

## BASE Project Workflow

**Thorough documentation of the collection procedures will ensure maintenance of sample value.**

1. Following acceptance of your samples by the selection group: Request unique identifiers for sample naming/labelling from Bioplatforms (Anna Fitzgerald email: [afitzgerald@bioplatforms.com](mailto:afitzgerald@bioplatforms.com))
2. Select a 25 x25m plot at the sample site in a reasonably homogenous environment that reflects the characteristics of the site (based on soil, vegetation and land use).
3. Collect soil (comprising between 9-30 samples) from the plot in a manner that adequately samples the whole plot and ensures biological integrity of the sample.  
These can be sampled regularly on a grid if you think there isn't much microgeographic variation, or the sample points could be stratified to take account of anything you think might be important.
4. Collect the samples as two depths (1) top 10cm; (2) 20cm and below (define).

Homogenise all within plot sub-samples to make a pooled sample for each of the two depths. Samples are best mixed in the field in a large ziplock plastic bags from which aliquots can easily be drawn. Sieve if needed.

5. Ensure collection of adequate soil for nucleic acid extraction and contextual data generation from each sampling unit (e.g., 1 kg from each depth).
6. Assign unique sample identifiers to each sample using the last digits after the "/" i.e. 102.100.100/8202 would be called **8202**. Each depth is to have a separate identifier.
7. Collect and record all other local contextual data listed in the 'BASE contextual data template spreadsheet'.
8. Take photos of plot – soil and surrounding environment (example below).



9. Send each sample for DNA analysis, chemical analysis and archiving as below:

### **A) DNA ANALYSIS:**

- Fill 50mL Falcon tube with soil for DNA analysis (leaving 1-2 cm of space at top of tube) and freeze as soon as possible.

- Contact Dr Leanne McGrath (AGRF) at the address below to organise soil transfer permit paperwork (Biosecurity SA)
- Send frozen samples (on dry ice) to AGRF Adelaide for DNA extraction and sequencing analysis.

Facility	Address	Contact person
<b>AGRF</b>	Australian Genome Research Facility Ltd Plant Genomics Centre Hartley Grove, Waite campus University of Adelaide Urrbrae SA 5064	Dr Leanne McGrath Phone: (08) 8313 7148 Email: Leanne.McGrath@agrif.org.au

- Note: Any samples received that are thawed/room temperature will be deemed inappropriate for extraction.

Gently air dry and bag remaining soil for:

**B) CHEMICAL ANALYSIS and PARTICLE SIZE (as below or equivalent):**

- For chemical analysis send sample 250g dry weight preferred [200g minimum required] to CSBP, Perth WA for the 'Comprehensive Test'.
- For particle size include an additional 180g dry weight of soil

<http://www.csbp.com.au/docs/default-source/csbp-lab/csbp-lab-methods-1118.pdf>

Facility	Address	Contact person
<b>CSBP</b>	CSBP Soil and Plant Laboratory 2 Altona Street BIBRA LAKE WA 6163	Phone: (08) 9434 4600 Email: analysis@csbp.com.au

**C) ARCHIVING:**

- Remaining soil to be sent to CSIRO National Soils Archive, Canberra.
- Samples must be air dried (or oven dried at 40 degrees Celsius)
- Minimum 200g dry weight to be sent in approved containers (Cospak 500mL or 1L polyethylene containers cat # A500 or A572) labelled with BPA provided unique identifier.
- Email Linda Karssies at the address below when you are sending samples for archive so they are aware of their impending arrival.

Facility	Address	Contact person
<b>CSIRO National Soils Archive</b>	National Soils Archive CSIRO Land and Water, Black Mountain, Canberra ACT 2601	Linda Karssies Phone: (02) 6246 5824 Email: <a href="mailto:linda.karssies@csiro.au">linda.karssies@csiro.au</a>

10. Submit all **contextual data** into the excel flat file sheet supplied by Anna Fitzgerald.