

Supplementary Table 1. Characterization of *Wolbachia* infection across beetle species and populations based on data in the literature.

Citation	Examined- infected species	taxonomy	Geography	<i>Wolbachia</i> genotyping	host genotyping	number of examined populations	number of examined individuals	species level	population level	individuals level	supergroup	effects on hosts	other effects
Kageyama et al. 2010	<i>Lasioderma serricorne</i>	Anobiidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Lasioderma serricorne</i>	Anobiidae	Canada,Europe,USA	wsp,MLST	n.n.	5	n.n.	all infected	n.n.	n.n.	n.n.	n.n.	n.n.
Kageyama et al. 2010	<i>Stegobium paniceum</i>	Anobiidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Stegobium paniceum</i>	Anobiidae	Canada,USA	wsp,MLST	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus arvensis lablloffi</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	F	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus ater</i>	Buprestidae	France	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus cyprescens</i>	Buprestidae	Germany	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus derasofasciatus</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus graminis</i>	Buprestidae	France	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Sontowski et al. 2015	<i>Agrilus ribesi</i>	Buprestidae	Germany	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Sontowski et al. 2015	<i>Anthaxia anatolica</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Sontowski et al. 2015	<i>Capnodis tenebricosa</i>	Buprestidae	Armenia, France	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Sontowski et al. 2015	<i>Chrysobothris affinis</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Sontowski et al. 2015	<i>Lamprodila mirifica nadezhdae</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Sontowski et al. 2015	<i>Sphaerobothris aghababiani</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	F	n.n.	n.n.
Sontowski et al. 2015	<i>Sphenoptera antiqua</i>	Buprestidae	Armenia	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Sontowski et al. 2015	<i>Trachys minutus</i>	Buprestidae	Germany	ftsZ	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Malloch et al. 2000	<i>Byturus tomentosus</i>	Byturiidae	Europe	ftsZ	n.n.	34	152	n.n.	24% or 99% infected	97% multiple infected	A	n.n.	n.n.
Heintzman et al. 2014	<i>Anona alpina</i>	Carabidae	Arctica	n.n.	n.n.	1	6	n.n.	n.n.	2 strains	AB	n.n.	n.n.
Kittayapong et al., 2003	<i>Chlaenius sp.</i>	Carabidae	Thailand	ftsZ,wsp	n.n.	1	3	1/3 infected	n.n.	n.n.	B	n.n.	n.n.
Frank et al. 2009	<i>Pheropsochus aequinoctialis</i>	Carabidae	S America	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Aikawa et al. 2009	<i>Monochamus alternatus</i>	Cerambycidae	Japan	ftsZ,wsp,16S,groEL	n.n.	2	25	4% population infected	22/25 infected	single ftsZ variant	A	14% of W. genes transferred into autosomes of the host - no living bacteria detected	n.n.
Clark et al. 2001	<i>Acalymma blandulum</i>	Chrysomelidae	N America	16S, ftsZ	n.n.	1	20	all infected	n.n.	n.n.	A	n.n.	n.n.
Clark et al. 2001	<i>Acalymma vittatum</i>	Chrysomelidae	N America	16S, ftsZ	n.n.	1	20	5% infected	n.n.	n.n.	A	n.n.	n.n.
Werren et al. 1995	<i>Acromis sparsa</i>	Chrysomelidae	Panama	ftsZ	n.n.	28S	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Pankewitz et al. 2007	<i>Agelastica alni</i>	Chrysomelidae	Germany	16S,wsp,ftsZ	n.n.	1	5	all infected	all infected	n.n.	A	n.n.	n.n.
Jäckel et al. 2013	<i>Alicia aenesces</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	3	n.n.	single strain (3/3 infected)	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia birmanensis</i>	Chrysomelidae	Taiwan	ftsZ	COI, ITS2, EF1a, msats	1	1	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia brevicollis</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	1	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia carinata</i>	Chrysomelidae	USA	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia cariniflora</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Xue et al. 2011	<i>Alicia cirsiola</i>	Chrysomelidae	East Asia	wsp	COI,ITS2,EF1a	2	23	all infected	all infected	single infected	n.n.	n.n.	n.n.
Jäckel et al. 2013	<i>Alicia engstroemi</i>	Chrysomelidae	Sweden	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain	single infected	B	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia ericeti</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Xue et al. 2011	<i>Alicia fragariae</i>	Chrysomelidae	East Asia	wsp	COI,ITS2,EF1a	4	47	all infected	all infected	single infected	n.n.	n.n.	n.n.
Jäckel et al. 2013	<i>Alicia helianthemi</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	1	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia impressicollis</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain (5/9 infected)	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia lybri</i>	Chrysomelidae	Germany; Poland; France	ftsZ	COI, ITS2, EF1a, msats	18	50	n.n.	single strain (19/50 infected)	single infected or uninfected females	AB	perfect LD between W. infection and mtDNA haplotype (SS), CI, sex ratio distortion	horizontal transmission?
Jäckel et al. 2013	<i>Alicia oleracea</i>	Chrysomelidae	Europe	ftsZ	COI, ITS2, EF1a, msats	4	24	n.n.	single strain (10/24 infected)	single infected or uninfected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia palustris</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	9	n.n.	single strain	single infected	A	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia quercetorum</i>	Chrysomelidae	Germany	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	two strains	double infected	AB	n.n.	horizontal transmission?
Jäckel et al. 2013	<i>Alicia tamaricis</i>	Chrysomelidae	France	ftsZ	COI, ITS2, EF1a, msats	1	2	n.n.	single strain	single infected	n.n.	n.n.	horizontal transmission?
Xue et al. 2011	<i>Alicia viridicyanea</i>	Chrysomelidae	East Asia	wsp	COI,ITS2,EF1a	3	57	all infected	all infected	single infected	n.n.	n.n.	n.n.
Roehrdanz et al. 2006	<i>Aphodius nigricaudis</i>	Chrysomelidae	USA, Canada	wsp,ftsZ	16S	3	214	c. 70% infected	60%-94% infected in populations	single strain	A	SS and reduction of host diversity	n.n.
Takano et al. 2017	<i>Brontispa longissima</i>	Chrysomelidae	East Timor	16S (Illumina),MLST	n.n.	2	12	n.n.	n.n.	n.n.	n.n.	CI	identification of new Alphaproteobacteria
