

COMPLEMENTARY SEX DETERMINATION IN HYMENOPTERAN PARASITOIDS AND ITS IMPLICATIONS FOR BIOLOGICAL CONTROL

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Abstract In haplodiploid Hymenoptera, unfertilized eggs produce haploid males while fertilized eggs lead to diploid females under most circumstances. Diploid males can also be produced from fertilization under a system of sex determination known as complementary sex determination (CSD). Under single-locus CSD, sex is determined by multiple alleles at a single sex locus. Individuals heterozygous at the sex locus are female while hemizygous and homozygous individuals develop as haploid and diploid males, respectively. In multiple-locus CSD, two or more loci, each with two or more alleles, determine sex. Diploid individuals are female if one or more sex loci are heterozygous, while a diploid is male only if homozygous at all sex loci. Diploid males are known to occur in 43 hymenopteran species and single-locus CSD has been demonstrated in 22 of these species. Diploid males are either developmentally inviable or sterile, so their production constitutes a genetic load. Because diploid male production is more likely under inbreeding, CSD is a form of inbreeding depression. It is crucial to preserve the diversity of sex alleles and reduce the loss of genetic variation in biological control. In the parasitoid species with single-locus CSD, certain precautionary procedures can prevent negative effects of single-locus CSD on biological control.

Key words Complementary sex determination (CSD), Hymenoptera, diploid males, biological control

1 INTRODUCTION

Biological control of insect pests and weeds frequently encounters the reduction of genetic diversity during the process of collection, rearing, release and ultimate establishment of natural enemies. This reduction may interfere with the success of classical biological control programs (Mackauer 1976, Unruh *et al.* 1983, Roush 1990, Hopper 1995, Hopper *et al.* 1993, Roush & Hopper 1995, Morjan *et al.* 1999) and contribute partially to failure of some biological control programs.

Parasitic wasps (parasitoids) are widely used as biological control agents. The most common reproduction mode in parasitic hymenopterans is arrhenotoky,

in which males develop from unfertilized, haploid eggs and females develop from fertilized, diploid eggs. Haploid eggs receive a single set of maternal chromosomes; diploid eggs contain two sets of chromosomes, one from each parent. Ovipositing females can determine the sex of their offspring by controlling the release of stored sperm from the spermatheca during reproduction. However, some hymenopterans employ other reproductive modes: deuterotoky and thelytoky. Unfertilized eggs can produce either males or females in deuterotoky, while under thelytoky, unfertilized eggs give rise exclusively to females.

A number of parasitoid species show variation of sex ratios, especially under laboratory conditions.

tions. Thus, efficient economic usage will benefit from an understanding of the inherent sex determination mechanisms in parasitoids (Stouthamer *et al.* 1992, Cook and Crozier 1995). A clear understanding of these complex mechanisms will also shed light on the variation of sex ratios.

The proposed genetic mechanisms of sex determination in Hymenoptera are diverse and complicated (Beukeboom 1995). Four general modes of sex determination have been proposed for the Hymenoptera: complementary sex determination (CSD) (Whiting 1939, 1943, Crozier 1971, 1977), genic balance (Cunha and Kerr 1957), nucleocytoplasmic balance (Crozier 1971), and genomic imprinting sex determination (GISD; Poire *et al.* 1992, Beukeboom 1995, Dobson and Tanouye 1998). CSD has been confirmed in several widely distributed species in Hymenoptera. Under CSD, sex is determined by multiple alleles located at one or more sex determining loci. Individuals that are heterozygous on at least one sex locus develop as diploid females and hemizygous or homozygous individuals develop as haploid or diploid males, respectively (Whiting 1939, 1943, Stouthamer *et al.* 1992, Cook 1993b). The genic balance model hypothesizes that male-determining genes do not have an additive effect, unlike female-determining genes. Under this scenario, diploidy would activate female-determining genes, but not male-determining genes. The nucleocytoplasmic balance model assumes that sex will be determined by a balance between nuclear and cytoplasmic products. The genomic imprinting model relies on a sex-determining locus that binds a product only when it is present in male gametes. The gene turning on the female male pathway is activated by the binding of this product to the sex locus, whereas nonbinding leads to male development. Unfertilized haploid eggs are always male because they arise from female gametes which do not bind product, and fertilized diploid eggs are female because the bound product is intro-

