

A re-appraisal of species diversity within the Australian grasswrens *Amytornis* (Aves: Maluridae)

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ABSTRACT

The Australian grasswrens (*Amytornis*) comprise a genus of cryptically plumaged species inhabiting the arid regions of southern, western, central, and northern Australia. Isolated, fragmented populations characterise the distributional pattern of several species, whereas others appear to show ecophenotypic clinal variation in plumage patterns. These features have made the species-level taxonomy of the genus a matter of ongoing debate. We undertook qualitative considerations of morphological, biogeographical and ecological features in combination with quantitative DNA distance measures from published studies, to provide a comprehensive species level revision of *Amytornis*. In addition to the ten species recognised by Schodde and Mason (1999) (*housei*, *textilis*, *goyderi*, *burnelli*, *ballarae*, *merrotsyi*, *woodwardi*, *dorotheae*, *striatus*, *barbatus*), we also recognise as species the following: *modestus*, *rowleyi*, *oweni* and *whitei*. These fourteen species are placed into four subgenera: *Amytornis*, *Magnamytis*, *Maluropsis* and *Cryptamytis* subgen. nov. The latter subgenus is erected for *A. merrotsyi*. The potential impacts that this new taxonomy will have on the conservation status of the various taxa are canvassed.

Key words: grasswrens, molecular systematics, avian taxonomy, conservation status

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Introduction

The Australian grasswrens (*Amytornis*) comprise a genus of cryptically plumaged species inhabiting the arid regions of southern, western, central and northern Australia (Rowley and Russell 1997, 2007). Isolated fragmented populations characterise the distributional pattern of several species whereas others appear to show ecophenotypic clinal variation in plumage differentiation (see Schodde and Mason 1999). The combination of subtle patterns of plumage variation, fragmented populations and clinal variation have made the species-level taxonomy of the genus a matter of ongoing debate (e.g. Parker 1972; Mayr 1986; Schodde 1982a,b; Schodde and Mason 1999; Christidis and Boles 2008; Christidis *et al.* 2010; Black *et al.* 2010).

Several species of grasswren occur in remote areas of arid Australia and it is not surprising that new species, subspecies and populations have continued to be discovered. For example, *Amytornis barbatus* (Grey Grasswren) was first described in 1968 by Favalaro and McEvey (1968) and the subspecies *A. b. diamantina* was described 19 years later (Schodde and Christidis 1987). Condon (1969) described the subspecies *A. textilis ballarae* from western Queensland (Qld), which was later included by Parker (1972) within *A. burnelli* (Dusky Grasswren), before being elevated to species status by Schodde and Mason (1999) as *A. ballarae* (Kalkadoon Grasswren). In

1997 and 1998, the range of *A. merrotsyi* (Short-tailed Grasswren) was extended to include the Gawler Ranges, South Australia (SA) (Baxter and Paton 1998) and this population was later described as a new subspecies *A. m. pedleri* (Christidis *et al.* 2008).

A good understanding of the species composition of *Amytornis* is yet to be established. Schodde and Mason (1999) provided an excellent framework of morphological differentiation in the genus but acknowledged that the species status of several taxa required further investigation. They recognised ten species (*A. housei* Black Grasswren, *A. textilis* Thick-billed Grasswren, *A. goyderi* Eyrean Grasswren, *A. burnelli*, *A. ballarae*, *A. merrotsyi*, *A. woodwardi* White-throated Grasswren, *A. dorotheae* Carpentarian Grasswren, *A. striatus* Striated Grasswren, *A. barbatus*). More recently, there has been a trend to treat *A. textilis* (Western Grasswren) and *A. modestus* (Thick-billed Grasswren) as separate species (e.g. Black 2004; Black *et al.* 2010). The distributions of the species and subspecies of *Amytornis* discussed in this paper are depicted in Figures 1, 2 and 3.

Christidis *et al.* (2010) examined DNA distances and relationships for all currently recognised species and most subspecies of *Amytornis*. Although their study had major

