



## TROPICANA GOLD PROJECT

### Targeted Mygalomorph Survey & DNA Study



*Providing sustainable environmental strategies,  
management and monitoring solutions  
to industry and government.*



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## Tropicana Joint Venture



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## EXECUTIVE SUMMARY

The Tropicana Joint Venture (TJV) is currently undertaking a pre-feasibility study and is working through the relevant State and Federal Environmental Assessment processes associated with the proposed Tropicana Gold Project (TGP), which is centred on the Tropicana and Havana gold prospects. The proposed TGP Operational Area is located approximately 330 km east north-east of Kalgoorlie, and 15 km west of the Plumridge Lakes Nature Reserve, on the western edge of the Great Victoria Desert biogeographic region of Western Australia.

*Ecologia* Environment (*ecologia*) was contracted to conduct a literature review of short-range endemism in Western Australia, and to undertake surveys for short-range endemic invertebrates (SRE) in the proposed operational area. Trapping conducted in 2006 and 2008 found three species of mygalomorph spider (*Aganippe* sp. 1, *Aganippe* sp. 4 and *Kwonkan* sp. 2) that were fully impacted by the proposed TGP mining and infrastructure footprint.

During autumn 2009, targeted surveys were conducted with the aim of collecting the aforementioned species, mapping their geographic distribution within and around the TGP Operational Area and defining their preferred habitat. In addition, a DNA study of all collected specimens of the genus *Aganippe* was conducted using the mitochondrial gene for cytochrome c oxidase 1 (COI) in order to unravel their phylogenetic relationships and provide additional information for a comparison with morphological taxonomy.

The results of the targeted survey showed direct and/or indirect evidence of the occurrence of all three species outside the proposed TGP Operational footprint.

It was concluded that *Aganippe* sp. 4 was no longer impacted by the proposed TGP as the outline of the infrastructure footprint was modified to exclude the habitat of the species. In addition, suitable habitat was also found available further west from the proposed Operational footprint.

Specimens of *Aganippe* sp. 1 have been collected outside the infrastructure footprint and the low genetic divergence indicated that they are part of the same population as specimens inside the infrastructure footprint. Moreover, following further taxonomic examination, *Aganippe* sp. 8 was synonymised with *Aganippe* sp. 1, thus the geographic range of *Aganippe* sp. 1 was further expanded. *Aganippe* sp. 1 would be, therefore, only partially impacted by the TGP, and this impact would be insignificant to the species.

Specimens of *Aganippe* sp. 7 (non-target species) were used for comparison with the target species. In addition, the species was also subjected to further taxonomic examination and it was found identical with *Aganippe* sp. 2. Coupled with the synonymisation of *Aganippe* sp. 1 and *Aganippe* sp. 8, the taxonomic revisions reduced the eight *Aganippe* species listed in the main SRE report to six species.

In the absence of live specimens of *Kwonkan* sp. 2, focus has been given to the identification of suitable habitat of the species and its geographic distribution. The habitat was identified using information from 2006 survey sampling results, published literature and comparisons with other species at TGP. Three habitat types were identified suitable for *Kwonkan* sp. 2, of which two occurred both inside and outside the Operational footprint and one occurred outside the footprint only. The habitats were partially overlapping with suitable habitats of *Aganippe* sp. 2/7 and a new TGP species, *Swolnpes darwini*. Given this similarity, the spatial distribution of *Kwonkan* sp. 2 is most likely to follow the same patterns as those of *Aganippe* sp. 2/7 and *Swolnpes darwini*. It was, therefore, concluded

that *Kwonkan* sp. 2 would be only partially impacted by the Operational footprint, and this impact would be insignificant to the species.

## 1.0 INTRODUCTION

### 1.1 Project Background

The Tropicana Joint Venture (TJV) is currently undertaking a pre-feasibility study and is working through the relevant State and Federal Environmental Assessment processes associated with the proposed on the viability of establishing the Tropicana Gold Project (TGP), which is centred on the Tropicana and Havana gold prospects. The proposed TGP Operational Area is located approximately 330 km east north-east of Kalgoorlie, and 15 km west of the Plumridge Lakes Nature Reserve, on the western edge of the Great Victoria Desert biogeographic region of Western Australia (Figure 1). The Tropicana and Havana prospects represent the first gold resource discovered in this remote portion of Western Australia. Drilling to date suggests that the resource represents a multi-million ounce discovery within a new Greenfields gold province. The Project is a joint venture between AngloGold Ashanti Australia Limited (70% stakeholder and Manager) and the Independence Group NL (30% stakeholder).

The TGP consists of three main components (Figure 1):

- operational area - this area contains the mine, processing plant, aerodrome, village and other associated infrastructure;
- water supply area - two basins have been investigated, the Minigwal Trough and Officer Basin; and
- infrastructure corridor - two options are under consideration (Tropicana/Transline and Pinjin Road options).

During a short-range endemic surveys in 2006 and 2008, three mygalomorph spider species, *Aganippe* sp.1 (Figure 2), *Aganippe* sp. 4 and *Kwonkan* sp. 2 (Figure 2), were found to be fully impacted by the proposed TGP mining and infrastructure footprint. *Ecologia Environment (ecologia)* was contracted to conduct a targeted survey in 2009 with the aim of collecting the aforementioned species, mapping their geographic distribution within and around the TGP and defining their preferred habitat. In addition, a DNA study of all collected specimens was to be conducted using the mitochondrial gene for cytochrome c oxidase 1 (COI) in order to unravel their phylogenetic relationships and provide additional information for a comparison with morphological taxonomy. Part A of the report describes the field survey undertaken during March and May 2009, including the analysis of the suitable habitat, and Part B describes the DNA study of the collected specimens

### 1.2 Survey Objectives

The objectives of the Environmental Protection Authority (EPA) with regards to invertebrate fauna management are to:

- maintain the abundance, species diversity and geographical distribution of Short-range endemic terrestrial invertebrate fauna; and
- protect Specially Protected (Threatened) fauna, consistent with the provisions of the *Wildlife Conservation Act 1950*.

Hence, the purpose of this survey was to provide sufficient information to allow the EPA to assess the impact of the TGP located within the operational area on the *Aganippe* sp.1, *Aganippe* sp. 4 and *Kwonkan* sp. 2.

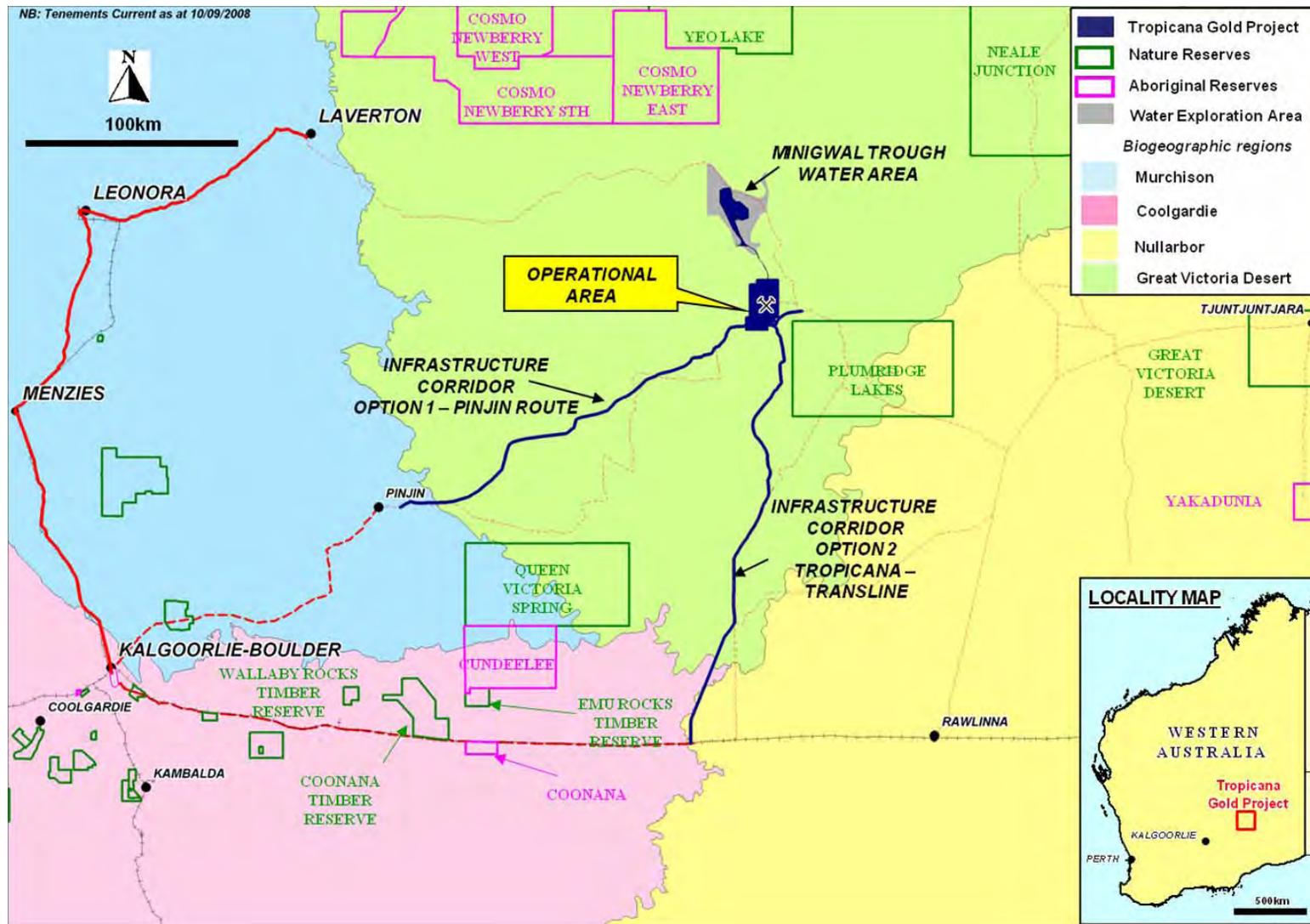


Figure 1 Location Plan of the Tropicana Joint Venture Operational Area in Western Australia



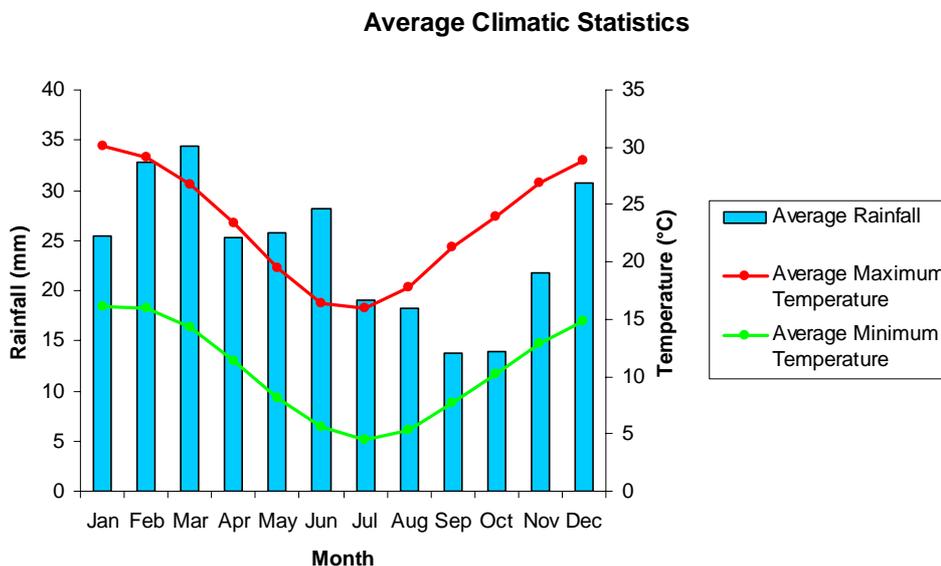
**Figure 2** *Aganippe* sp. 1 (left) and *Kwonkan* sp. 2 (right)

## 2.0 BIOPHYSICAL ENVIRONMENT

### 2.1 Climate

The operational area is located 330 km east-north-east of Kalgoorlie and 220 km east of Laverton. Average weather conditions in the area can be interpreted from data collected at weather stations in Laverton (to the north-west) and Balgair (to the south-east). A summary of the data is provided in Figure 3 and **Error! Reference source not found.**

The climate is described as arid, with summer and winter rain averaging 100 –180 mm (Barton *et al.* 2001b, a). The majority of rainfall occurs during the summer months between January and April and is generally associated with cyclonic rainfall extending inland.