duced with sperm. GISD was proposed as an alternative to CSD for those hymenopterans in which CSD was absent. Some species in Chalcidoidea, Chrysidoidea and Cynipoidea do not exhibit CSD and apparently have some other mechanisms of sex determination (Schmieder and Whiting 1947, Whiting 1960, Skinner and Werren 1980, Luck *et al.* 1992, Cook 1993a, b). Under the hypothesis of GISD (Poire *et al.* 1992, Beukeboom 1995), the paternal vs. maternal development involves different imprints by one or more sex loci. Sex is determined by the sex-specific imprinting of a sex-determining locus (S) binding a product (P) in the eggs or zygotes. Unfertilized eggs containing only maternally derived autosomes with the "maternal imprint" develop as haploid males. Fertilized eggs containing paternally imprinted autosomes and maternally derived autosomes develop as females. However, only *Nasonia vitripennis* has been tested for GISD (Dobson and Tanouye 1998). It is not clear to what extent GISD occurs in other taxa without CSD, and therefore, more tests in a wider scope are required. So far, there is good evidence for single-locus CSD in numerous systems (see table 1), and evidence consistent with genomic printing for *Nasonia vitripennis* (Dobson and Tanouye 1998). For the remainder of hymenopteran species, the mode of sex determination is unknown.

2 COMPLEMENTARY SEX DETERMINATION (CSD)

Two patterns of CSD, single-locus CSD (*s*2CSD) and multiple-locus CSD (*m*2CSD), have been proposed, of which *s*2CSD has been confirmed in numerous species in various hymenopteran taxa. In *s*2CSD, the sex ratio (proportion males) changes abruptly following one generation of inbreeding when mother-son or father-daughter mating is conducted and then stabilizes, while in *m*2CSD, the sex ratios increase gradually with subsequent generations of inbreeding.

Table 1 Diploid males tested in Hymenoptera to date (“+” or “-” indicates the species with or without diploid males, respectively. Higher level classification follows Goulet and Huber 1993, Whitfield 1998).

Taxon	Occurrence of diploid males	Explanation	Reference
Suborder Symphyta			
Tenthredinoidea			
Tenthredinidae			
<i>Athalia rosae</i>	+	s/CSD	Naito and Suzuki 1991
<i>Neodiprion nigroscutum</i>	+	s/CSD	Smith and Wallace 1971
<i>Neodiprion pinetum</i>	+	s/CSD ?	Stouthamer <i>et al.</i> 1992
Suborder Apocrita			
Infraorder Parasitica			
Ichneumonoidea			
Braconidae			
<i>Aphidius colemani</i>	+ ?	s/CSD	Ode <i>et al.</i> (unpublished data)
<i>Cotesia rubecula</i>	+	s/CSD	Stouthamer <i>et al.</i> 1992
<i>Habrobracon hebetor</i>	+	s/CSD	Inaba, 1939, Whiting 1961
<i>Habrobracon</i> sp. near <i>hebetor</i>	+	s/CSD	Holloway <i>et al.</i> 1999
<i>Habrobracon serinopae</i>	+	s/CSD	Clark and Rubin 1961, Clark <i>et al.</i> 1963
<i>Heterospilus prosopidis</i>	-		Wu <i>et al.</i> (unpublished data)
<i>Microplitis croceipes</i>	+	s/CSD	Steiner and Teig 1989
Ichneumonidae			
<i>Bathyplectus curculionis</i>	+	s/CSD ?	Unruh <i>et al.</i> 1984
<i>Diadegma amillata</i>	+	s/CSD	Butcher <i>et al.</i> 2000b
<i>Diadegma chrysostictos</i>	+	s/CSD	Butcher <i>et al.</i> 2000a
<i>Diadegma eucerophaga</i>	+	s/CSD	Butcher <i>et al.</i> 2000b
<i>Diadegma fabricianae</i>	+	s/CSD	Butcher <i>et al.</i> 2000b
<i>Diadegma fenestralis</i>	+	s/CSD	Butcher <i>et al.</i> 2000b
<i>Diadegma insulare</i>	+	s/CSD	Butcher <i>et al.</i> 2000b
<i>Diadegma semiclausum</i>	+	s/CSD	Butcher <i>et al.</i> 2000b, Noda 2000
<i>Diadromus pulchellus</i>	+	s/CSD	Hedderwick <i>et al.</i> 1985, Periquet <i>et al.</i> 1993
<i>Venturia canescens</i>	+	s/CSD	Beukeboom 2001
Chalcidoidea			
Eulophidae			
<i>Melittobia chalybii</i>	-		Schmieder 1938
<i>Melittobia</i> spp.	-		Schmieder and Whiting 1947, Whiting 1947
Pteromalidae			
<i>Dinamus vagabundus</i>	-		Rojas-Rousse <i>et al.</i> 1988
<i>Muscidifurax raptor</i>	-		Legner 1979, Fabritius 1984
<i>Muscidifurax zaraptor</i>	-		Legner 1979

