

**Genomics for Australian Plants (GAP):**

**Reference Genomes Request for Partnership 2022**

**GAP Background**

The [Genomics for Australian Plants Initiative (GAP)](https://www.genomicsforaustralianplants.com/) was catalysed by Bioplatforms Australia in partnership with researchers from the Australian State and National Herbaria and Botanic Gardens. This nationally-inclusive and collaborative initiativeis supported by Bioplatforms Australia (enabled by NCRIS), the Ian Potter Foundation, Royal Botanic Gardens Foundation (Victoria), Royal Botanic Gardens Victoria, the Royal Botanic Gardens and Domain Trust, the Council of Heads of Australasian Herbaria, CSIRO, Centre for Australian National Biodiversity Research and the Department of Biodiversity, Conservation and Attractions, Western Australia.

The central resource for this initiative is derived from herbaria and botanic gardens (living collections) around the country. The addition of genome sequencing data adds significant value to the collections and contribute to the development of new methods and capabilities. This project is aligned with and will help deliver on strategic actions identified in the [“Discovering biodiversity: a decadal plan for taxonomy and biosystematics in Australia and New Zealand 2018–2027”](http://www.science.org.au/support/analysis/decadal-plans-science/discovering-biodiversity-decadal-plan-taxonomy).

For GAP FAQ, [click here.](https://www.genomicsforaustralianplants.com/wp-content/uploads/2021/05/2021-05-11_GAP_webpage_FAQ.pdf)

**Reference Genomes Request for Partnership 2022**

We are now calling for a Request for Partnership (RFP) for the [GAP Reference Genomes](https://www.genomicsforaustralianplants.com/reference-genomes/) component. The aim of this RFP is to sequence and assemble Australian plant genome to fill in the gaps in the Australian Plant Tree of Life. The genomes generated may be a draft or complete.

The sequencing will be undertaken by Bioplatforms Australia genomics facilities through their Framework Initiative strategic investments (<https://bioplatforms.com/about/>) while the data assembly is to be supported by research community co-investment.

Successful teams will be required to undertake the following activities using their own resources:

1. Project design
2. Sample preparation and supply of metadata
3. DNA extraction from samples
4. Data analysis
5. Publication
6. Raw sequence data and assembled genome submission to international repository

Bioplatforms Australia will provide the following resources:

1. Sequencing at Bioplatforms facilities
2. Project management and data management (raw data storage and access, with associated metadata)

**Priority Plant families**

The GAP Reference Genomes component will be prioritising the plant families in the table below where there are no known or publicly available reference genomes.

We will also consider applications for other Australian plant families not listed in the table.

It should be noted that this is NOT a grant opportunity.

|  |  |  |
| --- | --- | --- |
| Alstroemeriaceae | Corsiaceae | Ripogonaceae |
| Austrobailyaceae | Dipentodontaceae | Smilacaceae |
| Berberidopsidaceae | Escalloniaceae | Stemonuraceae |
| Campynemataceae | Geraniaceae | Trimeniaceae |
| Cardiopteridaceae | Paracryphiaceae | Zygophyllaceae |
| Colchicaceae | Petermanniaceae |  |

Some species have large genomes. The current approaches we are currently using (e.g., long read sequencing) will not be practical. However, we are open to any innovative approach, should that be forthcoming.

**Recommendation for a successful outcome by the GAP Steering Committee**

**Plant**

1. Genome size and complexity
   * Almost all flowering plants are paleo-polyploids. Planning and ability to meet the challenges of large/polyploidy genome including personnel resources (e.g., bioinformatician time), compute resources and additional tools needs to be addressed.
   * Note: Compute resources can be provided by the Australian BioCommons for all successful applicants.
2. Availability of plant material
   * Plant material voucher samples for deposition in the herbarium are critical. If a voucher is not available, steps need to be taken to ensure voucher samples are secured before or when DNA is sampled.
   * Clones of the chosen plant in one or more location
   * Steps taken to protect the plant/clonal lineage
3. Nagoya Protocol compliance
   * For plant material not available in the botanic gardens, permission from local Indigenous groups and a benefit sharing agreement are required.

**Personnel**

1. Dedicated team leader - A team leader who can dedicate adequate time to manage the project is critical.

Team leader expectations:

* Point of contact with the GAP leadership team (Steering Committee, Project Manager)
* Actively manage both the wet lab and dry lab teams, communicating progress and issues with the GAP Project Manager
* Meet once a month with other teams to discuss project progress via video conference.

1. Dedicated personnel to extract DNA

* Expected time frame for DNA extraction – 4 months from project commencement
  + High molecular weight, good quality DNA extraction can pose a challenge, even for teams who routinely extract DNA for other purposes from the same species.
  + Successful projects have dedicated personnel who have spent months continuously trying new protocols and speaking to other experienced groups in extracting DNA and discussing the minimum QC requirement for the samples to be run.
  + Ability to genetically adapt material for appropriate DNA extraction, e.g., preparation / collection of haploid tissue; nuclear DNA preparations.
  + The DNA extraction methods successfully used by the GAP reference genome projects can be found [here.](https://www.genomicsforaustralianplants.com/protocols/)

1. Dedicated bioinformaticians
   * Expected time frame for Draft genome – 1 year from project commencement
   * Dedicated bioinformaticians who can commit time to perform the bioinformatics analysis and submit raw sequence data and assembled genomes to international repositories.
   * \*The GAP Steering Committee can assist in putting you in contact with relevant institutions if you need bioinformatics support.
   * \*It is expected that the reference genome bioinformaticians meet once a month with other bioinformaticians to discuss project progress (wet lab and dry lab) via video conference.