**Figure 3** Combined Average Climatic Statistics for Balgair and Laverton 1983 – 2009 (<http://www.bom.gov.au/>)

**Table 1** Climatic Statistics for Balgair and Laverton

Statistic	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
<b>Average Monthly Records Balgair (1983 – 2009)</b>												
Max Temp (°C)	32.9	31.9	29.2	26.1	22.4	19.1	18.6	20.5	24.2	26.8	29.2	30.9
Min Temp (°C)	16.3	16.6	14.7	11.9	9	6.2	5.1	5.9	8.2	10.5	12.8	14.7
Rainfall (mm)	20.2	27.3	29.9	21.4	21.6	25.3	17	18.3	16	16.2	23.9	36.2
<b>Average Monthly Records Laverton (1983 – 2009)</b>												
Max Temp (°C)	35.8	34.8	31.9	27.2	22.1	18.5	17.8	20	24.5	28	32.1	34.9
Min Temp (°C)	20.5	20	18	13.9	9.5	6.6	5.2	6.4	9.5	12.8	16.6	19.3
Rainfall (mm)	24.4	30	30.4	22.8	23.5	23.9	16.4	13.5	8.1	8.3	14.1	17.6
<b>Combined Average Records for Balgair and Laverton</b>												
Max Temp (°C)	34.35	33.35	30.55	26.65	22.25	18.8	18.2	20.25	24.35	27.4	30.65	32.9
Min Temp (°C)	18.4	18.3	16.35	12.9	9.25	6.4	5.15	6.15	8.85	11.65	14.7	17
Rainfall (mm)	22.3	28.65	30.15	22.1	22.55	24.6	16.7	15.9	12.05	12.25	19	26.9

## 2.2 Biogeography

The operational area of the TGP is located within the Great Victoria Desert bioregion, as defined by Thackway and Cresswell in the Interim Biogeographic Regionalisation of Australia (IBRA) Version 6.1. On a finer scale, it is located on the northern border of the Central and Shield sub-regions of the Great Victoria Desert.

The Central region of the Great Victoria Desert is described as an:

*“arid active sand-ridge desert with extensive dune fields of deep Quaternary aeolian sands overlying Permian strata of the Gunbarrel Basin. Landforms consist of salt lakes and major valley floors with lake derived dunes. Sand plains with extensive seif dunes running east west, occasional outcropping (breakaways) and quartzite hills provide minor relief”* (Barton *et al.* 2001a).

The subregion covers an area of 14,286,995 ha, of which 9.11 % is vested in conservation estates.

## 2.3 Flora and Vegetation

The operational area is situated in the Helms Botanical District, near the border of the Great Victoria Desert and the Nullarbor Plain, within the Eremaean Botanical Province. At a broad scale, Beard (1975) described three distinct vegetation units within close proximity to and including the Tropicana Gold Exploration Area:

1. *Acacia aneura* (mulga) low woodland between sand ridges;
2. Tree (*Eucalyptus gongylocarpa*, *E. youngiana*) and shrub steppe between sand hills with hummock grassland (*Triodia basedowii*); and
3. *Acacia aneura* / *Casuarina cristata* (*C. pauper*) woodland (Mulga and sheoak).

The survey area is primarily located within the Mulga between sandhill complexes with longitudinal sand ridges.

## 3.0 METHODS

The survey methods adopted by the *ecologia* biologist have been developed in consultation with Prof. B.Y. Main, The University of Western Australia

### 3.1 Sampling Methods

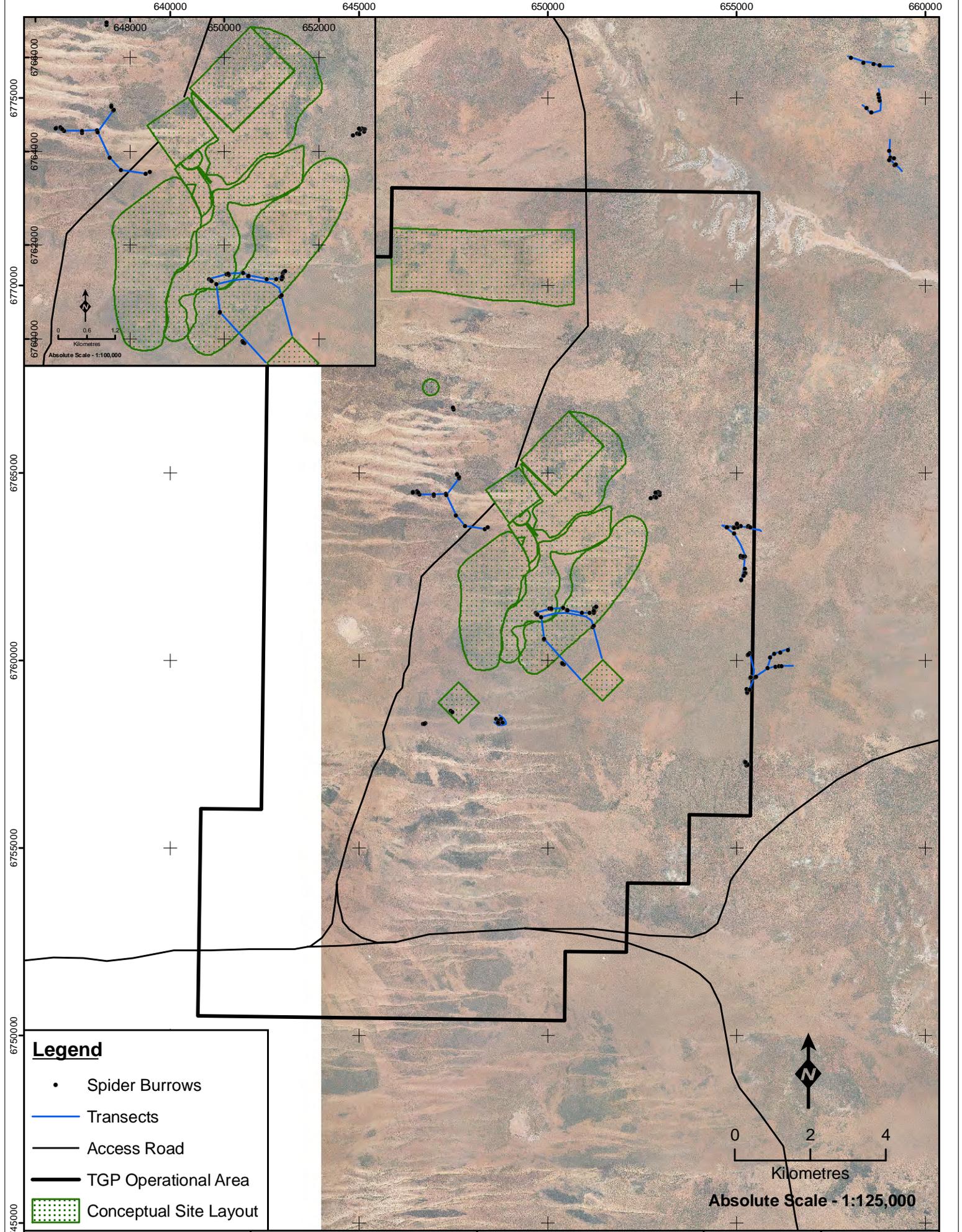
Two foraging surveys were conducted in March and May 2009. In order to determine habitat preference of each of the targeted species, transects were walked through various habitats with two people walking in parallel lines approximately 10-15 m apart. If a spider burrows was found, photographs were taken of the habitat and the burrow exterior. Some specimens were excavated for morphological identification and DNA analysis, in which case the burrow lid and food debris was also collected as these could be useful for taxonomic identification and information on behaviour. Apart from the target species, specimens of other *Aganippe* species (e.g. *Aganippe* sp. 7) were also collected to enable comparisons of habitat and DNA divergence.

### 3.2 Site Selection

Locations of transects were selected based on the data from the 2006 and 2008 surveys (see the main SRE report) and in the field. All transects walked are shown in Figure 4.

### 3.3 External Support

Professor Barbara York Main, an expert taxonomist for mygalomorph spiders, was involved in the identification of all collected specimens.



**Legend**

- Spider Burrows
- Transects
- Access Road
- TGP Operational Area
- Conceptual Site Layout

  
 0      2      4  
 Kilometres  
**Absolute Scale - 1:125,000**



**Targetted Myglomorph  
Survey Points & Habitat  
Transect Lines**

**Figure: 4**  
**Project ID: 1155**

**Drawn: SG**  
**Date: 24/07/09**  
 Unique Map ID: S004  
 Coordinate System  
 Name: GDA 1994 MGA Zone 51  
 Projection: Transverse Mercator  
 Datum: GDA 1994

## **PART A - SPECIES AND HABITAT ASSESSMENT**

## 4.0 RESULTS AND DISCUSSION

### 4.1 Overview

A total of 89 spiders were found, of which 24 were collected and identified. Table 2 and Figure 5 show the identification and location of all collected spiders.

### 4.2 Habitat Preference

#### *Aganippe* sp. 1

Seven specimens of *Aganippe* sp. 1 were collected from four sites, one of which was near the original site T5 inside the TGP mining and infrastructure footprint where the first specimen was collected in 2006, and three were located outside the TGP mining and infrastructure footprint (Figure 5). On the large scale, the species was found in two distinct vegetation units (Beard 1975):

1. Low woodland; *Acacia aneura* (mulga)
2. Hummock grasslands, open low tree steppe; *Acacia aneura* (mulga), *Casuarina pauper* (sheoak) [syn. *C. cristata*] over *Triodia basedowii* between sand ridges

On a small scale within the two vegetation units, however, the species was always associated with pockets of low-lying open ground subject to sheet-flooding and dominated by *Triodia*, with a surface crust on clay and loamy soils. For the purpose of this report, this habitat type was defined as either:

- **loamy open ground, spinifex & acacia;** and
- **loamy open ground, she-oak & acacia** (Table 3).

Transects walked from the original site T5 east and north-east across the proposed eastern waste dump and out of the TGP mining and infrastructure footprint showed that these pocket habitats extend a minimum of 6 km beyond the TGP mining and infrastructure footprint area (Figure 6 and Appendix 1).

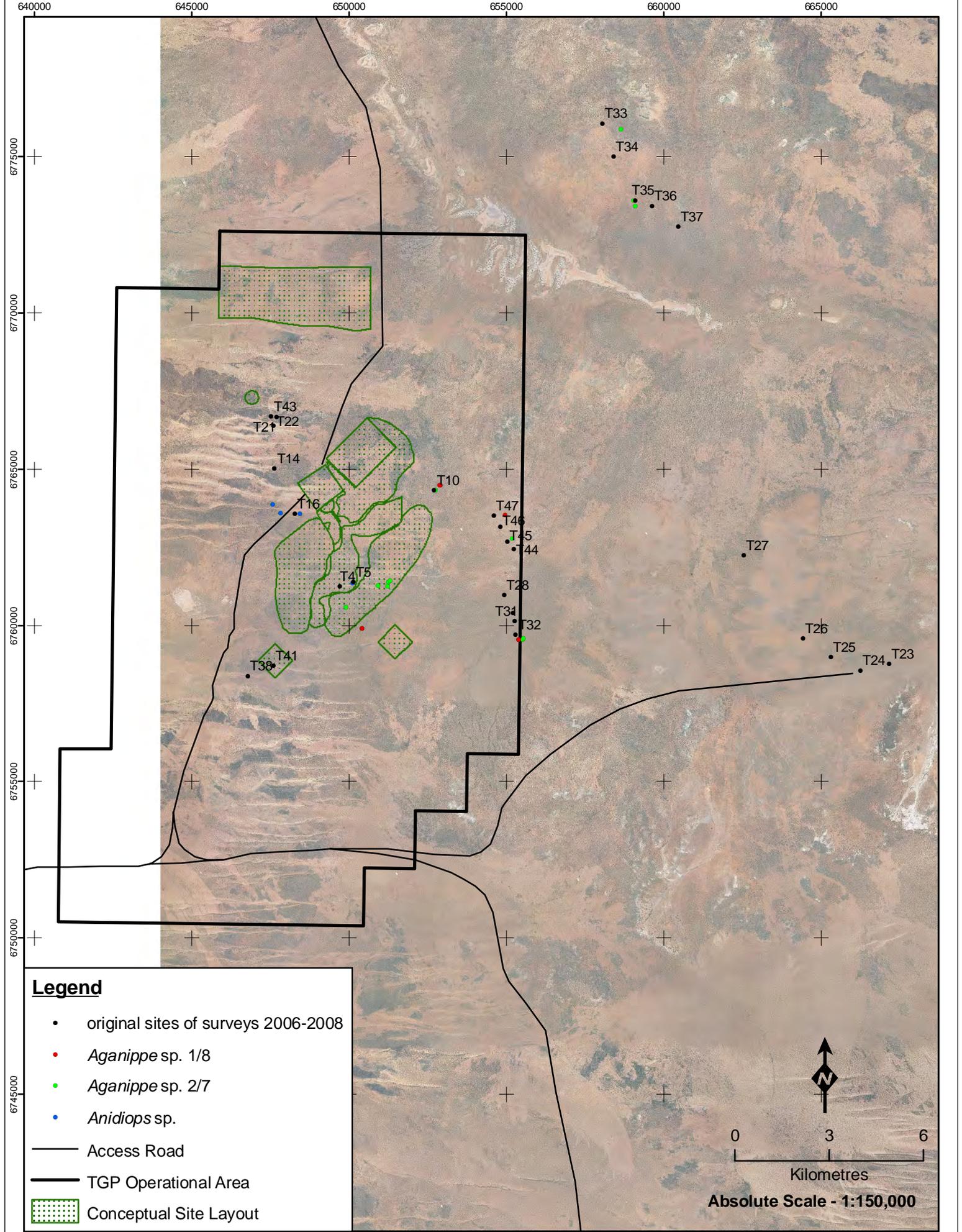
In addition, further taxonomic examination showed that *Aganippe* sp. 1 and *Aganippe* sp. 8 were identical species (B.Y. Main, pers. comm. 2009). The species is henceforth coded as *Aganippe* so. 1/8 and its geographic range now includes previous records of *Aganippe* sp. 1 as well as *Aganippe* sp. 8 from the 2008 survey at sites T30 and T47 (for details see the main SRE report).

