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RAD-Seq derived markers flank the shell colour and banding loci of the *Cepaea nemoralis* supergene

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Abstract

Studies on the classic shell colour and banding polymorphism of the land snail *Cepaea* played a crucial role in establishing the importance of natural selection in maintaining morphological variation. *Cepaea* is also a pre- eminent model for ecological genetics because the outward colour and banding phenotype is entirely genetically determined, primarily by a ‘supergene’ of at least five loci. Unfortunately, progress in understanding the evolution and maintenance of the *Cepaea* polymorphism stalled, partly because of a lack of genetic markers. With a view to re-establish *Cepaea* as a prominent model of molecular ecology, we made six laboratory crosses of *Cepaea nemoralis*, five of which segregated for shell ground colour (C) and the presence or absence of bands (B). First, scoring of colour and banding in 323 individuals found no recombination between the C and B loci of the supergene. Second, using restriction site–associated DNA sequencing (RAD-Seq) of two parents and 22 offspring, we identified 44 anonymous markers putatively linked to the colour (C) and banding (B) loci. The genotype of eleven of the most promising RAD-Seq markers was independently validated in the same 22 offspring, then up to a further 146 offspring were genotyped. The closest RAD-Seq markers scored are within ~0.6 centimorgan (cM) of the C-B supergene linkage group, with the combined loci together forming a 35.8 cM linkage map of markers that flank both sides of the *Cepaea* C-B supergene.

Keywords: colour polymorphism, *Heliconius*, RAD-Seq, restriction site–associated DNA sequencing, snail, supergene

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Introduction

It is over sixty years since Cain and Sheppard published the first of their seminal papers on adaptive variation in the shell colour and banding patterns of the land snail *Cepaea nemoralis* (Cain & Sheppard 1950, 1952, 1954). Classic work on the *Cepaea* polymorphism contributed to the establishment of the field of ecological genetics and has provided (Jones et al. 1977; Clarke et al. 1978) and continues to provide (Silvertown et al. 2011; Cameron & Cook 2012) compelling evidence for the fundamental role of natural selection in promoting and maintaining variation in natural populations. However, in contrast to other classic ecological genetic systems such as wing pattern variation in mimetic butterflies (Joron et al. 2011; Heliconius Genome Consortium 2012), nothing is known about the molecular genetics of the *Cepaea* polymorphism, despite the important mechanistic insights this could provide into how ecology and genetics interact to shape adaptive variation. The *Cepaea* polymorphism (Fig. 1; see Cook (1998), Clarke et al. (1978) and Jones et al. (1977) for reviews) is
defined by extensive phenotypic variation for shell ground colour, the presence of zero to five bands and the pigmentation patterns of these bands (Fig. 1A). Classical genetic studies (Murray 1975; Jones et al. 1977 and references therein) have identified nine loci that control this variation, at least five of which are tightly linked together on the same chromosome and so are inherited together as a 'supergene' (Fig. 1B). These loci interact epistatically with one another (e.g. the band presence locus with the band pigmentation, spreading and interruption loci) and with the unlinked loci (e.g. suppression of specific bands). Empirical estimates of the frequency of recombination within the supergene, although limited, suggest that shell ground colour (C), band presence (B) and band interruption (I) are in a very tight linkage group, with recombination frequencies typically towards the lower end of ~0–2% (Cain et al. 1960; Cook & King 1966; Cook 1967). Spread banding (S) and band pigmentation (P) may be more loosely linked to the C-B linkage group, with respective recombination frequency estimates of ~3–4% (Cain et al. 1960; Cook 1967) and ~4–15% (Cook 1967) reported. Certainly, additional estimates of linkage within the supergene would be beneficial.

A variety of processes may be involved in both the original evolution and maintenance of the polymorphism (Jones et al. 1977; Clarke et al. 1978; Cook 1998). Correlations between colour and banding phenotypes and selective factors, such as climate and predation, indicate a strong directional selection component (e.g. yellow snails are often more common in open grassland habitats, where they are better camouflaged and less liable to overheat than pink or brown snails). The observation that coadapted colour and banding alleles are often found in strong linkage disequilibrium with one another (e.g. yellow-banded in variegated hedgerow and grassland habitats) is consistent with the hypothesis that the supergene may have evolved as a means to prevent these adaptive allelic combinations from being broken up by recombination (Cain & Sheppard 1954; Cain et al. 1960; Cook 1967).
Indeed, given *C. nemoralis* has a haploid chromosome number of 22, the probability of finding five linked loci out of eight (excluding locus \(O\), which may or may not be linked) is low, around \(2 \times 10^{-4}\).