(to be continued on next page)

(continued)

Taxon	Occurrence of diploid males	Explanation	Reference
<i>Nasonia vitripennis</i>	+	Mutation	Whiting 1960, Skinner and Werren 1980, Dobson and Tanouye 1998
<i>Pteromalus puparum</i>	-		Whiting 1940
Cynipoidea			
Cynipidae			
<i>Cothonaspis bouardi</i>	-		Biemont and Bouletreau 1980
<i>Diplolepis rosea</i>	+	Gamete duplication	Stille and Davring 1980
<i>Leptopilina heterotoma</i>	-		Hey and Cargiulo 1985
Proctotrupoidea			
Scelionidae			
<i>Telonomus fariai</i>	-		Dreyfus and Breuer 1944, Cook 1993b
Infraorder Aculeata			
Apoidea			
Apidae			
<i>Apis cerana</i>	+	<i>sl2CSD</i>	Woyke 1979, Hoshiba <i>et al.</i> 1981
<i>Apis mellifera</i>	+	<i>sl2CSD</i>	Mackensen 1951, Woyke 1963, 1965
<i>Augochlorella striata</i>	+	<i>sl2CSD</i>	Parker and Owen 1990, Mueller 1993
<i>Bombus atratus</i>	+	<i>sl2CSD</i>	Garofalo 1973, Garofalo and Kerr 1975
<i>Lasioglossum zephyrum</i>	+	<i>sl2CSD</i> ?	Kukuk and May 1990
<i>Melipona compressipes</i>	+	<i>sl2CSD</i> ?	Kerr 1987
<i>Melipona quadrifasciata</i>	+	<i>sl2CSD</i>	de Camargo 1979
<i>Melipona scutellaris</i>	+	<i>sl2CSD</i>	Carvalho <i>et al.</i> 1995
<i>Trigona quadrangular</i>	+	<i>sl2CSD</i> ?	Cook 1993b
Chrysoidea			
Bethylidae			
<i>Goniozus nephantidis</i>	-		Cook 1993a
Vespoidea			
Formicidae			
<i>Doronomymex kutteri</i>	+	<i>sl2CSD</i> ?	Cook 1993b
<i>Epimyma stumperti</i>	+	<i>sl2CSD</i> ?	Cook 1993b
<i>Formica aquilonia</i>	+	<i>sl2CSD</i> ?	Cook 1993b
<i>Formica pressilabris</i>	+	<i>sl2CSD</i> ?	Pamilo and Rosengren 1984
<i>Harpagoxenus sublaevis</i>	+	<i>sl2CSD</i> ?	Cook 1993b
<i>Lasius alienus</i>	+	<i>sl2CSD</i> ?	Pearson, 1983
<i>Leptothorax muscorum</i>	+	<i>sl2CSD</i> ?	Loiselle <i>et al.</i> 1990
<i>Pseudolasius</i> sp. near <i>emeryi</i>	+	<i>sl2CSD</i> ?	Hung <i>et al.</i> 1972
<i>Rhytidoponera chalybaea</i>	+	<i>sl2CSD</i> ?	Ward 1980
<i>Rhytidoponera confusa</i>	+	<i>sl2CSD</i> ?	Ward 1980
<i>Solenopsis invicta</i>	+	<i>sl2CSD</i> ?	Hung <i>et al.</i> 1972, 1974
Vespidae			
<i>Liostenogaster flavolineata</i>	+	<i>sl2CSD</i> ?	Cook 1993b
<i>Mischocyttarus immarginatus</i>	+	<i>sl2CSD</i> ?	Queller <i>et al.</i> 1992

