

GAGA Sample Collection Summary - October 2017

A rough estimate of yield is 1-2 µg DNA/RNA per 10 small ants (~2 mm body length) or one large ant (~10 mm body length). Detailed guidelines and explanations are provided at antgenomics.dk/project-resources/. Samples for DNA/RNA extractions should be stored in RNAlater.

1. Samples for reference genome sequencing and assembly

- **Minimum:** Sufficient material to extract 12 µg of genomic DNA.
- **Optimum:** Sufficient material to extract 50 µg of genomic DNA.

2. Samples for transcriptome sequencing

- **Minimum:** Sufficient material to extract 1 µg of RNA from workers and 1 µg from gynes or queens.
- **Optimum:** Samples of various castes and life-stages, such as brood, different worker sub-castes, males, queens, gynes. (Required RNA: 1 µg per category)

3. Samples for metagenomics of ant-associated microbial communities

- **Minimum:** Samples of 10 workers (independent of size) from up to three colonies, not crushed.
- **Optimum:** Samples of 10 workers from three colonies from different geographic locations, not crushed.

4. Samples for parent-progeny sequencing

- **Optimum:** A reproductive queen and several of her male offspring. (Required DNA: 1 µg per individual)

5. Samples for population genomics

- **Optimum:** Samples (e.g. workers or gynes) from five to ten independent colonies from the same population. (Required DNA: 1 µg per colony)

6. Voucher samples

- **Minimum:** Several individuals sampled in EtOH, one individual sampled in RNAlater.
- **Optimum:** Two whole-nest series containing multiple individuals of workers, queens, gynes, larvae, pupae, eggs, symbionts. One series in EtOH and one series in RNAlater.

7. Life history data collection

- **Minimum:** Collector name, collection date, GPS coordinates, nesting site, habitat, sexual offspring found/missed, order of magnitude typical mature colony size ($10^2, 10^3$, etc.) – please download and use form available at <http://antgenomics.dk/wp-content/uploads/GAGA-traits.docx>.