

**Figure S1**. Dot plot showing the number and type of samples in each cluster. A) Altitudinal clusters, B) Latitudinal clusters.



**Figure S2**. Relative abundane of the metabolic pathways predicted with PICRUSt2 classified by the MetaCyc pathway ontology categories.

**Table S1.** Type and number of samples in each altitudinal cluster.

|  |  |  |  |
| --- | --- | --- | --- |
| Cluster | Source | Number of samples | Altitude range |
| 1 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 8 | | 20 | | 28 | | 0-2000 |
| 2 | |  | | --- | | Female | | Male | | |  | | --- | | 11 | | 4 | | 0-600, 800-2000 |
| 3 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 7 | | 8 | | 10 | | 400-600, 800-1400, 1600-1800 |
| 4 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 21 | | 10 | | 5 | | 0-2000 |
| 5 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 13 | | 1 | | 2 | | 0-200, 400-600, 800-1200, 1400-1800 |

**Table S2.** Type and number of samples in each latitudinal cluster.

|  |  |  |  |
| --- | --- | --- | --- |
| Cluster | Source | Number of samples | Latitude range |
| 1 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 4 | | 13 | | 11 | | 17, 18, 19, 20, 21, 22 |
| 2 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 16 | | 5 | | 10 | | 17, 18, 19, 20, 21, 22 |
| 3 | |  | | --- | | Larvae | | Female | | Male | | |  | | --- | | 10 | | 12 | | 9 | | 17, 18, 19, 20, 21 |

**Table S3**. Values of the nearest sequenced taxon index (NSTI) calculated by PICRUSt2 on the core ASVs.The Similarity column represent the sequence similarity of the ASV sequence with a given Species determined by the NSTI value.

|  |  |  |  |
| --- | --- | --- | --- |
| ASV ID | NSTI | Similarity | Species |
| 0ddf98a2987efff71c8bc2fbf64fa5ba | 0.033166 | 96.6834 | *Achromobacter aegrifaciens* (B) |
| 4d2dc5f5af056a13b46a2695f5b30587 | 0.00015 | 99.985 | *Gluconobacter cerevisiae* (L) (P) |
| 5c302056b95837009851259e229c6528 | 0.00015 | 99.985 | *Acetobacter lambici* (L) (P) |
| 65b901f569c3e1a0a2ba137cf1c8a062 | 0.010946 | 98.9054 | *Enterobacter hormaechei subsp. Xiangfangensis* (A) |
| 74d4069cbc73feae99a305de3cd76023 | 0.000101 | 99.9899 | *Gluconobacter frateurii (*L) |
| 7a76c2a0f7637c8e9168e81fe58a287e | 0.000101 | 99.9899 | *Brucella pseudogrignonensis* (A) |
| 7f605f61282fe9b25a0e900f3e27a081 | 0.010948 | 98.9052 | *Enterobacter mori* (A) |
| a68ace7d7ee4f50ad09513287f7ab7b8 | 0.00015 | 99.985 | *Phyllobacterium myrsinacearum* (B) |
| ae5315becdf1f3033fee7951440de6f9 | 0.135061 | 86.4939 | *Phyllobacterium endophyticum*(L) |
| b4d99952ced36febcddb9f39e9fe2dc8 | 0.00015 | 99.985 | *Acetobacter persici JCM 25330* (L) (P) |
| bcc0353ab537f2ce1577b5479b029610 | 0.000101 | 99.9899 | *Acetobacter suratthaniensis*( L) (P) |
| ea536311f4f59278af9d62817682bbb0 | 0.055351 | 94.4649 | *Acetobacter fabarum* (L) (P) |