Note: The question marks indicate the data are not conclusive.

211 Single-locus CSD (s1CSD)

Single-locus CSD was first proposed in the braconid wasp *Habrobracon* (= *Bracon*) *hebetor* by Whiting (1939, 1943). In s1CSD, sex is determined by multiple alleles at a single locus. Haploid (hemizygous) individuals are male with only one allele at the sex locus. Diploid individuals can be either homozygous or heterozygous at the sex locus. Individuals heterozygous at sex locus are females while homozygous individuals develop as diploid males (Cook and Crozier 1995).

There are three mating modes under s1CSD: unmatched mating, matched mating, and diploid male mating (Cook 1993b). In unmatched matings, females and haploid males do not share a sex allele and all diploid offspring are females. In matched matings, a female mates with a haploid male that carries a sex allele identical with one of her own, and 50% of diploid offspring are diploid males (Cook and Crozier 1995). In species, e. g. *Athalia rosae* and *Neodiprion nigroscutum*, which produce viable diploid males, diploid males frequently have difficulty in mating to females because of their bigger body size and incapability of inseminating females (Smith and Wallace 1971, Naito and Suzuki 1991). However, matings between female and diploid males may occur as well (*Diadromus pulchellus*; El Agoze and Periquet 1993, El Agoze *et al.* 1994). In this case, females have a lower fecundity compared to other females mated to diploid males or to virgin females. Only haploid sons are produced due to the failure of insemination by diploid sperm and the functional virginity of mated females, or if diploid males are successful in inseminating diploid females, the resultant offspring will be haploid males (e. g. *D. pulchellus*; El Agoze *et al.* 1994) or sterile triploids (e. g. *Athalia rosae*, Naito and Suzuki 1991; Stouthamer *et al.* 1992).

212 Multiple-locus CSD (m1CSD)

Crozier (1971) proposed single-locus CSD as a special case of multiple-locus CSD, in which sex is determined by multiple loci each with multiple alleles. Diploids are female if one or more sex loci

are heterozygous, whereas diploid individuals are male only if homozygous at all loci. Inbreeding leads to the production of diploid males but more gradually with continual generations of inbreeding under m1CSD than under s1CSD. Single-locus CSD can be tested by one inbreeding generation compared to outcross families, while more generations of inbreeding are required to test m1CSD. The number of sex loci can be estimated by the generations of sibmating required to cause diploid male production (Cook 1993a). Nevertheless, m1CSD has not been demonstrated in any species and therefore remains a hypothetical possibility.

