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Assessment of genetic markers for the determination of \textit{Coptotermes formosanus} × \textit{Coptotermes gestroi} (Isoptera: Rhinotermitidae) F1 hybrids

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The Formosan subterranean termite \textit{Coptotermes formosanus} Shiraki and the Asian subterranean termite \textit{Coptotermes gestroi} (Wasmann) (Isoptera: Rhinotermitidae) are 2 of the most invasive subterranean termite species in the world (Evans et al. 2013; Chouvenc et al. 2016a). These species are allopatric in their native area, but their distributions now overlap in a few locations with a subtropical climate, including Taiwan, Hawaii, Hainan, and south Florida (Grace 2014; Cao & Su 2015). Although both species are genetically distinct and the 2 lineages evolved independently for approximately 18 million yr (Bourguignon et al. 2015), it was recently shown that they had the potential for hybridization in Florida (Chouvenc et al. 2015). Interspecies mating between alates of both species was observed in the field in 2013, 2014, 2015, 2016, and 2017, and incipient F1 colonies were successfully established in the laboratory (T. Chouvenc, University of Florida, Institute of Food and Agricultural Sciences, Ft. Lauderdale Research and Education Center, Ft. Lauderdale, Florida). However, it is unknown if such F1 hybrids are established in the field, primarily because subterranean termites have a cryptic nest and the soldier morphology is highly conserved within the group (Scheffrahn & Su 2005), preventing rapid detection and identification from field samples.

These species have been introduced into Florida (1980–1990s), and we suspected that the potential for hybridization may have been limited to the past few years because the geographical overlap was first recorded in 2005 (Chouvenc et al. 2016b) and the first simultaneous dispersal flight was recorded in 2013. Currently, there are no reliable morphological markers to identify hybrids. Therefore, genetic markers that would allow for testing the potential hybridization in the field are needed. \textit{Coptotermes} colonies mature 8 yr after initial foundation (Chouvenc & Su 2014), which implies that the detection of field F1 hybrid colonies may only be possible years after the initial interspecies mating, and it may take decades before F2 may be recorded, if ever produced.

Gene flow among populations can be detected using microsatellite markers to determine if introgression events occurred in the past (Gaggiotti et al. 1999). The use of nuclear markers provides insight about the mating structures within a population that mitochondrial markers cannot, because the latter only provide information on maternal lineages. Creating a genetic library of nuclear markers for both \textit{C. gestroi} and \textit{C. formosanus} at overlapping locations would provide the background genetic information required to test for the detection of F1 hybrids as a diagnostic tool, with an initial emphasis on south Florida populations, the only location where interspecies mating was confirmed. However, the different genetic makeup of the 2 parental species implies that the nuclear markers used for genetic determination must be compatible for both species and their hybrids. Over the past few years, several studies have developed microsatellite primers to investigate genetic population structures of various \textit{Coptotermes} species (Thompson et al. 2000; Vargo & Henderson 2000; Yeap et al. 2011; Liu et al. 2012) but it is unknown if a marker developed for one species would be compatible with another species and their potential hybrids.

We screened 42 microsatellite primers previously developed for \textit{Coptotermes} and obtained a list of nuclear markers that can be used interchangeably among F1 individuals resulting from all mating combinations. Alates of \textit{C. formosanus} and \textit{C. gestroi} were collected during simultaneous swarming events in 2014 in Ft. Lauderdale, Florida. Pairings of males and females were placed in individual rearing units as described in Chouvenc et al. (2014), and all mating combinations were used for the establishment of incipient colonies: conspecific colonies (♀\textit{C. gestroi} × ♂\textit{C. gestroi}, ♀\textit{C. formosanus} × ♂\textit{C. formosanus}), and heterospecific colonies (♀\textit{C. gestroi} × ♂\textit{C. formosanus}, ♀\textit{C. formosanus} × ♂\textit{C. gestroi}). After 1 yr of rearing and colony growth in the laboratory, 5 workers from 5 colonies of each mating combination were sampled and processed for DNA extraction, as described in Chouvenc et al. (2015). In addition, 12 field samples from each parental species collected throughout south Florida were added to our laboratory samples to confirm that the alleles identified from our laboratory colonies matches the genetic diversity in the field.