**Table 2** A list of all specimens collected during the targeted surveys in March 2009 and May 2009

Species	Burrow	DNA	Site code	Habitat type	Area	Zone	Easting	Northing
Aganippe sp. 2/7	twig-lined	A	MDT05	sandy, eucalypts & acacias	E wastedump E of TROP 5	51J	650902.1	6761281
Aganippe sp. 2/7	twig-lined	A	MDT08	loamy, acacia	E wastedump E of TROP 5	51J	651245.4	6761393
Aganippe sp. 2/7	twig-lined	A	MDT12	sandy, eucalypts & acacias	E wastedump E of TROP 5	51J	649906.3	6760570
Aganippe sp. 2/7	twig-lined	A	MDT20A	loamy, acacia	E wastedump E of TROP 5	51J	655502.9	6759556
Aganippe sp. 2/7	twig-lined	A	MKT03	sandy, eucalypts & acacias	E wastedump E of TROP 5	51J	651224.3	6761273
Aganippe sp. 2/7	twig-lined	A	MKT108	sandy, she-oak & acacias	TROP 45	51J	655176	6762783
Aganippe sp. 2/7	twig-lined	A	MKT115	loamy open ground, she-oak & acacia	TROP 10 (Hat trick)	51J	652737.8	6764341
Aganippe sp. 2/7	twig-lined	A	SCT01	loamy, acacia	E wastedump E of TROP 5	51J	651294.5	6761436
Aganippe sp. 2/7	twig-lined	A	SCT06	loamy, acacia	E wastedump E of TROP 5	51J	655525.9	6759576
Aganippe sp. 2/7	twig-lined	B	MDT41	sandy, eucalypts & acacias	N of OA close to TROP 33	51J	658645.3	6775912
Aganippe sp. 2/7	twig-lined	B	MDT48	sandy, eucalypts & acacias	N of OA close to TROP 35	51J	659087.6	6773427
Aganippe sp. 2/7	twig-lined	B	SCT23	sandy, eucalypts & acacias	N of OA close to TROP 35	51J	659054.3	6773603
Aganippe sp. 2/7	twig-lined		MDT130	sandy, she-oak & acacias	TROP45	51J	655122.4	6762772
Aganippe sp. 1/8	mud-door	C	MDT114	loamy open ground, she-oak & acacia	TROP 10 (Hat trick)	51J	652887.2	6764485
Aganippe sp. 1/8	mud-door	C	MDT128	loamy open ground, she-oak & acacia	TROP 47	51J	654945.1	6763554
Aganippe sp. 1/8	mud-door	C	MDT14	loamy open ground, spinifex & acacia	E wastedump E of TROP 5	51J	650404.7	6759924
Aganippe sp. 1/8	mud-door	C	MDT17	loamy open ground, spinifex & acacia	Silhouette (SE of camp)	51J	655378.1	6759549
Aganippe sp. 1/8	mud-door	C	MDT54	loamy open ground, spinifex & acacia	Silhouette (SE of camp)	51J	655394.4	6759554
Aganippe sp. 1/8	mud-door	C	MKT114	loamy open ground, she-oak & acacia	TROP 10 (Hat trick)	51J	652861.3	6764488
Aganippe sp. 1/8	mud-door	C	SCT02	loamy open ground, spinifex & acacia	E wastedump E of TROP 5	51J	650403.1	6759919
Anidiops sp.	twig-lined	D	SCT14	sandy acacia thicket	W waste dump NE of TROP 16	51J	647814.2	6763597
Anidiops sp.	twig-lined	E	MDT30	sandy acacia thicket	W waste dump NE of TROP 16	51J	647568.3	6763874
Anidiops sp.	twig-lined		MDT01	sandy, eucalypts & acacias	SE havana, TROP 5	51J	650098.3	6761371
Anidiops sp.	twig-lined		SCT13	sandy acacia thicket	W waste dump NE of TROP 16	51J	648418.1	6763565

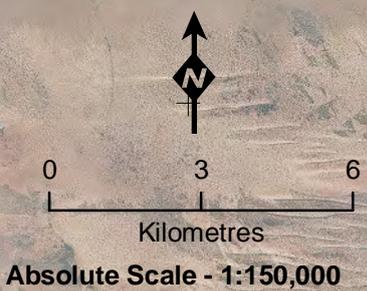
**Table 3** Association between species and habitats (colours as in Figure 6)

yellow	loamy open ground, spinifex & acacia	Aganippe sp. 1/8				
orange	loamy open ground, she-oak & acacia	Aganippe sp. 1/8				
red	loamy, acacia			Aganippe sp. 2/7		
purple	sandy, acacia thicket		Aganippe sp. 4	Aganippe sp. 2/7	Kwonkan sp. 2	
dark blue	sandy, eucalypts (& acacias)			Aganippe sp. 2/7	Kwonkan sp. 2	Swolnpes darwinii
pale blue	loamy, eucalypts & acacias					Swolnpes darwinii
light green	sandy, she-oak & acacias			Aganippe sp. 2/7		
dark green	sandy, she-oak & eucaypts				Kwonkan sp. 2	Swolnpes darwinii



**Legend**

- original sites of surveys 2006-2008
- *Aganippe* sp. 1/8
- *Aganippe* sp. 2/7
- *Anidiops* sp.
- Access Road
- TGP Operational Area
- ▨ Conceptual Site Layout

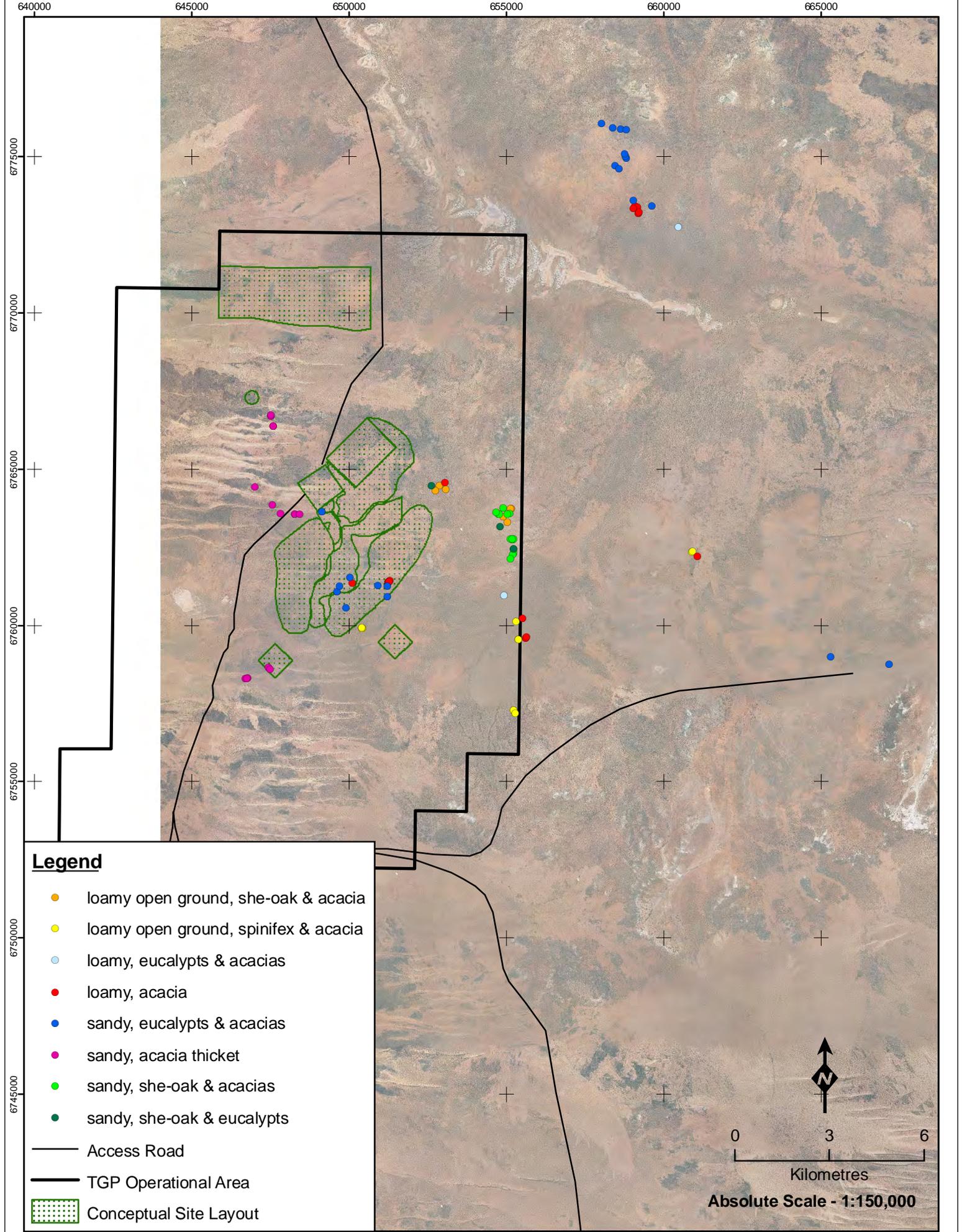


**Geographic distribution of species**

Figure: 5  
Project ID: 1155

Drawn: SG  
Date: 29/07/09

Coordinate System Name: GDA 1994 MGA Zone 51  
Projection: Transverse Mercator  
Datum: GDA 1994  
Unique Map ID: S007  
**A4**



**Legend**

- loamy open ground, she-oak & acacia
- loamy open ground, spinifex & acacia
- loamy, eucalypts & acacias
- loamy, acacia
- sandy, eucalypts & acacias
- sandy, acacia thicket
- sandy, she-oak & acacias
- sandy, she-oak & eucalypts
- Access Road
- TGP Operational Area
- Conceptual Site Layout

**Figure: 6**  
**Project ID: 1155**

**Drawn: SG**  
**Date: 29/07/09**

Coordinate System  
 Name: GDA 1994 MGA Zone 51  
 Projection: Transverse Mercator  
 Datum: GDA 1994

Unique Map ID: S006

**Habitats**



## ***Aganippe* sp. 4**

*Aganippe* sp. 4 was collected in 2006 at the original site T16, which was, at the time located within the TGP mining and infrastructure footprint. The outline of the proposed western waste dump was modified in 2009 in such a way that the site T16 is now located approximately 800 m west of its nearest boundary (Figure 7). The species *Aganippe* sp. 4 is therefore no longer directly impacted by the TGP.

Given the proximity of the site to the infrastructure border, however, additional habitat assessment was conducted in case the site T16 might be subject to indirect impact.

On the large scale, the site T16 lies within a low woodland *Acacia aneura* (mulga) vegetation unit (Beard 1975). On a small scale, twig-lined Idiopidae burrows (*Anidiops* sp.) were located within pockets of *Acacia aneura* thickets with loamy to sandy soils, surrounded by open woodland and / or low sand dunes. For the purpose of this report, this habitat was defined as:

- **sandy, acacia thicket** (Table 3)

In order to ensure that the habitat of this site was available further away from the TGP, transects were walked west and north-west from the site T16. The results showed that the habitat extended a minimum of 2 km beyond the TGP mining and infrastructure footprint area (Figure 6 and Appendix 1).

## ***Aganippe* sp. 7**

The species *Aganippe* sp. 7 was not one of the target species of this survey, however data on its distribution and genetic divergence were compiled in order to enable comparison with the target species. Twelve specimens of *Aganippe* sp. 7 were collected both inside and outside the TGP mining and infrastructure footprint (Figure 5). On the large scale, the species was found in two distinct vegetation units (Beard 1975):

3. Low woodland; *Acacia aneura* (mulga)
4. Hummock grasslands, open low tree steppe; *Acacia aneura* (mulga), *Casuarina pauper* (sheoak) [syn. *C. cristata*] over *Triodia basedowii* between sand ridges

On a small scale within the two vegetation units, however, the species was associated with pockets of habitat types which were defined for the purpose of this report as:

- **sandy, eucalypts & acacias;**
- **sandy, she-oak & acacias;**
- **loamy open ground, she-oak & acacia; and**
- **loamy, acacia.**

Transects walked within and outside the TGP mining and infrastructure footprint showed that these pocket habitats extended a minimum of 12 km beyond the TGP mining and infrastructure footprint. The comparison of specimens collected along Laverton track north of lake Rason palaeodrainage (Figure 6 and Appendix 1) and the group of specimens

collected south of the palaeodrainage revealed a deep split of approx. 7-8% of genetic divergence, contrasting with the 0.0-1.7% divergence within each group (for details see Part B). This suggests that the two groups belong to two separate populations.