3 HYMENOPTERAN SPECIES WITH DIPLOID MALES

Since the presence of diploid males was first discovered in *Habrobracon hebetor* by Whiting and Whiting (1925), diploid males have been reported from about 43 species in six out of eight hymenopteran superfamilies tested, and s1CSD was confirmed in at least 22 of these species (Stouthamer *et al.* 1992, Cook 1993b, Periquet *et al.* 1993, Cook and Crozier 1995, Butcher *et al.* 2000a, b, Beukeboom 2001) (see table 1). The diploid males in *Nasonia vitripennis* (Chalcidoidea) and *Diplolepis rosea* (Cynipoidea) were caused by mutation and gamete duplication respectively, not from inbreeding, and thus, cannot be attributed to CSD (Table 1). The s1CSD and m1CSD models have been explicitly tested only in *Nasonia vitripennis* (Skinner and Werren 1980), *Goniozus nephantidis* (Cook 1993a), *Diadromus pulchellus* (Periquet *et al.* 1993), and *Aphidius colemani* (Ode *et al.* unpublished data), but these four species were shown not to conform to m1CSD. However, m1CSD cannot be excluded from the Hymenoptera based on current evidence, because some biases may exist against detection of m1CSD, such as lethality of males homozygous at some of these loci (Cook 1993b). Another question is whether m1CSD can be excluded in species for which s1CSD exists. Only *Habrobracon hebetor* (= *juglandis*) (Whiting 1943), *Diadromus pulchellus* (Periquet

et al. 1993) and *Solenopsis invicta* (Ross and Fletcher 1985) have thus far been specifically examined, and *ml2CSD* was refuted in these three species.

Beukeboom *et al.* (2000) excluded *sl2CSD* from two braconid species, *Asobara tabida* and *Al2ysia manducator* based on the comparison of brood size and sex ratio between inbred and outbred families. But it is unknown whether there is *ml2CSD* in these two species without further testing even though their evidence shows no *sl2CSD* in these two species. It would be particularly interesting if further examination on *ml2CSD* is conducted, since *sl2CSD* is hypothesized to be ubiquitous in the superfamily Ichneumonoidea (containing families Braconidae and Ichneumonidae), a sister group of Aculeata, and these two braconid species are the first cases in this superfamily where *sl2CSD* is absent. Our strictly designed inbreeding test of CSD in another braconid species, *Heterospilus prosopidis*, showed that both *sl2* and *ml2CSDs* are absent from this species (Wu *et al.* unpublished data). No diploid males were observed, and the comparison of offspring size, sex ratio or proportion of all-male families between inbreeding and outbred lines over 13 consecutive generations did not conform to expectations under CSD.

Male-biased sex ratios were apparently not found in response to prolonged inbreeding in several species that presumably sib-mate in nature (Stouthamer *et al.* 1992), and CSD can be ruled out in these taxa (e. g., superfamilies Chalcidoidea, Chryridoidea, Cynipoidea and Proctotrupoidea) (Table 1). Based on theoretical and experimental evidence, *sl2CSD* seems unlikely to be present in those highly inbreeding species with female-biased sex ratios (Stouthamer *et al.* 1992, Cook 1993c) since CSD will lead to the production of diploid males and male-biased sex ratio under inbreeding systems.

4 DETECTION OF CSD AND DIPLOID MALES

Two methods can be used to identify CSD.

First, inbreeding effects on sex ratio and developmental mortality can be compared between inbred and outbred families. In inbred lines, mother-son matings can be set up by allowing virgin females to oviposit and mate to their haploid sons when they reach adulthood. If it is difficult to keep mothers alive long enough to mate with their sons, brother-sister crosses can be used instead. In this case, more inbreeding generations may be required to test CSD compared with the test initiated by mother-son mating because only one half of the matings are expected to be matched. Sex ratios (proportion males) produced by inbred females are expected to be higher than that produced by outbred females if CSD is operating. If started with a mother and son mating, 10 consecutive generations of sib-mating will be enough to detect a system of involving at least 15 independent loci (Cook 1993a).

In *sl2CSD*, the use of controlled matings between relatives permits easy and rapid quantitative predictions. For example, broods with no diploid males and broods with equal numbers of females and diploid males should be equally common following sib-matings if their parents did not share a sex allele. The diploid offspring of any mother and son mating should be 50% male. Furthermore, diploid males will be expected from any mating between females and their haploid male brothers from a brood that contains diploid males (Cook 1993b).