Kondo et al. 2011	<i>Callosobruchus analis</i>	Chrysomelidae	Britain, Sri Lanka, Bangladesh	wsp,ftsZ	mtDNA	3	8	all infected	n.n.	n.n.	B	n.n.	n.n.
Kageyama et al. 2010	<i>Callosobruchus analis</i>	Chrysomelidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Numajiri et al. 2017	<i>Callosobruchus analis</i>	Chrysomelidae	Sri Lanka	wsp	COI	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	CI, fitness decline in infected beetles	n.n.
Kageyama et al. 2010	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Nikoh et al. 2008	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan, Taiwan	wsp,ftsZ	n.n.	8 strains	14	n.n.	n.n.	n.n.	n.n.	30% of W. genes transferred into autosomes of the host	n.n.
Kondo et al. 2011	<i>Callosobruchus chinensis</i>	Chrysomelidae	Asia, Africa	wsp,ftsZ	mtDNA	37	184	all infected	n.n.	n.n.	AB	n.n.	n.n.
Kondo et al. 1999	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan	16S, wsp, ftsZ	mtDNA	6	409	all infected	all infected	n.n.	n.n.	n.n.	n.n.
Kondo et al. 2002	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan	wsp,ftsZ	n.n.	9	622	all infected	all infected	3 strains, infected: 93.7% triple , 6.1% double, 0.2% single, 1 strain in 90-100% ind.	AB	CI, W. populations (strains) controlled by the host	n.n.
Kondo et al. 2005	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Okayama et al. 2016	<i>Callosobruchus chinensis</i>	Chrysomelidae	Japan	n.n.	n.n.	1 (single strain)	1	n.n.	n.n.	n.n.	n.n.	infection affects the life history and sexual selection (CI)	n.n.
Goodyear et al. 2015	<i>Callosobruchus rhodesianus</i>	Chrysomelidae	Africa,Asia, Australia,N America	wsp	COI	4	4	n.n.	1/4 infected	n.n.	n.n.	n.n.	n.n.
Kondo et al. 2011	<i>Callosobruchus latitarsus</i>	Chrysomelidae	China, Taiwan	wsp,ftsZ	mtDNA	3	11	all infected	China, 2 ind. single infected, 2 ind. double infected	n.n.	AB	n.n.	n.n.
Werren et al. 2000	<i>Charidactylus purpuratus</i>	Chrysomelidae	USA	ftsZ,16S	n.n.	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Werren et al. 1995	<i>Chelymorpha alternans</i>	Chrysomelidae	Panama	ftsZ	28S	3	3	n.n.	n.n.	n.n.	B	n.n.	n.n.
Keller et al. 2004	<i>Chelymorpha alternans</i>	Chrysomelidae	Panama	16S, wsp, ftsZ	COI	24	753	747/753 infected	infected by two strains	99.2% and 53% of beetles infected by 2 strains, single or double infected	n.n.	CI	dry climate decrease infection frequency
Clark et al. 2008	<i>Chelymorpha alternans</i>	Chrysomelidae	Panama	16S, wsp	n.n.	2	n.n.	n.n.	n.n.	n.n.	n.n.	W. modification of sperm	n.n.
Werren et al. 1995	<i>Chersinella heteropunctata</i>	Chrysomelidae	Panama	ftsZ	28S	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Kubisz et al. 2012	<i>Crioceris quaterdecimpunctata</i>	Chrysomelidae	C.E Europe	ftsZ,hcpA	COI, ITS1	5	25	all infected	all infected	most double infected	AB	n.n.	n.n.
Kolasa et al. 2017	<i>Crioceris quaterdecimpunctata</i>	Chrysomelidae	C.E Europe	MLST	COL,ITS1	4	19	all infected	all infected	all double infected	AB	n.n.	n.n.
Kolasa et al. 2017	<i>Crioceris quinquepunctata</i>	Chrysomelidae	C.E Europe	MLST	COL,ITS1	2	10	all infected	all infected	all double infected	AB	n.n.	host plant transmission (Asparagus)
Mazur et al. 2014	<i>Crioceris quinquepunctata</i>	Chrysomelidae	C.E Europe	ftsZ,hcpA	COL,ITS1	2	10	all infected	all infected	most double infected	AB	n.n.	host plant transmission (Asparagus)
Roehrdanz & Levine 2007	<i>Diabrotica barberi</i>	Chrysomelidae	USA	16S, wsp, ftsZ	mtDNA	66	577	all infected	all infected	2 distinct strains	A	CI	n.n.
Roehrdanz & Wichmann 2013	<i>Diabrotica barberi</i>	Chrysomelidae	USA	wsp	n.n.	66	577	all infected	all infected	5 wsp variants	n.n.	n.n.	n.n.
Clark et al. 2001	<i>Diabrotica crinita</i>	Chrysomelidae	N America	16S,ftsZ	n.n.	1	25	12% infected	n.n.	n.n.	A	n.n.	n.n.
Clark et al. 2001	<i>Diabrotica lemniscata</i>	Chrysomelidae	N America	16S,ftsZ	n.n.	1	20	all infected	n.n.	n.n.	A	n.n.	n.n.
Clark et al. 2001	<i>Diabrotica virgifera virgifera</i>	Chrysomelidae	N America	16S,ftsZ	n.n.	1	40	all infected	n.n.	n.n.	A	n.n.	possible CI
Giordano et al. 1997	<i>Diabrotica virgifera virgifera</i>	Chrysomelidae	N America	16S,ftsZ	n.n.	15	60	13/15 populations infected	n.n.	n.n.	A	n.n.	n.n.
Barr et al. 2010	<i>Diabrotica virgifera virgifera</i>	Chrysomelidae	N America	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Kittayapong et al., 2003	<i>Diabrotica virgifera virgifera</i>	Chrysomelidae	Thailand	ftsZ,wsp	n.n.	1	12	1/12 infected	n.n.	n.n.	B	n.n.	W. down-regulate defence genes in maize
Pankewitz et al. 2007	<i>Galeruca tanacetii</i>	Chrysomelidae	Germany	16S,wsp,ftsZ	n.n.	1	5	all infected	all infected	n.n.	A	n.n.	n.n.
Jäckel et al. 2013	<i>Hermaeophaga mercuialis</i>	Chrysomelidae	n.n.	ftsZ	COL,ITS2,EF1a	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Kondo et al. 2011	<i>Megabruchidius sophorae</i>	Chrysomelidae	Japan	wsp,ftsZ	mtDNA	1	8	1/8 infected	n.n.	n.n.	B	n.n.	n.n.
Sintupachee et al. 2006	<i>Monolepta signata</i>	Chrysomelidae	Thailand	ftsZ,wsp	n.n.	1	19	1/19 infected	n.n.	n.n.	n.n.	n.n.	n.n.
Chafee et al. 2009	<i>Noctuidia hebbiana</i>	Chrysomelidae	N America	MLST	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Montagna et al. 2014	<i>Oreina bidantata</i>	Chrysomelidae	Italy	16S,wsp,MLST	COI	1	1	all infected	all infected	single strain	A	n.n.	n.n.
Montagna et al. 2014	<i>Oreina cacaliae</i>	Chrysomelidae	Italy	16S,wsp,MLST	COI	1	1	all infected	all infected	single strain	A	n.n.	n.n.
Montagna et al. 2014	<i>Oreina elongata</i>	Chrysomelidae	Italy	16S,wsp,MLST	COI	2	3	all infected	all infected	single strain	A	n.n.	n.n.
Montagna et al. 2014	<i>Oreina liturata</i>	Chrysomelidae	Italy	16S,wsp,MLST	COI	1	1	all infected	all infected	single strain	A	n.n.	n.n.
Montagna et al. 2014	<i>Oreina speciosa</i>	Chrysomelidae	Italy	16S,wsp,MLST	COI	3	5	all infected	all infected	single strain	A	n.n.	n.n.
Sintupachee et al. 2006	<i>Phyllotreta sp.</i>	Chrysomelidae	Thailand	ftsZ,wsp	n.n.	1	4	1/4 infected	n.n.	n.n.	n.n.	n.n.	n.n.
Jäckel et al. 2013	<i>Podagrica fuscipes</i>	Chrysomelidae	n.n.	ftsZ	COL,ITS2,EF1a	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Yun et al. 2011	<i>Propylea japonica</i>	Chrysomelidae	China	wsp	n.n.	44	n.n.	n.n.	n.n.	n.n.	B	n.n.	n.n.
Werren et al. 1995	<i>Priocera sp.</i>	Cleridae	Panama	ftsZ	28S	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Majerus et al. 2000	<i>Adalia bipunctata</i>	Coccinellidae	Russia	wsp									