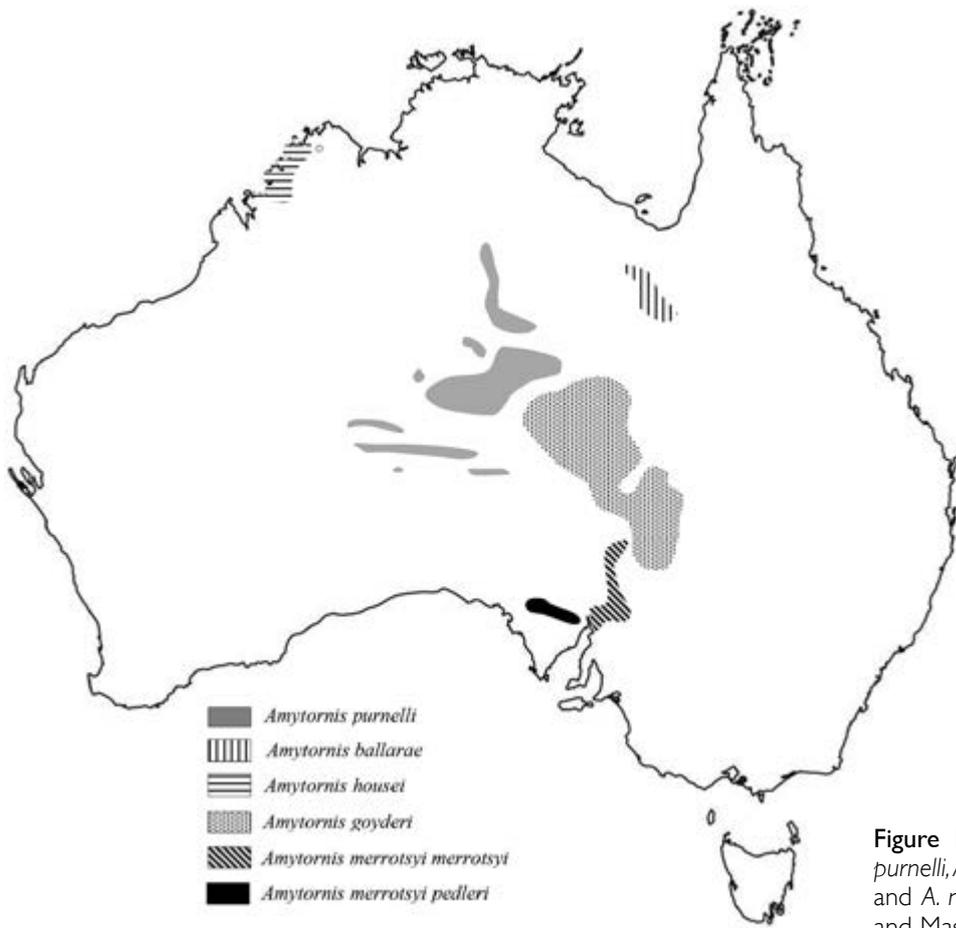


Figure 1. Distribution of *Amytornis purnelli*, *A. ballarae*, *A. housei*, *A. goyderi* and *A. merrotsyi*. Based on Schodde and Mason (1999)

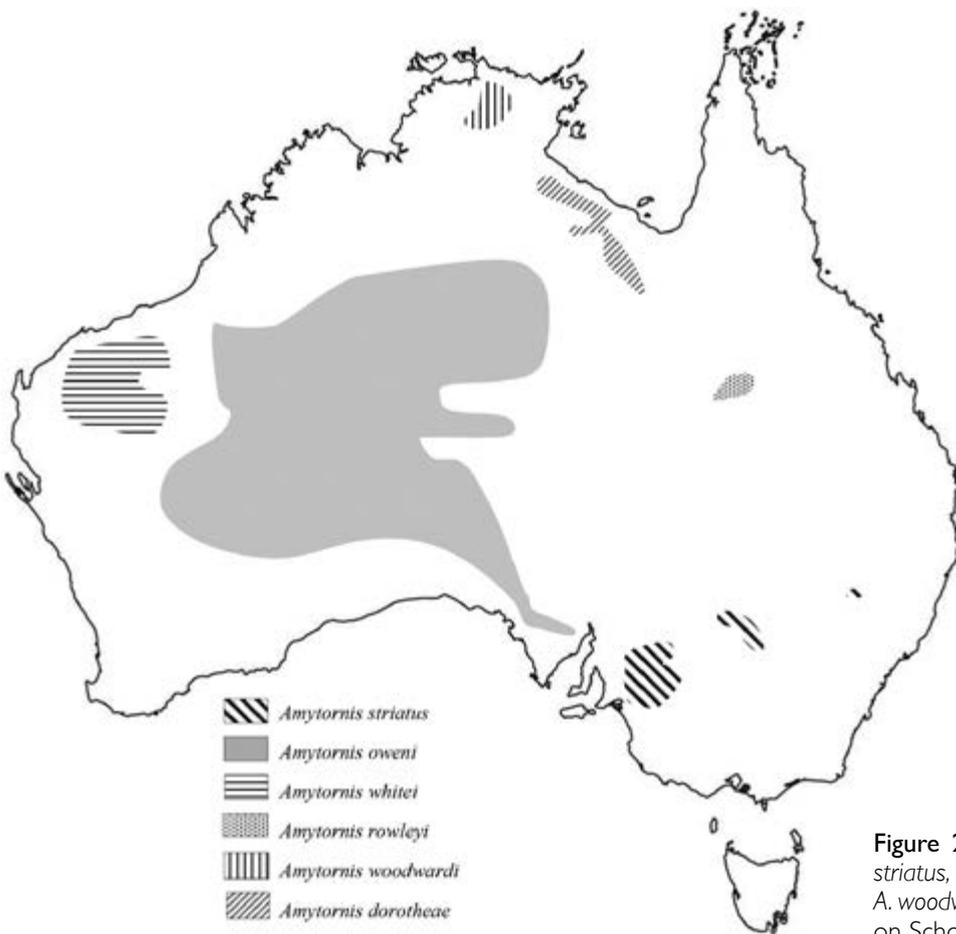


Figure 2. Distribution of *Amytornis striatus*, *A. oweni*, *A. whitei*, *A. rowleyi*, *A. woodwardi* and *A. dorotheae*. Based on Schodde and Mason (1999)