Inbreeding should increase diploid male production because it increases the incidence of matched mating and homozygosity. Diploid males produce diploid sperm and are effectively sterile, imposing a genetic load on the population (Cook and Crozier 1995). These diploid males are either inviable resulting in offspring mortality, or sterile if they reach adulthood. The survival of diploid males is rather common (Woyke 1962, 1969, Petters and Mettus 1980, de Camargo 1982, Kukuk and May 1990, El Agoze and Periquet 1993, Duchateau *et al.* 1994, Holloway *et al.* 1999, Beukeboom 2001) and diploid males are often capable of mating as well (El Agoze *et al.* 1994, Holloway *et al.* 1999). For instance, diploid males of *Diadromus*

pulchellus have normal viability, produce diploid sperm and are able to inseminate, but the resulting offspring are haploid sons due to the sterility of diploid males (El Agoze and Periquet 1993, El Agoze *et al.* 1994).

Second, the presence of CSD will be supported by the finding that diploid males are produced. Diploid males can be identified using the following methods: (1) Paternal inheritance of genetic markers, including visible genetic markers and dominant and codominant molecular markers. Visible recessive markers were used frequently to identify diploid males (Inaba 1939, Risman 1942, Whiting 1943, Grosch 1945, Whiting 1961, Holloway *et al.* 1999). All haploid male offspring have the recessive marker of their mother, whereas the diploid male offspring also have the dominant phenotype of their father. Diploid males can be recognized in crosses where females homozygous for a recessive marker are mated with males of dominant wild type. Diploid males can also be detected by the presence of two variants of one enzyme system using electrophoresis (Hung *et al.* 1972, Unruh *et al.* 1984, Hedderwick *et al.* 1985, Steiner and Teig 1989, Hunt and Page 1994, Noda 2000, Butcher *et al.* 2000a, Beukeboom 2001). Polymorphic RAPD PCR loci can also be used to assign paternity in male offspring (Hunt and Page 1994, Holloway *et al.* 1999, 2000). (2) Cytology, karyotyping of pupal or adult testes tissues can be used to directly identify diploid males (Naito and Suzuki 1991). (3) DNA quantitation. Butcher *et al.* (2000 a, b) used flow cytometry technique to compare the DNA content of single cell brain neuron between haploids and diploids. (4) Male size dimorphism (Inaba 1939, Grosch 1945, Smith and Wallace 1971, ChaudNetto 1975, Ross and Fletcher 1985, Naito and Suzuki 1991, Periquet *et al.* 1993). In some species, diploid males have larger cells and are bigger than haploid males. For example, diploid males of *Habrobracon hebetor* can be recognized by their larger cell size, as measured by hair density on the wings (Whiting 1943). Cell size of diploid male is larger than that of haploid male or diploid

female and this has been suggested as an explanation for the differential mortality of diploid males (Grosch 1945).

However, the above four methods cannot be applied to all hymenopteran species with diploid males, because diploid males may die during development or adult body size and coloration may be greatly dependent on the host species and rearing temperature (Fisher 1959, Butcher *et al.* 2000b). Butcher *et al.* (2000b) found that even wing hair density is also unreliable due to the overlap in the size distribution. Furthermore, Butcher *et al.* (2000a, b) were skeptical about the reliability of morphological characteristics for haploid/diploid discrimination, and suggested using flow cytometric neuronal cell DNA analysis to identify diploid males, since this DNA analysis can easily discriminate haploid and diploid individuals, and neuronal cell DNA content is not related to temperature or host status.

5 CSD AND EVOLUTION OF SEX DETERMINATION MECHANISMS

The wide distribution of CSD in the suborders Symphyta and Apocrita and in the infraorders Aculeata and Parasitica suggests that this form of sex determination may be ancestral in Hymenoptera (Cook 1993a, b). Butcher *et al.* (2000b) also supported the hypothesis that *sl2CSD* is the ancestral sex determination mechanism in Hymenoptera (Aculeata/Pichneumonoidea), in which Ichneumonoidea is recently considered by molecular evidences as a sister group of Aculeata (Whitfield 1998). However, our finding of absence of CSD in *Heterospilus prosopidis* raises an open question to this hypothesis, due to the relatively ancestral/basal phylogenetic status of the subfamily Doryctinae (in which *H. prosopidis* is located) in the family Braconidae (van Achterberg 1984). A plausible explanation of the absence of CSD in this primitive species might be that other unknown sex determining mechanism evolves and substitutes CSD.