Zhang et al. 2010	<i>Conotrachelus nenuphar</i>	Curculionidae	USA	wsp,ftsZ	COI	12	94	98% infected	n.n.	3 strains (double and single infected)	AB	possible CI	n.n.
Werren et al. 1995	<i>Cosmosus sp.</i>	Curculionidae	Panama	ftsZ	28S	n.n.	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Zchori-Fein et al. 2006	<i>Coccotrypes dactylipeda</i>	Curculionidae	Israel	16S		1	20	n.n.	all infected	n.n.	n.n.	role in oogenesis	n.n.
Toju & Fukatsu 2011	<i>Curculio sikkimensis</i>	Curculionidae	Japane	16S	EF1α	55	968	n.n.	82.5% infected	n.n.	n.n.	n.n.	coexistence with Rickettsia & Spiroplasma
Toju et al. 2013	<i>Curculio hachijoensis</i>	Curculionidae	Asia	16S		1	2	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Toju et al. 2013	<i>Curculio hilgendorfi</i>	Curculionidae	Asia	16S		2	3	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Toju et al. 2013	<i>Curculio morimotoi</i>	Curculionidae	Asia	16S		1	2	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Toju et al. 2013	<i>Curculio okumai</i>	Curculionidae	Asia	16S		2	4	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Kajtoch et al. 2017	<i>Cyanapion afer</i>	Curculionidae	Poland	MLST	COI, ITS2, EF1α	5	10	all infected	all infected	2 strains	A	n.n.	n.n.
Kajtoch et al. 2017	<i>Cyanapion syltenhalii</i>	Curculionidae	Poland	MLST	COI, ITS2, EF1α	6	12	all infected	all infected	single strain	A	n.n.	n.n.
Kajtoch et al. 2017	<i>Cyanapion spencii</i>	Curculionidae	Poland	MLST	COI, ITS2, EF1α	6	12	n.n.	5/6 infected	2 strains	AB	n.n.	n.n.
Werren et al. 2000	<i>Cyrtopistomus castaneus</i>	Curculionidae	USA	ftsZ,16S		n.n.	n.n.	n.n.	n.n.	n.n.	A	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Dorytomus carpaticus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Dorytomus rufatus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Ellescus bipunctatus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Eurytomus fallax</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single strain	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Eurytomus globosus</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single strain	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Eusomus ovalum</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	-	n.n.	A	n.n.	n.n.
Mazar et al. 2016	<i>Eusomus ovalum</i>	Curculionidae	C,SE.E Europe	MLST	COI, ITS2, EF1α	28	65	all infected	all infected, single strain	all infected, single strain	A	SS, possible pathogenesis induction	n.n.
Kawasaki et al. 2016	<i>Eusallaea interjectus</i>	Curculionidae	Japan	wsp,MLST	COI, EF1α	n.n.	20	n.n.	100% infected	single infected	A	haploidy induction uncertain	n.n.
Kawasaki et al. 2016	<i>Eusallaea validus</i>	Curculionidae	Japan	wsp,MLST	COI, EF1α	n.n.	21	n.n.	75% infected	single infected	A	haploidy induction uncertain	horizontal transmission?
Kittayapong et al. 2003	<i>Hydronomidius molitor</i>	Curculionidae	Thailand	ftsZ,wsp		1	1	n.n.	n.n.	n.n.	A	n.n.	horizontal transmission?
Berasategui et al. 2016	<i>Hyllobius abietis</i>	Curculionidae	Europe	16S NGS(454)		n.n.	6	54	all infected	0.2-100% abundance, 28-73% of reads	n.n.	n.n.	n.n.
O'Neill et al. 1992	<i>Hypera postica</i>	Curculionidae	n.n.	16S		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Iwase et al. 2015	<i>Hypera postica</i>	Curculionidae	Japane, Europe	wsp,ftsZ,coxA,hcpA	CyB	11	242	5/11 populations infected	0-100% infected	2 strains	B	n.n.	n.n.
Mariño et al. 2017	<i>Hypothenemus hampei</i>	Curculionidae	Puerto Rico	wsp		n.n.	1	n.n.	n.n.	n.n.	n.n.	CI	W. as biocontrol agent
Vega et al. 2002	<i>Hypothenemus hampei</i>	Curculionidae	S & C America, Asia, Africa	wsp		n.n.	17 countries	n.n.	11/17 populations infected	possibly only single strain	B	possible sex determination	n.n.
Toju et al. 2013	<i>Koreoculio minutissimus</i>	Curculionidae	Asia	16S		n.n.	2	3	n.n.	n.n.	n.n.	n.n.	n.n.
Chen et al. 2012	<i>Lissohoptrus oryzophilus</i>	Curculionidae	China, Texas	wsp,MLST		n.n.	6	127	all infected	all infected	B	W. necessary for oocyte production	n.n.
Lu et al. 2014	<i>Lissohoptrus oryzophilus</i>	Curculionidae	China, Texas	16S		n.n.	5	1421	all infected	all infected	n.n.	n.n.	n.n.
Rodríguez et al. 2010a	<i>Mimographus ocellatus</i>	Curculionidae	S America	MLST	COI	n.n.	1	n.n.	all infected	all infected	B	n.n.	n.n.
Prakash & Pattaraju 2006	<i>Myllocerus discolor</i>	Curculionidae	India	wsp		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus ambigua</i>	Curculionidae	S America	MLST	COI	n.n.	3	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus cervinus</i>	Curculionidae	S America	MLST	COI	n.n.	20	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010b	<i>Naupactus cervinus</i>	Curculionidae	S America	16S, wsp, coxA, fhpA	COI, ITS1.n.n.18S	39	309	all infected	all infected	single infected	B	LD	host bottleneck caused by W.
Rodríguez et al. 2010a	<i>Naupactus condecoratus</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus cyphoides</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus dissimilis</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus leucoloma</i>	Curculionidae	S America	MLST	COI	n.n.	3	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus minor</i>	Curculionidae	S America	MLST	COI	n.n.	3	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus peregrinus</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus purpureoviolaceus</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus tremolerasi</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Naupactus versicollis</i>	Curculionidae	S America	MLST	COI	n.n.	1	all infected	all infected	single infected	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Otiorynchus cocuus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Stenberg & Lundmark 2004	<i>Otiorynchus scaber</i>	Curculionidae	Austria, Slovenia	16S	COL,COII,CyB	2	28	all infected	infected: 5/10 ♂, 2/7 sexual ♀, 0 of clonal ♀	n.n.	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Otiorynchus singularis</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Son et al. 2008	<i>Otiorynchus sulcatus</i>	Curculionidae	USA	wsp		n.n.	5	96	all infected	all infected	B	W. necessary for egg development	n.n.
Rodríguez et al. 2010a	<i>Pantomorus auripes</i>	Curculionidae	S America	MLST	COI	n.n.	3	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Pantomorus cinerosus</i>	Curculionidae	S America	MLST	COI	n.n.	2	all infected	all infected	single infected	B	n.n.	n.n.
Rodríguez et al. 2010a	<i>Pantomorus viridisquamosus</i>	Curculionidae	S America	MLST	COI	n.n.	2	all infected	all infected	single infected	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Paophilus aflatu</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Paragoucartia squamulata</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Arthofer et al. 2009	<i>Phyogenes chalcographus</i>	Curculionidae	C,E.N.S Europe	wsp, MLST	COI, EF1α	31	344	35.5% infected	0-100% infected	3 strains (91% - A, 9% - B)(95% single infected, 5% double infected)	AB	n.n.	bacteria loss and horizontal transfer
Lachowska-Cierlik et al. 2010	<i>Polydrusus inustus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	A	n.n.	n.n.
Kajtoch et al. 2012	<i>Polydrusus inustus</i>	Curculionidae	C,E Europe	wsp,16S,ftsZ,hcpA	COI, ITS2,EF1α	9	40	all infected	all infected, 2 closely related strains	all infected, 2 closely related strains	A	probably SS	n.n.
Lachowska-Cierlik et al. 2010	<i>Polydrusus molit</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Kajtoch et al. 2012	<i>Polydrusus pilifer</i>	Curculionidae	Caucasus	wsp,16S,ftsZ,hcpA	COI, ITS2,EF1α	5	5	all infected	all infected	single infected	n.n.	probably SS	n.n.
Lachowska-Cierlik et al. 2010	<i>Polydrusus pilosus</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	AB	n.n.	n.n.
Campbell et al. 1992	<i>Rhinocyclus conicus</i>	Curculionidae	Italy	16S		n.n.	n.n.	n.n.	n.n.	n.n.	F	n.n.	n.n.
Toševski et al. 2015	<i>Rhinusa pilosa</i>	Curculionidae	Europe	coxA	COI, 16S,EF1α	6	47	n.n.	80.8% ind. Infected	n.n.	n.n.	n.n.	n.n.
Toševski et al. 2015	<i>Rhinusa rara</i>	Curculionidae	Europe	coxA	COI, 16S,EF1α	5	10	n.n.	60% ind. Infected	n.n.	n.n.	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Sciaphobus rubi</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
White et al. 2015	<i>Sitona obsoletus</i>	Curculionidae	New Zealand	16S(454),MLST		n.n.	2	36	all infected	all infected	A	n.n.	n.n.
Heddi et al. 1999	<i>Stiophilus granarius</i>	Curculionidae	France	16S		n.n.	3	30	2 out of 3 infected	40% infected	n.n.	n.n.	coexistence with Rickettsia
Heddi et al. 1999	<i>Stiophilus oryzae</i>	Curculionidae	Africa,Asia, Australia,N America	16S		n.n.	10	100	7 out of 10 infected	61% infected	B	n.n.	n.n.
Carvalho et al. 2014	<i>Stiophilus oryzae</i>	Curculionidae	America S, N, Asia, Australia	16S		n.n.	16	n.n.	7/16 infected	n.n.	n.n.	n.n.	horizontal transmission
Li et al. 2015	<i>Stiophilus oryzae</i>	Curculionidae	Canada	wsp,MLST		n.n.	7	n.n.	1/6 populations infected	n.n.	n.n.	n.n.	n.n.
Werren et al. 1995	<i>Stiophilus oryzae</i>	Curculionidae	Panama	ftsZ	28S	n.n.	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Carvalho et al. 2014	<i>Stiophilus zaemais</i>	Curculionidae	America S, N, Asia, Australia	16S	16S	11	n.n.	n.n.	9/11 infected	n.n.	n.n.	n.n.	horizontal transmission
Kageyama et al. 2010	<i>Stiophilus zaemais</i>	Curculionidae	Japane	wsp		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Stiophilus zaemais</i>	Curculionidae	Thailand	wsp,MLST		n.n.	3	n.n.	2/3 populations infected	n.n.	n.n.	n.n.	n.n.
Heddi et al. 1999	<i>Stiophilus zaemais</i>	Curculionidae	Asia, Africa, America,	16S		n.n.	10	100	4 out of 10 infected	40% infected	n.n.	n.n.	n.n.
White et al. 2015	<i>Stierophilus variabilis</i>	Curculionidae	New Zealand	16S(454),MLST		n.n.	18	all infected	all infected	W. = 8-12% of bacteria reads	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Strophosoma capitatum</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Lachowska-Cierlik et al. 2010	<i>Strophosoma melanogrammum</i>	Curculionidae	Poland	wsp,16S,ftsZ,hcpA	COI	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
Kawasaki et al. 2016	<i>Taphrorhynchus bicolor</i>	Curculionidae	Austria	wsp,MLST	COI,EF1α	n.n.	5	n.n.	80% infected	single infected	B	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xyleborinus schaufussi</i>	Curculionidae	Japan	wsp,MLST	COI,EF1α	n.n.	11	n.n.	85% infected	single infected	A	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xyleborus dispar</i>	Curculionidae	Austria	wsp,MLST	COI,EF1α	n.n.	5	n.n.	100% infected	6 strains, ind. multiple infected	A	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xyleborus seiryorensis</i>	Curculionidae	Japan	wsp,MLST	COI,EF1α	n.n.	7	n.n.	100% infected	single infected	A	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xylosandrus crassiusculus</i>	Curculionidae	Japan	wsp,MLST	COI,EF1α	n.n.	47	n.n.	95% infected	single infected	A	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xylosandrus germanus</i>	Curculionidae	Japane	wsp,MLST	COI	9	120	all infected	all infected, 5 strains, 1-4 strains/population	9 allele combinations	A	n.n.	horizontal transmission?
Kawasaki et al. 2016	<i>Xylosandrus germanus</i>	Curculionidae	Germany, Hungary	wsp,MLST	COI,EF1α	n.n.	130	n.n.	100% infected	4 strains, ind. multiple infected	A	n.n.	horizontal transmission?
Kageyama et al. 2010	<i>Anthonus verbasci</i>	Dermestidae	Japane	wsp		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Attagenus unicolor</i>	Dermestidae	USA	wsp,MLST		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Dermestes lardarius</i>	Dermestidae	Canada	wsp,MLST		n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
García-Vázquez & Ribera 2016	<i>Deronectes angelinii</i>	Dytiscidae	Italy	wsp	COL16S,NADH,H3,Wg	1	1	n.n.	n.n.	n.n.	B	n.n.	n.n.
García-Vázquez & Ribera 2016	<i>Deronectes aubei</i>	Dytiscidae	Italy, Germany, Spain, France	wsp	COL16S,NADH,H3,Wg	5	15	8/15 infected	n.n.	n.n.	A	n.n.	n.n.
García-Vázquez & Ribera 2016	<i>Deronectes delarouzei</i>	Dytiscidae	Spain	wsp	COL16S,NADH,H3,Wg	4	4	all infected	n.n.	n.n.	A	n.n.	n.n.
García-Vázquez & Ribera 2016	<i>Deronectes moestus</i>	Dytiscidae	Greece, Italy, Spain, Morocco	wsp	COL								

