|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| T-RF (bp) in T-RFLP profiles\* | T-RF\*\* (bp) | Accession No. | Closest relative (Gene bank accession no.) | Similarity (%) | **Taxonomic classification\*\*\*** | Group\*\*\*\* | Variety | Midgut | Hindgut | No. of clones |
| ***Actinobacteria*** |
| 65 | 66 | HE613272 | Uncultured *Bifidobacterium* sp. (HM113200)1 | 99 | ***Bifidobacteriales*** | “Bifido” | Phacelia |  | x | 1 |
| HE613273-77 | Uncultured *Bifidobacterium* sp. (HM113220)1 | 96-99 | “Bifido” | DKC 5143 |  | x | 5 (1\*\*\*\*\*) |
| 161/164 | 165 | HE613278 | Uncultured *Bifidobacterium* sp. (HM113243)1 | 99 | “Bifido” | Phacelia |  | x | 1 |
| HE613279 | Uncultured *Bifidobacterium* sp. (HM113099)1 | 99 | “Bifido” | Benicia |  | x | 1 |
| ***Firmicutes*** |
| 318-320 | 322 | HE613280 | Uncultured bacterium (HM111911)1 | 99 | ***Bacilli*,** ***Lactobacillales*** | F5 | Phacelia |  | x | 1 |
| HE613281-83 | Uncultured bacterium(HM113313)1 | 98-99 | F5 | Phacelia |  | x | 3 |
| HE613284-85 | Uncultured bacterium (HM113193)1 | 98 | F5 | DKC 5143 |  | x | 2 |
| HE613286-87 | Uncultured bacterium (HM111880)1 | 99 | F5 | DKC 5143 |  | x | 2 |
| HE613288 | Uncultured bacterium (HM113252)1 | 98 | F5 | DKC 5143 |  | x | 1 |
| ***Proteobacteria*** |
| 442 | 441 | HE613289-92 | Uncultured bacterium(HM112426)2 | 96 | ***Alphaproteobacteria*, *Acetobacteriacea*** | α-2 | BT | x |  | 4 (3\*\*\*\*) |
| 449 | 447 | HE613293-97 | Uncultured bacterium (HM113219)1 | 98 | ***Betaproteobacteria*, *Neisseriaeceae*** | β-1 | BT | x |  | 5 (3\*\*\*\*) |
| 448 | HE613298-99 | Uncultured bacterium (HM113170)1 | 98-99 | β-1 | Phacelia | x |  | 2 |
| 489 | 488 | HE613300 | Uncultured *Orbus* sp. (HM112036)1 | 98 | ***Gammaproteobacteria*, incertae sedis** | γ-1 | Benicia |  | x | 1 |
| 491/493 | 492 | HE613301 | Uncultured *Orbus* sp. (HM111973)1 | 98 | γ-1 | BT | x |  | 1 |
| HE613302 | Uncultured *Orbus* sp. (HM113151)1 | 98 | γ-1 | Phacelia | x |  | 1 |
| HE613303 | Uncultured *Orbus* sp. (HM112085)1 | 99 | γ-1 | Phacelia | x |  | 1 |
| ***Firmicutes*** |
| 568 | 567 | HE613304 | Uncultured bacterium(HM112042)1 | 99 | ***Bacilli*, *Lactobacillales*, *Lactobacillaceae* (F4, F5)** | F4 | Phacelia |  | x | 1 |
| 569 | HE613305-06 | Uncultured bacterium(HM112126)1 | 98 | F5 | Phacelia |  | x | 2 (1\*\*\*\*) |
| 570 | 570 | HE613307 | Uncultured bacterium(HM113344)1 | 98 | F4 | Phacelia |  | x | 1 |
| HE613308-09 | Uncultured bacterium(HM113214)1 | 99 | F5 | Phacelia | x |  | 2 (1\*\*\*\*) |
| HE613310 | Uncultured bacterium(HM113344)1 | 99 | F5 | Phacelia | x |  | 1 |
| 580 | 579 | HE613311 | Uncultured bacterium (HM112788)3 | 98 | F4 | Phacelia | x |  | 1 |

\*see Figure 5; \*\*T-RF as determined by *in silico* analyses of cloned DNA sequences; \*\*\*according to RDP classifier (see Materials and Methods), \*\*\*\*according to [23, 27]. \*\*\*\*\*PCR fragments were cloned in reverse orientation, so that the determination of T-RFs was not possible. The assignment of these clones was done according to DNA sequence similarities (>97 %) to clones with known terminal sequences. DNA-sequences of closest relatives originated from bees (Family: Apidae), index numbers indicate different hosts 1*Apis mellifera*, 2*Xylocapa californica*, or 3*Diadasia opuntiae* [25]