Bull (1981) suggested that *sl2CSD* might be ancestral to *ml2CSD*. Periquet *et al.* (1993) noted

that multi-locus CSD might evolve from *s*2CSD by tandem duplication of the sex locus closely linked on a chromosome, followed by dispersion of the repeated genes to other chromosomes. Other sex determining systems might be derived from CSD over time with the eventual loss of CSD. For naturally inbreeding species, sex determination mechanisms other than CSD will be expected to avoid the production of diploid males. A more complete understanding of the sex determination systems present in the Hymenoptera requires further tests in other superfamilies.

Relative to *s*2CSD, all of the proposed sex determination modes decrease or eliminate the production of diploid males and may therefore especially advantageous at low population densities, where sex alleles diversity may be low. Selection for sex determination mechanisms other than *s*2CSD may be stronger in parasitoid species that typically or periodically persist at low population densities. Therefore, the quest to find species exhibiting *m*2CSD or any modes of sex determination other than *s*2CSD might be focused by looking at the parasitoid complexes of cyclic defoliators such as the gypsy moth, populations of which can remain at very low levels for many years, then reach outbreak levels in a relatively short time (Elkinton and Liebhold 1990).

6 CSD AND BIOLOGICAL CONTROL

Diploid male production poses a potential threat to the success of biological control attempts using parasitoids. The occurrence of diploid males in a population reduces the potential growth rate of populations because some fertilized eggs become diploid male eggs that either die during development or become sterile males when they reach adulthood. In matched matings under *s*2CSD, 50% of fertilized eggs will develop as diploid males or die during development. CSD therefore increases the apparent sex ratio (proportion males). The production of diploid males is equivalent to increased mortality of females, and therefore is unfavorable for biological control. High ratio of males (i. e., less female in

dividuals) in a population has a strong, negative influence on the population growth, because only few males produce offspring and effectively contribute to the suppression of insect pests.

Allelic diversity at the sex locus and mating patterns of parasitic wasps will determine heterozygosity at the sex locus (Ross *et al.* 1993) and the population growth rate (Stouthamer *et al.* 1992). Large populations likely harbor more sex alleles and consequently decrease the probability of diploid male production. Estimates of the number of sex alleles in natural populations lie between 3 and 86 (Table 2). Limited initial field collections, genetic drift, inbreeding, population crashes in mass rearing or other population bottlenecks may facilitate loss of sex alleles and reduction of genetic diversity (Unruh *et al.* 1984), and might even result in a population with only two sex alleles at a single locus (Cook 1993a). Petters and Mettus (1980) suspected that many laboratory populations of *Habrobracon hebetor* might be in this state. Predictions based on *s*2CSD, i. e., an increasing frequency of all-male families in the offspring of laboratory populations and a low establishment rate of populations released as biological control agents, occurs in the families Braconidae and Ichneumonidae but not in some other parasitoid taxa (Stouthamer *et al.* 1992, Hopper 1995), e. g., the chalcidoids.

In response to these potential problems present in the practice of biological control, Stouthamer *et al.* (1992) proposed two solutions to overcome the loss of sex alleles during the laboratory augmentation: maintaining the parasitic wasps as a large population or keeping the wasps as a large number of isolated subpopulations (inbred lines). The first strategy reduces the rate at which sex alleles are lost, and the second strategy results in many alleles being lost in each subpopulation, but at least two sex alleles are retained per subpopulation that exists (e. g. Whiting 1943, Petters and Mettus 1980, Cook 1993c). However, Stouthamer *et al.* (1992) also pointed out there is a potential threat by CSD due to the population extinction caused by the production of diploid males and their matings with few

Table 2 Estimated number of sex alleles in Hymenoptera.

