Reproductive compensation favours male-killing Wolbachia in a live-bearing host

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Wolbachia are maternally inherited, cellular endosymbionts that can enhance their fitness by biasing host sex ratio in favour of females. Male killing (MK) is an extreme form of sex-ratio manipulation that is selectively advantageous if the self-sacrifice of Wolbachia in males increases transmission through females. In live-bearing hosts, females typically produce more embryos than can be carried to term, and reproductive compensation through maternal resource reallocation from dead males to female embryos could increase the number of daughters born to infected females. Here, we report a new strain of MK Wolbachia (wCsc2) in the pseudoscorpion, Cordylochernes scorpioides, and present the first empirical evidence that reproductive compensation favours the killing of males in a viviparous host. Females infected with the wCsc2 strain produced 26 per cent more and significantly larger daughters than tetracycline-cured females. In contrast to the previously described wCsc1 MK Wolbachia strain in G. scorpiones, wCsc2 infection was not accompanied by an increase in the rate of spontaneous brood abortion. Characterization of the wCsc1 and wCsc2 strains by multi-locus sequence typing and by Wolbachia surface protein ( wsp) gene sequencing indicates that the marked divergence between these two MK strains in their impact on host reproductive success, and hence in their potential to spread, has occurred in association with homologous recombination in the wsp gene.

Keywords: Wolbachia; male killing; reproductive compensation; Cordylochernes scorpioides; recombination; viviparity

1. INTRODUCTION

Wolbachia are obligate intracellular bacteria that infect an estimated 66 per cent of insect species (Hilgenboecker et al. 2008), and also occur in nematodes, amphipods, isopods and arachnids (Charlat et al. 2003; Rowley et al. 2004; Zeh et al. 2005; Baldo et al. 2007; Werren et al. 2008). As with other genetic elements present in the cytoplasm of animal cells, these cellular endosymbionts are transmitted to offspring only through eggs, and can therefore enhance their fitness by biasing host sex ratio in favour of females (Cosmides & Tooby 1981). Wolbachia employ diverse mechanisms for manipulating host sex ratio, including feminizing genetic males (Bouchon et al. 1998; Hiroki et al. 2002; Negri et al. 2006) and inducing parthenogenesis (Stouthamer et al. 1993). Alternatively, female bias can be achieved by killing male embryos early in development. Male killing (MK) by Wolbachia has been demonstrated in beetles (Hurst et al. 1999; Fialho & Stevens 2000), butterflies (Hurst et al. 1999; Dyson et al. 2002), fruit flies (Hurst et al. 2000; Dyer & Jaenike 2004) and a single pseudoscorpion species (Zeh et al. 2005; Zeh & Zeh 2006a).

While Wolbachia clearly benefit from feminization or parthenogenesis induction by converting dead-end males into microbe-transmitting females, the fitness gain derived from MK is less apparent. Kin selection theory predicts that MK can be favoured, if Wolbachia lethality in male embryos increases the transmission of clonally related Wolbachia lineages in female siblings (Werren 1987; Hurst 1991). Such fitness compensation may occur in egg-laying hosts through cannibalism, lowered risk of inbreeding or reduced sibling competition for resources (Hurst 1991; Hurst & Majerus 1993). In live-bearing hosts, females typically produce more embryos than can be carried to term. Reproductive compensation, a viviparity-specific form of fitness compensation in which maternal resources are reallocated from dead embryos to viable siblings (Charlesworth 1994), provides a direct, physiological mechanism that could increase the number and/or quality of daughters born to infected females, thereby promoting the spread of MK endosymbionts.

