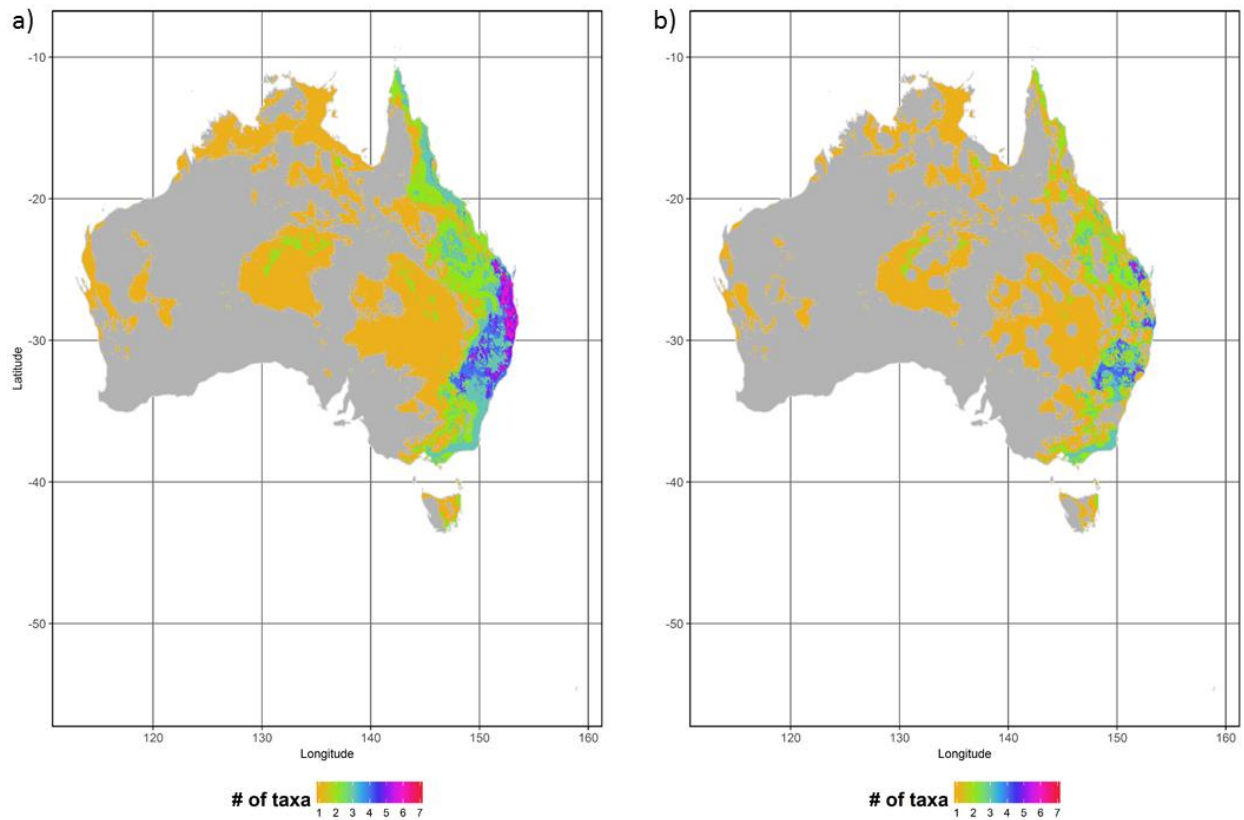


Figure S4. a) Potential species distribution richness of soybean crop wild relatives in Australia. The map displays overlapping potential distribution models for 10 assessed soybean crop wild relatives. Blue-purple-red colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 7 taxa potentially occurring within the same ca. 5 km² grid. b) Priority areas for further collecting of Australian soybean crop wild relatives. The map displays geographic regions where soybean crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Blue-purple-red colours indicate greater overlap of potential distributions of under-represented taxa. Blank circular areas (in comparison to (a)) represent regions where germplasm has already been collected, with accessions from these areas currently conserved in genebanks.