*Aganippe* sp. 7 was also subjected to further taxonomic examination and the species was found identical with *Aganippe* sp. 2 (B. Y. Main, pers. comm., 2009). The species is henceforth referred to as *Aganippe* sp. 2/7.

Importantly, coupled with the synonymisation of *Aganippe* sp. 1 and *Aganippe* sp. 8, the taxonomic revisions reduced the eight *Aganippe* species listed in the main SRE report to six species.

## ***Kwonkan* sp. 2**

Despite the repeated efforts during the surveys in March and May 2009, no live *Kwonkan* sp. 2 specimens could be collected. The following summary is based on literature information, habitat assessment and similarities with other species found at TGP.

There are currently six described species of *Kwonkan* in Australia: *K. wonganensis*, *K. anatolion*, *K. eboracum*, *K. goongarriensis*, *K. moriartii*, and *K. silvestris* (Main 1983). Only one of these species, *K. wonganensis*, prefers open ground of pebbly loam soils and constructs a turret of pebbles and soil at entrance resembling burrows of wolf spiders. The remaining species are found in loamy to sandy soils within the leaf litter of open Eucalyptus woodlands or heath, constructing cryptic burrows with small funnel entrance (Main 1983).

The site where the *Kwonkan* sp. 2 was collected in 2006 (T4) is located within the larger vegetation unit of low woodland; *Acacia aneura* (Beard 1975). On a small scale, however, *Acacia aneura* is interspersed with open low woodland of *Eucalyptus gongylocarpa*, over *Eucalyptus trivalvis* sparse mallee, over open low shrubs and *Triodia basedowii* moderately dense hummock grassland, or occasional *Casuarina* sp., with moderate leaf litter, mainly under trees and sparse wood litter, and with orange sand soils. For the purpose of this report, the habitat types were called:

- **sandy, eucalypts;**
- **sandy, acacias; and**
- **sandy, she-oak & eucalypts** (Table 3).

Transects walked from the original site T4 north-east, east, and south-east, across the proposed eastern waste dump and out of the TGP mining and infrastructure footprint, showed that pockets of this habitat extend a minimum of 6 km beyond the TGP mining and infrastructure footprint (Figure 6 and Appendix 1). This habitat is interspersed and partially overlapping with pockets of the open low-lying areas subject to sheet-flooding dominated by *Triodia* that is preferred by the *Aganippe* sp. 1/8, and also by open *Casuarina* sp. and/or *Acacia aneura* woodland over open low shrubs and *Triodia basedowii* that is preferred by *Aganippe* sp. 2/7.

The low genetic diversity of both *Aganippe* sp. 1/8 (0.0-0.3%) and *Aganippe* sp. 2/7 (0.0-1.7%) (see part B) within this area presents evidence that no barriers to dispersal exist across these habitat pockets and that the individual spiders belong to a larger population extending over a minimum of several kilometres beyond the TGP mining and infrastructure footprint. It is, therefore, reasonable to assume that the population of *Kwonkan* sp. 2 in this area is

subject to the same natural conditions and that it follows the same patterns of distribution and dispersal, both inside and outside the proposed TGP mining and infrastructure footprint.

This assumption is supported by the data on a geographic distribution of another species from the family Nemesidae, *Swolnpes darwinii* gen. nov. sp. nov. (B.Y. Main, pers. comm. 2009) found at Tropicana in 2008 (details in the original report on 2006 and 2008 surveys). This species, which was until recently unknown to science, prefers pockets of habitat with open *Casuarina* woodland and it inhabits areas outside the TGP mining and infrastructure footprint over a distance of 12 km (Figure 6 and Appendix 1).

In summary, the targeted survey of the habitat preferred by *Kwonkan* sp. 2 suggests that the species is not restricted to the TGP mining and infrastructure footprint area. The population of *Kwonkan* sp. 2 is, therefore, expected to be partially impacted by the proposed TGP, however this impact is likely to be insignificant to the species.

640000 645000 650000 655000 660000

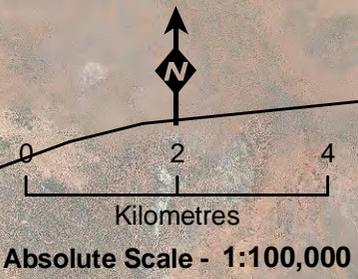
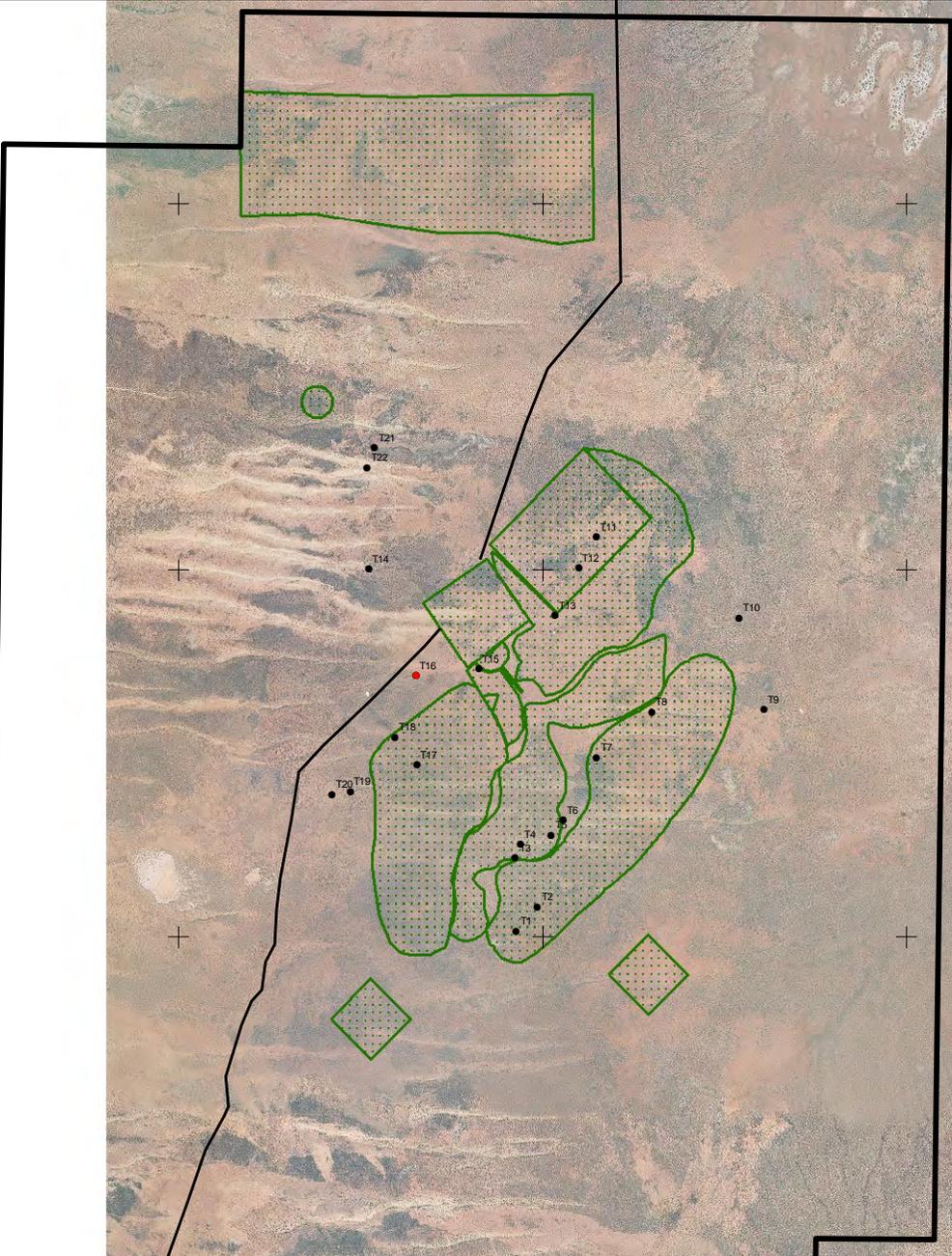
6770000

6765000

6760000

**Legend**

- Survey Site T16
- Survey Sites T1-22
- Access Road
- TGP Operational Area
- Conceptual Site Layout



**Modification of Western Waste Dump - T16 outside 2009 Conceptual Site Layout**

**Figure: 7**  
**Project ID: 716**  
 Coordinate System  
 Name: GDA 1994 MGA Zone 51  
 Projection: Transverse Mercator  
 Datum: GDA 1994

**Drawn: SG**  
**Date: 23/07/09**

Unique Map ID: S003

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## PART B - DNA STUDY



# Helix

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21 August 2009

Dr. Magdalena Davis  
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Ecologia  
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WEST PERTH WA 6005

Via email

**Re. Report on the molecular systematics of the trapdoor spiders *Aganippe* and *Anidiops***

Dear Magdalena,

Following is a summary of the results of the *Aganippe* study. Our data support the morphological designations as assigned by Dr. York Main, however, the data have also revealed divergence, associated with geographical locations, within *Aganippe* sp. 2/7. In addition, our data suggest the two specimens of *Anidiops* belong to two different species.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you would like to discuss the results in detail.

Sincerely,

Terrie Finston and Oliver Berry  
Helix Molecular Solutions



## Objective

The trapdoor spider fauna in WA is diverse, (Main, 1957; 1982), and many new species continue to be recovered (Schmidt, 2007). Morphological taxonomy can be difficult in this group of spiders especially where only one sex or adults have the diagnostic characters (Paquin & Hedin, 2004). Because morphological characters may not always capture true species diversity, DNA methodologies provide a rapid approach to this problem and are increasingly being employed. DNA sequencing allows a rapid assessment of genetic diversity and methods are readily transferred among taxa.

Twenty-three specimens of mygalomorph trap-door spiders collected from the Tropicana Gold Project (TGP; approximately 80 km east of Payne's Find, W.A.), and belonging to two genera (*Aganippe* and *Anidiops*), were sequenced for variation at the mitochondrial DNA gene cytochrome oxidase subunit 1 (COI). The samples were sequenced with the aim of providing complementary information to existing morphological identifications to validate the number of species/genera present in the collection, assess genetic diversity within assigned species, and assess relationships of the TGP specimens with other mygalomorphs from the region.

## Executive summary:

- Twenty-one specimens of trap-door spiders from the Tropicana Gold Project were sequenced for variation at the Cytochrome Oxidase subunit I (COI) gene. These included specimens assigned by morphology to *Anidiops*, *Aganippe* sp. 1/8 and *Aganippe* sp. 2/7.
- Four strongly divergent genetic lineages were recovered. These lineages were of sufficient divergence to classify as four distinct species.
- Morphological species assignments for *Anidiops*, *Aganippe* sp. 1/8 and *Aganippe* sp. 2/7 were supported by the genetic data.
- Genetic variation within *Aganippe* sp. 1/8 was low (<1% divergence between any pair of individuals).
- Genetic variation within *Aganippe* sp. 2/7 was moderate (approximately 7-8% divergence between any pair of individuals), with two divergent lineages corresponding to geographic locations approximately 20 km apart
- The observed moderate genetic divergence over 20 km likely reflects poor dispersal ability of these spiders, and in particular females. This level of divergence suggests the two lineages of *Aganippe* sp. 2/7 have been evolving independently for several million years
- The two *Anidiops* specimens had highly divergent haplotypes and are likely to represent two distinct species.

## Methods

Twenty-three specimens of mygalomorph spiders belonging to two genera (*Aganippe* and *Anidiops*) were sequenced for variation at the COI gene using primers M200 (GGAGGATTGGA AATTGATTAGTCC) and M205 (ACTGTAAATATATGATGAGCTCA) (Simon et al. 1994) (Table 1). Genetic distances between unique genetic types (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotides different between sequences). Maximum parsimony (MP) analysis and neighbour-joining (NJ) of uncorrected p-distances were used to construct phylogenetic trees. The robustness of the branching pattern was assessed using 100 and 500 bootstrap iterations, respectively. The funnel web spider *Euagrus chioseus* was used as an outgroup.

A second phylogenetic tree was constructed as above, using voucher specimens of *Gaius* and *Aganippe* from Goldfield and Wheatbelt sites (Mt. Jackson, Mt. Keith, Albion Downs, Mt. Gibson, Grasspatch, Koolyanobbing). As well as providing information on the relationships of the Tropicana specimens to other mygalomorphs of the region, this was done to test the validity of the *Anidiops* assignments.

