Appendix

Appendix A GenBank numbers of *Wolbachia* sequences.

| Location	*wsp*		*ftsZ*	
	Infected individuals	GenBank no.	Infection individuals	GenBank no.
HUBJZ	HUBJZ10	KP822801		
JXNC	JXNC6	KP822797		
JXGZ	JXGZ6	KP822803		
GZXY	GZXY5 GZXY6 GZXY8	KP822800	GZXY1 GZXY2 GZXY7 GZXY8 GZXY10	KP844451
	GZXY9	KP822798	GZXY3	KP844452
	GZXY1 GZXY2 GZXY3 GZXY4 GZXY7 GZXY10	KP822809	GZXY5	KP844453
			GZXY6	KP844450
			GZXY4 GZXY9	KP844449
GXGY	GXGY4	KP822799	GXGY4	KP844447
	GXGY5	KP822808		
GXYZ	GXYZ3 GXYZ10	KP822804	GXYZ7 GXYZ8 GXYZ10	KP844448
	GXYZ8	KP822802		
GXNN	GXNN2	KP822805		
YNZT	YNZT4	KP822807		
	YNZT7	KP822806		

Appendix B Haplotypes and GenBank number of mtDNA *COI* and *Cytb* genes.

COI		Cytb	
Haplotypes	GenBank no.	Haplotypes	GenBank no.
HapCOI1	KP859409	HapCytb1	KP868925
HapCOI2	KP859426	HapCytb2	KP868926
HapCOI3	KP859414	HapCytb3	KP868914
HapCOI4	KP859412	HapCytb4	KP868948
HapCOI5	KP859413	HapCytb5	KP868912
HapCOI6	KP859473	HapCytb6	KP868942
HapCOI7	KP859421	HapCytb7	KP868899
HapCOI8	KP859448	HapCytb8	KP868949
HapCOI9	KP859411	HapCytb9	KP868950
HapCOI10	KP859447	HapCytb10	KP868933
HapCOI11	KP859423	HapCytb11	KP868951
HapCOI12	KP859475	HapCytb12	KP868952
HapCOI13	KP859424	HapCytb13	KP868915
HapCOI14	KP859474	HapCytb14	KP868916
HapCOI15	KP859468	HapCytb15	KP868917
HapCOI16	KP859429	HapCytb16	KP868918
HapCOI17	KP859431	HapCytb17	KP868910
HapCOI18	KP859430	HapCytb18	KP868903
HapCOI19	KP859419	HapCytb19	KP868919
HapCOI20	KP859445	HapCytb20	KP868965
HapCOI21	KP859446	HapCytb21	KP868966
HapCOI22	KP859450	HapCytb22	KP868967

|			
HapCOI23	KP859415	HapCytb23	KP868911
HapCOI24	KP859427	HapCytb24	KP868913
HapCOI25	KP859451	HapCytb25	KP868909
HapCOI26	KP859465	HapCytb26	KP868953
HapCOI27	KP859501	HapCytb27	KP868938
HapCOI28	KP859460	HapCytb28	KP868939