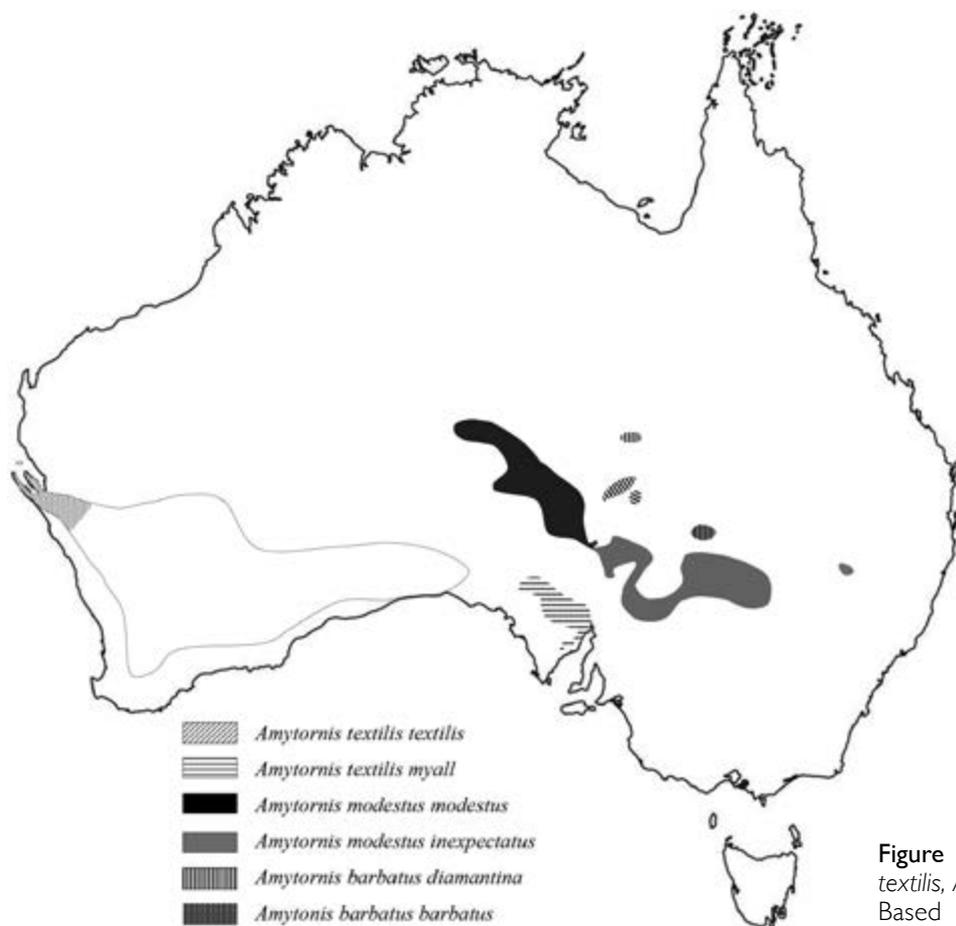


Figure 3. Distribution of *Amytornis textilis*, *A. modestus* and *A. barbatus*. Based on Schodde and Mason (1999)

taxonomic implications, this was not the focus of the paper, and no taxonomic recommendations were made. Here we interpret the levels of DNA differentiation recorded by Christidis *et al.* (2008, 2010) and Austin *et al.* (2013) in context with published morphological, biogeographical and ecological features (e.g. Schodde and Mason 1999; Black 2004, 2011a,b; Black *et al.* 2010) to provide a comprehensive species and subspecies level revision of *Amytornis*.

Methods

Taxonomic decisions based on mitochondrial DNA (mtDNA) differentiation are best made in the context of the level of distances separating well-established species on a genus-by-genus basis, in order to account for differing evolutionary rates (e.g. Norman *et al.* 1998; Bradley and Baker 2001; Baker and Bradley 2006; Garnett and Christidis 2007; Christidis and Norman 2010). Bradley and Baker (2001) outlined five criteria that needed to be met by DNA studies in order to assess reliably species status of taxa: (1) phylogenetic methods employed to test genetic distance patterns; (2) use of stable and constantly evolving coding genes; (3) inclusion of known species-level “bench marks” for evaluating different levels of sequence divergence; (4) comparisons restricted to single speciation events; and (5) comprehensive inclusion of sister taxa.