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All 42 microsatellite primers were tested and optimized for PCR amplification from 4 original studies (Thompson et al. 2000; Vargo & Henderson 2000; Yeap et al. 2011; Liu et al. 2012). The primers were subjected to a series of gradient polymerase chain reaction (PCRs) to determine the best annealing temperature that would amplify products from both Coptotermes species as well as their respective hybrids. The PCRs were comprised of standard Taq buffer (New England Biolabs, Inc., Ipswich, Massachusetts), 1.25 U Taq DNA polymerase (New England Biolabs, Inc., Ipswich, Massachusetts), 200 mM each dNTP, 0.4 µM each primer, 2 µL of template DNA, and sterile molecular grade water to a final reaction volume of 50 µL. The microsatellite loci were amplified with either Mastercycler Gradient Thermocycler (Eppendorf North America, Hauppauge, New York) or Arktik Thermocycler (Thermo Fisher Scientific, Inc., Waltham, Massachusetts) using the following cycling conditions: initial denaturation step at 95 °C (90 s), followed by 34 cycles at 95 °C (30 s), annealing at 53 °C to 61.4 °C (60 s), 72 °C (2 min), and a final extension at 72 °C (8 min). Amplification products (5 µL) were separated on an 8% polyacrylamide gel using electrophoresis, stained with ethidium bromide and visualized using UV illumination.

Upon analysis, 6 primer pairs successfully provided polymorphic alleles for genotyping individuals from the 2 Coptotermes species and their F1 hybrids where the allele size was different in each parental species but expressed jointly in F1 hybrids. The forward primers of all 6 markers are summarized in Table 1.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Reference</th>
<th>Primer sequence</th>
<th>Motif</th>
<th>T_a (°C)</th>
<th>Target Qubit (ng/µL)</th>
<th>Allele size (bp) C. gestroi</th>
<th>Allele size (bp) C. formosanus</th>
</tr>
</thead>
<tbody>
<tr>
<td>CopF6</td>
<td>Liu et al. 2012</td>
<td>F: CAGTGGCAGCGAGTATA R: ATCTGGAGTGCTCAGAGGC</td>
<td>(AC)_5, (AC)_5</td>
<td>56.9</td>
<td>1.5</td>
<td>168, 174</td>
<td>176, 184</td>
</tr>
<tr>
<td>CopF14</td>
<td>Liu et al. 2012</td>
<td>F: CTACAAGGCTACCATGGGAGGAGGACGAT</td>
<td>(CT)_5</td>
<td>55.0</td>
<td>0.7</td>
<td>194</td>
<td>208, 226</td>
</tr>
<tr>
<td>CopF10</td>
<td>Liu et al. 2012</td>
<td>F: AGGTGTGTAAGGCTGTT G: CACAGCTGCGACAAAGT</td>
<td>(AC)_5</td>
<td>61.4</td>
<td>1.5</td>
<td>302</td>
<td>326</td>
</tr>
<tr>
<td>Cg33</td>
<td>Yeap et al. 2011</td>
<td>F: TTTCATCGAAAGTCCAGTGT G: TGTCGATGAGGAAGATGCT</td>
<td>(CATAA)_5</td>
<td>56.0</td>
<td>1.5</td>
<td>202, 205, 208, 211</td>
<td>193</td>
</tr>
<tr>
<td>CF10-4</td>
<td>Vargo &amp; Henderson 2000</td>
<td>F: GGCATGTGGACGTGAAAAA R: TCAAATGCTGCTCGAGTCATGG</td>
<td>(AGT)_5</td>
<td>61.4</td>
<td>3.0</td>
<td>162, 165, 168, 171</td>
<td>126, 150, 153</td>
</tr>
<tr>
<td>Clac1</td>
<td>Thompson et al. 2000</td>
<td>F: CAGAGTGACATCGAAATG R: GCACATAACAGTAAACCTGCTG</td>
<td>(AGA)AA(AGA)</td>
<td>53.0</td>
<td>1.5</td>
<td>186, 172, 175</td>
<td>191</td>
</tr>
</tbody>
</table>

Allele sizes displayed represent observed values from 12 specimens from each species collected in south Florida.

* F = forward primer, R = reverse primer
* T_a = annealing temperature

This study investigated nuclear markers in Coptotermes formosanus Shiraki and Coptotermes gestroi (Wasmann) (Isoperta: Rhinotermitidae) that can be used as a diagnostic tool to detect F1 hybrids from field samples. Six microsatellite markers were compatible for both parental species and hybrid termites and were optimized so that a standard gene library can be built for the south Florida Coptotermes populations.

Key Words: termite; microsatellite; interspecies; optimization

**References Cited**


Scientific Notes