Sintupachee et al. 2006	<i>Onthophagus vaulongeri</i>	Scarabaeidae	Thailand	ftsZ,wsp	n.n.	1	6	1/6 infected	n.n.	n.n.	n.n.
Yun et al. 2011	<i>Paederus fuscipes</i>	Staphylinidae	China	wsp	n.n.	n.n.	7		n.n.	B	n.n.
Bili et al. 2016	<i>Aleochara bilineata</i>	Staphylinidae	France	16S NGS(454), fbpA	n.n.	2	40	n.n.	n.n.	A	n.n.
Bili et al. 2016	<i>Aleochara bipustulata</i>	Staphylinidae	France	16S NGS(454), fbpA	n.n.	2	40	n.n.	n.n.	B	n.n.
Li et al. 2015	<i>Oryzaephilus mercator</i>	Sylvanidae	Canada	wsp,MLST	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	coexistence with Rickettsia & Spiroplasma
Sharaf et al. 2010	<i>Oryzaephilus surinamensis</i>	Sylvanidae	Israel	16S	n.n.	2	94	69-86% infected	n.n.	n.n.	coexistence with Spiroplasma
Sharaf et al. 2013	<i>Oryzaephilus surinamensis</i>	Sylvanidae	Israel	16S	COI,16S	3	n.n.	n.n.	n.n.	n.n.	possible CI
Li et al. 2015	<i>Oryzaephilus surinamensis</i>	Sylvanidae	Canada,Europe,USA	wsp,MLST	n.n.	5	n.n.	all infected	n.n.	n.n.	n.n.
Kageyama et al. 2010	<i>Oryzaephilus surinamensis</i>	Sylvanidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Kageyama et al. 2010	<i>Tribolium confusum</i>	Tenebrionidae	Japan	wsp	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Goodacre et al. 2015	<i>Tribolium confusum</i>	Tenebrionidae	USA, China, Uganda	wsp	COI	9	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2016	<i>Tribolium confusum</i>	Tenebrionidae	Canada	wsp	n.n.	colonies	80	all infected?	100% infected?	n.n.	CI
Ming et al. 2015	<i>Tribolium confusum</i>	Tenebrionidae	China	wsp	EF-2	1	numerous	n.n.	n.n.	n.n.	CI
Fialho & Stevens 1997	<i>Tribolium confusum</i>	Tenebrionidae	Asia, USA, Europe	ftsZ,ITS	n.n.	11	-	all infected	all infected	n.n.	B
Fialho & Stevens 1996	<i>Tribolium confusum</i>	Tenebrionidae	Asia, USA, Europe	16S	n.n.	8 strains	n.n.	n.n.	n.n.	n.n.	CI
O'Neill et al. 1992	<i>Tribolium confusum</i>	Tenebrionidae	n.n.	16S	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.	n.n.
Li et al. 2015	<i>Tribolium confusum</i>	Tenebrionidae	Canada,Europe,USA	wsp,MLST	n.n.	16	n.n.	15/16 populations infected	n.n.	n.n.	n.n.
Fialho & Stevens 2000	<i>Tribolium madens</i>	Tenebrionidae	n.n.	ftsZ,wsp,ITS,groEL	n.n.	3 strains	n.n.	2 strains infected	n.n.	n.n.	male-killing

