Supplementary Material

Supplementary Tables

Table S1. The morphological characteristics information of ten Mantidis Ootheca representative samples

Sample ID	Shape	Color
SPX6-A	fusiform	brown
SPX6-B	barrel-like	brown
SPX12-A	fusiform	brown
SPX12-B	barrel-like	brown
SPX13-A	ellipsoid	reddish
SPX13-B	barrel-like	brown
SPX14-A	fusiform	brown
SPX15-A	barrel-like	brown
SPX15-B	ellipsoid	black
SPX17-A	fusiform	black

Table S2. Primer tag sequence

tag	Tag sequence
1	TCGTAGCA
2	TGAGACGT
3	TGCTCACT
4	CAGCTGAG
5	ATACGCTC
6	CTGTCTCG
7	ATAGAGCG
8	ATCACTGC
9	ACTAGCAG
10	CATGCTGT
11	CTCATGCT
12	CTCTACGA
13	CTAGTAGC
14	AGCGTATG
15	AGATCGAC
16	AGTCTGCA
17	ACGCGAGA
18	ACGATGTC

Table S3. Mantidis COI records from GenBank

Species	Accession number	Each haplotype label in the haplotype network map
Tenodera sinensis	KT036561.1	ASV_TS1
	MT129400.1	ASV_TS2
	MN447996.1	ASV_15
	MK829299.1	ASV_16
Tenodera angustipennis	MT129147.1	ASV_TA1
	MT129420.1	ASV_TA2
	MW085479.1	ASV_TA3
	MT129197.1	ASV_TA4
	MZ049121.1	ASV_132
Hierodula patellifera	MT129374.1	ASV_H
	KX611803.1	ASV_4
	MW085419.1	ASV_4
	NC_034283.1	ASV_4
	MT439617.1	ASV_9
Statilia maculata	KM362717.1	ASV_S1
	KM362718.1	ASV_S1
	KM362722.1	ASV_S1
	KM362720.1	ASV_S1
	MW085640.1	ASV_S1
	KM362723.1	ASV_S2
	KT036560.1	ASV_S3
	NC_056840.1	ASV_S4
	KM362721.1	ASV_S5
	KM362719.1	ASV_S6

Table S4. 54 ASVs and Blast-Megan results

ASV_ID	Best Blast Results	Percent Identity (%)
ASV_4	*Hierodula patellifera*	100
ASV_9	*Hierodula patellifera*	100
ASV_21	*Hierodula patellifera*	99
ASV_22	*Hierodula patellifera*	99
ASV_27	*Hierodula patellifera*	99
ASV_28	*Hierodula patellifera*	99
ASV_24	*Hierodula patellifera*	98
ASV_25	*Hierodula patellifera*	98
ASV_29	*Hierodula patellifera*	98
ASV_40	*Hierodula patellifera*	98
ASV_43	*Hierodula patellifera*	98
ASV_51	*Hierodula patellifera*	98

ASV_42	*Hierodula patellifera*	97
ASV_2	*Tenodera sinensis*	94
ASV_3	*Tenodera sinensis*	99
ASV_132	*Tenodera sinensis*	100
ASV_20	*Tenodera sinensis*	97
ASV_36	*Tenodera sinensis*	93
ASV_41	*Tenodera sinensis*	98
ASV_15	*Tenodera sinensis*	100
ASV_16	*Tenodera sinensis*	100
ASV_17	*Tenodera sinensis*	98
ASV_26	*Tenodera sinensis*	98
ASV_35	*Mantidae sp. DIMC031-09*	97
ASV_12	*Tenodera sinensis*	97
ASV_39	*Mantidae sp. DIMC031-09*	96
ASV_46	*Mantidae sp. DIMC031-09*	96
ASV_52	*Mantidae sp. DIMC031-09*	96
ASV_14	*Tenodera sinensis*	97
ASV_55	*Tenodera sinensis*	95
ASV_47	*Tenodera sinensis*	96
ASV_13	*Tenodera sinensis*	97
ASV_30	*Hierodula patellifera*	92
ASV_54	*Tenodera sinensis*	95
ASV_31	*Tenodera sinensis*	92
ASV_49	*Tenodera sinensis*	92
ASV_187	*Tenodera angustipennis*	99
ASV_10	*Argentinatachoides balli*	91
ASV_11	*Trogoderma variabile*	99
ASV_136	*Trogoderma variabile*	100
ASV_167	*Stegobium paniceum*	100
ASV_18	*Lasioderma serricorne*	100
ASV_19	*Stegobium paniceum*	94
ASV_33	*Dicladispa armigera*	88
ASV_34	*Blattisocius tarsalis*	99
ASV_37	*Blattisocius tarsalis*	98
ASV_38	*Tribolium castaneum*	100
ASV_44	*Tribolium castaneum*	100
ASV_45	*Anthrenus scrophulariae*	88
ASV_48	*Podagrion bouceki*	91
ASV_5	*Trogoderma variabile*	100
ASV_50	*Tydeidae sp*	87
ASV_53	*Trogoderma variabile*	97
ASV_88	Chrysomelidae sp.	86

Table S5. Number of reads available for each sample

Sample ID	Total reads	Reads determined as Mantis	Coverage (Mantis reads per individual)
spx01	17,095	12,198	76.24
spx02	23,815	19,731	82.21
spx03	82,827	15,771	39.33
spx04	110,805	31,351	125.40
spx05	65,813	39,713	93.88
spx06	25,215	23,173	66.59
spx07	91,632	40,207	155.84
spx08	50,016	11,536	33.34
spx09	68,638	8,698	29.19
spx10	32,296	28,109	119.61
spx11	81,248	5,239	15.14
spx12	27,935	11,761	44.89
spx13	111,815	40,290	110.38
spx14	119,999	32,809	218.73
spx15	135,279	17,551	117.01
spx16	77,340	44,539	291.10
spx17	9,792	8,762	74.89
spx18	25,452	21,995	281.99

