

A floral gem: A review of the conservation status of Bauer's Midge Orchid, *Genoplesium baueri* R.Br (Orchidaceae)

Brian Towle^{1*} and Robert K. Humphries¹

¹ Ecoplanning Pty Ltd, 428 Princes Highway Woonona, 2517

* Corresponding author: brian.towle@ecoplanning.com.au

Abstract

Genoplesium baueri (family Orchidaceae), Bauer's Midge Orchid is a cryptic, terrestrial orchid species endemic to eastern NSW and listed as endangered under state and Commonwealth threatened species legislation. The legislative protections afforded to the species require land managers and determining authorities to have up to date information on the range and total population size of the species. However, this information is not readily available and the information that is available is rapidly becoming outdated as additional populations of the species are identified and reported. This review presents the results of combined searches for records of *Genoplesium baueri* occurrences from multiple databases to collate information on the range and population size of the species and compares the results with previous conservation assessments.

Genoplesium baueri has an even more restricted range than previously thought (Extent of Occurrence reduced from 11,500 km² to 6,398 km²). Despite the reduced range of the species, a small increase in the Area of Occupancy of the species is estimated (increased from 168 km² to 180 km²) and a four to eight-fold increase in total population size is estimated. The results of this review suggest that the total population size, number of populations, and occurrence within conservation reserves are greater than previously estimated, although the extinction risk of the species remains unchanged. As the increase in known population size is largely attributed to increased detection and reporting of occurrences of the species, in real terms the species, and its habitat, may have continued to decline in recent decades from ongoing habitat loss and disturbance. Additionally, management actions at known populations have been shown to be effective at protecting and maintaining some populations, although have not produced any quantifiable increases in population size or extent, such that any loss of individuals may be irreplaceable. Future research priorities for the species should include identifying management actions which are effective at protecting and enhancing the size and extent of populations of the species.

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Introduction

Genoplesium baueri (family Orchidaceae), Bauer's Midge Orchid is a cryptic, terrestrial, myco-heterotrophic orchid which is endemic to eastern coastal New South Wales, Australia (Jones 1993; NSW Scientific Committee 2004; Weston *et al.* 2005). The species is inconspicuous with the entire plant commonly less than 150 mm tall (Jones 1993). The colour of the leaf and inflorescence scape contribute to the inconspicuous nature of the species, ranging from pale green, to yellow and red-brown (Jones 1993; **Figure 1**). The inflorescence typically includes between one and six flowers, although maybe up to 18 (Grimm *et al.* 2020a; pers. obs; **Figure 1**), with individual flowers approximately 15 mm wide (Jones 1993).

Shortly following the first collection of *Genoplesium baueri* by Robert Brown and Ferdinand Bauer in 1805, the rarity of the species was recognised with the species (as *Prasophyllum deaneanum*) described as being "...extremely rare" (Fitzgerald 1888). The recognition of *Genoplesium baueri* as being 'rare' and with a narrow range has been maintained by numerous authors describing the species and its habitat (e.g. Jones 1988; Bishop 1996), with Grimm (2022) describing the species as a "floral gem". In 2004 *Genoplesium baueri* was listed as 'vulnerable' in NSW under the former NSW *Threatened Species Conservation Act 1995* (TSC Act; NSW Scientific Committee 2004). The listing under this Act was upgraded to 'endangered' in 2012 (NSW Scientific Committee 2012) and the species was also listed as

'endangered' under the Commonwealth *Environment Protection and Biodiversity Conservation Act 1999* (EPBC Act) in 2014 (DOE 2014). In 2022 *Genoplesium baueri* was also listed on the IUCN Red List as endangered, based upon the DOE (2014) assessment.

When the TSC Act was repealed in 2017, its listing as endangered was maintained under the current NSW *Biodiversity Conservation Act 2016* (BC Act). The species is also recognised as an entity at risk of 'Serious and Irreversible Impacts' (SAIL) in accordance with Section 6.5 of the BC Act and Section 6.7 of the NSW *Biodiversity and Conservation Regulations 2017* (BC Reg). Therefore, where impacts on *Genoplesium baueri* or its habitat are proposed as part of any development, impacts to the species must be assessed against Section 9.1.1 of the NSW Biodiversity Assessment Method (DPIE 2020; the 'SAIL assessment'). The SAIL assessment for *Genoplesium baueri* requires accurate details of the number of individuals, or areas of habitat within any proposed development sites and as a percentage of the total population. However, up to date information on the population size of the species is not readily available, the only data being available is that within the respective threatened species listing determinations (NSW Scientific Committee 2012; DOE 2014) and a small number of monitored populations in the north of its range (Grimm *et al.* 2020a). This review has been prepared to summarise contemporary information on the occurrences of the species across NSW to better inform conservation assessments and assessments against relevant legislative requirements.