The discovery of an MK strain of Wolbachia in a highly female-biased line of the harlequin beetle-riding pseudoscorpion Cordylochernes scorpioides (henceforth, the wCsc1-infected line; Zeh et al. 2005; Zeh & Zeh 2006a) afforded a unique opportunity to assess the capacity of reproductive compensation to favour MK in a live-bearing host. Unlike most terrestrial arthropods, pseudoscorpions are viviparous, with embryos developing in an external, translucent brood sac overlying the female’s genital aperture (Weygoldt 1969; Zeh & Zeh 2006b). Although wCsc1-infected females that carried broods to term produced 10 per cent more daughters than uninfected females, this reproductive compensation was heavily outweighed by a high rate of spontaneous brood abortion in infected females, thereby limiting the spread of the wCsc1 strain (Zeh & Zeh 2006a).
Here, we report a second strain of MK \textit{Wolbachia} (henceforth, wCsc2) in \textit{C. scorpioides} that can potentially spread through populations by means of reproductive compensation. Using a combination of inheritance studies, antibiotic treatment, early-stage embryo counts and assessment of female reproductive success, we show that the killing of male embryos in wCsc2-infected females significantly increases the number and size of female offspring, relative to those produced by tetracycline-cured females, but does not increase the rate of spontaneous brood abortion. Although wCsc1 and wCsc2 differ extensively in their \textit{wsp} gene sequences, characterization by multi-locus sequence typing (MLST; Baldo et al. 2006b) revealed a close evolutionary relationship between the two strains. Phylogenetic and recombination analyses indicate that the marked divergence between these two MK strains in their impact on host reproductive success, and hence in their potential to proliferate, has occurred in association with homologous recombination in the \textit{wsp} gene of the wCsc2 strain.

2. \textbf{MATERIAL AND METHODS}

(a) \textbf{Pseudoscorpions}

Experimental females were derived from an iso-female line characterized by extremely female-biased sex ratios through four generations in the laboratory. This wCsc2-infected line was established from a field-collected dam that produced 18 females and zero males in the laboratory, following the collection of 174 \textit{C. scorpioides} individuals from the Parque Nacional Soberanía (PNS) in the Republic of Panamá in January 2006. In each generation, the line was maintained at a population size of 250–300 adults by outcrossing wCsc2-infected females from approximately 15 full-sib families to males from a large laboratory population (800–1000 adults per generation), also established from the PNS collections in 2006. These males were randomly selected from approximately 30 full-sib families whose sex ratios were not significantly female biased (\(p > 0.05\)). Four generations of outcrossing to unrelated males resulted in a set of wCsc2-infected, full-sib families that differed substantially in their nuclear genetic backgrounds.

(b) \textbf{Phenotypic and fitness consequences of wCsc2 infection}

(i) \textbf{Tetracycline treatment}

To determine the effect of \textit{Wolbachia} curing on female fecundity (number of early-stage embryos produced), female reproductive success (number of nymphs born) and offspring sex ratio in the wCsc2-infected line, we performed a split-brood experiment in which the first-instar nymphs (protonymphs) produced by each of 13 wCsc2-infected-line females (the parental or P generation) were randomly assigned at birth to either an untreated (control) or a tetracycline-treated rearing regime (for details of rearing methods and tetracycline treatment, see Zeh et al. 2005; Zeh & Zeh 2006a). Dietary supplementation with tetracycline was terminated when the treated offspring (the F1 generation) reached sexual maturity. Four untreated and four treated F1 female offspring from each P-generation female were then mated to males from the laboratory population. To control for the effects of nuclear genetic background across treatments, within-full-sib families, the tetracycline-treated and untreated females were mated to the same set of four males, i.e. males were mated in random order to one untreated female and one treated female.

After mating, \textit{C. scorpioides} females exhibit one of the three possible outcomes: (i) failure to produce a brood of embryos; (ii) production of a brood of embryos but subsequent spontaneous abortion of the entire brood, or (iii) brood production and carrying of embryos to term, with all protonymphs birthing simultaneously. In order to determine whether sex-ratio distortion in the wCsc2-infected line occurs through feminization or MK, we exploited the ‘external womb’ form of viviparity in \textit{C. scorpioides}, and obtained within-female counts of both early-stage embryos produced by and protonymphs born to the F1 females. Broods were permitted to develop to the stage at which individual embryos were first clearly distinguishable (approx. 5 days after mating) before being photographed, using an Olympus SZ60 stereomicroscope equipped with a Ultra 20 digital camera. For this early-stage brood photomicroscopy, each female was gently restrained on her dorsum under a glass slide, and a digital image of the entire brood recorded for subsequent embryo counting, using NIH \textsc{ImageJ} (v. 1.37). Females were then returned to their individual vials for continued monitoring of their reproductive status.