The question of how supergenes evolve and subsequently remain protected from recombination is a long-standing one in population genetics. The problem is certainly more complicated than gene duplication, because typically the linked loci seem to have diverse biochemical and developmental roles (Jones et al. 1977; Barrett et al. 2000; Nijhout 2003). A further key problem is that bringing coadapted loci together in the genome will also generate irrelevant or harmful allelic combinations. Theoretically, it has been proposed that loci could be brought together as supergenes by chromosomal rearrangements (Sheppard 1953; Charlesworth & Charlesworth 1975; Kirkpatrick & Barton 2006), or a ‘sieve’ mechanism, whereby linkage is tightened between loci that are already located near one another (Turner 1977; D’Ennequin et al. 1999). Interestingly, recent molecular evidence suggests a role for both mechanisms in the evolution of a butterfly supergene (Joron et al. 2011; Jones et al. 2012). Certainly, empirical molecular evidence from *Cepaea* could shed further light on this problem.

While directional selection has undoubtedly played an important role in the evolution of the *Cepaea* polymorphism, the situation is complex because balancing selection (e.g. predation-driven apostatic selection) also acts on the polymorphism, such that rare recombinants may be sometimes favoured (Allen 1988; Cameron & Cook 2012). The mechanisms that continually maintain this variation remain difficult to disentangle (Jones et al. 1977; Cook 1998). Arguably, however, the evolution of the *Cepaea* polymorphism, of which the supergene is an inherent component, centres on the tension between balancing selection favouring the novel phenotypes created by rare recombination events within the supergene and directional selection favouring the suppression of recombination and maintenance of coadapted allele combinations. To identify and characterize the supergene and better understand the evolution of the polymorphism will require a set of linked molecular markers. Combining genetic knowledge with the wealth of historical and contemporary population genetic data available online as part of the citizen science project, the Evolution Megalab (http://www.evolutionmegalab.org/) (Silvertown et al. 2011; Cameron & Cook 2012), would greatly facilitate new angles of research.

Until recently, mapping adaptive loci in *Cepaea*, and other nonmodel organisms, has been inhibited by technological and cost constraints. However, a number of recently developed, rapid and cost-effective genotyping-by-sequencing methods, including restriction site–associated DNA sequencing (RAD-Seq), now meet the demands for de novo mapping in nonmodel organisms (Baird et al. 2008; Davey & Blaxter 2010; Amores et al. 2011; Baxter et al. 2011; Davey et al. 2011, 2013; Rowe et al. 2011). Consequently, with an ultimate view to identify and dissect the individual components of the *Cepaea* supergene, and to understand their evolution, we used RAD-Seq to construct a local map of markers linked to the shell ground colour (\(C\)) and banding presence (\(B\)) loci. We also present new data on the frequency of recombination between these two tightly linked loci, based on our own crosses. The map and the resource that are the segregating offspring should form the foundation of future work to re-establish *Cepaea* as a contemporary model of molecular ecology.

**Methods**

**The culture of Cepaea**

Snails were fed a hydrated grass pellet, oat and chalk mix, supplemented with lettuce. Generally, large juvenile virgin snails were raised to adulthood in isolation and then introduced to a partner. Pairs of snails were then kept in tanks with \(-4\) cm soil until egg laying began. As *Cepaea nemoralis* is a simultaneous hermaphrodite, offspring from both parents were used, except for crosses C100 × C101 and C108 × C109, where a nonvirgin snail (C100 and C108 respectively) was removed after mating. Egg batches were isolated, and the offspring reared to adulthood under the same feeding regime, with the time from egg to adult being \(-6\) months. Mature offspring and parents were then frozen at \(-20\) °C. The shell ground colour (\(C\)) and presence or absence of bands (\(B\)) phenotypes of all snails were then scored.

Segregation, including phase, of the colour and band presence loci was inferred from the parental and offspring phenotypes, where shell colour is pink (\(C^cC^c\) or \(C^cC^s\)) or yellow (\(C^cC^s\) homozygous recessive) and bands absent (\(B^bB^b\) or \(B^bB^b\)) or present (\(B^bB^b\) homozygous recessive). For each cross (Table 1), Mendelian segregation ratios were tested using chi-square goodness-of-fit tests.