Abbreviations: W – *Wolbachia*, LD - linkage disequilibrium, SS- selective sweep, CI - cytoplasmic incompatibility, MLST – multilocus sequence typing, gatB - aspartylglutamyl-tRNA (Gln) amidotransferase, subunit B, coxA - cytochrome c oxidase, subunit I, hcpA - conserved hypothetical protein, rfsZ - cell division protein, fbpA - fructose-bisphosphate aldolase, wsp – *Wolbachia* surface protein, 16S/18S/28S rDNA - 16S/18S/28S ribosomal DNA, groEL - heat-shock protein 60, COI – cytochrome oxidase subunit I, ITS – internal transcribed spacer, EF1 α – elongation factor 1 α , Wg - wingless, H3 - histone H3, msats – microsatellites.

References to Supplementary table 1.

Aikawa T, Anbutsu H, Nttoh N, Kikuchi T, Shibata F, Fukatsu T. 2009. Longicorn beetle that vectors pinewood nematode carries many *Wolbachia* genes on an autosome. *Proceedings of the Royal Society B: Biological Sciences* **276**: 3791–3798. DOI: 10.1098/rspb.2009.1022.

Arbuthnot W, Richter M, Arizvi D, Stauffer C. 2009. Evidence for low-titre infections in insect symbiosis: *Wolbachia* in the bark beetle *Pityogenes chalcographus* (Coleoptera: Scolytinae). *Environmental Microbiology* **11**: 1923–33. DOI: 10.1111/j.1462-2920.2009.01914.x.

Barr KL, Hearne LB, Brisseacher S, Clark TL, Davis GE. 2010. Microbial Symbionts in Insects: Influence Down-Regulation of Defense Genes in Maize. *PLoS ONE* **5**: e11339. DOI: 10.1371/journal.pone.0011339.

Berastegui A, Axelsson K, Nordlander G, Schmidt A, Berg-Karlson A-K, Gershenzon J, Terenius O, Kallersjö M. 2016. The gut microbiota of the pine weevil is similar across Europe and resembles that of other 649 conifer beetles. *Molecular Ecology* **25**: 4014–4031. DOI: 10.1111/mec.14186.

Bill M, Cortesero AM, Mougé Y, Gauthier JP, Ermel G, Simon JC, Outreman Y, Terrat S, Mahéo F, Polsoot D. 2016. Bacterial Community Diversity Harboured by Interacting Species. *PLoS ONE* **11**: e0155392. DOI:10.1371/journal.pone.0155392.

Campbell BC, Bragg TS, Turner C. E. 1992. Phylogeny of symbiotic bacteria of four weevil species (Coleoptera: Curculionidae) based on analysis of 16s ribosomal DNA. *Insect Biochemistry and Molecular Biology* **22**: 415–421. DOI: 10.1016/0965-1748(92)90136-3.

Carvalho GA, Correa AS, Oliveira LO, Guedes RNC. 2014. Evidence of horizontal transmission of primary and secondary endosymbionts between the maize and rice weevils (*Stophilus zeamais* and *S. oryzae*) and the parasitoid *Theoclastus elegans*. *Journal of Stored Products Research* **59**: 61–65. DOI: 10.1016/j.jspr.2014.05.004.

Chafee ME, Funk DJ, Harrison RG, Bordenstein SR. 2010. Lateral phage transfer in obligate intracellular bacteria (*Wolbachia*): Verification from natural populations. *Molecular Biology and Evolution* **27**: 501–505. DOI: 10.1093/molbev/msp275.

Chen SJ, Lu F, Cheng JA, Jiang MX, Way MO. 2012. Identification and Biological Role of the Endosymbiont *Wolbachia* in Rice Water Weevil (Coleoptera: Curculionidae). *Environmental Entomology* **41**: 469–477. DOI: 10.1603/EN11195.

Clark ME, Bailey-Jourdain C, Ferree PM, England SJ, Sullivan W, Windsor DM, Werren JH. 2008. *Wolbachia* modification of sperm does not always require residence within developing sperm. *Heredity* **101**: 420–428. DOI: 10.1038/hdy.2008.71.

Clark TL, Meinke LJ, Skoda SR, Foster JE. 2001. Occurrence of *Wolbachia* in Selected Diabroticid (Coleoptera: Chrysomelidae) Beetles. *Annals of the Entomological Society of America* **94**: 877–885.

Dudek K, Humnińska K, Wójcickiewicz J, Tryjanowski P. 2017. Metagenomic survey of bacteria associated with the invasive ladybird *Harmonia axyridis* (Coleoptera: Coccinellidae). *European Journal of Entomology* **114**: 312–316. DOI: 10.14411/eje.2017.038.

Elmady S, Majerus MEN, Gardener M, Lawson-Handley L. 2013. The direct effects of male-killer infection on fitness of ladybird hosts (Coleoptera: Coccinellidae). *Journal of Evolutionary Biology* **26**: 1816–1825. DOI: 10.1111/jeb.12186.