Within 48 h of birth, nymphs were collected from the female’s brood nest and counted. As males and females are indistinguishable as nymphs, we reared 25 protonymphs to the adult stage (the F2 generation) from each of 12 treated and 12 untreated females in order to assess offspring sex ratio in the two treatments. These adult offspring were photographed, again using an Olympus SZ60 stereomicroscope equipped with an Ultra 20 digital camera. NIH \textsc{ImageJ} (v. 1.37) was then used to measure cephalothorax length, the trait most closely correlated with female reproductive success (Newcomer et al. 1999).

To assess the efficacy of tetracycline treatment in curing wCsc2 infection, \textit{Wolbachia}-specific PCR, using the MLST \textit{ftsZ} primer pair (see below), was performed on DNA samples extracted from 12 of the F1 tetracycline-treated dams, as well as both positive and negative controls. We confirmed that the quality of the DNA samples was suitable for amplification by carrying out a second PCR, using a primer pair designed from an approximately 600 bp region of \textit{C. scorpioides} mitochondrial COI gene (GTAGG\textsuperscript{C}\textsuperscript{TTTTGTGCTATAGAA}\textsuperscript{AGTTCTAAAATTTCGATCAGT} \textsuperscript{W AGAAG}).

(ii) \textbf{Test for paternal inheritance of female-biased sex ratio}

To determine whether female-biased sex ratio in the wCsc2-infected line is inherited exclusively through females, surviving males from the untreated feeding regime were mated to females from the laboratory population. From each successful brood, 25 protonymphs were reared to adults to estimate offspring sex ratio.

(iii) \textbf{Statistical analyses}

Tetracycline effects on brood sex ratio, number of early-stage embryos, number of protonymphs, number of female protonymphs produced per F1 female (see below) and the size of adult F2 females were analysed using a general linear mixed model (GLMM) approach, as implemented in PROC GLIMMIX in \textsc{SAS}, v. 9.2 (SAS 2008). Antibiotic treatment was modelled as a fixed effect, with the P-generation dam included as a random effect to avoid pseudoreplication. To control for possible effects of tetracycline treatment on...
female fecundity, the number of early-stage embryos produced by each female was included as a covariate in analyses of the number of protonymphs born and the number of female protonymphs born. The few treated and untreated females that did not produce a brood sac within 45 days of mating were excluded from analyses of early-stage embryo and nymph production because such females never became gravid (Newcomer et al. 1999). To assess the potential for reproductive compensation to enhance Wolbachia transmission through increased embryonic survival of females, we restricted comparison of the number of daughters born (proportion of female adult offspring × number of nymphs born) to untreated and tetracycline-treated dams to only those broods for which we had directly determined offspring sex ratio by rearing 25 nymphs to the adult stage.

(c) Multi-locus sequence typing and wsp gene sequencing of wCsc1 and wCsc2 Wolbachia strains

(i) DNA extraction, polymerase chain reaction and sequencing DNA was extracted from whole individuals, using the Invitrogen Chargeswitch gDNA Micro Tissue Kit, following the manufacturer’s instructions. PCR was carried out, using the standard primers for the five Wolbachia MLST loci, gatB, coxA, hcpA, fisZ and fbpA (Baldo et al. 2006b; http://pubmlst.org/wolbachia/). For PCR amplification of the wsp gene, a conserved primer pair (CTACRTTCGCTT RCAAATACAACG and TTCTGCAACAYATGCTGT AAAS) was designed from the alignment of published wsp sequences from 34 Wolbachia strains (Zeh et al. 2005).

PCR reactions were carried out in a 25 μl volume containing approximately 10 ng of genomic DNA, 2.5 μl of Expand Long Template buffer 2 (Roche), 350 μM dNTPs, 750 nM primers, and 1 U of a 5 : 1 mixture of TITANIUM Taq (ClonTech) and PfX Ultra (Stratagene) DNA polymerases. PCR amplification conditions involved a 1 min hot start at 95°C, followed by 34 iterations of the following cycle: melting at 93°C for 25 s, annealing at 52, 54 or 58°C for 40 s (52°C for gatB, coxA, hcpA, fisZ, 54°C for wsp; 58°C for fbpA) and extension at 68°C for 60 s.