Figure 1. *Genoplesium baueri* inflorescence (left) and entire above ground portions of the plant (right) – B. Towle

Methods

A review was undertaken of voucher specimens and observational records of *Genoplesium baueri* contained within the Atlas of Living Australia (ALA); the Australasian Virtual Herbarium (AVH); BioNet Atlas and iNaturalist (iNat). It is noted that the ALA database includes records from all other databases listed above, however searches of individual databases were undertaken to obtain 'as held' data (prior to location information being denatured) from the BioNet Atlas (provided under licence ASH2006) and AVH records. Most recent searches were performed on the 19 December 2024. Additional reviews of records of *Genoplesium baueri* were from relevant social media (Facebook) sites, specifically the 'Australian Native Orchids' and 'NSW Native Plant Identification' Facebook groups (where the species was confidently identified), and those contained within previous conservation assessments (NSW Scientific Committee 2004; 2012; DOE 2014) and references cited therein (Jones 1993; Jones 2006; Riley & Banks 2002; Copeland 2008; Stephenson 2010).

Data audit

All records from the sources outlined above were compiled into a single dataset and reviewed to eliminate duplicate records. Duplicate records were determined based upon catalogue numbers, collection dates, spatial data, observers, and site information. Where uncertainty existed in relation to the accuracy of records, the sources of records were contacted (where known) for clarification. Records identified as being made from the same site, but on different dates, were retained as independent entries, although were excluded when estimating population size to avoid double counting.

Unique records were categorised as 'uncertain' or 'likely extant' based upon the spatial accuracy, age and location relative to contemporary mapping of native vegetation extent. Specifically, records were categorised as 'uncertain' where the following was true: spatial accuracy was reported as greater than 10 km; spatial accuracy was greater than 1 km with no detailed location description; records were greater than 50 years old at locations where no subsequent records of the species had been made; and records which were from locations where native vegetation was not mapped on the State Vegetation Type Map (NSW DCCEEW 2024a), including an uncertainty buffer matching the spatial accuracy of the record. All remaining records were categorised as 'likely extant'.

Population size and habitat association

Where records were located within 2 km of each other these were assumed to represent the same population including where clusters of multiple records extended across a distance of greater than 2 km, but with the distance between individual records was less than 2 km. It is noted that the use of the term 'population' follows the common biological usage and varies from the specific usage in the Red List Criteria. The 2 km distance was selected based upon the definitions of populations as geographically distinct groups between which there is little demographic or genetic exchange, typically one successful migrant individual or gamete per year or less (IUCN 2024). No detailed studies have been undertaken on the dispersal of *Genoplesium* seeds, although orchid seeds in general are

considered well equipped for effective wind dispersal due to their small size and large volume to weight ratio (Rasmussen 1995) and examples of colonisation across large distances support this conclusion. However, most studies investigating spatial genetic structure within terrestrial orchid populations have found a significant pattern, which in most cases was explained by limited seed dispersal (Machon *et al.* 2003; Jersáková and Malinová 2007; Kotlínek *et al.* 2020). In a study of two European terrestrial orchid species, Kotlínek *et al.* (2020) found that most seeds landed very close to maternal plants (95% of captured seeds were within 7.2 m), although gene flow at greater distances was frequent at up to 2 km in *Cephalanthera rubra* and up to 125 km in *Epipactis atrorubens*. As dispersal distances of terrestrial orchids are influenced by inflorescence height and the density of surrounding vegetation (Brzosko *et al.* 2017), seed dispersal and gene flow in *Genoplesium baueri* are thought to be far less than the species for which detailed studies have occurred (e.g. Kotlínek *et al.* 2020). Considering the shorter height of its inflorescence, the increased density of surrounding vegetation in typical *Genoplesium baueri* habitat, and its low reproductive success (Grimm *et al.* 2020a), it was considered that seed dispersal beyond 2 km would be very infrequent.