Fialho RF, Stevens L. 1996. *Wolbachia* infections in the flour beetle *Tribolium confusum*: evidence for a common incompatibility type across strains. *Journal of Invertebrate Pathology* **67**: 195–197. DOI: 10.1006/jip.1996.0052.

Fialho RF, Stevens L. 1997. Molecular evidence for single *Wolbachia* infections among geographic strains of the flour beetle *Tribolium confusum*. *Proceedings of the Royal Society B: Biological Sciences* **264**: 1065–1068. DOI: 10.1098/rspb.1997.0147.

Fialho RF, Stevens L. 2000. Male-killing *Wolbachia* in a flour beetle. *Proceedings of the Royal Society B: Biological Sciences* **267**: 1469–1474. DOI: 10.1098/rspb.2000.1166.

Floate KD, Coghlin PC, Dossall L. 2011. A Test using *Wolbachia* Bacteria to Identify Eurasian Source Populations of Cabbage Seedpod Weevil, *Centorhynchus obstrictus* (Marsham), in North America. *Environmental Entomology* **40**: 818–823. DOI: 10.1603/EN10315.

Frank JH, Erwin TL & Honeynaw JC. 2009. Economically Beneficial Ground Beetles. The specialized predators *Pterostichus acquinoidalis* (L.) and *Stenopatus ruficornis* (Morawitz): Their laboratory behavior and descriptions of immature stages (Coleoptera, Carabidae, Brachininae). *Zookeys* **14**: 1–36. DOI: 10.3897/zookeys.14.188.

García-Vázquez D, Rihera L. 2016. The origin of widespread species in a poor dispersing lineage (diving beetle genus Deronectes). *PeerJ* **4**: e2514. DOI: 10.7717/peerj.2514.

Giordano R, Jackson JJ, Robertson HM. 1997. The role of *Wolbachia* bacteria in reproductive incompatibilities and hybrid zones of *Diabrotica* beetles and *Gryllus* crickets. *Proceedings of the National Academy of Sciences of the USA* **94**: 11439–11444.

Goodacre SL, Fricke C, Martin OY. 2015. A screen for bacterial endosymbionts in the model organisms *Tribolium castaneum*, *T. confusum*, *Callosobruchus maculatus*, and related species. *Insect Science* **22**: 165–177. DOI: 10.1111/1744-7917.12096.

Goryacheva II, Bikhman AV, Andrianova BV, Gorelova IV, Zakharaov IA. 2015. Genotypic Diversity of *Wolbachia* pipientis in Native and Invasive *Harmonia axyridis* Pall., 1773 (Coleoptera, Coccinellidae) Populations. *Russian Journal of Genetics* **8**: 731–736.

Heddi A, Grenier AM, Khachatourian Ch, Charles H, Nardon P. 1999. Four intracellular genomes direct weevil biology: Nuclear, mitochondrial, principal endosymbiont, and *Wolbachia*. *Proceedings of the National Academy of Sciences of the USA* **96**: 6814–6819. DOI: 10.1073/pnas.96.12.6814.

Heintzman PD, Elias SA, Moore K, Paszkiewicz K, Barnes I. 2014. Characterizing DNA preservation in degraded specimens of *Anura alpina* (Carabidae: Coleoptera). *Molecular Ecology Resources* **14**: 606–615. DOI: 10.1111/1755-0998.12205.

Hurst GDD, Jiggins FM, von der Schlenburg JHG, Bertrand D, West SA, Goriacheva II, Zakharaov IA, Werren JH, Stouthamer R, Majerus MEN. 1999b. Male-killing *Wolbachia* in two species of insect. *Proceedings of the Royal Society B: Biological Sciences* **266**: 735–740. DOI: 10.1098/rspb.1999.0698.

Iwase S, Tani S, Sareki Y, Tuda M, Haran J, Shuhrove J, Takagi M. 2015. Dynamics of infection with *Wolbachia* in Hyperparasitoid (Coleoptera: Curculionidae) during invasion and establishment. *Biological Invasions* **17**: 3659–3668. DOI: 10.1007/s10530-015-0985-1.

Jäckel R, Morit D, Dohler S. 2013. Evidence for selective sweeps by *Wolbachia* infections: Phylogeny of *Adicia* leaf beetles and their reproductive parasites. *Molecular Ecology* **22**: 241–255. DOI: 10.1111/mec.12389.

Jeyaprabak A, Hoy MA. 2006. Long PCR improves *Wolbachia* DNA amplification: wsp sequences found in 76% of 63 arthropod species. *Insect Molecular Biology* **9**: 393–405. DOI: 10.1046/j.1365-2583.2006.00203.x.

Jeong G, Kang T, Park H, Choi J, Hwang S, Kim W, Choi Y, Lee K, Park I, Sim H. 2009. *Wolbachia* infection in the Korean endemic firefly, *Luciola umunusana* (Coleoptera: Lampyridae). *Journal of Asia-Pacific Entomology* **12**: 33–36. DOI: 10.1016/j.aspen.2008.11.001.

Kageyama D, Norita S, Imamura T, Miyashita A. 2010. Detection and identification of *Wolbachia* endosymbionts from laboratory stocks of stored-product insect pests and their parasitoids. *Journal of Stored Products Research* **46**: 13–19. DOI: 10.1016/j.jspr.2009.07.003.

Kajtoch L, Karotysev B, Lachowska-Cierlik D. 2012. Genetic distinctness of pathogenic forms of European *Polysphrus* weevils of the subgenus *Scythodraus*. *Insect Science* **19**: 183–194. DOI: 10.1111/j.1744-7917.2011.01448.x.

Kajtoch L, Montagna M, Wanat M. 2017. Species delimitation within the Bothryerhyachaeon weevils: multiple evidence from genetics, morphology and ecological associations. *Molecular Phylogenetics and Evolution*. DOI: 10.1016/j.ympev.2017.12.022.

Kawasaki Y, Schuler H, Stauffer C, Lakatos F, Kajimura H. 2016. *Wolbachia* endosymbionts in haplodiploid and diploid scolytine beetles (Coleoptera: Curculionidae: Scolytinae). *Environmental Microbiology Reports* **8**: 680–688. DOI: 10.1111/1758-2229.12425.

Keller GP, Windsor DM, Scucedo JM, Werren JH. 2004. Reproductive effects and geographical distributions of two *Wolbachia* strains infecting the Neotropical beetle, *Chelymophora alternans* Boh. (Chrysomelidae, Cassidinae). *Molecular Ecology* **13**: 2405–2420. DOI: 10.1111/j.1365-294X.2004.02213.x.

Kittayapong P, Jammongluk W, Tiplakson A, Milne JR, Sindhussake C. 2003. *Wolbachia* infection complexity among insects in the tropical rice-field community. *Molecular Ecology* **12**: 1049–1060. DOI: 10.1046/j.1365-294X.2003.01793.x.

Kolasa M, Montagna M, Meregheiti V, Kubisz D, Mazur MA, Kajtoch L. 2017. Preliminary evidence of *Wolbachia* horizontal transmission between *Cricocaris* leaf beetles and *Asparagus* host plants. *European Journal of Entomology* **114**: 446–454. DOI: 10.14411/eje.2017.057.

Kondo N, Ijichi N, Shimada M, Fukatsu T. 2002. Prevailing triple infection with *Wolbachia* in *Callosobruchus chinensis* (Coleoptera: Bruchidae). *Molecular Ecology* **11**: 167–180. DOI: 10.1046/j.0962-1083.2001.01432.x.