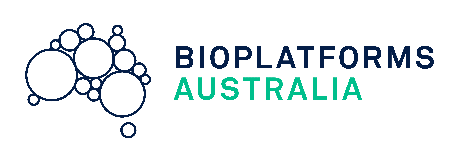
**Lessons learnt from the Reference Genomes pilot**

Three species were chosen for the GAP reference genome pilot: *Acacia pycnantha*, Telopea speciosissima and Areocleome oxalidea. More details [here](https://www.genomicsforaustralianplants.com/2018/12/18/dec-2018-plants-launch/). The aim was to assemble DNA sequence data into published annotated draft genomes, that could act as a platform for ongoing genome analysis.

The pilot projects were chosen for GAP to identify the potential challenges and pitfalls working with Australian native plants. After 15 months, the Areocleome project was unable to continue due to difficulties in obtaining plant material. Both *Acacia* and Telopea have generated long and linked read data and are currently preparing manuscripts for publications.

The Telopea plant chosen for the pilot perished in the 2019 bushfires (and subsequently re-generated), highlighting the need to prepare clonal material and ensure that strategies are in place to preserve nominated specimen plants for future sampling. Another major hurdle was the difficulty in obtaining plant material (heat stress due to extreme weather conditions, timing of plant growth) and challenges in extracting high molecular weight DNA suitable for long read sequencing. Ongoing challenges in obtaining sufficient plant material and voucher specimens of identical genotype underscore the importance of formal collections in managing and characterising the Australian flora.

For more details on the lessons learnt, please click [here.](https://docs.google.com/document/d/1RNghfr5Ivs2Bxo-_CTCCfAWWq67g7oRs0ROYM6dCPyU/edit) It is recommended that all RFP submitters familiarise themselves with the potential challenges and address these in their RFP submissions.



**Genomics for Australian Plants:**

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**Instructions for filling in this document:**

1. Complete one document for each species.
2. Address all the criteria listed.
3. Provide a short 1 paragraph answer for each question.
4. Answers to all the criteria should not exceed 4 pages.

**Dateline:** COB Monday, 4th July 2022

Please email your completed documents to Mabel Lum [mlum@bioplatforms.com](mailto:mlum@bioplatforms.com)

**Contact information:**

David Cantrill | Project information | T: +61 3 9252 2301 | [David.Cantrill@rbg.vic.gov.au](http://www.bioplatforms.com/australian-plants/David.Cantrill@rbg.vic.gov.au)  
Mabel Lum | Project Manager | T: +61 2 9850 1174 | [mlum@bioplatforms.com](mailto:mlum@bioplatforms.com)

**Please fill in your details below:**

|  |  |
| --- | --- |
| Name: |  |
| Affiliation: |  |
| Contact details: | Email:  Phone: |
| Species: |  |
| Family: |  |
| Genome size:  (in Gigabase, not c-value) |  |
| Interest in the project: |  |
| Expertise: |  |
| Conflict of interest to  declare: |  |

**List of criteria to be addressed:**

|  |
| --- |
| 1. Is the species currently being worked on? If so, in what way? How can an additional reference genome add value to the research? |
| 2. How will the genome that is generated be used for other applications by the team in the following 12 months? Please outline. |
| 3. Does this genome represent a taxonomic gap in available Australian genomes?  If so, at what taxonomic level?  Is the gap important to fill in from a systematic perspective and why? |
| 4. Does the species resonate with the public or have political value in additional to scientific value? |
| 5. What is the ecosystem value of the species?  Is it a key species or vital to conservation / regeneration of an ecosystem?  What is the conservation status? Is the species threatened or endangered? |
| 6. Does the species have commercial value? In what industry does this species have commercial value? |
| 7. Is the species of a genome ploidy and size that makes a 'reference' genome feasible?  Ploidy:  Genome size (in Gigabase, not c-value): |
| 8. Is there access to repeatable samples of required quality and quantity for reference genome generation, continuing research and voucher samples.  Provide photo evidence and living accession number of the plant that will be used for the project.  Provide herbarium accession of the plant. |

|  |
| --- |
| 9. Are these samples available from an accessioned collection and an institution that has a  commitment to maintain and clonally propagate if necessary?  Outline the plans to maintain and/or clonally propagate the plant.  Outline the steps taken to protect the plant. |
| 10. What resources does the group have available (laboratory, equipment and staff time / expertise) for high quality DNA and RNA extractions? |
| 11. Is the group able to commit time required for genome assembly and attending monthly teleconference meetings? |
| 12. Are there any other factors to be considered for this species? |
| 13. Have you and all your named collaborators read and understood the GAP Agreements and Policies?  Please contact Mabel Lum [mlum@bioplatforms.com](mailto:mlum@bioplatforms.com) if you have any questions.  Link: <https://www.genomicsforaustralianplants.com/agreements-policies/> | |
| 14. Do you agree to access all data from the [Data Portal](https://data.bioplatforms.com/organization/about/bpa-plants)?  Data generated through GAP cannot be accessed directly from the sequencing facility. | |
| 15. Is the team leader able to commit the time required for the project?  Please see page 2 for an outline for the team leader expectations from GAP. | |
| 16. Can you commit to the expected time frames below?   1. DNA extraction – 4 months from project commencement 2. Draft genome – 1 year from project commencement | |
| 17. How quickly can you submit samples for sequencing?  Please outline any experiences you have with plant high molecular weight DNA extraction or if you have DNA extracts ready and suitable for (long read) sequencing. | |
| 18. Do you agree to submit all the raw sequence data AND assembled genome to the international repository? | |