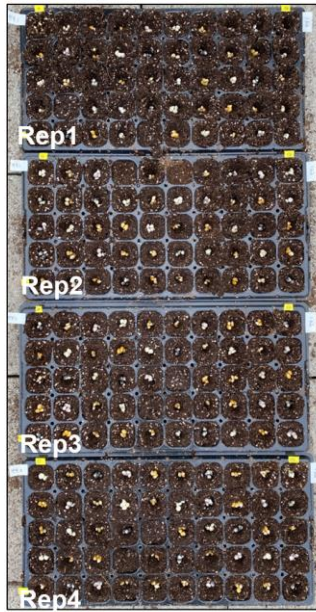


Figure S1: The morphological features of commercialized six maize corn and *Spodoptera frugiperda* larvae that fed on them. (A1) mebaek 2-ho, whitish color (B1) heukjeom 2-ho, blue color (C1) dreamok, yellow color (D1) oryun popcorn, yellow color (E1) oryun 2-ho, yellow color and (F1) meheukchal, purple color. Three (n=3) commercially available waxy corn cultivars (mebaek 2-ho, heukjeom 2-ho, and meheukchal), two (n=2) popcorn cultivars (oryun popcorn, oryun 2-ho), and one (n=1) processing purpose cultivar (dreamok). The six different larvae are depicted as A2-F2. A2 larvae consumes A1 corn-seedlings; similarly, B2, C2, D2, E2 and F2 consume corn varieties: B1, C1, D1, E1 and F1, respectively.

A



B

5x10 in each tray, 6x8+2 blanks

Arbitrary arrangement of six maize corn varieties

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|------|---|-------|---|-------|-------|-------|---|---|---|----|
| Rep1 | D | E | C | D | B | A | D | B | F | E |
| | C | B | E | A | F | C | F | E | C | B |
| | A | E | F | D | E | B | D | A | F | D |
| | D | blank | A | B | F | A | E | C | E | C |
| | B | F | C | F | blank | C | A | D | B | A |
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| Rep2 | A | D | B | blank | E | blank | E | F | B | A |
| | F | C | F | A | C | A | B | D | C | B |
| | B | A | E | C | B | D | E | B | F | E |
| | F | C | B | D | E | F | A | D | A | C |
| | D | A | D | F | C | D | E | C | E | F |
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| Rep3 | F | D | B | A | E | D | B | C | D | F |
| | D | A | E | C | A | F | E | A | E | B |
| | E | F | A | F | B | blank | C | E | A | C |
| | C | B | D | A | blank | E | D | C | B | F |
| | F | C | E | C | D | B | F | A | D | B |
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| Rep4 | A | D | F | B | C | E | F | E | D | A |
| | C | B | D | A | E | A | B | C | B | F |
| | E | A | E | F | blank | C | A | F | C | D |
| | A | D | C | blank | E | F | E | B | A | B |
| | D | F | B | D | C | D | B | C | E | F |

Cultivar (code and name)

| | |
|---|---------------|
| A | Mebaek 2-ho |
| B | Heukjeom 2-ho |
| C | Dreamok |
| D | Oryun popcorn |
| E | Oryun 2-ho |
| F | Meheukchal |

Figure S2: Random selection and arbitrary arrangement of six corn varieties (A) Actual early-stage view of maize seedlings in a plastic tray on commercial bed soil (replication as rep1–4). (B) Six corn variety deployment layers. Random selection was executed over four replications for seven days, sowing eight corn seeds of six corn varieties in 5 × 10 trays (including two blank spots). (2022.06.21 – 2022.06.27);



Figure S3: Six commercialized maize corn cultivars were grown in a greenhouse at Chuncheon campus, Kangwon National University, in order to understand the host preferences of *Spodoptera frugiperda*. (A) The experiment was conducted in a BugDorm-2400 Insect Rearing Tent (75 × 75 × 115) mebaek 2-ho, (B) heukjeom 2-ho, (B1-B3) Top view after two weeks (each variety of corn reached a height of approximately 50 cm), (C1-C3) side view after two weeks (each variety of corn reached a height of approximately 50 cm);