Estimates of population size were made using the quantitative count data associated with the records of *Genoplesium baueri*. Where no count data was provided, the population was assumed to be a single individual. Where the same population was counted on multiple dates and years, the maximum observed population size was used to estimate the population size.

The habitat associations (Plant Community Types [PCTs]; NSW DCCEEW 2024a) of the records of *Genoplesium baueri* were identified using GIS software to determine intersection of the records with regional vegetation mapping (State Vegetation Type Map [SVTM]; NSW DCCEEW 2024a). These associations were reviewed and updated where the regional mapping did not reflect the: observations by the authors (who have directly observed the species at the majority of populations); information included within database records (where a vegetation description or PCT was included in the record information); or based on discussions with the record observer. Land tenure was also determined using GIS software to identify intersections with NPWS estate boundaries (DCCEEW 2024b), Local Council Reserves, Crown land reserves and other statutory authority land such as Roads and Maritime and WaterNSW (DCS 2024).

Results

A total of 1,058 records of *Genoplesium baueri* were returned from the searches of the nominated databases and reviews of conservation assessments. Following the removal of duplicate records, 445 unique records of the species were identified. Records ranged in age from 1881 to 2024, with the majority of records having been made in the time since the last conservation assessment of the species in 2012 (NSW Scientific Committee 2012; **Figure 2**). Considering all unique records, 45 populations of *Genoplesium baueri* were identified, with the status of 12 populations categorised as uncertain and 33 populations categorised as likely to be extant (**Table 1**).

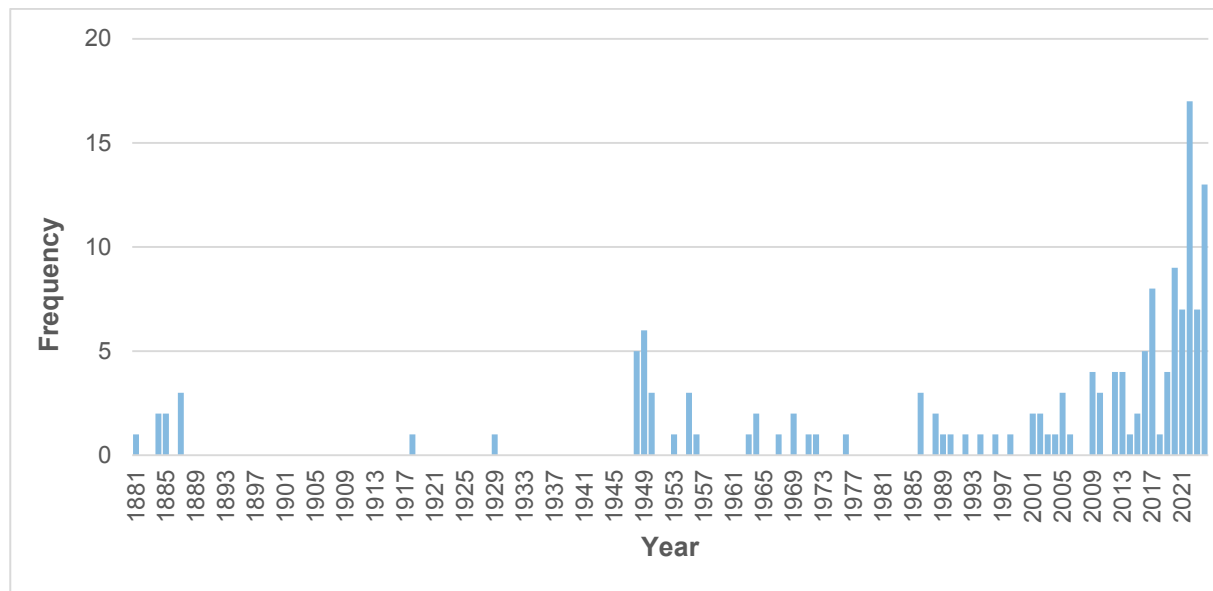


Figure 2. The number of voucher collections and observations for *Genoplesium baueri* for each year from 1880 and 2024. Records by the same observer, on the same date and from the same population were combined into single records (n = 146).