Kondo N, Shimada M, Fukatsu T. 1999. High prevalence of *Wolbachia* in the azuki bean beetle *Callosobruchus chinensis* (Coleoptera, Bruchidae). *Zoological Science* **16**: 955–962. DOI: 10.2108/zsj.16.955.

Kondo N, Shimada M, Fukatsu T. 2005. Infection density of *Wolbachia* endosymbiont affected by co-infection and host genotype. *Biology Letters* **1**: 488–491. DOI: 10.1098/rsbl.2005.0340.

Kondo N, Tuda M, Tsunemitsu Y, Lau MC, Buranapanichavan S, Hwang SB, Shimada M, Fukatsu T. 2011. *Wolbachia* infections in world populations of bean beetles (Coleoptera: Chrysomelidae: Bruchinae) infecting cultivated and wild legumes. *Zoological Science* **28**: 501–508. DOI: 10.2108/zsj.28.501.

Kubisz D, Kajtoch L, Mazur MA, Lis A, Holecová M. 2012. Conservation genetics of highly isolated populations of xenothermic *Cricocaris quatuordecimpunctata* (Coleoptera: Chrysomelidae). *Invertebrate Biology* **131**: 333–344. DOI: 10.1111/j.1744-7410.2012.00276.x.

Lachowska-Cierlik D, Kajtoch L, Knutelski S. 2010. Occurrence of *Wolbachia* in central European weevils: correlations with host systematics, ecology and biology. *Entomologia Experimentalis et Applicata* **14**: 105–118. DOI: 10.1111/j.1570-7458.2010.00974.x.

Li YY, Fields PG, Pang B, Coghlin PC, Floate KD. 2015. Prevalence and diversity of *Wolbachia* bacteria infecting insect pests of stored products. *Journal of Stored Products Research* **62**: 93–100. DOI: 10.1016/j.jspr.2009.07.003.

Li YY, Fields PG, Pang BP, Floate KD. 2016. Effects of tetracycline and rifampicin treatments on the fecundity of the *Wolbachia*-infected host, *Tribolium confusum* (Coleoptera: Tenebrionidae). *Journal of Economic Entomology* **109**: 1458–1464. DOI: 10.1093/jee/tow067.

Lu F, Kang XY, Lorenz G, Espino L, Jiang MX, Way MO. 2014. Culture-independent analysis of bacterial communities in the gut of rice water weevil (Coleoptera: Curculionidae). *Annals of the Entomological Society of America* **10**: 592–600. DOI: 10.1603/AN13145.

Majerus MEN, Majerus TMO. 2000. Multiple causes of male-killing in a single sample of the 2-spot ladybird, *Adalia bipunctata* (Coleoptera: Coccinellidae) from Moscow. *Heredity* **84**: 605–609. DOI: 10.1046/j.1365-2540.2000.00710.x.

Malloch G, Fenton B, Butcher RD. 2000. Molecular evidence for multiple infections of a new subgroup of *Wolbachia* in the European raspberry beetle *Byturus tomentosus*. *Molecular Ecology* **9**: 77–90.

Mariño Y, Verle Rodrigues JC, Bayman P. 2017. *Wolbachia* Affects Reproduction and Population Dynamics of the Coffee Berry Borer (*Hypothenemus hampei*): Implications for Biological Control Insects **8**: 8. DOI: 10.3390/insects8010008.

Mazur M.A., Holecová M., Lachowska-Cierlik D., Lis A., Kubisz D., Kajtoch L. 2016. Selective sweep of *Wolbachia* and pathogenetic host genes on the example of the weevil *Eusomus ovalum*. *Insect Molecular Biology* **25**: 701–711. DOI: 10.1111/imb.1225.

Mazur MA, Kubisz D, Kajtoch L. 2014. Restricted geographic distribution and low genetic distinctiveness of steppe *Cricocaris quinquepunctata* (Coleoptera: Chrysomelidae) populations in central-east Europe. *Entomologia Fennica* **25**: 103–111.

Ming QL, Shen JF, Cheng C, Liu CM, Feng ZJ. 2015. *Wolbachia* infection dynamics in *Tribolium confusum* (Coleoptera: Tenebrionidae) and their effects on host mating behavior and reproduction. *Journal of Economic Entomology* **108**: 1408–1415. DOI: 10.1093/jee/tov053.

Montagna M, Chouaib B, Sacchi L, Porretta D, Martin E, Giorgi A, Lozza GC, Epiš SA. 2014. New Strain of *Wolbachia* in an Alpine Population of the *Viviparus oreina calcaica* (Coleoptera: Chrysomelidae). *Environmental Entomology* **43**: 913–922. DOI: 10.1603/EN13228.

Nttoh N, Tanaka K, Shibata F, Kondo N, Hiyama M, Shimada M, Fukatsu T. 2008. *Wolbachia* genome integrated in an insect chromosome: evolution and fate of laterally transferred endosymbiont genes. *Genome Research* **18**: 272–280. DOI: 10.1101/jg.7144908.

Nirjamsaki A, Banks GK, Frohlich DR, Yowell Z, Braig HR, Miller TA, Bedford JD, Markham PC, Sawalick C, Bourdais K. 2003. *Wolbachia* Infections of the Whitefly *Bemisia tabaci*. *Current Microbiology* **47**: 0093–0101. DOI: 10.1007/s00284-002-3969-1.

Nijmaji Y, Kondo N, Tsunemitsu Y. 2017. Moltic mutation causes a fitness decline in bean beetles infected by *Wolbachia*. *Entomologia Experimentalis et Applicata* **164**: 54–65. DOI: 10.1111/eea.12588.

O'Neill SL, Giordano R, Colbert AM, Karr TL, Robertson HM. 1992. 16S rRNA phylogenetic analysis of the bacterial endosymbionts associated with cytoplasmic incompatibility in insects. *Proceedings of National Academy of Sciences of the USA* **89**: 2699–2702.

Okayama K, Katsuki M, Sumida Y, Okada K. 2016. Costs and benefits of symbiosis between a bean beetle and *Wolbachia*. *Animal Behaviour* **119**: 19–26. DOI: 10.1016/j.anbehav.2016.07.004.

Pankewitz F, Zöllner A, Hilker E, Griseir Y. 2007. Presence of *Wolbachia* in Insect Eggs Containing Antimicrobially Active Anthraquinones. *Microbial Ecology* **54**: 713–721. DOI: 10.1007/s00248-007-9230-5.

Perrotti MA, Young DK, Braig HR. 2016. The ghost sex-life of the paedogogic beetle *Micromalthus debilis*. *Scientific reports* **6**: 27364. DOI: 10.1038/srep27364.

Piper RW, Compton SG, Rasplus JY, Piry S. 2001. The species status of *Cathormocerus britannicus*, an endemic, endangered British weevil. *Biological Conservation* **101**: 9–13. DOI: 10.1016/S0006-3207(01)00048-9.

Pourali P, Roayaei Ardakani M, Jolodar A, Razi Jalali MH. 2009. PCR screening of *Wolbachia* in some arthropods and nematodes in Khuzestan province. *Iranian Journal of Veterinary Research* **10**: 216–222.

Prakash BM & Puttaraju HP. 2006. *Wolbachia* endosymbiont in some insect pests of sericulture. *Current Science* **90**: 1671–1674.