The DNA study of Christidis *et al.* (2010) provides a sound framework on which to apply the DNA-based criteria of Bradley and Baker (2001) in determining species limits within *Amytornis*. The three mitochondrial genes ND2, ND3 and CO1 fit the criteria of stable, constantly evolving coding genes and have been successfully used to define genus and species limits in other Australian songbird families (Norman *et al.* 2007; Jönsson *et al.* 2008; Driskell *et al.* 2011; Christidis *et al.* 2011). Although Christidis *et al.* (2010) lacked DNA data for *A. striatus whitei*, the coverage of all other taxa in this complex allows its taxonomic status to be discussed in a relative context.

The taxa under consideration here have been defined at species and subspecies levels based on plumage, morphology and ecology by Schodde and Mason (1999), Black (2004) and Black *et al.* (2010).

Results and Discussion

DNA differentiation and species taxonomy of *Amytornis*

Applying a mtDNA-distance approach to species status assessment requires comparison with the lowest mtDNA divergences recorded between well-accepted sister species (Norman *et al.* 1998; Garnett and Christidis 2007; Christidis and Norman 2010). According to the DNA phylogeny for *Amytornis* (Christidis *et al.* 2010),

the most relevant distances are those recorded between *Amytornis woodwardi* and *A. dorotheae* which were 2.6% for ND2 and ND3, and 1% for CO1 (Table 1). At the other extreme, the sister species *A. ballarae* and *A. purnelli* differed by 7.6%, 5.7% and 4.2% for ND2, ND3 and CO1 respectively (Table 1). Within-species calibrations are provided by *A. barbatus* where distances between the two subspecies (*barbatus* and *diamantina*) were 1.8%, 1.2% and 1.5% for ND2, ND3 and CO1 respectively (Table 1), and *A. merrotsyi* where the ND3 distance between the two subspecies was 2.1%. Within-taxon variation was not evaluated by Christidis *et al.* (2010). However, Christidis *et al.* (2008) recorded intra-subspecific ND3 genetic distances of 0.6% and 0.9% within *A. merrotsyi pedleri* and *A. m. merrotsyi*, respectively.

Based on these comparisons (Table 1), and the criteria advocated by Norman *et al.* (1998) and Bradley and Baker (2001), we argue that within *Amytornis*, DNA distances for ND2, ND3 and CO1 of approximately 2% or less are reflective of subspecies-level recognition. Species-level distances are more gene specific, with CO1 being the slowest diverging gene. The minimum DNA distance between the sister species *A. ballarae* and *A. purnelli* was 4.2%. Consequently, distances above 4% can be argued to be reflective of species-level recognition in *Amytornis*. Species that fall in this well differentiated category were *A. housei*, *A. goyderi*, *A. purnelli*, *A. ballarae*, *A. merrotsyi* and *A. barbatus*.

There were three cases where DNA distances between taxa within genetically well-defined complexes fell in the range of 2–4%: (1) *Amytornis woodwardi* and *A. dorotheae*; (2) *Amytornis modestus* and *A. textilis*; and (3) *A. striatus*. Here, more detailed morphological and ecological considerations are discussed below in order to determine the number of species in each complex.

Table 1. mtDNA divergences based on Kimura distances (Kimura 1980). Species recognition and composition of the subgenera follows the revision advocated in the current study: *Amytornis* (*housei*, *textilis*, *modestus*, *goyderi*, *purnelli*, *ballarae*); *Magnamytis* (*woodwardi*, *dorotheae*, *striatus*, *rowleyi*, *oweni*, *whitei*); *Cryptamytis* (*merrotsyi*); and *Maluropsis* (*barbatus*).

Comparisons	mtDNA gene region		
	ND2	ND3	COI
Between subgenera			
<i>Amytornis</i> – <i>Magnamytis</i>	12.6%-15.45%	10.6%-14.2%	6.7%-10.8%
<i>Amytornis</i> – <i>Cryptamytis</i>	14.2%-16.3%	11.6%-14.4%	8.4%-10.2%
<i>Amytornis</i> – <i>Maluropsis</i>	15.3%-17.6%	12.5%-15.1%	9.2%-10.8%
<i>Magnamytis</i> – <i>Cryptamytis</i>	13.6%-13.8%	9.6%-10.9%	8.1%-10.7%
<i>Magnamytis</i> – <i>Maluropsis</i>	13.8%-15.2%	8.2%-12.5%	10.4%-11.5%
<i>Cryptamytis</i> – <i>Maluropsis</i>	16.0%-16.3%	11.8%-12.5%	9.0%-9.2%
Between closely related and sister taxa			
<i>A. ballarae</i> v <i>A. purnelli</i>	7.6%	5.7%	4.2%
<i>A. textilis</i> v <i>A. modestus</i>	4.4%	3.5%	4.0%
<i>A. textilis textilis</i> v <i>A. t. myall</i>	0.4%	1.7%	1.2%
<i>A. textilis myall</i> v <i>A. modestus</i>	4.8%	2.9%	4.4%
<i>A. striatus</i> v <i>A. rowleyi</i>	4.0%	4.5%	3.8%
<i>A. striatus</i> v <i>A. oweni</i>	na	4.2%	na
<i>A. dorotheae</i> v <i>A. woodwardi</i>	2.6%	2.6%	1.0%
<i>A. merrotsyi merrotsyi</i> v <i>A. m. pedleri</i>	na	2.1%	na
<i>A. barbatus barbatus</i> v <i>A. b. diamantina</i>	1.8%	1.2%	1.5%