The likely extant populations ranged from Berowra in the north, Buxton in the west, and Ulladulla in the south (**Figure 3**). Interrogation of previous records outside this range including records from Penrose State Forest (CBG 9407714 and CBG 9517048) and Woodford (MEL 0054530A; MEL 1530914A; MEL 0054529A; MEL 0054488A) found these records to be erroneous. In the case of the Penrose State Forest record, no locality information was provided with the specimen and “Penrose State Forest” was incorrectly copied from other collections accessioned at the same time (Anna Monro, Parks Australia, pers. comm. 2024). It is not possible to determine where the specimens were collected. Similarly, the records of the species from Woodford were found to be duplicates of records from the ‘Wahroonga’ and ‘Pennant Hills’ regions, based upon the collector (I. Bowden) and collection dates (March, April 1948 and February, March 1949), and as detailed in Rupp (1948). The attributing of these species to the ‘Woodford’ region appears to be an error arising from the address of the collector (I. Bowden lived at Woodford). Records of the species north of the

Hawkesbury River, including Port Stephens (Riley & Banks 2002) and the Hunter Valley (Jones 1993; Bishop 2000), were found to erroneous in 2008 (Copeland 2008).

Using the likely extant records compiled as part of this review, the Extent of Occurrence (EOO) for *Genoplesium baueri* based on a minimum convex polygon enclosing all mapped occurrences (IUCN 2024) is estimated to be 6,398 km² (**Figure 3**). The Area of Occupancy (AOO) for *Genoplesium baueri* based on a 2 x 2 km grid cell (IUCN 2024) is estimated to be 180 km² (45 grid cells; **Figure 3**). Using the maximum single season count data for each of the 33 likely extant populations, a total of 1,953 flowering individuals has been observed, or estimated by the observers, across these populations (**Table 1**). The size of likely extant populations of *Genoplesium baueri*, using the maximum single season count data associated with the relevant records, ranged from single individuals up to approximately 300 individuals, with an average population size of ~57 individuals (**Table 1**).

Table 1. Populations of *Genoplesium baueri* considered likely to be extant, including size, land tenure and Plant Community Types.

Population	Count	Land tenure	PCT associations in SVTM (NSW DCCEW 2024a)
Ku-ring-gai NP	~500*	National Park; Crown land	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest
St Ives			3595 - Sydney Coastal Sandstone Gully Forest
Duffys Forest	2	Private land	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest
Newport	1	Private land	3814 - Woronora Plateau Heath-Mallee
Galston	6	Private land	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest*
Hornsby	1	Private land	3789 - Coastal Headland Clay Heath
North Wahroonga	15	Crown land;	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest
Terrey Hills	89	Private land	3176 - Sydney Enriched Sandstone Moist Forest
		National Park; Private Land	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest*
			3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest
			3814 - Woronora Plateau Heath-Mallee

Population	Count	Land tenure	PCT associations in SVTM (NSW DCCEEW 2024a)
Davidson	7	National Park; Private land	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest 3595 - Sydney Coastal Sandstone Gully Forest
Frenchs Forest	1	Private Land	3595 - Sydney Coastal Sandstone Gully Forest
Pennant Hills	2	Private Land	3592 - Sydney Coastal Enriched Sandstone Forest 3621 - Sydney Hinterland Turpentine-Apple Gully Forest
Baulkham Hills	4	Private Land	3592 - Sydney Coastal Enriched Sandstone Forest
Malabar	16	National Park	3811 - Sydney Coastal Headland Cliff Scrub 3812 - Sydney Coastal Sandstone Headland Heath
Royal NP	2	National Park	3593 - Sydney Coastal Sandstone Bloodwood Shrub Forest*
Lucas Heights	~300	Private Land	3619 - Sydney Hinterland Enriched Sandstone Bloodwood Forest 3813 - Sydney Hinterland Dwarf Apple Low Woodland
Heathcote	6	National Park;	3619 - Sydney Hinterland Enriched Sandstone Bloodwood Forest
Helensburgh	90	Metropolitan Special Area	3590 - Southern Sydney Scribbly Gum Woodlan
Appin	22	Crown land	3619 - Sydney Hinterland Enriched Sandstone Bloodwood Forest
Cordeaux	80	Metropolitan Special Area	3619 - Sydney Hinterland Enriched Sandstone Bloodwood Forest 3598 - Woronora Plateau Scribbly Gum Woodland
Buxton	1	Private land	3598 - Woronora Plateau Scribbly Gum Woodland
Bargo	5	Private land	3616 - Sydney Hinterland Grey Gum Transition Forest
Yanderra	1	Upper Nepean SCA	3598 - Woronora Plateau Scribbly Gum Woodland
Yerrinbool	100	Upper Nepean SCA	3619 - Sydney Hinterland Enriched Sandstone Bloodwood Forest
North Nowra	29	Private land	3588 - Shoalhaven Foothills Bloodwood Heathy Forest
West Nowra	25	Nature Reserve	3654 - Shoalhaven Lowland Bloodwood Shrub Forest
Yerriyong	68	Crown land reserve	3588 - Shoalhaven Foothills Bloodwood Heathy Forest
Jerrawangala NP	20	National Park	3588 - Shoalhaven Foothills Bloodwood Heathy Forest
Kinghorne	30	BioBank Site	3273 - South Coast Lowland Shrub-Grass Forest *
Callala Bay	200	BioBank Site	3273 - South Coast Lowland Shrub-Grass Forest*
Culburra	35	BioBank Site	3273 - South Coast Lowland Shrub-Grass Forest*
Worrawing Heights	143	Council land	3545 - Coastal Sands Bloodwood Low Forest
Bendalong	31	National Park; Crown land reserve	3267 - Shoalhaven Foothills Turpentine Forest
Ulladulla	120	Crown land; Private land	3267 - Shoalhaven Foothills Turpentine Forest 3654 - Shoalhaven Lowland Bloodwood Shrub Forest
Dolphin Point	1	National Park	3805 - Southern Sandplain Heath
Total	1,953	-	-