PCR templates were prepared for sequencing by electrophoresing 12 μl of the reaction mixture through a 0.8 per cent agarose gel stained with ethidium bromide. Amplification products were excised from gels and purified with Promega Wizard minicolumns. BigDye reactions (6 μl) containing approximately 100 ng of purified PCR product and 3.2 pmol of PCR primer were sequenced with both forward and reverse PCR primers, using an Applied Biosystems Prism 3730 DNA Analyser. Sequences were edited from the chromatograms using the FinchTV v. 1.4.0 viewer (Geospiza Inc.), and contig sequences were assembled from forward and reverse sequences in Geneious Pro 4.5 (Biomatters Ltd). For both the wCsc1 and wCsc2 strains, stable inheritance of Wolbachia gene sequences was confirmed by sequencing the DNA of at least one individual from each of three generations of the infected C. scorpioidei lines.

(ii) Phylogenetic analyses and tests for recombination DNA sequences of individual MLST genes, the concatenated MLST genes and the wsp gene for each wCsc1 and wCsc2 Wolbachia strains were compared with sequence data for Wolbachia strains infecting 28 other host taxa (see electronic supplementary material, table S1). MLST sequences were obtained from the Wolbachia MLST website (http://pubmlst.org/wolbachia/; Jolley et al. 2004), and we selected only strains for which both MLST and wsp gene sequences were available. Representatives from the A, B, D and F Wolbachia supergroups, including five MK strains from lepidopteran and dipteran hosts, were included in the phylogenetic analyses. Sequences were aligned in Geneious with CLUSTALW (Larkin et al. 2007), and phylogenetic analyses were conducted using maximum parsimony and maximum-likelihood (ML) methods in PAUP v. 4.0b10 (Swofford 2002). For ML, the best-fit evolutionary model for each dataset was determined through AIC likelihood ratio tests, using MODELTEST 3.7 (Posada & Crandall 1998). Comparison of MLST and wsp ML tree topologies was performed using 1000 bootstrap replications of the Shimodaira–Hasegawa (SH) test (Shimodaira & Hasegawa 1999), as implemented in the LSCORES command in PAUP. The SH test involved fitting the MLST- and wsp-derived tree topologies to the MLST dataset to determine whether they were significantly different in their likelihood (−ln L) scores. To facilitate visual comparison of trees, Wolbachia phylograms were rooted with the Brugia malayi Wolbachia sequence (Fenn et al. 2006). It should be noted, however, that the most appropriate taxon for rooting arthropod Wolbachia sequences remains in question (Bordenstein et al. 2009).

Tests for homologous recombination between the 30 Wolbachia strains, that is, recombination involving replacement in a recipient sequence by homologous DNA from a donor genome (Baldo et al. 2006a), were performed with the RECOMBINATION DETECTION Program, v. 3 (Martin et al. 2005b), using the following methods to identify horizontal gene transfer (HGT) events: 3Seq (Boni et al. 2007), Bootscaan (Martin et al. 2005a), Chimaera (Posada & Crandall 2001), GENECONV (Pidam et al. 1999), MaxChi (Maynard Smith 1992), Phylypro (Weiller 1998), RDP (Martin & Rybicki 2000) and SiScan (Gibbs et al. 2000).

(d) Polymerase chain reaction assays for presence of non-Wolbachia male-killing bacteria

To test for possible multiple infections in the wCsc1- and wCsc2-infected lines, we performed PCR assays for non-Wolbachia bacteria known to be associated with MK in other arthropod species (Duron et al. 2008). Using DNA samples that tested positive for wsp and all five MLST loci, PCR reactions were performed with the following primer pairs: R1 and R2 for Richettia sp.; ArsF and ArsR2 for Arsenophonus nasoiae; FlavF and FlavR for Flavobacterium sp.; SpixoF and SpixoR for Spiroplasma isodetis, and SpoulF and SpoulR for Spiroplasma poultonii. The sequences and annealing temperatures for these primer pairs are described in table 2 of Duron et al. (2008).