Amytornis woodwardi and *A. dorotheae*

Condon (1951) combined *A. woodwardi* (White-throated Grasswren) and *A. dorotheae* (Carpentarian Grasswren) as a single species, and on the basis of the low levels of mtDNA differentiation recorded between the two (2.6% for ND2 and ND3, and 1% for CO1; Table 1), this might appear to be appropriate. Nevertheless, the two differ greatly in overall morphology (Schodde and Mason 1999; Higgins *et al.* 2002). In terms of plumage patterns and size, *A. woodwardi* more closely resembles *A. housei* whereas *A. dorotheae* is more similar to *A. striatus*. There are also subtle differences in habitat preferences (summarised in Higgins *et al.* 2002). The optimal habitat for *A. woodwardi* is flat, unbroken plateaux that are sparsely vegetated with *Triodia* hummocks. In the north of its range, *A. dorotheae* occurs in dissected plateaux and slopes with *Triodia* hummocks whereas in the south it occurs in less dissected siltstone ranges, with *Triodia* cover. Two taxonomic options are possible here. First, the extent of plumage and ecological differences are ignored and the two taxa are combined based on low DNA divergence. Conversely, the DNA distances are interpreted as representing recent speciation. Christidis and Norman (2010) argued that low levels of DNA differentiation, on their own, are not sufficient to combine taxa and this approach is taken here. Consequently, we here retain *A. woodwardi* and *A. dorotheae* as recently evolved species.

Amytornis modestus and *A. textilis*

Schodde and Mason (1999) treated *Amytornis modestus* (Thick-billed Grasswren) as a subspecies of *A. textilis* (Western Grasswren), although the two had been kept separate by Schodde (1982b). The pattern of mtDNA distances recorded for the complex by Christidis *et al.* (2010) is more consistent with species-level status for both

forms. The north-easterly form *A. modestus* differed by up to 4.8% (ND2) from *A. t. myall* and 4.4% (ND2) from *A. t. textilis*. Comparable distances were also evident in ND3 and CO1 (Table 1). Black *et al.* (2010) and Black (2004) presented detailed arguments based on a consideration of plumage, morphology and habitat preferences for treating *A. modestus* as separate species to *A. textilis*, with *myall* being aligned with the latter. This alignment is consistent with the DNA data of Christidis *et al.* (2010). DNA distances between *A. t. textilis* (Western Australia [WA]) and *A. t. myall* (northern Eyre Peninsula, SA) ranged from 0.4% to 1.7% (Table 1) and these are comparable to those recorded between subspecies of *A. barbatus* and *A. merrotsyi* (Table 1). The two are also similar in plumage and morphology (Schodde 1982a; Schodde and Mason 1999; Black 2004). Black (2004) advocated use of the vernacular names Western Grasswren and Thick-billed Grasswren for *A. textilis* and *A. modestus* respectively, which is in keeping with previous usage. North (1902) gave the name Thick-billed Grasswren to *Amytis modesta* when he originally described that taxon, while the name Western Grasswren has previously been applied to *Amytornis textilis* (RAOU 1926; Parker 1972).

Black (2011a) recognised seven taxa within *A. modestus*, of which six were formally treated as subspecies. Four of these taxa referred to previously named subspecies (*modestus*, *indulkanna*, *inexpectatus*, *obscurior*), two were newly described (2011a) (*raglessi*, *curnamona*), and the population from northeast of Lake Eyre was mooted as a possible unnamed seventh subspecies. This revision was primarily based on plumage and morphological analyses. Specimens from the two NSW taxa (*inexpectatus*, *obscurior*) were not examined. When summarising the plumage and morphological data used to define *modestus*, *indulkanna*, *raglessi* and *curnamona*, Black (2011a) acknowledged that the differences were relatively slight and that the presence or absence of sexual dimorphism was especially fraught, given the limited samples of female specimens for some populations. An examination of the plumage based Scatterplot depicted in Black (2011a: Fig. 5) reveals that almost all the variation observed in *curnamona* is circumscribed by that observed within *raglessi*. Furthermore, one of the defining bill characters for *curnamona* is described as “variably finer bill”, which is more suggestive of ecophenotypic variation rather than taxonomic diversity. Differences between *raglessi* and *curnamona* from South Australia and the adjacent NSW forms *inexpectatus* and *obscurior* were not evaluated by Black (2011a), except to note strong plumage similarities between them.