Crosses were generated for three linked purposes: (i) to construct RAD-Seq libraries and generate candidate supergene-linked loci; (ii) to provide further offspring to validate candidate RAD-Seq loci as being linked or not; and (iii) to assess the frequency of recombination within the supergene.

**DNA extractions**

Genomic DNA was extracted from frozen snail foot tissue as follows. In brief, slices of snail tissue were
incubated at 65 °C in extraction solution (3% CTAB, 100 mM Tris-HCl, pH 7.5, 25 mM EDTA, pH 8, 2 M NaCl) with 0.2 mg/mL proteinase K and 80 l g/mL RNase. Upon lysis, a chloroform extraction was performed, then three volumes of CTAB dilution solution (1% CTAB, 50 mM Tris-HCl, pH 7.5, 10 mM EDTA, pH 8). Samples were mixed until a precipitate appeared, then the supernatant removed. The pellet was washed twice in 0.4M NaCl in TE (0.4 M NaCl, 10 mM Tris-HCl, pH 8), redisolved in 1.42M NaCl in TE (1.42 M NaCl, 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, pH 8), then precipitated in ethanol. For RAD library construction, precipitated DNA was spooled out, then washed in 70% ethanol; otherwise, centrifugation was used.

**Table 1** Summary of *Cepaea nemoralis* crosses. Cross 1 was used for linkage mapping; crosses 1 and 6 were used to validate RAD-Seq-derived linked markers; crosses 1–5 were used to estimate frequency of recombination between the ground colour (C) and band presence (B) supergene loci. All sites are UK unless otherwise stated. Key to phenotypes: Pink-unbanded Ø; pink-banded Ø; yellow-unbanded Ø; yellow-banded Ø. Note: some of the snails used are derived from previous laboratory crosses, so it was not possible to infer the geographic origin of each one of the pair of chromosomes that contain the supergene. Shell colour and banding phenotype data for all individuals from the six crosses are archived in DRYAD under doi:10.5061/dryad.560r4

<table>
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<th>Parent chromosomes</th>
<th>Genotype</th>
<th>Chromosome origin</th>
<th>F1 offspring genotypes</th>
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<tr>
<td></td>
<td>Parent Genotype</td>
<td></td>
<td></td>
<td>C&lt;sup&gt;0&lt;/sup&gt; B&lt;sup&gt;0&lt;/sup&gt;</td>
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<tr>
<td>Test cross repulsion 1</td>
<td>C100</td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
<td>Wye Valley</td>
</tr>
<tr>
<td></td>
<td>C101</td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
<td>Wye Valley</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
<td>Slieve Carron, Ireland</td>
</tr>
<tr>
<td></td>
<td>C108</td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
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<tr>
<td></td>
<td>C111</td>
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<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
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<td>C112</td>
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<tr>
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<td>C115</td>
<td>Ø</td>
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<td>Segmenting for colour (C) only 1</td>
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<tr>
<td></td>
<td>C117</td>
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<tr>
<td></td>
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<td>Ø</td>
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<td>Nottingham</td>
</tr>
<tr>
<td></td>
<td>C119*</td>
<td>Ø</td>
<td>C&lt;sup&gt;B&lt;/sup&gt; B&lt;sup&gt;B&lt;/sup&gt;</td>
<td>Nottingham</td>
</tr>
</tbody>
</table>

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### RAD-Seq library construction

For a single cross (C100 × C101; Table 1; Fig. 2), Restriction site–associated DNA sequencing libraries were constructed as in Baird et al. (2008), but with some minor modifications. Briefly, genomic DNA from each individual was separately digested with SbfI and then ligated to a P1 adapter containing a five-base barcode unique to each individual, with a minimum of two-base differences between each barcode. Samples were then pooled and sheared to ~400 bp fragments on a Covaris S2 sonicator. The fraction of 300–600 bp sheared DNA fragments was size selected from an agarose gel and ligated to a P2 paired-end adapter with the following sequences: P2 top oligo 5'–/5Phos/CTCAGGCATCACTCGATTCCTCCGA-
GAACAA-3' ; P2 bottom oligo 5'-CAAGCAGAGACGGCATACGAGGGAATCGATGCCTGAG*T-3', where * denotes a phosphorothioate bond; both oligos of the P1 adapters were also modified with a phosphoro-
thioate bond at the same position. The adapter-ligated DNA was subject to 20 cycles of PCR enrichment fol-
lowed by gel purification of the 400- to 700-bp fraction of
PCR product. Each library was paired-end sequenced on
an Illumina GAIIx flow cell, producing 101 base reads.

