

CORRECTION

Correction: A Metatranscriptomic Approach to the Identification of Microbiota Associated with the Ant *Formica exsecta*

The PLOS ONE Staff

In [Table 1](#), there is an error in the title. Additionally, there are errors in the numbers of the FIMM and BGI columns of the New Stage in Caste/sex Queen. Please view a corrected version of [Table 1](#) here.

Table 1. Number of individuals pooled in each of the total of 14 libraries sequenced by FIMM or BGI.

Caste/sex	Stage	FIMM	BGI
Queen	Old overwintered	6 (6)	4 (4)
	New	10 (5)	8 (4)
	Old cocoon	8 (4)	6 (3)
	Intermediate cocoon	8 (4)	6 (3)
	Young cocoon	8 (4)	6 (3)
Worker	Old overwintered	18 (6)	30 (8)
	New	10 (5)	15 (6)
	Old cocoon	8 (4)	6 (3)
	Intermediate cocoon	8 (4)	6 (3)
	Young cocoon	8 (4)	6 (3)
Male	Adult	3 (3)	3 (3)
	Old cocoon	3 (3)	3 (3)
	Intermediate cocoon	3 (3)	3 (3)
	Young cocoon	3 (3)	3 (3)

Castes and developmental classes of *F. exsecta* are given together with number of source colonies in parentheses.

doi:10.1371/journal.pone.0121606.t001



OPEN ACCESS

Citation: The PLOS ONE Staff (2015) Correction: A Metatranscriptomic Approach to the Identification of Microbiota Associated with the Ant *Formica exsecta*. PLoS ONE 10(3): e0121606. doi:10.1371/journal.pone.0121606

Published: March 13, 2015

Copyright: © 2015 The PLOS ONE Staff. This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Reference

1. Johansson H, Dhaygude K, Lindström S, Helanterä H, Sundström L, Trontti K (2013) A Metatranscriptomic Approach to the Identification of Microbiota Associated with the Ant *Formica exsecta*. PLoS ONE 8(11): e79777. doi: [10.1371/journal.pone.0079777](https://doi.org/10.1371/journal.pone.0079777) PMID: [24260298](https://pubmed.ncbi.nlm.nih.gov/24260298/)