3. RESULTS

(a) Phenotypic and fitness consequences of wCsc2 infection

(i) Tetracycline treatment

Wolbachia-specific PCR confirmed the efficacy of tetracycline treatment, with all 12 of the tested, treated F1 dams failing to produce an ftsZ amplification product. Untreated (wCsc2-infected) and tetracycline-treated (cured) females did not differ in the proportion that failed to become gravid, spontaneously aborted their entire broods or gave birth to protonymphs (Fisher

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exact test, \( p = 0.825 \)). Dam mortality, exclusion of females that did not become gravid and, in a few cases, failure to obtain an accurate embryo or proonymph count reduced the number of females included in analyses of fecundity and reproductive success to 37 untreated and 41 tetracycline-treated females. After controlling for the effect of female body size by including cephalothorax length as a covariate in the GLMM (\( p < 0.001 \)), tetracycline treatment resulted in a marginally significant reduction in the number of early-stage embryos produced by treated dams (T) compared with untreated controls (C) (\( \bar{x}_T \pm \text{s.e.} = 80.15 \pm 2.45 \), \( \bar{x}_C = 87.64 \pm 2.45 \), \( F_{1,12} = 4.77 \), \( p = 0.05 \)). Despite this slight reduction in fecundity, tetracycline treatment significantly increased female reproductive success. With the number of early-stage embryos included as a covariate (\( F_{1,51} = 21.35 \), \( p < 0.001 \)), treated dams gave birth to a least-squares mean of 53.90 \( \pm \) 2.51 nymphs, compared with 33.42 \( \pm \) 2.64 for untreated females (\( F_{1,12} = 32.11 \), \( p < 0.001 \)). As the rate of spontaneous brood abortion did not differ between treated (8.70%) and \( \nu \)Csc2-infected females (9.52%) (Fisher exact test, \( p = 1.000 \)), the lower reproductive success of the untreated dams was attributable to a higher rate of embryonic mortality in broods that were successfully carried to term (\( \bar{x}_C \) of embryos dying before birth = 56.8 \( \pm \) 2.6\% \( \bar{x}_T = 32.0 \pm 2.5\% \), \( F_{1,22} = 46.52 \), \( p < 0.001 \)).

Tetracycline treatment also restored offspring sex ratio to 1 : 1. In the subset of nymphs reared to the adult stage from 12 untreated and 12 treated females, untreated females produced a highly significant excess of female offspring (paired \( t_4 = 0.864 \), \( p = 0.4363 \)), indicating that female-biased sex ratio in the \( \nu \)Csc2-infected line is not transmitted through males.

(b) Assays for multiple infections in \( \nu \)Csc1 and \( \nu \)Csc2 lines

Within each C. scorpions Wolbachia strain, \( wsp \) and MLST sequences obtained from pseudoscorpion individuals across three matrilineal generations were identical and sequence traces were free of multiple peaks, suggesting infection by a single Wolbachia strain. In addition, PCR tests for the presence of non-Wolbachia MK bacteria (Rickettsia sp., A. nasonium, Flavobacterium sp.; S. ixodetis and S. poulsonii) were all negative.

(c) Multi-locus sequence typing and \( wsp \) gene sequencing of \( \nu \)Csc1 and \( \nu \)Csc2 Wolbachia strains

