

**Table S1. Summary of clone library derived from the midgut crypts of *Cavelerius saccharivorus*.**

Locality	Instar	Sex <sup>a</sup>	OTUs identified with		<i>Burkholderia</i> clade <sup>d</sup>	Accession No.
			99% identity <sup>b</sup>	No. of clones <sup>c</sup>		
Okinawa Island	adult	F	OK-1	7	PBE	AB916362-AB916368
	adult	M	OK-2	10	SBE	AB916369-AB916378
	adult	M	OK-3	10	PBE	AB916379-AB916388
Kita-Daito Island	5th	-	KD-1	10	SBE	AB916425-AB916434
	5th	-	KD-2	10	SBE	AB916435-AB916444
Minami-Daito Island	adult	M	MD-1	6	SBE	AB916406-AB916411
	adult	F	MD-2	6	BCC	AB916412-AB916417
	adult	F	MD-3	7	SBE	AB916418-AB916424
Ishigaki Island	5th	-	IG-1	7	SBE	AB916389-AB916395
	5th	-	IG-2	10	BCC	AB916396-AB916405
Yonaguni Island	5th	-	YG-1	12	SBE	AB916445-AB916456
	5th	-	YG-2	7	SBE	AB916457-AB916463

<sup>a</sup> F, female; M, male; -, undetermined.

<sup>b</sup> A single phylotype was detected from each individual.

<sup>c</sup> Total amount of sequenced clones.

<sup>d</sup> Each clade was defined in Fig. 2.

**Table S2. Illumina deep sequencing of *Burkholderia* phylotypes in the midgut crypts of *Cavelerius saccharivorus*.**

Insect ID	No. of sequences (No. of OTUs)					
	Bacteria Total	<i>Burkholderia</i> Total	SBE <sup>a</sup>	BCC <sup>a</sup>	PBE <sup>a</sup>	Unclassified <sup>b</sup>
MD-I-1	34,734 (104)	34,682 (99)	31,070 (3)	0	254 (1)	3,358 (95)
MD-I-2	38,957 (126)	38,781 (115)	34,747 (3)	0	0	4,034 (112)
MD-I-3	26,208 (83)	26,154 (74)	23,878 (2)	0	0	2,276 (72)
MD-I-4	31,290 (85)	31,075 (67)	19 (2)	0	29,437 (2)	1,619 (63)
MD-I-5	29,446 (96)	29,281 (79)	26,075 (3)	0	2 (1)	3,204 (75)
MD-I-6	36,851 (118)	36,462 (90)	32,909 (2)	0	3 (1)	3,550 (87)
MD-I-7	16,767 (37)	16,723 (27)	17 (2)	0	16,214 (1)	492 (24)
MD-I-8	20,372 (42)	20,248 (31)	0	0	19,711 (1)	537 (30)
MD-I-9	30,331 (79)	30,316 (74)	27,449 (2)	0	0	2,867 (72)
MD-I-10	34,705 (91)	34,473 (76)	31,604 (3)	0	2 (1)	2,867 (72)

<sup>a</sup> *Burkholderia* spp. classified with 99% identity against reference sequences shown in Fig. 2.

<sup>b</sup> *Burkholderia* spp. unclassified with less than 99% identity against reference sequences shown in Fig. 2.