## Results

*Phylogenetic analysis and morphotype associations*

A 616 base-pair (bp) fragment of COI was isolated from 21 of the 23 specimens. Sequences for each specimen are shown in Appendix 1. Of the 616 bp alignment, 406 characters were constant, 83 were variable but parsimony-uninformative, and 127 were parsimony informative. Both tree building methods produced similar trees (Figure 1; only the NJ tree is shown). Five well-supported genetic lineages were identified (A-E, Figure 1), and these corresponded to morphological designations. Lineages A and B formed a well-supported monophyletic clade, corresponding to *Aganippe* sp. 2/7 (hereafter referred to as *Aganippe* sp. 2/7-A and *Aganippe* sp. 2/7-B). Lineage C was also well-supported, and corresponded to *Aganippe* sp. 1/8. Lineages D and E corresponded to *Anidiops* morphotypes, but they did not form a monophyletic clade. While there was broad agreement between morphological designations and the genetic data, the DNA showed further distinctions within the morphological designations (see below).

#### *Divergence between lineages*

Genetic divergence between the five lineages was moderate to high, ranging from 7.0% between lineages A and B to 18.1% between lineages C and E (Table 2). It should be noted that that p-distance is a conservative estimate, in that it doesn't account for mutational saturation. Hence these distances should be considered minimum estimates and could in fact be higher. Lineages D and E (*Anidiops* sp.) were highly divergent, differing from one another by 17.4% sequence divergence.

#### *Divergence within morphotypes*

Haplotype diversity within morphotypes and lineages was substantially lower than divergences between morphotypes and lineages (Figure 2). Diversity within morphotypes ranged from low (<1% - *Aganippe* sp. 1/8) to moderate (up to nearly 8% - *Aganippe* sp. 2/7). The observed divergence within *Aganippe* sp. 2/7 was a result of the variation between lineages A and B, which ranged from 7.0 to 7.8 % (Table 3; Figure 2). Haplotype diversity within the two lineages of *Aganippe* sp. 2/7 was substantially lower, ranging from 0 to 1.7% in lineage A and from 0.2 to 1.2% in lineage B. Haplotype diversity within *Aganippe* sp. 1/8 ranged from 0 to 0.3 % sequence divergence (Table 3). All pair-wise divergences between haplotypes are shown in Appendix 2.

#### *Geographic distribution of lineages*

The lineages had relatively well-defined geographical distributions. Lineages A (*Aganippe* sp. 2/7-A), C (*Aganippe* sp. 1/8), D and E (*Anidiops* sp.) are found clustered at the southern sites, with lineages A and C having overlapping distributions, and lineages D and E being found west of the A/C group. Lineage B (*Aganippe* sp. 2/7-B) is found approximately 20 km to the northeast (Figure 3).

#### *Relationships of TGP fauna to other mygalomorph groups*

Both the TGP *Aganippe* and *Anidiops* were contained within a well-supported clade containing *Aganippe castellum* and other *Aganippe* species from Wheatbelt and Goldfields sites (Figure 4). In particular, *Aganippe* sp. 1/8 and the *Anidiops* specimen from SCT14 formed a clade with *Aganippe* sp. 'MG014' from Albion Downs, with the relationship between *Anidiops* sp. and *Aganippe* sp. 'MG014' being particularly well-supported. *Aganippe* sp. 2/7 formed a clade with specimens of *Aganippe* from Mt. Jackson, Koolyanobbing and Forrestainia, although the relationship was not particularly well-supported. The haplotypes of *Gaius* formed a separate, well-supported clade.

## **Conclusions**

Correspondence between morphology and genetics provides a robust foundation for the identification of distinct species. Morphotypes *Aganippe* sp.1/8 and *Aganippe* sp. 2/7 form monophyletic clades that are highly divergent. This reflects a long history of evolutionary isolation and thus their status as distinct species is supported by this study. Similarly, while specimens SCT14 and MDT30 were both identified as *Anidiops*, genetic differentiation between them was high (17.4%). This level of divergence suggests that they are unlikely to belong to the same species.

Variation within *Aganippe* sp. 2/7 requires further consideration. Sequence divergence between lineages A and B is substantially higher (approximately 7-8%) than within lineages (<2%), and the lineages are geographically separated from one-another. Further, the Lake Rason

paleodrainage separates the sites where the A and B lineages are found (M. Davis, pers. comm.). While this level of divergence is sometimes seen between distinct spider species (Barrett & Hebert, 2005), the biology of trapdoor spiders is conducive to producing variation at maternally-inherited mitochondrial genes such as COI. Female trapdoor spiders rarely leave their burrow; it is the male of the species that tends to disperse (Main, 1982). Furthermore, unlike many spider groups, juveniles do not disperse aerially (Main, 1995). Trap door spiders are thus a group likely to show genetic divergence over small spatial scales, which may not be reflected in morphological variation. Whether they are considered "species" or not, they have a long-independent evolutionary history, corresponding to several millions of years of isolation.

*Aganippe* sp. 1/8 and 2/7 showed affinities to other *Aganippe* specimens from Goldfield and Wheatbelt sites, however the large genetic distances between genetic groups (represented by long branch lengths) suggests that *Aganippe* sp. 1/8 and 2/7 represent new species.

The taxonomic status of the *Anidiops* specimens needs further investigation. Both *Anidiops* haplotypes were contained within the *Aganippe* clade. It is believed that *Aganippe* evolved from *Anidiops* (B. York Main, pers. comm. to M. Davis) hence, this might explain the affinity of the *Anidiops* specimens to the genus *Aganippe*. However, without DNA sequences of *Anidiops* we cannot fully resolve the taxonomic status of the TGP specimens. Based on the current data set, the *Anidiops* specimens appear to have no close affinity to the genus *Gaius*.

### Acknowledgements

Many thanks to Western Areas, Cliffs Natural Resources and BHP-Billiton for kindly sharing their *Aganippe* and *Gaius* data. Thanks to Kate Loynes for laboratory and analytical assistance.

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Table 1. Specimens sequenced for COI and their morphological assignments.

Organism	Code	zone	Easting	Northing
<i>Anidiops</i> sp.	MDT01	51J	650098.3	6761371
<i>Aganippe</i> sp. 2/7	MDT05	51J	650902.1	6761281
<i>Aganippe</i> sp. 2/7	MDT08	51J	651245.4	6761393
<i>Aganippe</i> sp. 1/8	MDT114	51J	652887.2	6764485
<i>Aganippe</i> sp. 2/7	MDT12	51J	649906.3	6760570
<i>Aganippe</i> sp. 1/8	MDT128	51J	654945.1	6763554

Aganippe sp. 1/8	MDT14	51J	650404.7	6759924
Aganippe sp. 1/8	MDT17	51J	655378.1	6759549
Aganippe sp. 2/7	MDT20A	51J	655502.9	6759556
Anidiops sp.	MDT30	51J	647568.3	6763874
Aganippe sp. 2/7	MDT41	51J	658645.3	6775912
Aganippe sp. 2/7	MDT48	51J	659087.6	6773427
Aganippe sp. 1/8	MDT54	51J	655394.4	6759554
Aganippe sp. 2/7	MKT03	51J	651224.3	6761273
Aganippe sp. 2/7	MKT108	51J	655176	6762783
Aganippe sp. 1/8	MKT114	51J	652861.3	6764488
Aganippe sp. 2/7	MKT115	51J	652737.8	6764341
Aganippe sp. 2/7	SCT01	51J	651294.5	6761436
Aganippe sp. 1/8	SCT02	51J	650403.1	6759919
Aganippe sp. 2/7	SCT06	51J	655525.9	6759576
Anidiops sp.	SCT13	51J	648418.1	6763565
Anidiops sp.	SCT14	51J	647814.2	6763597
Aganippe sp. 2/7	SCT23	51J	659054.3	6773603

Table 2. Genetic diversity (uncorrected p-distances) between the major lineages A-E.

Lineage	A	B	C	D	E
A	X				
B	7.0-7.8	X			
C	13.9-15.1	13.9-14.4	X		
D	13.6-14.1	13.6-14.1	13.3-13.4	X	
E	16.6-18.4	16.6-17.1	17.9-18.1	17.4	X

Table 3. Genetic diversity (uncorrected p-distances) within morphotypes.

Morphotype	Range of genetic divergence
<i>Aganippe</i> sp. 2/7	0.0 - 7.8 %
<i>Aganippe</i> sp. 2/7-A	0.0 - 1.7%
<i>Aganippe</i> sp. 2/7-B	0.2 - 1.2%
<i>Aganippe</i> sp. 1/8	0.0 - 0.3%
<i>Anidiops</i> sp.	17.4%

Figure 1. Neighbour-joining tree of uncorrected p-distances for a 616 bp alignment of COI. Numbers on major nodes correspond to NJ and MP bootstrap support, respectively Letters on branches correspond to lineages as referred to in the text. Morphological designations are indicated to the right of the haplotypes, and coloured bars correspond to map of lineages (Figure 2).

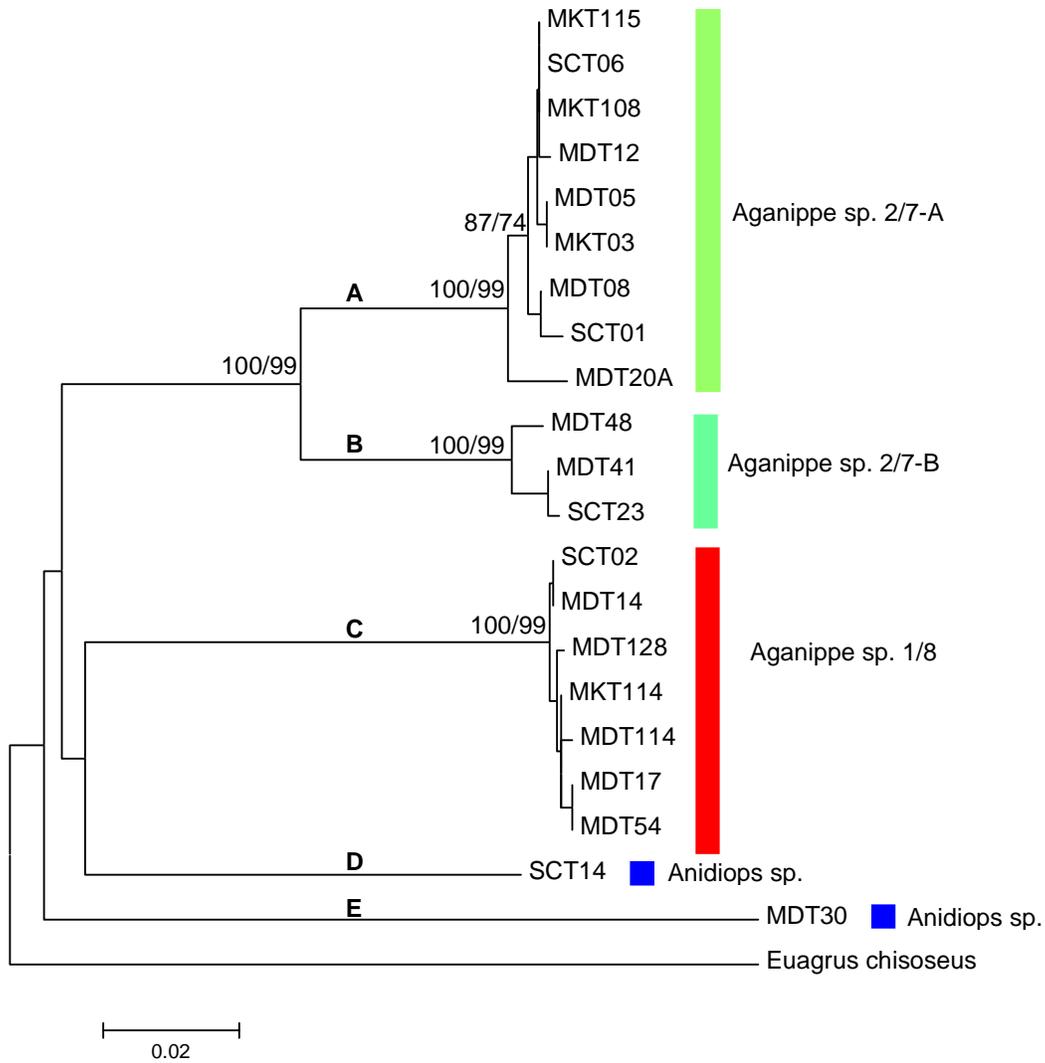


Figure 2. Histogram showing the distribution of pair-wise sequence divergence between haplotypes (uncorrected p-distances), highlighting differences within and between morphotypes.