Appendix C Median-joining network of *Sesamia inferens* (A) mtDNA (*COI*) and (B) mtDNA (*Cytb*) haplotypes associated with *Wolbachia* infection status based on *ftsZ* gene. The area within the circles are proportional to haplotype frequency.
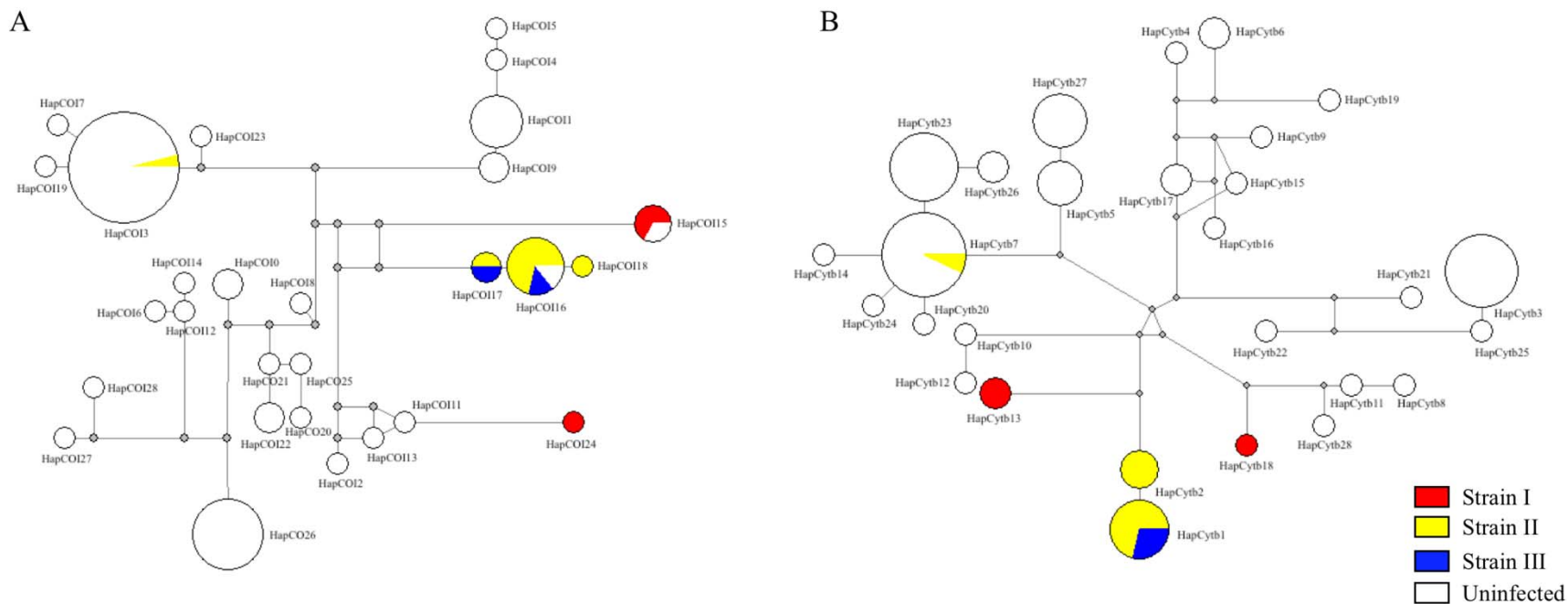
Appendix D Observed and simulated mismatch distributions of *Sesamia inferens*. The horizontal axis represents the number of pairwise differences, and the vertical axis shows relative frequency. (A) Infected group based on *COI* gene. (B) Uninfected group based on *COI* gene. (C) Infected group based on *Cytb* gene. (D) Uninfected group based on *Cytb* gene.
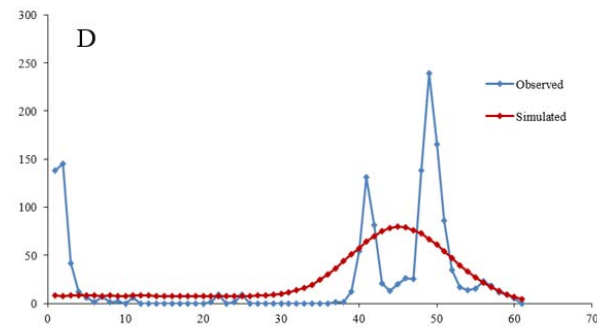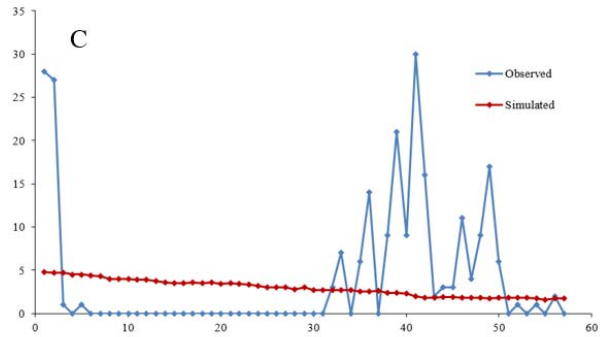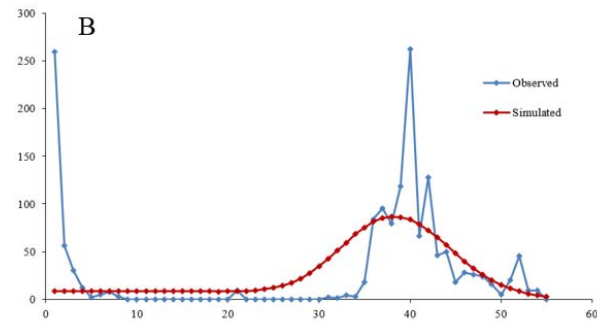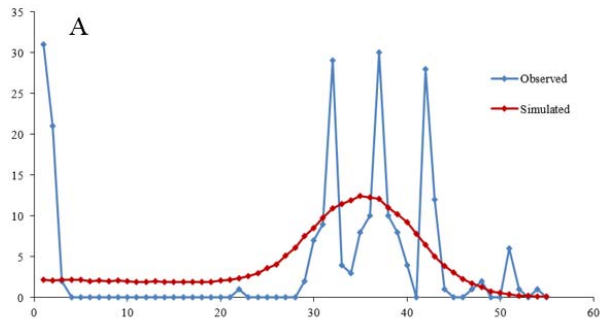
Appendix E Fixation index (F_{ST}) values of *COI* gene inferred from pairwise compared *wsp* strains.

