**(Supporting Information)**

**Sublethal and Transgenerational Effects of Nitenpyram on *Acyrthosiphon* gossypii and Its Impacts on Symbiotic Bacteria**

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**Supporting information legends**

**Table A1.** Bacterial community composition (%) of *A. gossypii* at different taxonomic levels in treatment and control groups (only showed proportion > 5%)

**Table A2.** Changes of major symbiotic taxa in three successive generations of *A. gossypii* at the family level(top 15 abundance).

**Table A3.** Top 15 abundant bacterium in *A. gossypii* G0–G2 at the genus level following 48 h exposure of initial adults (G0) to LC20 of nitenpyram.

**Table A1. Bacterial community composition (%) of *A. gossypii* at different taxonomic levels in treatment and control groups (only showed proportion > 5%)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Taxonomic categories | Taxa | G0 (Proportion%) | G1(Proportion %) | G2 (Proportion %) |
| CKG0 | NG0 | CKG1 | NG1 | CKG2 | NG2 |
| Phylum | Proteobacteria | 97.69 | 90.53 | 95.53 | 98.10 | 97.01 | 97.57 |
| Class | Gammaproteobacteria | 96.60 | 78.63 | 88.64 | 96.79 | 93.46 | 96.31 |
| Order | Enterobacterales | 94.63 | 62.52 | 57.73 | 96.10 | 52.72 | 95.63 |
| Family | Morganellaceae | 94.31 | 62.16 | 57.10 | 95.98 | 52.44 | 95.21 |
| Genus | *Buchnera**Acinetobacter* | 85.490.04 | 51.9712.97 | 47.4229.06 | 87.670.15 | 46.9732.72 | 88.140.22 |

**Table A2. Changes of major symbiotic taxa in three successive generations of *A. gossypii* at the family level(top 15 abundance).**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Taxonomy | CK-G0(%) | N-G0(%) | CK-G1(%) | N-G1 | CK-G2(%) | N-G2(%) |
| Morganellaceae | 94.31 | 62.16 | 57.10 | 95.98 | 52.44 | 95.21 |
| Moraxellaceae | 0.05 | 12.99 | 29.09 | 0.15 | 32.73 | 0.23 |
| Sphingomonadaceae | 0.25 | 7.05 | 4.42 | 0.41 | 2.41 | 0.33 |
| Xanthomonadaceae | 1.55 | 0.18 | 0.05 | 0.03 | 6.62 | 0.02 |
| Lachnospiraceae | 0.39 | 0.51 | 0.47 | 0.29 | 0.45 | 0.37 |
| Enterobacteriaceae | 0.32 | 0.36 | 0.63 | 0.12 | 0.28 | 0.41 |
| Hyphomonadaceae | 0.18 | 0.85 | 0.26 | 0.20 | 0.14 | 0.17 |
| Comamonadaceae | 0.04 | 0.30 | 0.99 | 0.08 | 0.08 | 0.06 |
| Gemmatimonadaceae | 0.09 | 0.65 | 0.20 | 0.09 | 0.05 | 0.07 |
| Dongiaceae | 0.09 | 0.47 | 0.27 | 0.09 | 0.10 | 0.09 |
| Bacteroidaceae | 0.13 | 0.48 | 0.18 | 0.10 | 0.12 | 0.10 |
| Muribaculaceae | 0.14 | 0.14 | 0.35 | 0.10 | 0.16 | 0.20 |
| Pseudomonadaceae | 0.02 | 0.10 | 0.14 | 0.01 | 0.80 | 0.01 |
| Saprospiraceae | 0.05 | 0.54 | 0.15 | 0.13 | 0.09 | 0.09 |
| Microscillaceae | 0.08 | 0.44 | 0.24 | 0.06 | 0.09 | 0.08 |

**Table A3. Top 15 abundant bacterium in *A. gossypii* G0–G2 at the genus level following 48 h exposure of initial adults (G0) to LC20 of nitenpyram.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Taxonomy | CK-G0(%) | N-G0(%) | CK-G1(%) | N-G1(%) | CK-G2(%) | N-G2(%) |
| *Buchnera* | 85.49 | 51.97 | 47.42 | 87.67 | 46.97 | 88.14 |
| *Acinetobacter* | 0.04 | 12.97 | 29.06 | 0.15 | 32.72 | 0.22 |
| *Arsenophonus* | 8.82 | 10.19 | 9.68 | 8.31 | 5.47 | 7.07 |
| *Sphingomonas* | 0.17 | 6.18 | 4.06 | 0.31 | 2.17 | 0.24 |
| *Stenotrophomonas* | 1.52 | 0.03 | 0.01 | 0.00 | 6.58 | 0.00 |
| SWB02 | 0.16 | 0.63 | 0.18 | 0.14 | 0.10 | 0.13 |
| *Dongia* | 0.09 | 0.47 | 0.27 | 0.09 | 0.10 | 0.09 |
| *Bacteroides* | 0.13 | 0.48 | 0.18 | 0.10 | 0.12 | 0.10 |
| *Pseudomonas* | 0.02 | 0.10 | 0.14 | 0.01 | 0.80 | 0.01 |
| *Escherichia-Shigella* | 0.14 | 0.21 | 0.29 | 0.03 | 0.18 | 0.21 |
| *Muribaculaceae* | 0.14 | 0.14 | 0.35 | 0.10 | 0.15 | 0.19 |
| *Comamonas* | 0.00 | 0.01 | 0.68 | 0.00 | 0.01 | 0.00 |
| *Paracoccus* | 0.00 | 0.13 | 0.42 | 0.00 | 0.07 | 0.02 |
| TRA3-20 | 0.04 | 0.37 | 0.07 | 0.05 | 0.04 | 0.04 |
| *Enterobacter* | 0.07 | 0.10 | 0.23 | 0.07 | 0.04 | 0.07 |
| others | 3.17 | 16.02 | 6.96 | 2.95 | 4.47 | 3.46 |