Rodríguez MS, Confalonieri VA, Guedes JVC, Lanteri AA. 2010a. *Wolbachia* infection in the tribe Naupactini (Coleoptera, Curculionidae): association between phylogenetic pathogenesis and infection status. *Insect Molecular Biology* **19**: 631–640. DOI: 10.1111/j.1365-2583.2010.01018.x.

Rodríguez MS, Lanteri AA, Confalonieri VA. 2010b. Mito-nuclear genetic comparison in a *Wolbachia* infected weevil: insights on reproductive mode, infection age and evolutionary forces shaping genetic variation. *BMC Evolutionary Biology* **10**: 340. DOI: 10.1186/1471-2148-10-340.

Rochelandet R & Levine E. 2007. *Wolbachia* bacterial infections linked to mitochondrial DNA reproductive isolation among populations of northern corn rootworm (Coleoptera: Chrysomelidae). *Annals of the Entomological Society of America* **100**: 522–531. DOI: 10.1603/0013-8746(2007)100[522:WBBLTM]2.0.CO;2.

Rochelandet R, Olson D, Bourchier R, Sears S, Corfield A, Fauske G. 2006. Mitochondrial DNA diversity and *Wolbachia* infection in the flea beetle *Aphthona nigricincta* (Coleoptera: Chrysomelidae): an introduced biocontrol agent for leafy spurge. *Biological Control* **37**: 1–8. DOI: 10.1016/j.biocontrol.2005.12.004.

Rochelandet RL, Wichmann SGS. 2013. *Wolbachia* wsp gene clones detect the distribution of *Wolbachia* variants and wsp hypervariable regions among 160 individuals of a multistrain infected population of *Diabrotica barberi* (Coleoptera: Chrysomelidae). *Annals of the Entomological Society of America* **106**: 329–338. DOI: 10.1603/AN12118.

Sharaf K, Hadid Y, Pavlíček T, Nevo E. 2013. Local genetic population divergence in a saw-toothed grain beetle, *Oryzaephilus surinamensis* (L.) (Coleoptera, Cucujidae). *Journal of Stored Products Research* **53**: 72–76.

Sharaf K, Horová L, Pavlíček T, Nevo E, Bureš P. 2010. Genome size and base composition in *Oryzaephilus surinamensis* (Coleoptera: Sylvanidae) (Ckleotera: Sylvanidae) and differences between native (feral) and silo pest populations in Israel. *Journal of Stored Products Research* **46**: 34–37.

Sintupachee S, Milne JR, Poonchaisri S, Balañal V, Kittayapong P. 2006. Closely Related *Wolbachia* Strains within the Pumpkin Arthropod Community and the Potential for Horizontal Transmission via the Plant. *Microbial Ecology* **51**: 294–301. DOI: 10.1007/s00248-006-9036-x.

Son Y, Luckhart S, Zhang X, Lieber MJ, Lewis EE. 2008. Effects and implications of antibiotic treatment on *Wolbachia* - infected vine weevil (Coleoptera: Curculionidae). *Agricultural and Forest Entomology* **10**: 147–155. DOI: 10.1111/j.1461-9563.2008.00369.x.

Sontowski R, Bernhard D, Bleidorn C, Schlegel M, Gerth M. 2015. *Wolbachia* distribution in selected beetle taxa characterized by PCR screens and MLST data. *Ecology and Evolution* **5**: 4345–4353. DOI: 10.1002/eec3.1641.

Stenberg P., Lundmark M., 2004. Distribution, mechanisms and evolutionary significance of clonality and polyplody in weevils. *Agricultural and Forest Entomology* **6**: 259–266. DOI: 10.1111/j.1461-9555.2004.00231.x.

Takano SI, Tuda M, Takasu K, Furuya N, Imamura Y, Kim S, Tashiro K, Tavares M, Amaral AC. 2017. Unique clade of alpharetroviral endosymbionts induces complete cytoplasmic incompatibility in the coconut beetle. *Proceedings of National Academy of Sciences USA* **114**: 6110–6115. DOI: 10.1073/pnas.1618094114.

Toju H & Fukatsu T. 2011. Diversity and infection prevalence of endosymbionts in natural populations of the chestnut weevil: Relevance of local climate and host plants. *Molecular Ecology* **20**: 853–868. DOI: 10.1111/j.1365-294X.2010.04980.x.

Toju H, Tanaka K, Saito Y, Sata T, Fukatsu T. 2013. Diversification of endosymbiotic replicons: co-speciation and practicality of bacteriocyte symbionts in weevils. *The ISME Journal* **7**: 1378–1390. DOI: 10.1038/ismej.2013.27.

Tolwinski L, Caldera R, Jovic J, Hernandez-Vera G, Baviera C, Gasman A, Emerson BC. 2015. Host associated genetic divergence and taxonomy in the *Bhimusa pilosa* (Gyllenhal) species complex: an integrative approach. *Systematic Entomology* **40**: 268–287. DOI: 10.1111/syen.12109.

Vega FE, Benavides P, Stuart J, O'Neill SL. 2002. *Wolbachia* infection in the coffee berry borer (Coleoptera: Scolytidae). *Annals of the Entomological Society of America* **95**: 374–378. DOI: 10.1603/0013-8746(2002)95[374:WITTCB]2.0.CO;2.

Weinert LA, Tinsley MC, Temperley M, Jiggins FM. 2007. Are we underestimating the diversity and incidence of insect bacterial symbionts? A case study in ladybird beetles. *Biology Letters* **3**: 678–681. DOI: 10.1098/rsbl.2007.0373.

Werren JH, Windsor D, Guo L. 1995. Distribution of *Wolbachia* among neotropical arthropods. *Proceedings of the Royal Society B: Biological Sciences* **262**: 197–204. DOI: 10.1098/rspb.1995.0196.

Werren JH, Windsor DM. 2000. *Wolbachia* infection frequencies in insects: evidence of a global equilibrium? *Proceedings of the Royal Society B: Biological Sciences* **1450**: 1277–1285. DOI: 10.1098/rspb.2000.1139.

White JA, Richards NK, Laugrand A, Saeed A, Curry MM, McNeill MK. 2015. Endosymbiotic candidates for parasitoid defense in exotic and native New Zealand weevils. *Microbial Ecology* **70**: 274–286. DOI: 10.1007/s00248-014-0561-8.

Xue H-J, Li W-Z, Nie R-E, Yang X-K. 2011. Recent Speciation in Three Closely Related Sympatric Species: Inferences Using Multi-Locus Sequence, Post-Mating Isolation and Endosymbiont Data. *PLoS ONE* **6**: e27834. DOI: 10.1371/journal.pone.0027834.

Yun Y, Peng Y, Liu FX, Lei C. 2011. *Wolbachia* screening in spiders and assessment of horizontal transmission between predator and prey. *Neotropical Entomology* **40**: 164–169. DOI: 10.1590/S1519-566X2011000200002.

Zehori-Fein E, Borad C, Harari AR. 2006. Oogenesis in the date stone beetle, *Coccotrypesdactylipera*, depends on symbiotic bacteria. *Physiological Entomology* **31**: 164–169. DOI: 10.1111/j.1365-3032.2006.00504.x.

Zhang X, Luckhart S, Tu J, Pfeiffer DG. 2010. Analysis of *Wolbachia* strains associated with *Conotrachelus nenuphar* (Coleoptera: Curculionidae) in the eastern United States. *Environmental Entomology* **39**: 396–405. DOI: 10.1603/EN