Austin *et al.* (2013) examined mitochondrial differentiation in all forms of *A. modestus* recognised by Black (2011a) and identified an eastern and western clade that differed by a genetic distance of 1.7%. The western clade comprised the forms *modestus* and *indulkanna*, and the eastern clade comprised *obscurior*, *raglessi*, *curnamona* and the unnamed ‘eyre’ form. The most easterly extinct form *inexpectatus* was not examined. There was no phylogeographic structure in the eastern clade, whereas the western clade had two subgroups that differed by a genetic distance of 0.5%.

Although DNA data is not available for *inexpectatus*, it is very similar to adjacent *obscurior* in appearance. On the available morphological and genetic evidence a conservative, but robust, treatment of subspecies in *A. modestus* would recognise two forms: (1) *modestus* (including *indulkanna*) west of Lakes Eyre and Torrens extending north to the MacDonnell Ranges; (2) and *inexpectatus* (including *raglessi*, *curnamona*, *obscurior* and the population from northeast of Lake Eyre) to the east and extending into NSW. Further research is needed to assess whether the shallow phylogeographic structure separating *indulkanna* and nominate *modestus* represents population subdivision or subspecific differentiation.

A further question that needs to be addressed is whether further subspecies are recognisable within *A. textilis textilis*. Black (2011b) reassessed the taxonomic history of the complex and analysed morphometric measurements of 23 to 27 individuals. Based on this sample he further divided *A. t. textilis* into four subspecies: *textilis*, *carteri*, *giganturus* and *macrorous* (including *varius* and *morgani*). The morphological analysis of Black (2011b) was limited due to small sample sizes. Reinstatement of the southern form *giganturus* was based on only 3 individuals and it was argued that they were darker and larger than northern populations, but this could equally be reflective of ecophenotypic variation. Black (2011b) also acknowledged that the reported darker plumages in *carteri* were only apparent in specimens from the HLW collection (Museum Victoria).

In their DNA study Austin *et al.* (2013) found only minor levels of genetic divergence within *A. t. textilis*. Two subgroups were recognised. The first comprised *textilis* and *carteri* from the Shark Bay region and Dirk Hartog Island, while the second comprised *macrorous* and *giganturus* from southern WA and southern SA. A case could be made for recognising two subspecies *A. t. textilis* (including *carteri*) and *A. t. macrorous* (including *giganturus*). Given that the genetic distances separating the two groups are more equivalent to levels recorded within subspecies, we refrain from recognising them as subspecies at this stage.

A. striatus complex

The *Amytornis striatus* complex comprises several isolated forms. Schodde and Mason (1999) segregated the central Queensland population as a new subspecies, *rowleyi*, distinguished by its small size and russet plumage. In genetic distances, *rowleyi* differs from nominate *striatus* by 3.8–4.5% across the three mitochondrial genes (Table 1). This divergence is higher than that observed for subspecific differentiation and more comparable with that recorded between *A. modestus* and *A. textilis*. The form *rowleyi* is geographically isolated, being restricted to the Cooper–Diamantina drainage and over 600 km distant from other populations of *striatus* (based on Barrett *et al.* 2003). The geographical isolation in combination with the genetic distances is indicative of a long-independent evolutionary trajectory for *rowleyi* relative to nominate *striatus*. When taken in context with the morphological and plumage differentiation (Schodde and Mason 1999), we conclude that the

form *rowleyi* is best treated as a separate species to *A. striatus*. *Amytornis rowleyi* is a newly elevated species with no previous vernacular name. Consequently, we apply the name Rusty Grasswren in reference to its russet plumage.

Excluding *rowleyi*, there has been considerable debate on how many other forms exist within the *A. striatus* complex. Mayr (1986) recognised three forms: (1) *whitei* in the Pilbara of WA, which is large and rufous; (2) *oweni* in the sand deserts of WA, SA and the Northern Territory (NT), which is small and rufous but with a white belly; and (3) *striatus* in the south-eastern Australian mallee through to central New South Wales (NSW), which is large and grey-brown. Condon (1951), Keast (1958), Mees (1961) and Ford and Parker (1974) combined the first two whereas Schodde (1982a) and Schodde and Mason (1999) combined the latter two. Christidis *et al.* (2010) provided ND3 DNA data for *A. striatus oweni*. The DNA distances between *A. s. oweni* and *A. s. striatus* and *A. rowleyi* were 4.2% and 4.5% respectively. These levels are comparable to species-level recognition as defined previously for *Amytornis*.

