Project Plan SP 2018-041

Molecular characterisation of stinking passionflower (*Passiflora foetida*)

BCS Plant Science and Herbarium

Project Core Team

X X **Supervising Scientist** Tara Hopley
Data Custodian Tara Hopley

Project status as of Sept. 5, 2023, 8:23 a.m.

X X Update requested

Document endorsements and approvals as of Sept. 5, 2023, 8:23 a.m.

X X
Project Team granted
Program Leader granted
Directorate granted
Biometrician granted
Herbarium Curator not required
Animal Ethics Committee not required

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Program

BCS Plant Science and Herbarium

Departmental Service

Service 7: Research and Conservation Partnerships

Project Staff

X	X	X	Role	Person	Time allocation (FTE)
			Research Scientist	Margaret Byrne	0.1

Related Science Projects

Proposed period of the project

July 1, 2017 – Dec. 31, 2020

Relevance and Outcomes

Background

At the top of many emerging weed threat lists for the Pilbara and Kimberley regions of Western Australia is stinking passionflower (*Passiflora foetida* var. *hispida* DC. ex Triana & Planch. Killip; Passifloraceae), a perennial vine from South and Central America. In the Pilbara, the weed is rapidly expanding its abundance in areas with slightly higher moisture availability than the surrounding landscape, including coastal reserves in the Roebourne sub-region (e.g. Cape Range National Park, Murujuga National Park), riparian habitats across the region in particular at the Millstream-Chichester National Park. The Fortescue Marsh and Karijini National Park are considered highly suitable for invasion, although no records have yet been reported from high conservation value habitat in these areas. Recent work by CSIRO and the Department of Parks and Wildlife has clearly shown that this emerging threat tag is warranted for stinking passionflower (Webber et al. 2014).

A significant impediment for implementing effective weed management strategies for stinking passionflower is that very little is known about its biology and life history, particularly in countries where it has been introduced. Ecological and genetic characterisation of the weed is required in order to guide the search for suitable biological control agents. Stinking passionflower has a broad native range in South and Central America, a widespread cosmopolitan introduced distribution, and is believed to be a species complex comprised of numerous entities. Molecular analysis of Australian collections, in the context of samples from the native range and other regions and countries where the weed is introduced, will be used to identify and characterise the genetic entity(ies) present in the Pilbara, whether there are multiple origins of the Pilbara invasions, and to confirm the level of relatedness to native *Passiflora* species and commercial varieties. Based on the ecological and genetic characterisation we will be able to identify and prioritise a suite of promising candidate biological control agents from stinking passionflower's native range.

In recent times, stinking passionflower in the Pilbara and Kimberley has been significantly more invasive than in the Northern Territory and Queensland, suggesting the existence of different forms adapted to local conditions. We will test this hypothesis by molecular characterisation of Pilbara populations relative to less invasive populations to identify any signal of adaption (given the high selective pressure induced by the ecological traits) and to inform which populations to preferentially target for biological control.

Aims

- Use molecular analysis of Australian collections, in the context of samples from the native range and other regions and countries where the weed is introduced, to identify and characterise the genetic entity(ies) present in the Pilbara.
- Elucidate whether there are multiple origins of the Pilbara invasions.

- Confirm the level of relatedness of the invasive *Passiflora foetida* to native *Passiflora* species and commercial varieties.
- Characterisation of Pilbara populations relative to less invasive populations to identify any signal of adaption (given the high selective pressure induced by the ecological traits) and to inform which populations to preferentially target for biological control.

Expected outcome

- Provide essential information on the potential taxonomic entities and origin to inform identification of putative agents matched to the target weed.
- Guide how to prioritise the search for agents (when combined with ecological insight).
- Inform how local adaptation within invasive populations may influence the effectiveness of control between different shortlisted agents.

Knowledge transfer

Tasks and Milestones

- Commence collection of samples for genetic work from across study populations and the native range - 1 October 2017
- Commence extractions of DNA from collected material, and develop methods to investigate taxonomic identity, invasion history and local adaptation - 1 December 2017
- Complete collection of samples for genetic work from across study populations and the native range - 1 December 2018
- Complete ongoing genetic analyses and generate initial results to clarify weed's taxonomic identity and invasion history - 1 December 2018
- Complete genetic analyses to clarify weed's taxonomic identity and invasion history - 1 December 2019
- Undertake analyses to determine adaptation signals in invasive populations - 1 December 2019
- Prepare and submit draft publication(s) on genetic analyses to date - 1 December 2020

References

Webber B.L., Yeoh P.B. & Scott J.K. (2014b) *Invasive* Passiflora foetida *in the Kimberley and Pilbara: understanding the threat and exploring solutions*. Phase 1 final report. CSIRO, Australia. 27pp.

Study design

Methodology

Phylogenetic characterisation of the Australian entities with respect to the native range sampling of *Passiflora foetida* will be undertaken using whole chloroplast sequencing methods. Samples from across the invaded range in Australia will be compared to samples acquired from specimens at the Missouri botanical gardens herbarium representing the native range (Central and South America) of *Passiflora foetida*. Results from whole genome sequencing will subsequently be aligned to the *Passiflora edulis* chloroplast reference genome and individual assembled chloroplast sequences will be used for maximum likelihood and bayesian phylogenetic analysis.

For more detailed population analyses, leaf material from approximately 20 individuals from populations across the climatic gradients will be sampled. Samples will be typed using next generation sequencing genomics methods to identify single nucleotide polymorphism (SNPs) markers. Levels of genetic diversity between sites and climatic zones will be compared to identify any genetic structure present. SNP's will also be analysed to identify adaptive variation between populations and climatic zones.

Biometrician's Endorsement

granted

Data management

No. specimens

Herbarium Curator's Endorsement

granted

Animal Ethics Committee's Endorsement

not required

Data management

As this project will create large data sets, active data sets will be kept on the Pawsey group file storage. Raw and final data will be stored on the Pawsey long term storage and be backed up on external hard drives.

Budget

Consolidated Funds

to | X | X | X |

Source	Year 1	Year 2	Year 3
FTE Scientist			
FTE Technical			
Equipment			
Vehicle			
Travel			
Other			
Total			

External Funds

to | X | X | X |

Source	Year 1	Year 2	Year 3
Salaries, Wages, Overtime			
Overheads			
Equipment			
Vehicle			
Travel			
Other			
Total	130000	368000	245000