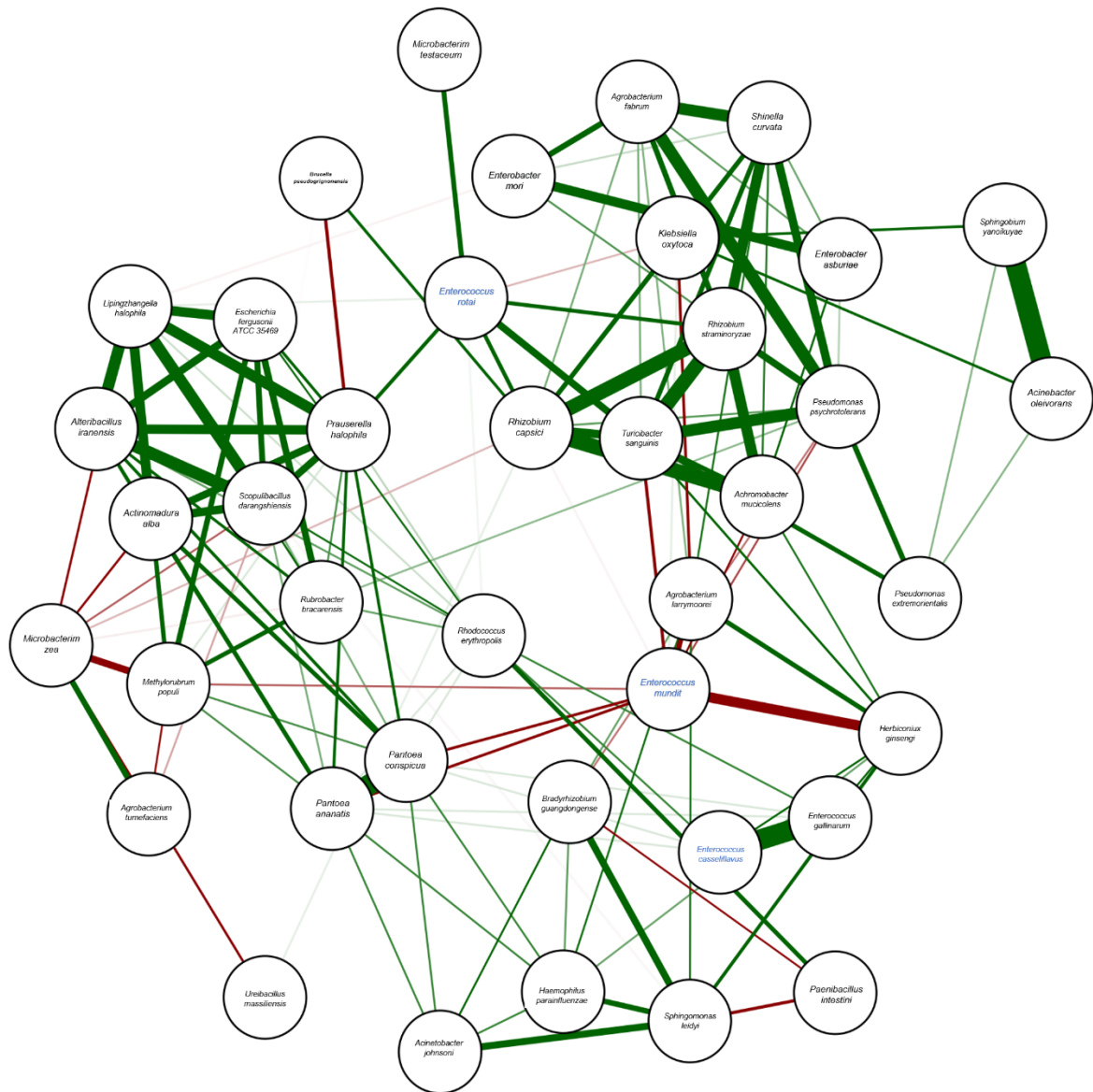


Figure S4: Species richness and network analysis of bacterial species shows a interction to the bacterial community up to top forty species. The most dominant *Enterococcus* spp. are presented in the middle of each circle by blue color and rest of the bacteria are presented by black color. Green line indicates a positive relationship, red line indicates a negative relationship. The arbitrary line thickness shows the relation level of each bacterial population.

Table S1 The information of paired reads, filtered and trimmed reads from 18 insect gut samples

| Sample | Input reads (paired) | Filtered reads¹⁾ | Merged reads²⁾ | Non-chimeric reads³⁾ | Contaminant removal⁴⁾ |
|---------------|---------------------------------|--|--------------------------------------|--|---|
| FAW_A1 | 95,076 | 26,951 | 26,863 | 26,842 | 20,410 |
| FAW_A2 | 75,636 | 26,079 | 25,724 | 25,454 | 19,188 |
| FAW_A3 | 92,702 | 29,579 | 29,241 | 28,542 | 23,271 |
| FAW_B1 | 105,281 | 33,819 | 33,662 | 33,588 | 30,657 |
| FAW_B2 | 110,780 | 31,127 | 30,880 | 30,782 | 27,673 |
| FAW_B3 | 131,126 | 46,091 | 45,828 | 45,724 | 43,224 |
| FAW_C1 | 120,800 | 43,303 | 43,188 | 43,110 | 40,480 |
| FAW_C2 | 119,016 | 26,263 | 26,032 | 25,793 | 23,943 |
| FAW_C3 | 116,073 | 29,433 | 29,292 | 29,243 | 26,703 |
| FAW_D1 | 141,109 | 48,816 | 48,535 | 48,425 | 43,990 |
| FAW_D2 | 116,627 | 31,123 | 30,882 | 30,667 | 26,659 |
| FAW_D3 | 127,434 | 36,192 | 35,900 | 35,723 | 31,995 |
| FAW_E1 | 129,657 | 44,942 | 44,878 | 44,800 | 43,082 |
| FAW_E2 | 111,958 | 35,774 | 35,568 | 34,926 | 31,135 |
| FAW_E3 | 121,062 | 44,057 | 43,929 | 43,737 | 42,705 |
| FAW_F1 | 99,374 | 33,880 | 33,829 | 33,826 | 31,634 |
| FAW_F2 | 108,559 | 37,605 | 37,509 | 37,456 | 36,119 |
| FAW_F3 | 51,542 | 15,178 | 15,130 | 15,112 | 13,919 |

¹⁾ Calculate the q-value based on the trimmed length set for the input reads, and remove reads that do not meet the criteria.

²⁾ Merge the two reads, which must overlap by at least 12 bp to merge.

³⁾ Compare ASV(amplicon sequence variant)s to select only non-chimeric reads.

⁴⁾ Remove contaminants (almost human-derived sequences) of 400 bp or less that are significantly smaller than the size of the target region (about 450 bp) and rRNA sequences derived from plastids, including chloroplasts and mitochondria.