* PCT associations updated from SVTM based upon observations of author(s) of records

Habitat associations

Extant records of *Genoplesium baueri* are associated with 19 PCTs which generally belong to the Dry Sclerophyll Forests (Shrubby sub-formation) and Heathlands vegetation formations (Keith 2004; **Table 1**). At the southern limit of the species range, records of the species occur within PCTs which are taller and wetter plant community types, including PCTs classified as part of the Wet Sclerophyll Forests (Grassy sub-formation; Keith 2004; **Table 1**). Sites are generally on shallow low nutrient sandstone soils sometimes with residual shale influence.

Land tenure

Of the 33 identified populations of *Genoplesium baueri*, 10 populations or approximately one third of the identified populations are at least partially located within NPWS estate. Specifically, the AOO intersects the following National Park Estates: Ku-ring-gai Chase National Park, Garigal National Park, Malabar Headland National Park, Royal National Park, Heathcote National Park, Upper Nepean State Conservation Area, Jervis Bay National Park, Triplarina Nature Reserve, Jerrawangala National Park, Conjola National Park and Meroo National Parks.

Additionally, two populations are located within the Metropolitan Special Area, an area jointly managed by WaterNSW and NPWS and are afforded similar protection to those populations within NPWS estate. A further three populations are within formal offset properties established under the BC Act or TSC Act

(BioBank sites or Biodiversity Stewardship Sites) which involve in-perpetuity management for the conservation of biodiversity values. The remaining populations occur within private land, or land managed by local councils or crown land reserves.



Figure 3. Area of Occupancy and Extent of Occurrence of *Genoplesium baueri*

Discussion

Species range

Using all the likely extant records compiled as part of this review, the range of *Genoplesium baueri* is more restricted than previously thought. The EOO for *Genoplesium baueri* based on the likely extant records compiled as part of this review (6,398 km²) represents a decrease of approximately 45 % compared to previous estimate of 11,500 km² (NSW Scientific Committee 2012; DOE 2014). The identification of the most western records (Penrose State Forest and Woodford) as erroneous means that the species has a more coastal distribution and lower altitudinal limit (approximately 400 m asl) than previously thought. The northern limit of the species using the likely extant records compiled as part of this review is consistent with that utilised in the most recent conservation assessments (NSW Scientific Committee 2012; 2014 and DOE 2014), although excludes previous records north of the Hawkesbury River (e.g. the Hunter Valley, Port Stephens and even Coffs Harbour; Jones 1993; Bishop 2000; Riley & Banks 2002) with previous reviews (Copeland 2008) having established that these northerly records are erroneous. The AOO calculated from this review (180 km² equivalent to 45 grid cells [2 x 2 km as per IUCN 2024]) represents a slight increase compared to the previous estimate of 168 km² (42 grid cells; NSW Scientific Committee 2012; DOE 2014), despite the much smaller EOO.