(i) Phylogenetic affinities of the C. scorpions Wolbachia strains

Bidirectional sequencing yielded nucleotide data ranging from 422 to 478 bp for the five MLST loci. While the \( \nu \)Csc1 and \( \nu \)Csc2 strains are very similar or identical at these loci, with pair-wise identities ranging from 97 to 100 per cent, NCBI BLAST searches revealed that the two C. scorpions strains show considerable divergence from other Wolbachia strains in GenBank. Across the five loci, the sequences with the highest BLAST similarity scores ranged from 89 to 93 per cent identical to the C. scorpions Wolbachia sequences (data not shown). Gene fragments for MLST loci were aligned and trimmed, consistent with sequences recorded in the Wolbachia MLST database, to a length of 369–444 bp, depending on the locus. The loci were combined in order of their location within the \( \nu \)Mel Wolbachia reference genome (\( \text{gatB}–\text{coxA}–\text{hcpA}–\text{fpsZ}–\text{fbpA} \); Baldo et al. 2006b), resulting in a concatenated MLST sequence alignment of 2079 bp. Likelihood and parsimony methods yielded broadly concordant phylogenies, with the \( \nu \)Csc1 and \( \nu \)Csc2 strains clustering as monophyletic sister taxa for all MLST loci. The phylogeny based on concatenated MLST sequences placed the pseudoscorpion Wolbachia clade near the base of the tree, as the sister group to A + B supergroup clades (figure 1). This topology was largely consistent with phylogenies based on individual MLST loci, with the exception of \( \text{coxA} \), which clustered both the pseudoscorpion and F-group clades with supergroup B strains.

For the \( \nu \)sp gene, sequences from the 30 Wolbachia strains were aligned across a 495 bp region. In contrast to MLST loci, \( \nu \)sp sequences from the \( \nu \)Csc1 and \( \nu \)Csc2 strains are highly divergent (uncorrected \( 'p' = 0.200 \)), with the two strains widely separated in the \( \nu \)sp phylogeny (figure 2). As the basal arthropod-infecting strain in this tree, \( \nu \)Csc1 is most similar in its \( \nu \)sp sequence to Wolbachia from B. malayi and Ephesia kuehniella, with uncorrected \( p \) distances of 0.158 and 0.148, respectively. By contrast, the more-derived \( \nu \)Csc2 \( \nu \)sp sequence exhibits the greatest similarity to the Wolbachia strain infecting Telogryllus taitianenma (uncorrected \( p = 0.180 \)). Comparison of the MLST and \( \nu \)sp trees revealed a highly significant difference in their topologies.
the significant recombination events, 13 of which involved the entire dataset, the analyses identified 19 statistically significant recombinant sequence was particularly strong, with the diverged group of seven very similar wsp sequences (A. encedon, A. oklahoma, B. texana, P. sialia, S. invicta, T. taiwanemma and T. confusum).

4. DISCUSSION
To our knowledge, this is the first study to demonstrate empirically that reproductive compensation in a live-bearing host provides a selective advantage to MK by a cellular endosymbiont. Cordylochernes scorpioides females infected with the newly identified wspCsc2 Wolbachia strain gave birth to an average of 20 daughters for every son. This highly female-biased sex ratio was restored to 1 : 1 in cured females and was attributable to the killing of male embryos during development. Infected females suffered no reduction in the number of early-stage embryos produced but gave birth to 38 per cent fewer protonymphs than cured females. MK thus appears to be a highly adaptive strategy of maternal resources from dead male embryos to female siblings. MK thus appears to be a highly adaptive strategy.

(ii) Tests for recombination
For the recombination tests, the wsp sequence was inserted between the ftsZ and fbpA gene fragments in the concatenated MLST sequence for each strain. For the entire dataset, the analyses identified 19 statistically significant recombination events, 13 of which involved the wsp gene. Evidence for the wspCsc2 wsp gene as a recombinant sequence was particularly strong, with the 3Seq, Chimera, MaxChi and RDP algorithms all yielding p-values of <0.001. The single, major parental sequence in the wspCsc2 wsp recombinant was identified as wspCsc1, with minor parental sequences from a highly diverged group of seven very similar wsp sequences (A. encedon, A. oklahoma, B. texana, P. sialia, S. invicta, T. taiwanemma and T. confusum).

Figure 1. Maximum-likelihood phylogram of the 30 Wolbachia strains based on a 2079 bp alignment of the concatenated MLST loci. Wolbachia strains are identified by their host taxon. The single most likely tree was determined using a GTR + G + I model of substitution (−ln L score = 8965.36, tree length = 1233, consistency index = 0.562). Wolbachia strains implicated in MK are indicated by 'MK.' Values at nodes denote per cent support for clades based on 500 bootstrap replicates.