Although Schodde and Mason (1999) argued that plumage differences between *oweni* and nominate *striatus* are clinal, they point out that the available specimen material is meagre and the interpretation is provisional. Furthermore, such a cline does not fit in with the large distributional break between the two taxa, which includes the biogeographically significant Eyrean and Murravian Barriers in south-eastern SA. Accordingly, *A. oweni* is recognised here as a species with the vernacular name Sandhill Grasswren in reference to its preferred habitat. The vernacular name Striated Grasswren is restricted to the nominate form in the mallee regions of SA, Victoria (Vic) and central NSW. Further work, including DNA analysis, is required to assess the status of the “transitional populations” around the northern Eyre Peninsula identified by Schodde and Mason (1999). These could represent ecophenotypic variants or a separate subspecies within *A. oweni* (as defined here).

DNA data are not available for the form *A. striatus whitei*, which is restricted to the Pilbara region of WA. Nevertheless, we believe that it also represents a separate species for two reasons. First, it is the most morphologically distinct member of the *A. striatus* complex (Schodde and Mason 1999). Secondly, it is the only member of the complex to inhabit rocky outcrops; all other members inhabit flatlands. Given that no other species of *Amytornis* occurs in both rocky outcrops and flatlands, it is highly unlikely that the form *whitei* is conspecific with *A. oweni*, the geographically most proximate member of the complex. Schodde and Mason (1999) in fact suggested that the significance of this habitat differentiation needed be further investigated as it could point to sibling species status. Furthermore, species of *Amytornis* have been found to be tightly definable in terms of habitat preferences (Christidis *et al.* 2010). Accordingly, we recognise *A. whitei* as a separate species and apply the vernacular name Pilbara Grasswren in reference to its geographical isolation.

Subgenera within *Amytornis*

Schodde and Christidis (1987) erected the subgenus *Maluropsis* for *Amytornis barbatus* arguing that it was basal to all the other species in *Amytornis*. This assertion was based on considerations of plumage pattern and preliminary protein allozyme data. Following on from this, Schodde and Mason (1999) placed all other species of *Amytornis* into the nominate subgenus. In contrast, the DNA data of Christidis *et al.* (2010) consistently identified four equally diverged lineages within *Amytornis*: (1) *barbatus*; (2) *ballarae*, *purnelli*, *goyderi*, *textilis-modestus*, *housei*; (3) *dorotheae*, *woodwardi*, *striatus*; and (4) *merrotsyi*. DNA distances between subgenera (Table 1) ranged from 12.6% to 17.6% (ND2), 8.2% to 15.1% (ND3) and 6.7% to 11.5% (CO1). Furthermore, the DNA phylogeny of Christidis *et al.* (2010) indicated that the four lineages diverged in rapid succession from each other, and that if subgenera are recognised then these should correspond with each of the lineages. This is the action that is recommended here. In addition to *Maluropsis* (lineage 1) and *Amytornis* (lineage 2), the name *Magnamytis* Mathews, 1912 is available for lineage 3. No subgeneric name is available for lineage 4. Accordingly we here distinguish a new subgenus for *Amytornis merrotsyi*.

Amytornis subgenus *Cryptamytis*, subgen. nov. Christidis, Rheindt, Boles and Norman, this study

Type species: *Amytornis merrotsyi* Mellor, 1913

Diagnosis: Face patterned with an obscure supra-loral bar and vestigial black malar stripe. Tail is disproportionately short.

Etymology: The original generic name *Amytis* Lesson, 1831 was shown to be preoccupied and so was replaced by *Amytornis* Stejneger, 1885. *Cryptamytis* combines *kruptos*, (Greek, hidden) and *amytis*, from the original name (that of a Persian princess). The name is figuratively ‘secret princess’ alluding to the bird’s secretive habits and long hidden identity.

Taxonomic revision of *Amytornis*

In considering the DNA, plumage, morphological, ecological and geographical data, we here divide the genus *Amytornis* into four subgenera comprising 14 species. Four of these species are further divided into subspecies. The shallow phylogeographic structure recorded by Austin *et al.* (2013) in *A. textilis textilis* and *A. modestus modestus* is here interpreted as representing population subdivision rather than subspecific differentiation. With this caveat we propose the following taxonomy for the genus *Amytornis*:

Amytornis Stejneger, 1885

Maluropsis Schodde and Christidis, 1987

A. barbatus Grey Grasswren

A. b. barbatus

A. b. diamantina

Magnamytis Mathews, 1912*A. woodwardi* White-throated Grasswren*A. dorotheae* Carpentarian Grasswren*A. striatus* Striated Grasswren*A. whitei* Pilbara Grasswren*A. oweni* Sandhill Grasswren*A. rowleyi* Rusty Grasswren**Cryptamytis subgen nov***A. merrotsyi* Short-tailed Grasswren*A. m. merrotsyi**A. m. pedleri***Amytornis Stejneger, 1885***A. ballarae* Kalkadoon Grasswren*A. pumelli* Dusky Grasswren*A. goyderi* Eyrean Grasswren*A. housei* Black Grasswren*A. textilis* Western Grasswren*A. t. textilis* (includes *carteri*, *giganturus* and *macrorous*)**A. t. myall**A. modestus* Thick-billed Grasswren*A. m. modestus* (includes *indulkanna*)**A. m. inexpectatus* (includes *raglessi*, *curnamona* and *obscurior*)** *Subspecific composition may require further assessment***Conservation implications**

The taxonomic revision outlined here has several conservation implications. At the higher end are considerations of phylogenetic diversity. Erwin (1991) and Vane-Wright *et al.* (1991) argued that conservation priorities should take into consideration the phylogenetic or evolutionary distinctiveness of the taxa under consideration. Higher priority would be given to taxa belonging to ancient or species-poor groups because these contribute more to overall taxonomic diversity. Several approaches to measuring phylogenetic diversity have been proposed (e.g. Faith 1992; Krajewski 1994). A common theme in each of these approaches is that the phylogenetic relationships of a taxon directly influence its conservation priority ranking. As such, taxonomic revision can have a significant bearing on conservation ranking.

The case of *Amytornis merrotsyi* provides an interesting case study. Although originally described as a new species (Mellor 1913), the Chestnut-mantled Grasswren, it was subsequently included as a subspecies of *A. striatus* (e.g. Keast 1958; Parker 1982; Schodde 1982a), before again being elevated to species status on the basis of genetic (Christidis 1999) and morphological (Schodde and Mason 1999) assessments. The latter considered it part of the *A. striatus* group whereas the former identified it as a distinct lineage. Mitochondrial and nuclear DNA

sequence data (Christidis *et al.* 2010) confirmed that *A. merrotsyi* represents a monospecific lineage which is formally recognised here as the subgenus *Cryptamytis*. Under a phylogenetic diversity approach, *A. merrotsyi* has the same conservation value as the other three *Amytornis* subgenera *Amytornis*, *Magnamytis*, and *Maluroopsis* with six, six and one species respectively. In terms of phylogenetic diversity status, the conservation value of *A. merrotsyi* has increased as a result of its placement in a new subgenus. However, there has been no change to its actual conservation status in terms of threats.

A second taxonomic change advocated that has major conservation implications concerns the status of the forms *oweni* and *striatus* within the *Amytornis striatus* complex. Schodde (1982a) and Schodde and Mason (1999) treated *oweni* and *striatus* as a single form, in contrast to Mayr (1986), who kept them as separate subspecies. Garnett *et al.* (2011) followed the arrangement of Schodde and Mason (1999), and subsequently listed *A. s. striatus* as 'Near Threatened'. This listing took into consideration the wide geographical range of the taxon stretching from WA through to NSW. According to Garnett *et al.* (2011), "the habitat in the south-east of the subspecies' range has been historically reduced and fragmented, and such losses continue at a slow rate in NSW". According to the taxonomy adopted here, this latter region corresponds to the distribution of *A. striatus sensu stricto*. Clearly a reappraisal of the conservation status of *A. striatus* as defined here is required. The western form *A. oweni* is more widespread and the 'Near Threatened' listing may still be applicable but this also needs to be revisited.

In their assessment of conservation status, Garnett *et al.* (2011) accepted the taxonomy proposed for *Amytornis modestus* by Black (2011a). The western forms *modestus* and *indulkanna* were listed as 'Extinct' and 'Least Concern', respectively. Here the two are kept in *modestus* which would now be listed as 'Least Concern'. The eastern forms *inexpectatus*, *raglessi*, *curnamona* and *obscurior* were listed as 'Extinct', 'Vulnerable', 'Near Threatened' and 'Critically Endangered', respectively. Given that they are all treated here under *inexpectatus*, a reappraisal of the conservation status of this taxon is also required.

Black (2011b) divided *Amytornis textilis textilis* into four subspecies with only the nominate form being extant. Consequently, the conservation implications for the extant populations will not change irrespective of whether one or more subspecies are recognised in this complex.

Garnett *et al.* (2001) listed *Amytornis barbatus diamantina* as 'Least Concern' and *A. b. barbatus* as 'Endangered'. They noted that the subspecific identity of populations from south-western Queensland and South Australia, while assumed to belong to *diamantina* (Schodde 1990), required further confirmation (Carpenter 2002). However, Christidis *et al.* (2010) demonstrated that genetically, these populations were aligned with *diamantina* as argued by Schodde (1990). This taxonomic resolution does not affect the current conservation status of either subspecies.

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