Population estimates

The 1,953 flowering individuals observed, or estimated by the recorders, across the 33 likely extant populations (**Table 1**) represents a likely minimum estimate of population size, with counts across all populations not accounting for dormant (but mature) individuals. Considering the cryptic nature of the species, that flowering and detection are stimulated by fire (Towle 2023), the large areas of habitat where access is restricted (e.g. Metropolitan Special Area), and the lack of detailed counts from many of the known extant populations, the total population size is likely to be much greater than 1,953 individuals. Notwithstanding the likely underestimate of total population size associated with the counts of only flowering individuals across single seasons, the population estimate of 1,953 individuals is approximately four to eight times greater than previous population estimates which range from 250 to 488 individuals (Copeland 2008; Stephenson 2011; NSW Scientific Committee 2012; DOE 2014).

Habitat associations

The use of habitat associations as a predictor of the likely distribution of threatened species is embedded into the environmental impact assessment framework in NSW as part of the Biodiversity Assessment Method (DPIE 2020) and the accompanying Threatened Biodiversity Database Collection ('TBDC'; NSW DCCEEW 2025). The habitat associations for *Genoplesium baueri* included within the TBDC (presented as a list of associated PCTs) in combination with the mapping of these PCTs by the SVTM (NSW DCCEEW 2024a) represent a surrogate-based habitat model for predicting where the species is likely to occur and where assessment under relevant legislation is required. Recent reviews have identified that habitat associations within the TBDC are poorly correlated with the habitat in which records of species have been made (Bell 2025). However, records collated as part of this review largely support the habitat model for *Genoplesium baueri*

formed by the associated PCTs included within the TBDC (NSW DCCEEW 2025; **Figure 4**). Records of *Genoplesium baueri* are most frequently associated with heathlands and open shrubby woodlands commonly dominated by one of the scribbly gums (e.g. *Eucalyptus racemosa* and *Eucalyptus haemastoma*) and *Corymbia gummifera* (Red Bloodwood). There are also a small number of records of the species from taller forests at the northern and southern limits of its range.

Assessment of extinction risk

Previous assessments of extinction risk and listing as endangered under NSW and Commonwealth legislation have been based upon a restricted geographic extent (AOO < 500 km²), severe fragmentation and an inferred and projected ongoing decline (NSW Scientific Committee 2012; DOE 2014). The revised AOO calculated herein is sufficient for maintaining the listing of *Genoplesium baueri* as endangered due to a restricted range where there is also evidence of an ongoing decline and severe fragmentation of habitat.

The increased number of known individuals and populations presented herein, compared to previous conservation assessments (NSW Scientific Committee 2012; DOE 2014), may be interpreted as the species having increased, or at least not decreased, in population size or the key indicators of population size as detailed in IUCN (2024). However, it is considered more likely that the observed increase is the result of greater awareness of the species following listing of the species under relevant legislation, more targeted surveys for the species (as a result of more prescriptive threatened flora survey guidelines associated with the BC Act), as well as more reporting of observations of the species via publicly available databases and special interest social media groups. If the observed increases in known individuals and populations are attributed only to increased detection and reporting, then despite the increased number of individuals identified in recent years and collated herein, in real terms the species, and its habitat, may have continued to decline in recent decades as a result of habitat loss and disturbance. Therefore, the results of this review are insufficient to conclude that the species is not subject to an ongoing decline driven by ongoing loss of habitat quality or diversity, particularly due to the location of many new populations within track and easement margins and areas subject to vegetation slashing.

Despite the increased number of populations identified as part of this review, habitat for the species (where habitat is used in the strict sense as areas habitable by the species and not in a generic sense referring to broader vegetation types) can still be considered severely fragmented according to the definitions of IUCN (2024) and the NSW Scientific Committee (2020). The majority of populations of *Genoplesium baueri* are separated by large distances relative to dispersal distance of the species. As discussed in relation to the determination of populations, despite the suitability for orchid seed to be dispersed by wind, available evidence suggests that actual seed dispersal is typically only very short distances from parent plants (Machon *et al.* 2003; Jersáková and Malinová 2007; Kotlínek *et al.* 2020). For *Genoplesium baueri*, dispersal across distances greater than 2 km is thought to occur very infrequently. In contrast, the majority of its populations, and confirmed habitat for the species, is separated by more than double this estimated dispersal distance, such that chances of recolonisation of habitat patches from adjacent habitat patches are low.