(MLST tree: −ln L score = 8965, wsp tree = 10 696, ln L difference = 1731, SH test, p < 0.001).
male = 0.53), and to the offspring sex ratio of \( wCsc1 \)-infected females cured with tetracycline in a previous study (proportion male = 0.51; Zeh et al. 2005). In addition, survival from the protonymph to the adult stage in the study reported here was high and nearly identical in the control (mean survivorship = 0.86) and tetracycline treatments (mean survivorship = 0.88). As the two treatments differed markedly in sex ratio but not in survivorship, there is essentially no scope for gender-based differences in post-embryonic mortality associated with tetracycline treatment. The finding that population sex ratio deviates only slightly from 1 : 1 is consistent with the results of a published PCR survey (Zeh et al. 2005), indicating low \( Wolbachia \) infection frequency (approx. 10%) in \( C. scorpioides \) from central Panama. Although this previous survey did not distinguish between strain types, preliminary results from a survey currently in progress suggest an overall \( Wolbachia \) infection rate of 8.6 per cent, with the \( wCsc2 \) strain four times as abundant as the \( wCsc1 \) strain (D. W. Zeh 2009, unpublished data).

Phylogenetic analysis of the five MLST loci indicates that \( wCsc2 \) and the previously described \( wCsc1 \) strain from \( C. scorpioides \) (Zeh et al. 2005; Zeh & Zeh 2006a) diverged only recently from a common ancestor. Over the 2063 nucleotides that constitute their MLST concatenated sequences, the two strains exhibit only 14 substitutions. Despite this close evolutionary relationship, \( wCsc1 \) and \( wCsc2 \) differ substantially in their capacity to benefit from reproductive compensation in \( C. scorpioides \) female hosts. While both strains are effective killers of male embryos that bias sex ratio in favour of females, in the \( wCsc1 \) strain, any gain from reproductive compensation in broods carried to term is strongly outweighed by a high rate of spontaneous brood abortion and the resultant overall reduction in the number of daughters born to infected females compared with uninfected controls (Zeh & Zeh 2006a). By contrast, in this study, rate of spontaneous brood abortion among \( wCsc2 \)-infected females was low and unaffected by tetracycline treatment.

Interestingly, this difference between the \( wCsc1 \) and \( wCsc2 \) strains in their impact on female reproductive success in \( C. scorpioides \) is associated with extensive divergence in their \( wsp \) gene sequences, with 112 nucleotide substitutions, several indels and 48 amino acid differences over 521 aligned nucleotides. Phylogenies based on MLST and \( wsp \) gene sequences were topologically highly incongruent, suggesting HGT, a hypothesis that was strongly supported by our recombination detection analyses. Evidence indicates that \( wCsc2 \) \( wsp \) gene is a
mosaic sequence derived from recombination between the wspC1 wsp sequence and the wsp sequence from one or more closely related wsp genes present in Wolbachia strains that infect insects and spiders. The ensemble of seven wsp gene sequences identified as minor parental sequences in the recombinant wspC2 sequence may signify that the true minor parental sequence was not present in the 30 analysed strains but is very similar to the sequences of these seven strains. Phylogenetic and recombination analyses thus indicate that the marked divergence between the wspC1 and wspC2 MAK strains in their impact on host reproductive success, and hence in their potential to proliferate, has occurred in association with homologous recombination in the wsp gene.

Comparative studies of arthropod-infecting Wolbachia strains have revealed the highly chimaeric nature of Wolbachia genomes, with extensive evidence for recombination in wsp (Baldo et al. 2005), as well as within and between housekeeping genes such as gltA, dnaA, fltZ and groEL (Baldo et al. 2006a). Comparative sequencing studies also suggest strong diversity, diversifying selection acting on the wsp locus (Baldo et al. 2005), reflecting a history of antagonistic coevolution between arthropod hosts and their Wolbachia endosymbionts (Jiggins et al. 2002). In C. scorpiorides, it remains to be determined whether wsp recombination is the cause of the reduced rate of spontaneous brood abortion in wspC2-infected females or is simply a diagnostic marker of evolutionary divergence between the wspC1 and wspC2 Wolbachia strains.

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