**Table S3. Illumina deep sequencing profiles of the most dominant *Burkholderia* OTUs in each insect.**

Sequence ID <sup>a</sup>	No. of sequences	Relative abundance (%) <sup>b</sup>	BLASTn search		
			Closest sequences <sup>c</sup> (Accession No. <sup>d</sup> )	Identity %	Clade <sup>e</sup>
MD-I-1	30,985	89.2	<i>Burkholderia</i> sp. BurkA_pop5 (JQ993996)	100	SBE
MD-I-2	34,741	89.2	<i>Burkholderia</i> sp. MD-1 (AB916406)	100	SBE
MD-I-3	23,873	91.1	<i>Burkholderia</i> sp. MD-1 (AB916406)	100	SBE
MD-I-4	29,435	94.1	<i>Burkholderia</i> sp. OK-1 (AB916362)	100	PBE
MD-I-5	26,044	88.4	<i>Burkholderia</i> sp. MD-3 (AB916418)	100	SBE
MD-I-6	32,907	89.3	<i>Burkholderia</i> sp. MD-1 (AB916406)	100	SBE
MD-I-7	16,214	96.7	<i>Burkholderia</i> sp. OK-3 (AB916379)	100	PBE
MD-I-8	19,711	96.8	<i>Burkholderia</i> sp. OK-3 (AB916379)	100	PBE
MD-I-9	27,442	90.5	<i>Burkholderia</i> sp. BurkA_pop5 (JQ993996)	100	SBE
MD-I-10	31,558	90.9	<i>Burkholderia</i> sp. MD-3 (AB916418)	100	SBE

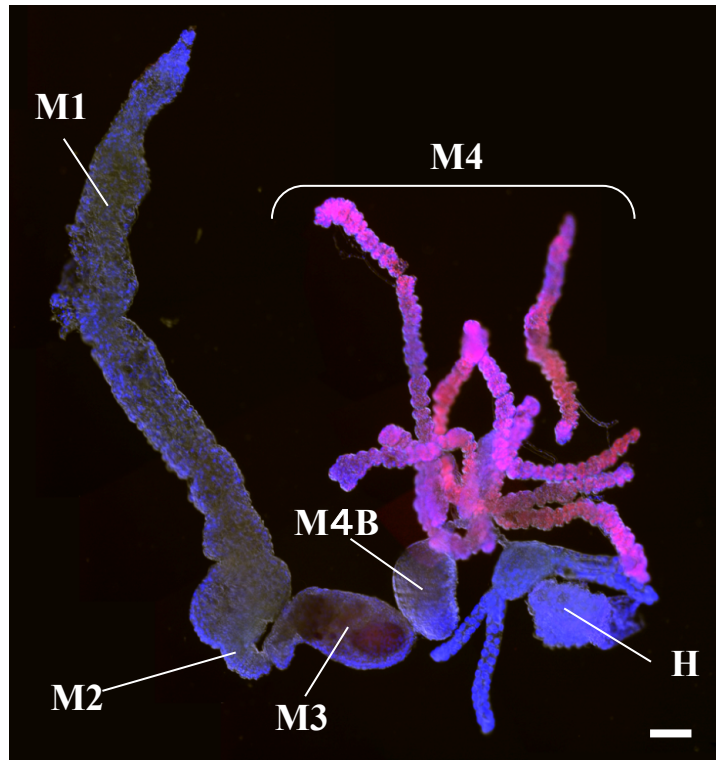
<sup>a</sup> Same as the insect ID shown in Table S2.

<sup>b</sup> % rate of the given sequences/total numbers of sequences.