	Uninfected	wDro	wCam	wOri	wPip	wInf	wCon
Uninfected		+	−	−	+	−	+
wDro	0.12366		−	−	+	−	+
wCam	-0.37212	0.05690		−	−	−	−
wOri	-0.37212	0.05690	0.00000		−	−	−
wPip	0.22000	0.33375	0.40849	0.40849		−	−
wInf	0.10683	-0.02723	1.00000	1.00000	-0.68352		−
wCon	0.21237	0.23413	0.37313	0.37313	-0.02162	-1.00000	

Values below the diagonal represent F_{ST} values; Symbols above the diagonal are significance tests of F_{ST} *P*-values: '+' represent significant and '-' represent non-significant (significance level = 0.05).

Appendix F Fixation index (F_{ST}) values of *Cytb* gene inferred from pairwise compared *wsp* strains.

	Uninfected	wDro	wCam	wOri	wPip	wInf	wCon
Uninfected		−	−	−	+	−	+
wDro	0.03310		−	−	+	−	−
wCam	-0.27851	-0.06500		−	−	−	−
wOri	-0.30689	-0.07395	1.00000		−	−	−
wPip	0.20622	0.21373	0.43548	0.41667		−	−
wInf	0.09129	-0.17248	1.00000	1.00000	-0.70732		−
wCon	0.18473	0.13576	0.44444	0.43038	-0.05009	-0.91489	

Values below the diagonal represent F_{ST} values; Symbols above the diagonal are significance tests of F_{ST} *P*-values: '+' represent significant and '-' represent non-significant (significance level = 0.05).

Appendix G Fixation index (F_{ST}) values of concatenated sequences (*COI*+*Cytb*) inferred from pairwise compared *ftsZ* strains.

	Uninfected	Strain I	Strain II	Strain III
Uninfected		+	+	+
Strain I	0.25833		+	–
Strain II	0.31314	0.60371		–
Strain III	0.27281	0.43056	-0.29616	

Values below the diagonal represent F_{ST} values; Symbols above the diagonal are significance tests of F_{ST} *P*-values: '+' represent significant and '-' represent non-significant (significance level = 0.05).