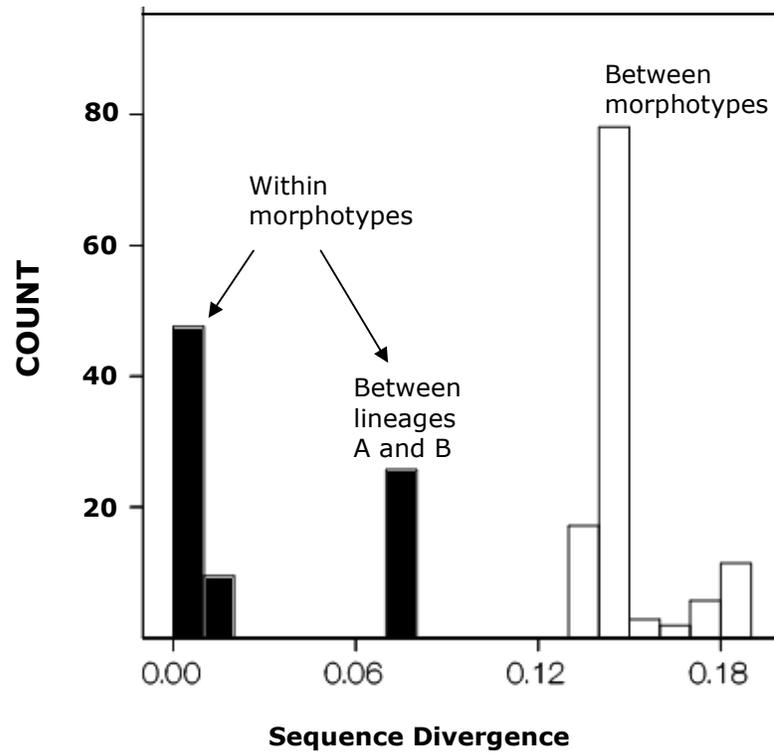


Figure 3. Distribution of genetic lineages as shown if Figure 1.

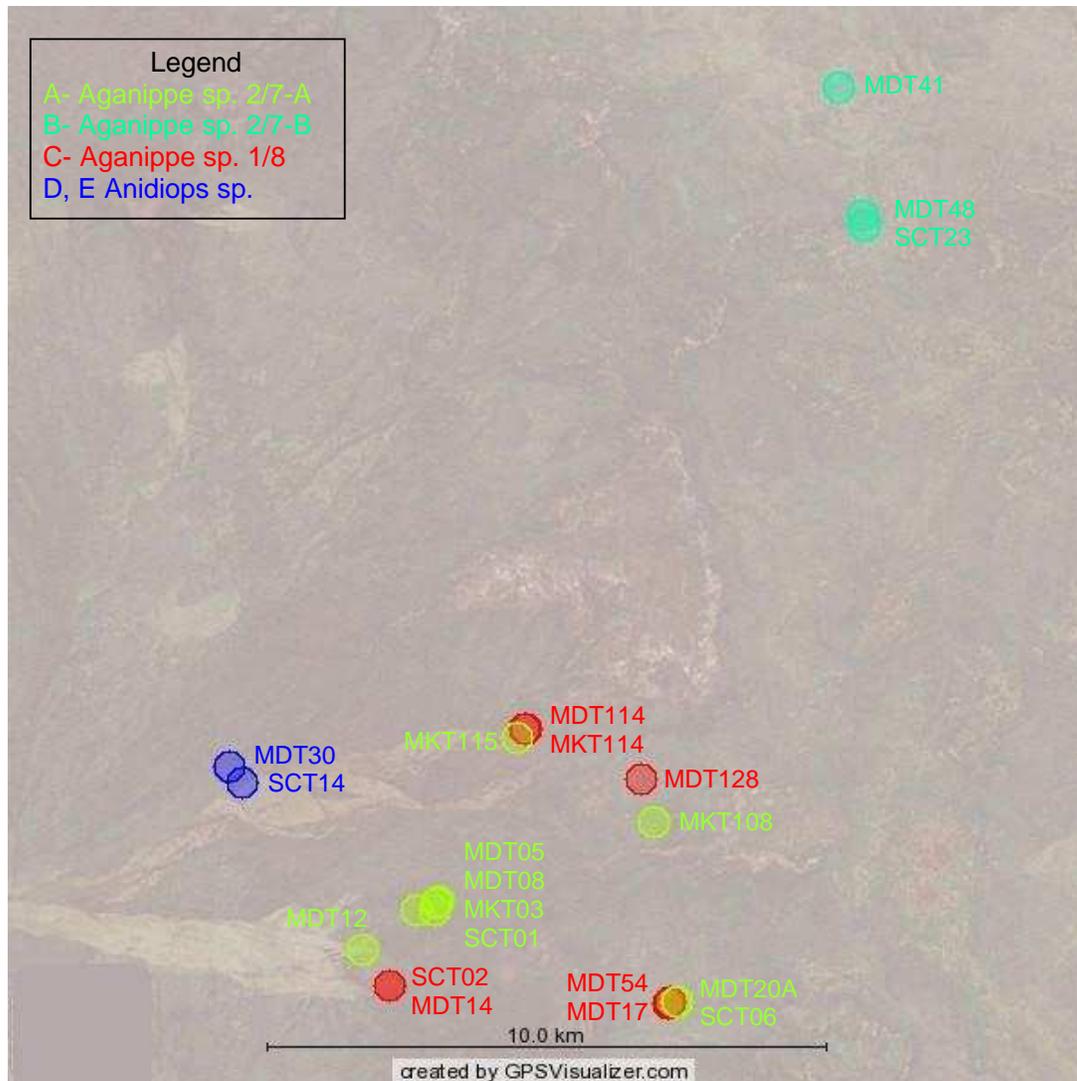
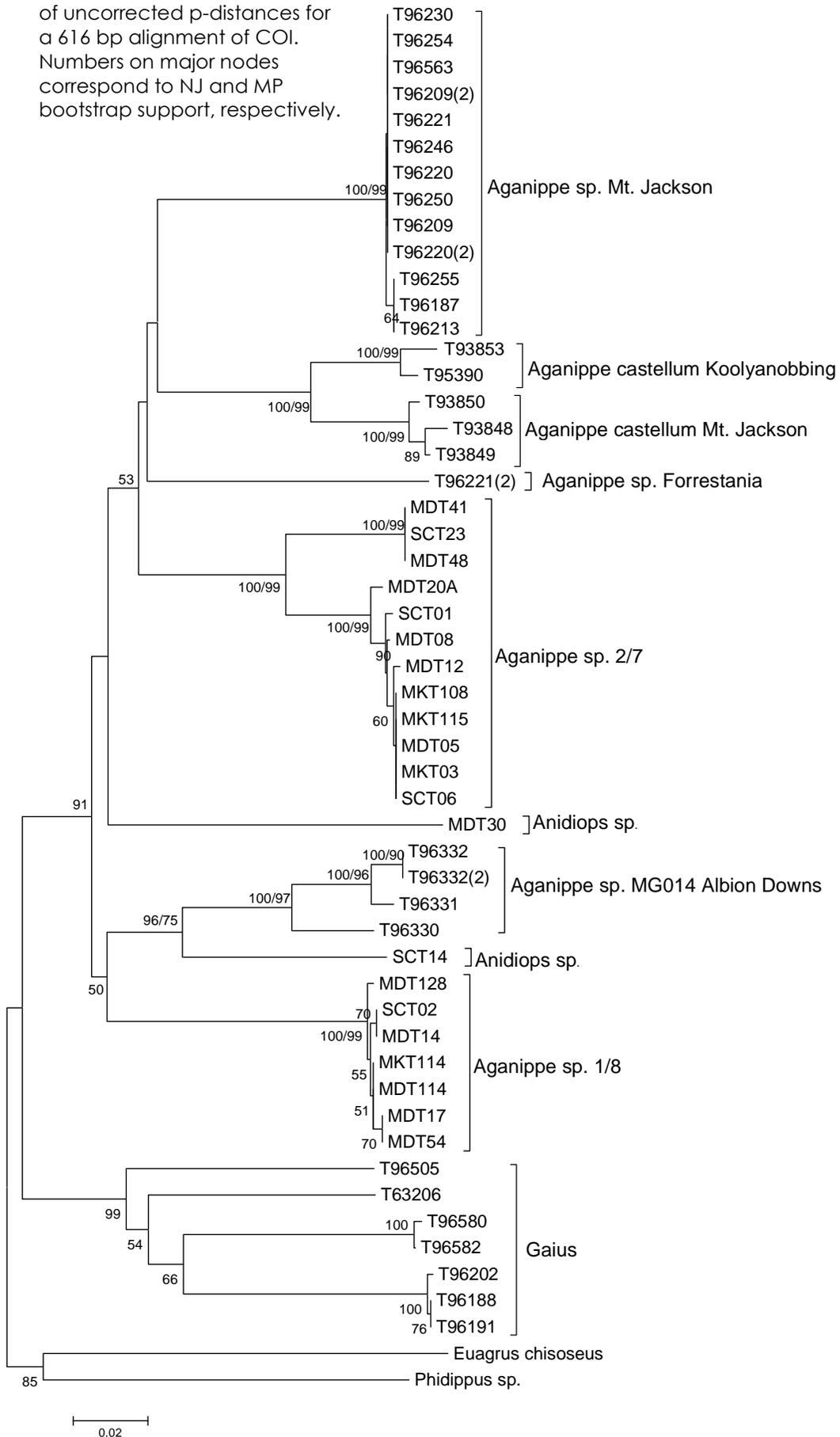


Figure 4. Neighbour-joining tree of uncorrected p-distances for a 616 bp alignment of COI. Numbers on major nodes correspond to NJ and MP bootstrap support, respectively.



Appendix 1. Complete sequences for 21 specimens of mygalomorphs for a 616 bp fragment of COI.

MDT41  
TGATTAGTTCCTTTGATGTTAGGTTGCGCTGATATGGCTTTTCCTCGGATAAATAATTTGAGATTTTGATTGTTGCCT  
SCT02  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MDT05  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
MDT08  
TGATTAGTTCCTTTGATGCTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
MDT114  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MDT12  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
MDT128  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MDT14  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MDT17  
TGATTAGTTCCTT-GATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MDT20A  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTACCT  
MDT30  
TGATTAGTTCCTATAACGTTAGGGGCTCCTGATATAGCTTTCCCTCAGATAAATAATTTGAGATTTTGATTATTACCT  
MDT48  
TGATTAGTTCCTTTGATGTTAGGTTGCGCTGATATGGCTTTTCCTCGGATAAATAATTTGAGATTTTGATTGTTGCCT  
MDT54  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MKT03  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
MKT108  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
MKT114  
TGATTAGTTCCTTTGATGTTAGGAGCTCCAGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCA  
MKT115  
TGATTAGTTCCTTTGATGTTAGGTTACCTGATATGGCTTTTCCTCGAATAAATAATTTGAGATTTTGATTATTGCCT  
SCT01  
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SCT06  
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SCT14  
TGATTAGTTCCTTAATGTTAGGGGCACCTGATATGGCTTTTCCTCGGATGAATAATTTGAGATTTTGATTATTACCT  
SCT23  
TGATTAGTTCCTTTGATGTTAGGTTGCGCTGATATGGCTTTTCCTCGGATAAATAATTTGAGATTTTGATTGTTGCCT

MDT41  
CCTTCTTTGTTTTTTTGGATGGTTTCTTCTTAATTGAGGTTGGGGTGGGGGCTGGTTGAACATTTATCCTCCATTG  
SCT02  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MDT05  
CCTTCTTTGTTTTTTTGGATGGTTTCTTCTTTGATTGAGGTTGGGGTAGGGGCTGGTTGGACTATTTATCCTCCATTG  
MDT08  
CCTTCTTTGTTTTTTTGGATGGTTTCTTCTTTGATTGAGGTTGGGGTAGGGGCTGGTTGGACTATTTATCCTCCATTG  
MDT114  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MDT12  
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MDT128  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MDT14  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MDT17  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MDT20A  
CCTTCTTTGTTTTTTTGGATGGTTTCTTCTTTGATTGAGGTTGGGGTAGGGGCTGGTTGGACTATTTATCCTCCATTG  
MDT30  
CCTTCTTTATTTTTTTAATGGTTTCTCGTTGATACAGATTGGGCTTGGGGTGGGATGAACCATTTATCCTCCTTTG  
MDT48  
CCTTCTTTGTTTTTTTGGATGGTTTCTTCTTAATTGAGGTTGGGGTGGGGGCTGGTTGAACATTTATCCTCCATTG  
MDT54  
CCTTCTTTATTTTTTTGTTATTATCTTCAGTAATTGAGGTTGGTGTGGGGGCTGGGTGAACAATTTATCCTCCTTTG  
MKT03  
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MKT108  
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MKT114  
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MKT115  
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SCT01  
CCTTCTTTGTTTTTTTTGATGGTTCTTCTTTGATTGAGGTTGGGGTAGGGGCTGGTTGACTATTTATCCTCCATTG  
SCT06  
CCTTCTTTGTTTTTTTTGATGGTTCTTCTTTGATTGAGGTTGGGGTAGGGGCTGGTTGACTATTTATCCTCCATTG  
SCT14  
CCTTCTTTGTTTTTTTTATTGGTTTCGTCTTTGATTGAGGTAGGAGTGGGAGCAGGATGAACGATTTATCCTCCTTTG  
SCT23  
CCTTCTTTGTTTTTTTTGATGGTTCTTCTTTAATTGAGGTTGGGGTAGGGGCTGGTTGAACTATTTATCCTCCATTG

