

GAGA Sample Collection Summary – June 2018

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. Not crushed.
- **Optimum:** Sufficient material to extract 50 µg of genomic DNA. Not crushed.

2. Samples for transcriptome sequencing

- **Minimum:** Sufficient material to extract 1 µg of RNA from workers and 1 µg from gynes or queens. Not crushed.
- **Optimum:** Samples of various castes and life-stages, such as brood, different worker sub-castes, males, queens, gynes. (Required RNA: 1 µg per category). Not crushed.

3. Samples for metagenomics of ant-associated microbial communities

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

4. Samples for parent-progeny sequencing

- **Optimum:** A reproductive queen and several of her male offspring. (Required DNA: 1 µg per individual). Not crushed.

5. Samples for population genomics

- **Optimum:** Samples (e.g. workers or gynes) from three to ten independent colonies from the same population. (Required DNA: 1 µg per colony). Not crushed.

6. Voucher samples

- **Minimum:** One individual worker sampled in EtOH, one individual worker sampled in RNAlater. Not crushed.
- **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. Not crushed.

7. Life history & collection data records

- **For each collected colony (i.e. “collection event”) we ask you to record the following:** Collector name; collection date; GPS coordinates; collection id; (micro-)habitat; approx. colony size; queen number; sampled material – please use the online submission form available at <http://antgenomics.dk/gaga-submission> or the excel file available at http://antgenomics.dk/wp-content/uploads/GAGA_rawSampleSubmission.xlsx.