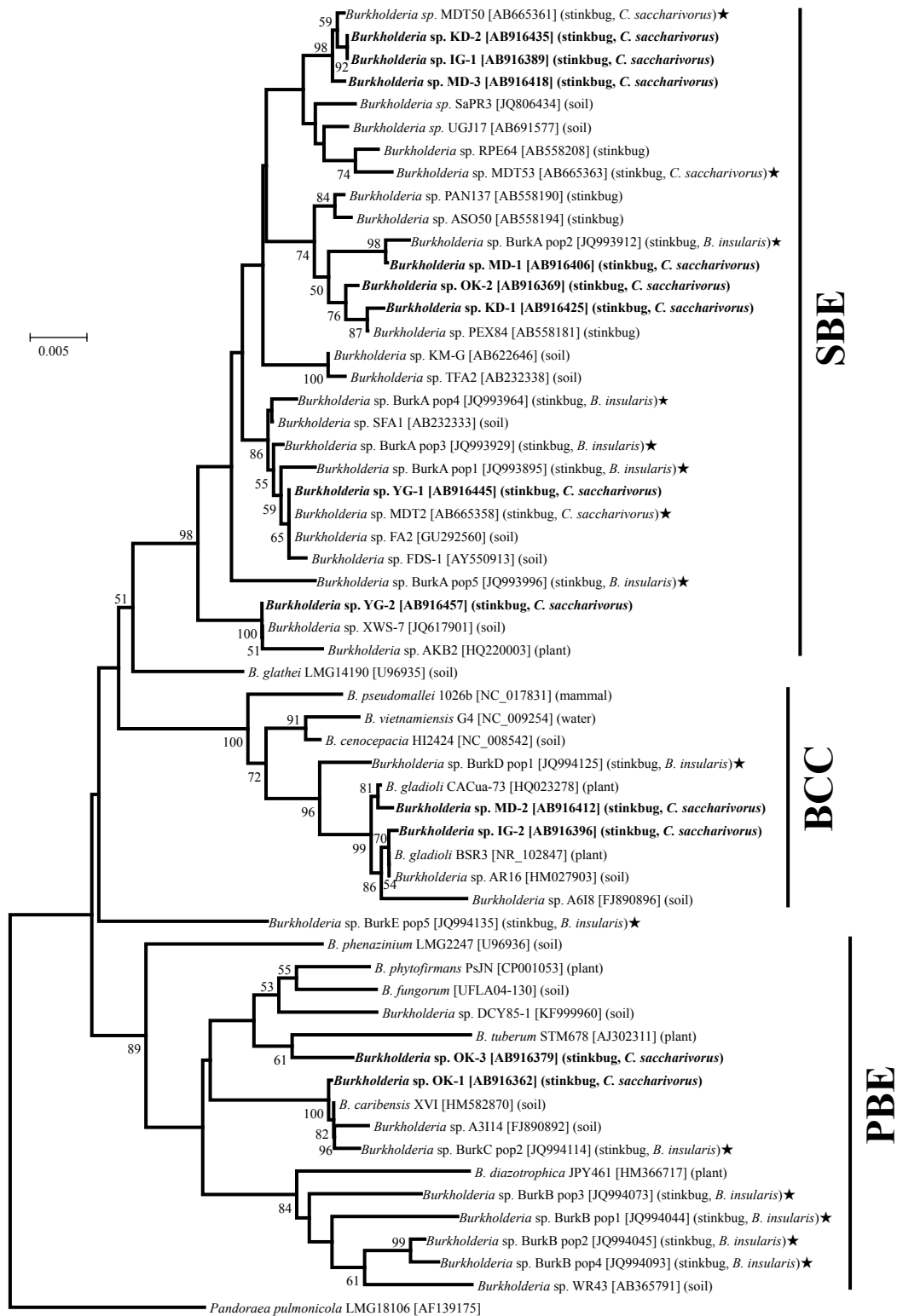
<sup>c</sup> Phylogenetic positions of the sequences are shown in Fig. 2.

<sup>d</sup> Accession numbers for the DNA database (DDBJ/EMBL/GenBank).

<sup>e</sup> These clades are shown in Fig. 2.



**Fig. S1.** Fluorescent in situ hybridization targeting 16S rRNA of *Betaproteobacteria* in a dissected midgut. *Betaproteobacteria* is visualized in red by hybridizing an Alexa555-conjugated BET940 probe, whereas blue signals show host insect nuclei stained with DAPI. Abbreviations: M1, midgut first section; M2, midgut second section; M3, midgut third section; M4, midgut fourth section with crypts; M4B, bulbous section before M4; H, hindgut. Bar shows 250  $\mu$ m.



**Fig. S2.** Phylogenetic placement of the gut symbiotic bacteria of *C. saccharivorus* on the basis of the 16S rRNA gene sequences. A neighbor-joining tree inferred from aligned 1372 bp sequences of 16S rRNA gene is shown. For explanatory notes, see Fig. 2.