MDT41  
TCTTCAGGTGTTGGACATAGAGGGGAGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
SCT02  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCGGGGGCTTCTTCAATT  
MDT05  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MDT08  
TCTTCAGGTGTTGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MDT114  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCTGGGGCTTCTTCAATT  
MDT12  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MDT128  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCTGGGGCTTCTTCAATT  
MDT14  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCGGGGGCTTCTTCAATT  
MDT17  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCTGGGGCTTCTTCAATT  
MDT20A  
TCTTCAGGTGTTGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MDT30  
TCTTCTAGTGTTGACCATAGAGGTGGGGG-ATAGATTTTGTGTTTATTCTTCTTCAATTAGCTGGTGCTTCTTCAATT  
MDT48  
TCTTCAGGTGTTGGACATAGAGGGGAGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MDT54  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCTGGGGCTTCTTCAATT

MKT03  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MKT108  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
MKT114  
TCTTCAGGGGTAGGTCATAGAGGTGGAGGAATAGATTTTGTGTGTTTTCTTTACATTTGGCTGGGGCTTCTTCAATT  
MKT115  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
SCT01  
TCTTCAGGTGTTGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
SCT06  
TCTTCAGGTGTCGGGCATAGAGATGGGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT  
SCT14  
TCTTCTAGTGTCGGTCATAGTGGGGGTGGGATGGATTTTGTGTTTTTCTTTACATTTGGCTGGTGCTTCTTCAATT  
SCT23  
TCTTCAGGTGTTGGACATAGAGGGGAGGGATAGATTTTGTGTTTTTCTTTGCATTTAGCGGGTGCTTCTTCAATT

MDT41  
ATAGGAGCTATTAATTTTATTTCTACTGTAATTAATATGCGAACTAAGGGAATAGAGTTTGAACGCGTCCCTTTGTTT  
SCT02  
ATAGGTGCTATTAATTTTATTTCTACTATTATAAACATACGAGCTTTAGGAATGAGGTTTGAACGCGTTCCTTTGTTT  
MDT05  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTACCTTTGTTT  
MDT08  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTACCTTTGTTT  
MDT114  
ATAGGTGCTATTAATTTTATTTCTACTATTATAAACATACGAGCTTTAGGAATGAGGTTTGAACGCGTTCCTTTGTTT  
MDT12  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTACCTTTGTTT  
MDT128  
ATAGGTGCTATTAATTTTATTTCTACTATTATAAACATACGAGCTTTAGGAATGAGGTTTGAACGCGTTCCTTTGTTT  
MDT14  
ATAGGTGCTATTAATTTTATTTCTACTATTATAAACATACGAGCTTTAGGAATGAGGTTTGAACGCGTTCCTTTGTTT  
MDT17  
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MDT20A  
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MDT30  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGCGTACCTTTGTTT  
MDT48  
ATAGGAGCTATTAATTTTATTTCTACTGTAATTAATATGCGAACTAAGGGAATAGAGTTTGAACGCGTCCCTTTGTTT  
MDT54  
ATAGGTGCCATTAATTTTATTTCTACTATTATAAACATACGAGCTTTAGGAATGAGGTTTGAACGCGTTCCTTTGTTT

MKT03  
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MKT108  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTACCTTTGTTT  
MKT114  
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MKT115  
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SCT01  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTTCCTTTGTTT  
SCT06  
ATGGGGGCTATTAATTTTATTTCTACTGTAATTAATATGCGGACTAAGGGGATAGAGTTTGAACGGGTACCTTTGTTT  
SCT14  
ATAGGGGCTATTAATTTTATTTCTACTATTGTAATATACGAGCTATAGGGATGGTGTGTTGAACGTGTTCCTTTGTTT  
SCT23  
ATAGGAGCTATTAATTTTATTTCTACTGTAATTAATATGCGAACTAAGGGAATAGAGTTTGAACGCGTCCCTTTGTTT

MDT41  
GTATGGTCGGTGATGGTAACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTGGCTGGGGCGATTACTATGTTATTG  
SCT02  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTACCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MDT05  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MDT08  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MDT114  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTACCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MDT12  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MDT128  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTGCCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MDT14  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTACCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MDT17  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTACCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MDT20A  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MDT30  
GTATGGTCTGTAATAACTGCAATTTTATTGTTGTTGTCTCTTCAGTATTGGCTGGTGCTATTACTATATTGTTA  
MDT48  
GTATGGTCGGTGATGGTAACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTGGCTGGGGCGATTACTATGTTATTG  
MDT54  
GTTTGATCTGTTATAGTACTACGGTGTTATTGTTATTATCTTTACCAGTATTGGCTGGGGCTATTACTATATTGTTG  
MKT03  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MKT108  
GTATGGTCAGTAATGGTGACTGCTGTTTTATTATTGTTGTCTCTTCCTGTATTAGCTGGGGCAATTACTATATTATTG  
MKT114  
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MKT115  
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SCT06  
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SCT14  
GTATGGTCTGTTATAGTAACTACAGTGTGTTGCTATTATCTCTACCTGTGTTAGCTGGAGCTATTACTATGTTGTTA  
SCT23  
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MDT41  
ACTGATCGAAATTTAATACTTCTTTTTTTGACCCGGCTGGGGGAGGAGATCCTGTATTATTTTCAGCATTTATTTTGG  
SCT02  
ACTGATCGTAATTTAATACTTCTTTTTTTGATCCGGCTGGTGGGGGTGATCCTGTGTTATTTCAACATTTGTTTTGA  
MDT05  
ACTGATCGAAATTTAATACTTCTTTTTTTGATCCTGCTGGGGGTGGAGATCCTGTTTTATTTTCAGCATTTATTTTGA  
MDT08  
ACTGATCGAAATTTAATACTTCTTTTTTTGATCCTGCTGGGGGTGGAGATCCTGTTTTATTTTCAGCATTTATTTTGA  
MDT114  
ACTGATCGTAATTTAATACTTCTTTTTTTGATCCGGCTGGTGGGGGTGATCCTGTGTTATTTCAACATTTGTTTTGA  
MDT12  
ACTGATCGAAATTTAATACTTCTTTTTTTGATCCTGCTGGGGGTGGAGATCCTGTTTTATTTTCAGCATTTATTTTGA  
MDT128  
ACTGATCGTAATTTAATACTTCTTTTTTTGATCCGGCTGGTGGGGGTGATCCTGTGTTATTTCAACATTTGTTTTGA  
MDT14  
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MDT17  
ACTGATCGTAATTTAATACTTCTTTTTTTGATCCGGCTGGTGGGGGTGATCCTGTGTTATTTCAACATTTGTTTTGA  
MDT20A  
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MDT30  
ACTGACCATAATTTCAATACTTCTTTTTTTGATCCGGCCGGGAGGGGGGATCCTGTGTTATTCCAACATTTGTTTTGG  
MDT48  
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MDT54  
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MKT03  
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MKT108  
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MKT114  
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MKT115  
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SCT01  
ACTGATCGAAATTTAATACTTCTTTTTTTGATCCTGCTGGGGGTGGAGATCCTGTTTTATTTTCAGCATTATTTTGA  
SCT06  
ACTGATCGAAATTTAATACTTCTTTTTTTGATCCTGCTGGGGGTGGAGATCCTGTTTTATTTTCAGCATTATTTTGA  
SCT14  
ACTGATCGAACTTTAATACTTCTTTTTTTGACCCAGCAGGGGGTGGTATCCTGTTTTATTTCAACATTTATTTTGG  
SCT23  
ACTGATCGAAATTTAATACTTCTTTTTTTGACCCGGCTGGGGGAGGAGATCCTGTATTATTTTCAGCATTATTTTGG

MDT41  
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SCT02  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MDT05  
TTTTTTGGTCATCCTGAGGTTTATATCTTGATTTTACCAGGGTTTGGTATAGTGTCTCATATCGTTAGAGGTTCCGGTA  
MDT08  
TTTTTTGGTCATCCTGAGGTTTATATCTTGATTTTACCAGGGTTTGGTATAGTGTCTCATATCGTTAGAGGTTCCGGTA  
MDT114  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MDT12  
TTTTTTGGTCATCCTGAGGTTTATATCTTGATTTTACCAGGGTTTGGTATAGTGTCTCATATCGTTAGAGGTTCCGGTA  
MDT128  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MDT14  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MDT17  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MDT20A  
TTTTTTGGTCATCCTGAGGTTTATATCTTGATTTTACCAGGGTTTGGTATAGTGTCTCATATCGTTAGAGGTTCCGGTA  
MDT30  
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MDT48  
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MDT54  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MKT03  
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MKT108  
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MKT114  
TTCCTTTGGTCATCCTGAGGTTTATATTTAATTTTGCCAGGGTTTGGGATAGTGTCTCATATTGTTAGAGGTTTCAGTT  
MKT115  
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SCT01  
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SCT06  
TTTTTTGGTCATCCTGAGGTTTATATCTTGATTTTACCAGGGTTTGGTATAGTGTCTCATATCGTTAGAGGTTCCGGTA  
SCT14  
TTTTTTGGTCATCCTGAGGTTTATATTTTGATTTTACCTGGTTTTGGAATAGTGTCTCATATTGTGAGAGGTTCCGGTA  
SCT23  
TTTTTTGGTCATCCTGAAGTTTATATTTTGATTTTGCCCTGGGTTTGGTATGGTATCTCATATTGTTAGAGGTTCCGGTA

MDT41      GGCAAGCGAGAACCCTTTTGGATTATTAGGAATGATTTATGCGATGGTTGGGATTGGCGGAATAGGGTTTTG  
SCT02      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MDT05      GGGAAAGCGTGAACCTTTTGGGTTATTAGGAATGATTTATGCGATAGTTGGAATTGGTGGGATGGGATTTG  
MDT08      GGGAAAGCGTGAACCTTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
MDT114      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MDT12      GGGAAAGCGTGAACCTTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
MDT128      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MDT14      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MDT17      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MDT20A      GGGAGGCGTGAACCTTTTGGGTTATTAGGAATGATTTATGCAATAGTAGGAATTGGTGGGATGGGATTTG  
MDT30      GGTAAAGCAAGAACCCTTTTGGGTCATTGGGGATAATTTATGCGATGGCTGGTATTGGGGGATAGGGTTTTG  
MDT48      GGCAAGCGAGAACCCTTTTGGATTATTAGGAATGATTTATGCGATGGTTGGAAATTGTTGGTATAGGATATG  
MDT54      GGGAGGCGAGAACCCTTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGAAATAGGATTTG  
MKT03      GGGAAAGCGTGAACCTTTTGGGTTATTAGGAATGATTTATGCGATAGTTGGAATTGGTGGGATGGGATTTG

MKT108 GGAAGCGTGAACCTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
MKT114 GGGAGGCGAGAACCTTTGGGTTATTAGGAATGATTTATGCTATGGTAGGTATTGGTGGGAATAGGATTTG  
MKT115 GGAAGCGTGAACCTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
SCT01 GGAAGCGTGAACCTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
SCT06 GGAAGCGTGAACCTTTGGGTTATTAGGAATGATTTATGCAATAGTTGGAATTGGTGGGATGGGATTTG  
SCT14 GGGAGGCGAGAACCTTTGGATCATTGGAATGATTTATGCAATAGTAGGAATTGGTGGTATAGGATTTG  
SCT23 GCAAGCGAGAACCTTTGGATTATTAGGAATGATTTATGCGATGGTTGGGATGGGCGGAATAGGGTTTG

Appendix 2. Pair-wise sequence divergence (uncorrected p-distances) for individual mygalomorph specimens for a 616 bp fragment of COI. Green shaded cells correspond to divergence within morphotype *Aganippe* sp. 2/7. Red shaded cells correspond to divergence within morphotype *Aganippe* sp. 1/8.

lineage	A								
	1	2	3	4	5	6	7	8	9
[ 1] MKT115	x								
[ 2] SCT06	0.000	x							
[ 3] MKT108	0.000	0.000	x						
[ 4] MDT12	0.002	0.002	0.002	x					
[ 5] MDT05	0.002	0.002	0.002	0.003	x				
[ 6] MKT03	0.002	0.002	0.002	0.003	0.000	x			
[ 7] MDT08	0.003	0.003	0.003	0.005	0.005	0.005	x		
[ 8] SCT01	0.007	0.007	0.007	0.008	0.008	0.008	0.003	x	
[ 9] MDT20A	0.013	0.013	0.013	0.015	0.015	0.015	0.013	0.017	x
[10] MDT48	0.071	0.071	0.071	0.073	0.070	0.070	0.071	0.073	0.075
[11] MDT41	0.073	0.073	0.073	0.075	0.071	0.071	0.073	0.075	0.076
[12] SCT23	0.075	0.075	0.075	0.076	0.073	0.073	0.075	0.076	0.078
[13] SCT02	0.144	0.144	0.144	0.146	0.144	0.144	0.146	0.146	0.148
[14] MDT14	0.144	0.144	0.144	0.146	0.144	0.144	0.146	0.146	0.148
[15] MDT128	0.146	0.146	0.146	0.148	0.146	0.146	0.148	0.148	0.149
[16] MKT114	0.146	0.146	0.146	0.148	0.146	0.146	0.148	0.148	0.149
[17] MDT114	0.148	0.148	0.148	0.149	0.148	0.148	0.149	0.149	0.151
[18] MDT17	0.148	0.148	0.148	0.149	0.148	0.148	0.149	0.149	0.151
[19] MDT54	0.148	0.148	0.148	0.149	0.148	0.148	0.149	0.149	0.151
[20] SCT14	0.138	0.138	0.138	0.139	0.139	0.139	0.141	0.141	0.136
[21] MDT30	0.181	0.181	0.181	0.181	0.179	0.179	0.181	0.184	0.182