Species	Estimated sex alleles number	References
<i>Apis mellifera</i>	19	Adams <i>et al.</i> 1977
<i>Bombus terrestris</i>	24 - 46	Dutchateau <i>et al.</i> 1994
<i>Habrobracon hebetor</i>	9 - 20	Whiting 1943 , Heimpel <i>et al.</i> 1999
<i>Diadegma armillata</i>	17 - 19	Butcher <i>et al.</i> 2000b
<i>Diadegma chrysosctictos</i>	17 - 19	Butcher <i>et al.</i> 2000a
<i>Diadegma eucerophaga</i>	7 - 10	Butcher <i>et al.</i> 2000b
<i>Diadegma fabricianae</i>	14 - 15	Butcher <i>et al.</i> 2000b
<i>Diadegma fenestralis</i>	4 - 6	Butcher <i>et al.</i> 2000b
<i>Diadegma insulare</i>	4 - 6	Butcher <i>et al.</i> 2000b
<i>Diadegma semiclausum</i>	4 - 6	Butcher <i>et al.</i> 2000b
<i>Diadromus pulchellus</i>	15	Periquet <i>et al.</i> 1993
<i>Lasioglossum zephyrum</i>	10 - 25	Kukuk and May 1990
<i>Melipona compressipes</i>	20	Kerr 1987
<i>Melipona scutellaris</i>	7 - 36	Carvalho 2001
<i>Neodiprion nigroscutum</i>	3	Smith and Wallace 1971
<i>Solenopsis invicta</i>	15 - 86	Ross and Fletcher 1985 , Ross <i>et al.</i> 1993

males, if the second strategy is employed. Cook (1993c) argued that inbred lines under CSD can be maintained without population crash provided that the populations are reared in large enough colonies to avoid extinction, and stated that inbred lines may be used as an additional resources of sex alleles to a single large population, not just as an alternative suggested by Stouthamer *et al.* (1992). Maintenance of genetic diversity by maintenance of multiple isofemale lines has been confirmed for insects in general by Roush and Hopper (1995).

Combining samples from different geographic regions may increase the sex alleles, provided that wasps from different geographical origins do not show crossing incompatibility. The success of established populations with few sex alleles can be enhanced by importing and releasing additional wasps from other populations (Stouthamer *et al.* 1992). Cook and Crozier (1995) stated that taking a good initial sampling of natural allelic diversity and minimizing loss of genetic variation in the rearing and release will be more practical for a biological control

program. Keeping large populations, maintaining multiple inbred lines, reducing between-family variance in offspring production and avoiding population crashes are very important practices.

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膜翅目寄生蜂的互补性别决定机制及其在生防上的意义

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在膜翅目中,未受精卵形成单倍体的雄蜂,而在大多数情况下受精卵将产生双倍体的雌蜂。但是,因互补性别决定机制(CSD)的作用,受精卵有时也会产生双倍体雄蜂。这种性别决定机制包括单位点的CSD和多位点的CSD。在单位点的CSD作用下,唯一的一个性位点上的多个等位基因决定后代个体的性别。性位点上杂合的个体将是雌性,半合或同型结合的个体将分别形成单倍体或双倍体的雄性。在多位点的CSD作用下,两个或两个以上的性位点控制后代的性别,每个性位点上包含两个或两个以上的等位基因。如果一个或一个以上的性位点是杂合的,形成的双倍体后代都是雌性的,但若是所有的性位点都为同型合子,则将产生双倍体的雄蜂。在膜翅目中,目前已知43种具有双倍体雄蜂,其中22种发现存在单位点的CSD,但是多位点的CSD还有待于确认。双倍体的雄性个体或者不能存活,或者不育,这样的个体形成将对寄生蜂种群的增长带来一定的遗传负担。在生物防治上,保护寄生蜂种群的性等位基因的多样性及减少其遗传多样性的损失极其重要。如果利用具有单位点CSD的种类,采取一定的措施将可避免由于双倍体雄性的形成所带来的负面影响。

关键词 互补性别决定(CSD) 膜翅目 二倍体雄性 生物防治