Supplementary Figures

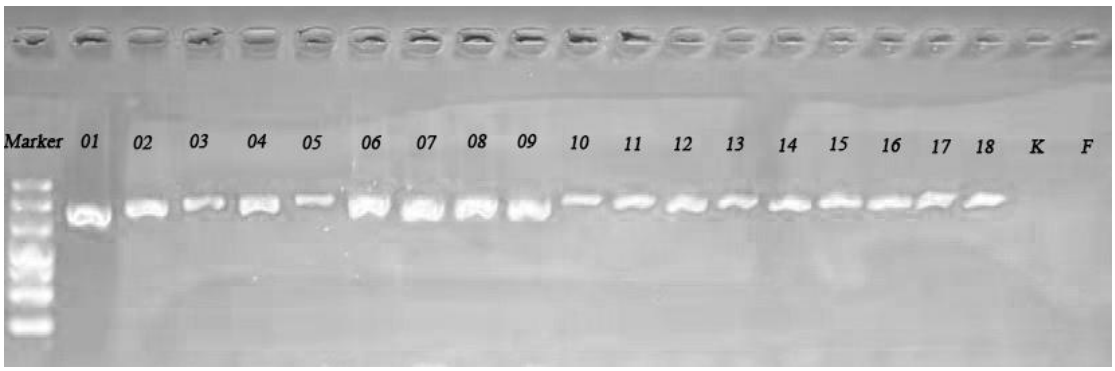

Figure S1 The gel electrophoresis diagram of the PCR products of 18 samples. From left to right: DL500 marker, 01-18 were samples spx01-spx18 respectively, K and F were negative controls during the experiment.

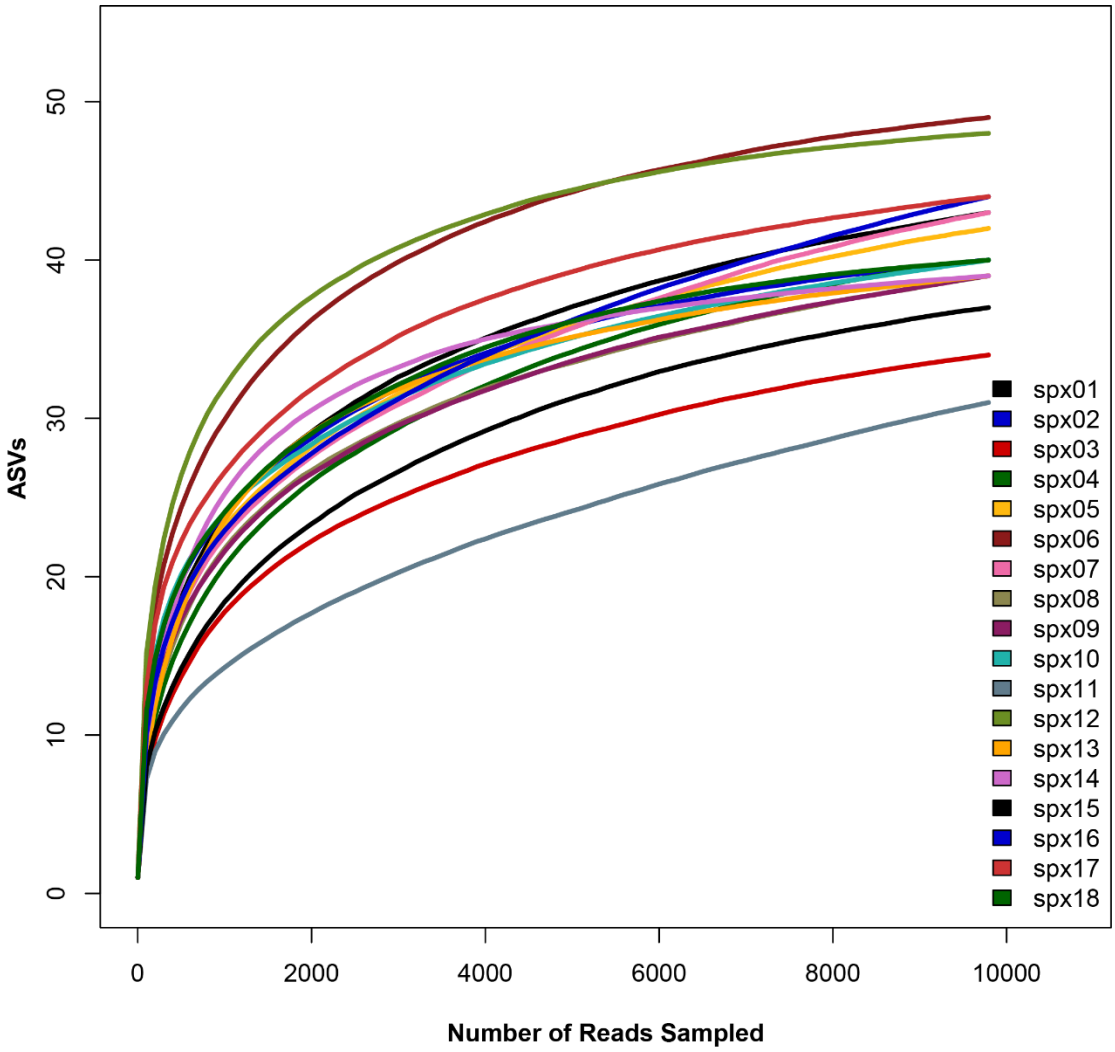

Figure S2 Rarefaction curves. The rarefaction curve reached a plateau, indicating that the sequencing depth was adequate.