Previous determinations of *Genoplesium baueri* being at risk of extinction due to extreme fluctuations in number of mature individuals (DOE 2014) are not supported by available data. Results of a decade long study of two of the largest known populations of *Genoplesium baueri* (Grimm et al. 2020a) found that population size did not fluctuate significantly through time, with the final counts approximating the ten-year means. Whilst not forming part of the determinations of previous conservation assessments, *Genoplesium baueri* does not appear to have an increased extinction risk due to its occurrence at a low number of locations. The term ‘location’ defines a geographically or

ecologically distinct area in which a single threatening event can rapidly affect all individuals of the taxon present (IUCN 2024). For *Genoplesium baueri* recognised threats include habitat loss and habitat disturbance (NSW Scientific Committee 2012; DOE 2014) and therefore locations are interpreted as areas where a single habitat clearing event can rapidly eliminate or severely reduce the population (NSW Scientific Committee 2020). Consequently, each population is considered a ‘location’, and the number of locations exceeds the relevant IUCN criteria for having a small number of locations (IUCN 2014).

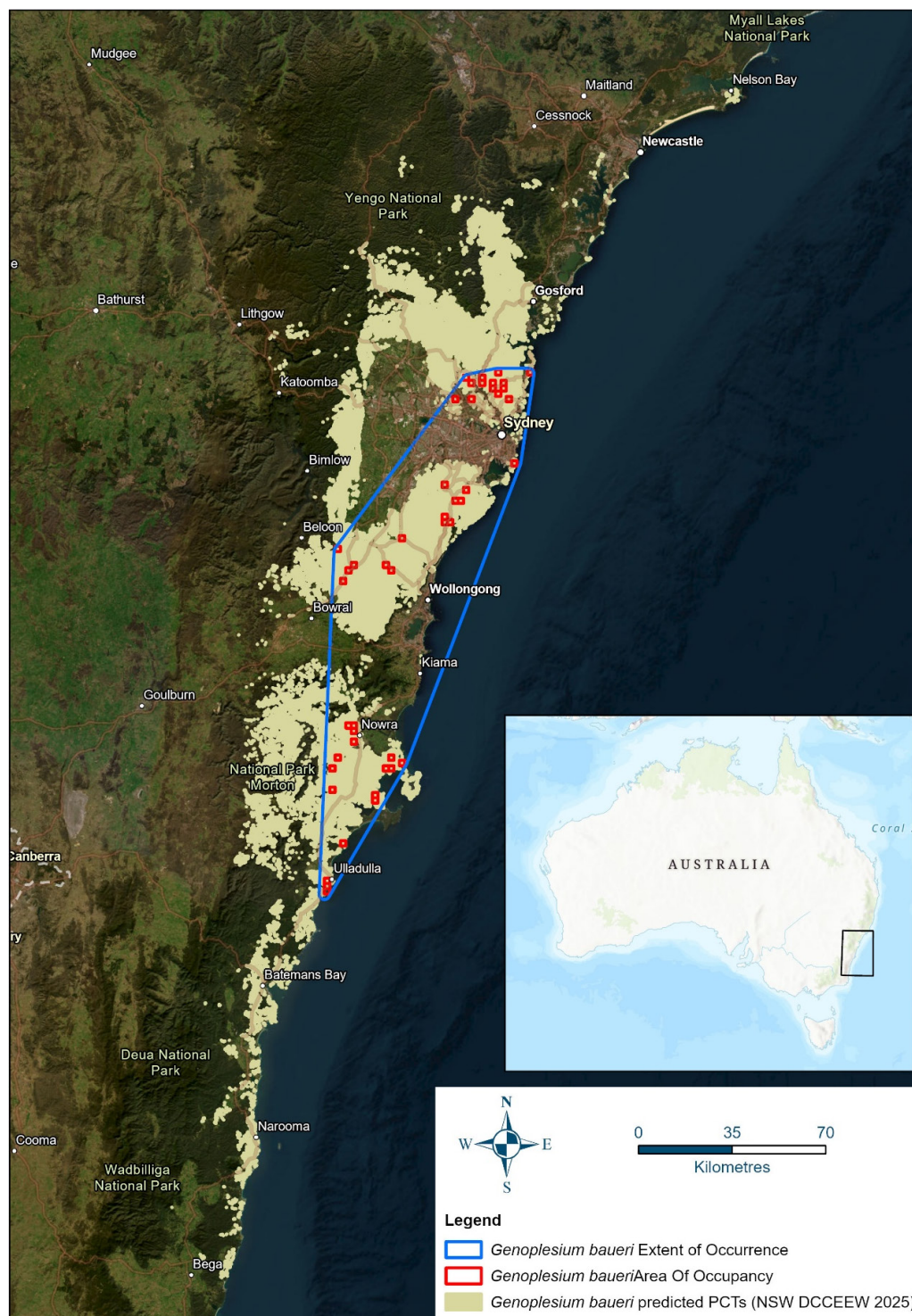


Figure 4. Mapped extent of Plant Community Types (NSW DCCEEW 2024a) with which *Genoplesium baueri* is predicted to occur under the Threatened Biodiversity Database Collection (NSW DCCEEW 2025)

Risk of Serious and Irreversible Impacts (SAIL)

The concept of SAIL is a central component of the NSW biodiversity offsets scheme established under Part 6 of the BC Act. SAIL on biodiversity values are defined in Section 6.7 of the BC Reg as impacts likely to contribute significantly to the risk of a threatened species or ecological community becoming extinct. SAIL is determined based upon four principles, three of which broadly align with criteria prepared by IUCN (2024; Keith *et al.* 2013) to assess the extinction risk of species and ecological communities. In 2019, *Genoplesium baueri* was assessed and recognised as a species at risk of SAIL (DPIE 2019). This recognition was initially based upon Principle 2 of the guidance for listing entities as SAIL (DPIE 2019) which recognises species with very small population size defined as: “fewer than 50 mature individuals independent of whether there are any threats”; or “fewer than 250 mature individuals and the species has an observed, estimated or projected continuing decline”. While not explicitly stated, this initial recognition of *Genoplesium baueri* as an entity at risk of a SAIL appears to be based upon the estimated population size being less