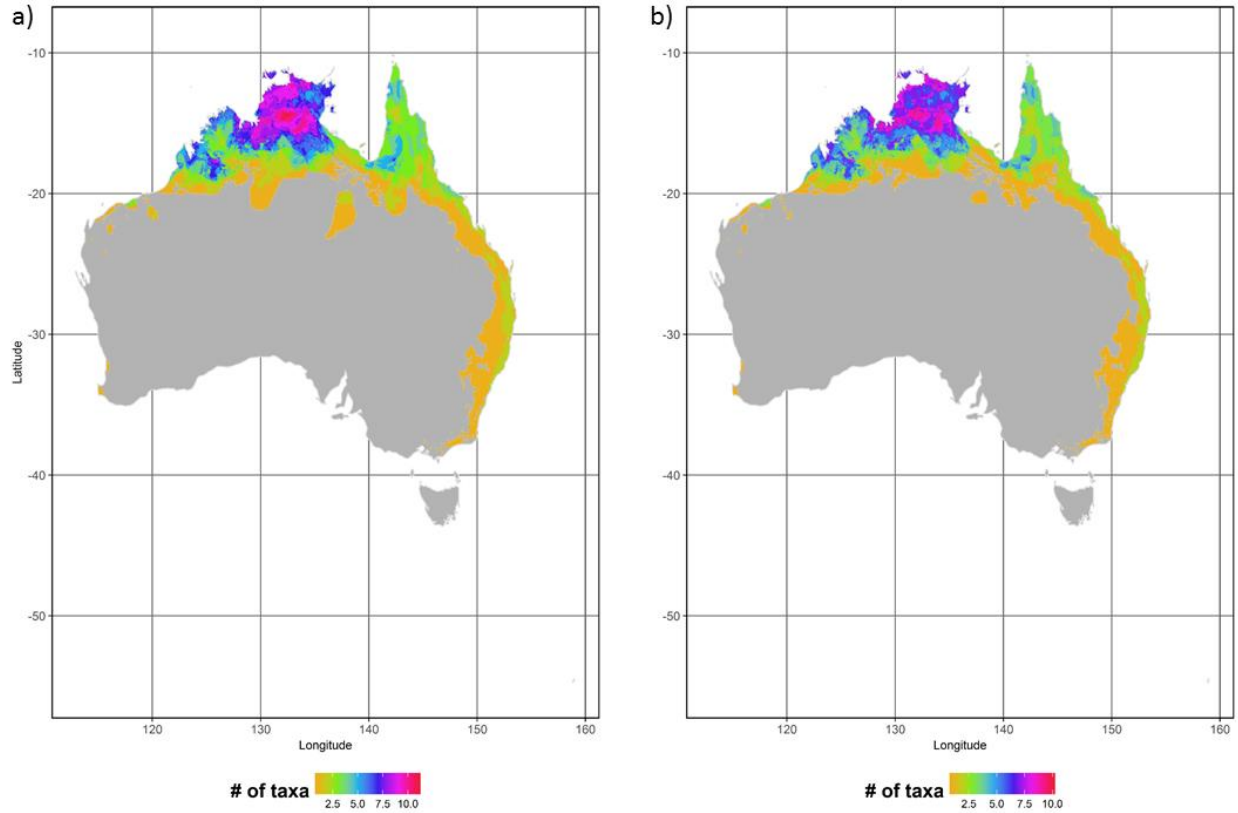


Figure S5. a) Potential species distribution richness of sorghum crop wild relatives in Australia. The map displays overlapping potential distribution models for 16 assessed sorghum crop wild relatives. Blue-purple-red colours indicate areas where greater numbers of taxa potentially occur in the same geographic localities, with up to 10 taxa potentially occurring within the same ca. 5 km² grid. b) Priority areas for further collecting of Australian sorghum crop wild relatives. The map displays geographic regions where sorghum crop wild relative taxa are expected to occur and have not yet been collected and conserved in genebanks. Blue-purple-red colours indicate greater overlap of potential distributions of under-represented taxa.