

## GAGA Sample Collection Summary - May 2017

### **Minimum requirement for reference genomes**

**Sufficient biomass to extract 12 µg of genomic DNA and 2 x 1 µg of RNA (workers/gynes).**

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/](http://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**

- **Optimum:** Worker samples from three colonies from different geographic locations. (Required DNA: 1 µg per colony)

#### **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:** One individual 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.), population density (rare, uncommon, abundant) – please download and use form available at <http://antgenomics.dk/wp-content/uploads/GAGA-traits.docx>.
- **Optimum:** More extensive notes life history traits and social characteristics (see the life history data sheet at <http://antgenomics.dk/wp-content/uploads/GAGA-traits.docx>).