Aganippe sp. 2/7

Aganippe sp. 1/8

Appendix 1, continued

B			C						
10	11	12	13	14	15	16	17	18	19
x									
0.010	x								
0.012	0.002	x							
0.141	0.139	0.141	x						
0.141	0.139	0.141	0.000	x					
0.143	0.141	0.143	0.003	0.003	x				
0.143	0.141	0.143	0.002	0.002	0.002	x			
0.144	0.143	0.144	0.003	0.003	0.003	0.002	x		
0.144	0.143	0.144	0.003	0.003	0.003	0.002	0.003	x	
0.144	0.143	0.144	0.003	0.003	0.003	0.002	0.003	0.000	x
0.136	0.139	0.141	0.134	0.134	0.134	0.133	0.134	0.134	0.134
0.171	0.166	0.167	0.181	0.181	0.179	0.179	0.181	0.181	0.181

Aganippe sp. 2/7  
 Aganippe sp. 1/8



**Appendix 1**

**Habitats**



## Type habitat of *Aganippe* sp. 1/8 inside TGP area

<p><b>Site T5</b></p> <p><b>Habitat type:</b> loamy open ground, Spinifex &amp; acacia</p> <p><b>Description:</b> <i>Acacia jamesiana</i> sparse medium shrubs, over <i>Triodia basedowii</i>. Sparse leaf litter, mainly under shrubs and sparse wood litter. Open ground; red-orange sandy loam.</p> <p><b>Type specimen (male)</b></p> 	
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## Habitat of *Aganippe* sp. 1/8 located outside TGP

<p><b>Burrow (right)</b></p> <p><b>Female at the entrance of her burrow (below).</b> Third left leg collected for DNA analysis.</p> 	
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<p><b>SE of T5</b> Sites MDT13, MDT14, MDT15 and SCT02</p> <p><b>Habitat type: loamy open ground, Spinifex &amp; acacia</b></p> <p><b>Description:</b> Mixed mulga (<i>Acacia aneura</i>) open tall shrubland over <i>Triodia basedowii</i> open hummock grass.</p> <p>Undulating plain. Sparse leaf litter, mainly under shrubs. Loose soil and surface crust</p> <p>Red-orange sandy clay</p>	
<p><b>T28 &amp; T30-32 (Silhouette)</b> Sites MDT17, MDT54, MDT123, MDT135 and MDTA4</p> <p><b>Habitat type: loamy open ground, Spinifex &amp; acacia</b></p> <p><b>Description:</b> <i>Eucalyptus</i> sp. woodland with some <i>Acacia</i>. Mature Spinifex.</p> <p>Thick leaf litter under Eucalypts.</p> <p>Patches of bare earth with gravely soil at surface. Sediment cemented.</p>	
<p><b>T10 (W of Hat trick Hill)</b> Sites MDT114 and MKT114</p> <p><b>Habitat type: loamy open ground, she-oak &amp; acacia</b></p> <p><b>Description:</b> <i>Acacia aneura</i> over sparse <i>Eucalyptus concinna</i> mallee, over open <i>Senna artemisioides</i> subsp. <i>petiolaris</i> medium shrubs</p> <p>Open ground, red sandy clay, calcrete bedrock</p>	

**T46 & 47 (WS of Hat trick Hill)**

Sites MDT126, MDT128, MDT129 & MKT 105

**Habitat type: loamy open ground, she-oak & acacia**

**Description:** She-oak open woodland with diverse understorey. Heavy leaf litter under trees.

Bare earth between trees and shrubs, calcrete bedrock.



**Airstrip Rd. West**

Sites MDT 146 and MDT 147

**Habitat type: loamy open ground, Spinifex & acacia**

**Description:** *Acacia aneura* over mature Spinifex.

Patches of bare earth with gravely soil at surface. Sediment cemented.



## Type habitat of *Aganippe* sp. 2/7 inside TGP

Burrow (right)

Female spider (below)



### East of T4

Sites MDT08, MDT09, MDT10, MDT20A,  
MDT136, SCT01, SCT06

**Habitat type:** loamy, acacia

**Description:** Mixed mulga (*Acacia aneura*)  
shrubland over *Triodia basedowii*

Abundant leaf litter, mainly under shrubs.  
Loose soil and surface crust

Red-orange sandy clay



**South-East of T4**

Sites MDT05, MDT12 and MKT03

**Habitat type: sandy, eucalypts & acacias**

**Description:** *Eucalyptus gongylocarpa* open low woodland, over *Eucalyptus trivalvis* sparse mallee, over open low shrubs and *Triodia basedowii* moderately dense hummock grassland.

Moderate leaf litter, mainly under trees and sparse wood litter

Orange sand



**Type habitat of *Aganippe* sp. 2/7 outside TGP**

**T33 & 34 (Laverton track)**

Sites MDT41, MDT42, MDT43, MDT44, MDT45, MDT46, MDT47, SCT16, SCT19

**Habitat type: sandy, eucalypts & acacias**

**Description:** *Acacia aneura* – sparse woodland. Grass under-storey with mixed shrubs.

Coarse sand



**T35 Laverton track)**

Site SCT23

**Habitat type: sandy, eucalypts & acacias**

**Description:** *Acacia aneura* low woodland. Grass under-storey with mixed shrubs.

Coarse sand



<p><b>T36 (Laverton track)</b> Sites MDT48, MDT49, MDT50, SCT25, SCT26</p> <p><b>Habitat type: loamy, acacia</b></p> <p><b>Description:</b> <i>Acacia aneura</i> woodland</p>	
<p><b>T47 (S of Hat trick Hill)</b> Sites MDT124, MDT125, MDT127, MKT102, MKT103, MKT104</p> <p><b>Habitat type: sandy, she-oak &amp; acacias</b></p> <p><b>Description:</b> She-oak open woodland with diverse understorey.</p> <p>No Spinifex.</p> <p>Heavy leaf litter under trees.</p> <p>Bare earth between trees and shrubs</p>	

**Other habitat of *Aganippe* sp. 2/7 outside TGP**

<p><b>T44 &amp; 45 (S of Hat trick Hill)</b> Sites MDT131, MDT132, MDT133, MDT134, MKT106, MKT107, MKT108, MKT109, MKT110</p> <p><b>Habitat type: sandy, she-oak &amp; acacias</b></p> <p><b>Description:</b> She-oak open woodland with diverse understorey.</p> <p>No Spinifex</p> <p>Lots of bare earth and calcrete</p>	
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**T10 (b); SW of Hat trick Hill**

Site MKT115

**Habitat type: loamy open ground, she-oak & acacia**

**Description:** *Acacia aneura* and sparse *Eucalyptus concinna* mallee over open *Senna artemisioides* subsp. *petiolaris* medium shrubs

Undulating Plain. Moderate leaf litter, mainly under shrubs and sparse wood litter.

Red sandy clay, Calcrete bedrock



## Habitat of *Aganippe* sp. 4 (outside TGP)

### East of T16

Site SCT13

**Description:** *Acacia aneura* low shrubland, over *Triodia desertorum* open hummock grass.

Dune valley. Sparse leaf litter, mainly under shrubs and sparse wood litter.

Red-orange fine sand



### West of T16

Sites SCT14 and MDT30

**Description:** *Acacia aneura* low shrubland; abundant leaf litter, mainly under shrubs and wood litter. Patches of open ground

Red-orange fine sand



### NW of T16

Site SCT15

**Description:** *Acacia aneura* low shrubland; abundant leaf litter, mainly under shrubs and wood litter.

Red-orange fine sand



<p><b>T21,22 &amp;43</b> Sites MDT 115 and MDT116</p> <p><b>Description:</b> <i>Acacia aneura</i> low shrubland, over <i>mature Spinifex</i> Dune valley. Sparse leaf litter, mainly under shrubs and sparse wood litter. Red-orange fine sand</p>	
<p><b>T38</b> Sites MDT118, MDT119, MKT101</p> <p><b>Description:</b> East-west facing dune. Eucalypts present mid to peak. Diverse understorey of shrubs to 1.5m. Spinifex mature and sand very soft. Leaf litter thick under <i>Eucalyptus</i> and <i>Acacia</i>.</p>	
<p><b>T41</b> MDT 117 and MDT120</p> <p><b>Description:</b> North facing, gently sloping dune base. <i>Acacia</i> over sparse shrubs and <i>Triodia</i> sp.  Red-orange fine sand.</p>	

## Type habitat of *Kwonkan* sp. 2 inside TGP area

### Site T4

**Description:** *Eucalyptus gongylocarpa* open low woodland, over *Eucalyptus trivalvis* sparse mallee, over open low shrubs and *Triodia basedowii* moderately dense hummock grassland.

Moderate leaf litter, mainly under trees and sparse wood litter

Orange sand



## Potential habitat of *Kwonkan* sp. 2 outside TGP area

### Site T10 (a)

**Description:** *Casuarina pauper* (sheoak) open medium woodland, over sparse *Eucalyptus concinna* mallee, over open *Senna artemisioides* subsp. *petiolaris* medium shrubs

Undulating Plain. Moderate leaf litter, mainly under shrubs and sparse wood litter

Red sandy clay, Calcrete bedrock



### Site T14

**Description:** Post-fire: *Eucalyptus ewartiana* open medium mallee, over *Codonocarpus cotinifolius* and *Callitris preissii* trees-shrubs, over other shrubs such as *Aluta maisonneuvei* subsp. *auriculata* and *Solanum plicatile*, with *Amphipogon caricinus* and *Triodia basedowii* grasses.

Inter-dune swale. Red sand. Post-fire: *Acacia acanthoclada* subsp. *acanthoclada* and other mixed sparse to scattered low or dwarf shrubs and grasses. Linear dune crest and slope. Yellow sand



**Sites T16 (a)**

**Description:** *Callitris columellaris* scattered trees, over *Eucalyptus youngiana* sparse mallee, over *Anthotroche pannosa* / *Pityrodia loricata* open low shrubland, over *Triodia desertorum* open hummock grass.

Dune Crest. Sparse leaf litter, mainly under shrubs and sparse wood litter. Burnt a long time ago

Red-orange fine sand



**Site T22 (a)**

**Description:** Mixed *Acacia aneura* (mulga) mid-dense low woodland, over mid-dense tall shrubs of dominantly *Eremophila latrobei* subsp. *latrobei* / *Dodonaea rigida*, over *Triodia basedowii* hummock grass.

Rocky sandstone slope. Sparse leaf litter, mainly under shrubs and sparse wood litter

Pale orange sand.



**Type habitat of *Swolnpes darwinii* gen nov. sp. nov. (outside TGP)**

**Site T 46**

**Description:** She-oak open woodland with diverse understorey with Spinifex starting to appear.  
Lots of bare earth and calcrete



**Other habitat of *Swolnpes darwinii* gen nov. sp. nov. (outside TGP)**

**Site T23**

**Description:** *Eucalypt* and *Acacia* dominated to 3 m over grasses, sand and small shrubs.  
Leaf litter with lots of twig and stick debris.  
Red-orange sand



**Site T25**

**Description:** Large, white *Eucalypts* and *Acacia*, dense thicket. Some Spinifex but mostly grasses and other low shrubs. Lots of leaves and debris under trees with around 30% bare earth outside of tree cover.  
Plentiful leaf litter.



**Site T28**

**Description:** *Eucalypt* sp. woodland with some *Acacia*. Mature Spinifex.

Thick leaf litter under Eucalypts.

Patches of bare earth with gravely soil at surface. Sediment cemented.



**Site T36**

**Description:** Weeping, small '*Calistomen*' and large *Eucalypt* to 6 m – white/salmon bark.

Variety of shrub understorey and grasses 70%.

Bare earth between trees.

100% leaf litter and debris under trees.

Course sands suggesting ancient river channel.



**Site T37**

**Description:** Dominated by mature Spinifex – 50%.

Bare sand over-storey, large *Acacia* sp. with accumulated leaf litter beneath.

Red sand and a few mature *Eucalyptus*.



**Site T44**

**Description:** She-oak open woodland with diverse understorey.

No Spinifex

Lots of bare earth and calcrete