than 250 individuals (as per DOE 2014) and one or more of the sub-criteria (e.g. population decline, small populations, extreme fluctuations etc.). Subsequent to the initial listing of *Genoplesium baueri* as an entity at risk of a SAIL under Principle 2, the species was identified as qualifying for this recognition under Principle 4. Principle 4 recognises species that cannot be offset because the entity is unlikely to respond to management.

Assessment against the listing principles for SAIL, suggests that SAIL and significant contributions to extinction risks are unlikely to occur for *Genoplesium baueri* based upon Principles 1 to 3. That is, there is limited evidence to show that *Genoplesium baueri* is undergoing a rapid decline ($\geq 80\%$), has a sufficiently small population size (< 250 individuals), and has a sufficiently restricted geographic distribution (known from ≤ 3 locations and/or AOO $< 10\text{km}^2$ or EOO $< 100\text{km}^2$). However, the species may be at risk of SAIL as any loss of individuals may be irreplaceable, as the species cannot with confidence be predicted to increase with appropriate management.

Genoplesium baueri, and related terrestrial orchid species, have been monitored within conservation management sites for various periods, without evidence of population response or recovery (e.g. Grimm *et al.* 2020a; Towle *et al.* 2022). In a decade long study of the *Genoplesium baueri* occurring within a National Park and Council Managed Wildflower Reserve, Grimm *et al.* (2020a) found that population size did not fluctuate significantly through time. Similarly, Towle *et al.* (2022) in a four-year monitoring period found that for *Genoplesium insigne* occurring across four populations in areas subject to active management, the number of flowering individuals observed each season remained relatively constant. Generally, conservation management for *Genoplesium baueri* and related species has been shown to be effective at protecting and maintaining existing populations, although have not been shown to produce a quantifiable increase in the size of populations or the area of habitat under conservation management. Therefore, any loss of individuals or populations may be irreplaceable, as under current management practices the species cannot with confidence be predicted to increase. Future research priorities for the species should include studies of the reproductive ecology and effective habitat management for the species. In particular, the effectiveness of techniques

such as hand-pollination and increased seed supply should be investigated given the comparatively low reproductive success of the species (Grimm *et al.* 2020a).

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