**Generation of RAD loci**

Restriction site-associated DNA sequence analysis was
performed using RADtools version 1.2.4 (http://www.
RAD-Seq.info) as described in Baxter *et al.* (2011).
Briefly, for each library, the raw reads were separated
into pools, according to the unique five-base barcode
assigned to each individual; reads were discarded
where sequence quality was not sufficient to recover
the barcode or restriction site. Barcodes were then
trimmed from the reads to leave 96 base sequences. For
each parent, the pooled reads from each library were
then concatenated, ready for analysis. For each individ-
ual, first read data were clustered into candidate RAD
loci comprising one or more candidate RAD alleles; a
default clustering distance of up to five bases was
allowed between alleles that were grouped together as
a single RAD locus, allowing for diversity between the
alleles. Only bases with quality scores >20 were used to
assess similarity during clustering, and alleles with a
read depth <2 were discarded. To account for PCR
duplication bias, read counts per allele, per individual,
were converted into estimated counts of the actual
number of DNA fragments in the original sample (frag-
ment counts); where the associated paired-end reads
were duplicated, first reads were collapsed into a single
unique sequence. RAD loci appearing in only a single
individual were then discarded and the remaining loci
merged across individuals, allowing for up to a 3-base
mismatch. Merged RAD loci exhibiting >4 alleles were
then discarded, because only a maximum of four alleles
can segregate for a given locus; loci with >4 alleles are
likely to be false positives, resulting from erroneously
clustered loci such as repeat regions. The resulting data
set of putative RAD loci was used to search for can-
didate loci linked to the supergene. Read counts and
coverage for each individual are given in Table 2.

**Identification of candidate-linked RAD loci**

A combination of Excel and Unix commands were used
to search for RAD loci that exhibited segregation pat-
terns consistent with linkage to the supergene. Data
from two individuals were excluded at this stage due
to them having substantially lower fragment counts
than the other individuals (Table 2). Details of the can-
didate segregation patterns found are given in Table 1
and Table S1, Supporting information.

Searches were conducted by first identifying all RAD
loci where one of the alleles exhibited a presence/
absence pattern across the parents and offspring, which
was consistent with linkage in phase with the dominant
colour allele (pink *C*<sup>0</sup>) or the dominant banding allele
(absent *B*<sup>0</sup>) (Fig. 2). A threshold of allelic dropout in
two offspring was used to account for insufficient
sequencing depth. Two putative recombinant offspring
were also allowed, to account for the possibility that a
recombination event could have occurred close to the
colour or banding loci in one or more offspring. Then,
for each of the RAD loci in this subset, the presence/
absence patterns of the alternative alleles were assessed
to see whether they exhibited a segregation pattern con-
sistent with linkage in phase. Again, in these alternative
alleles, dropouts were allowed in some individuals
(maximum of five where an allele is expected to present
in all 24 individuals and a maximum of two where an
allele is expected to present in 14, or less, individuals).

One problem was that RADtools is not able to deal with
indels in the tag sequence. Another potential problem is
in identifying pairs of tags where the polymorphism
between alleles exceeds that defined by the clustering
parameters. To find these missing loci, singleton RAD
loci that had been identified in the initial search were
compared against all RAD alleles using BLASTN. Signifi-
cant matches with ≥90% identities were then manually
aligned to see whether the alleles grouped into a locus
that cosegregated with either colour or banding (using
the same dropout thresholds). RAD loci meeting the
aforementioned criteria were considered as potential can-
didate-linked markers for further investigation.

**Marker development strategy**

We aimed to prioritize the development of those candi-
date markers suspected to be most closely linked to the
*C*-band supergene. However, we also developed some lesser
linked markers to aid in orientating the closest linked
markers with respect to *C*-band and to facilitate rapid valida-
tion of other candidate markers (see below). Conse-
quentially, of 44 markers (see Results), 11 (Cne_RAD01 to
Cne_RAD11) were developed through to an assay. For
the remaining 33 candidate markers, we compared the
existing RAD-Seq data for each marker to the segregation
of the first 11 developed markers. By comparison with
individual snails known to have received a recombinant
chromosome (between the *C*-band supergene and a RAD-
Seq marker), it was possible to infer likely orientation
and linkage of new markers relative to the *C*-band.
supergene. A four step procedure was used—(i) the segregation patterns of the snails that were used to create the RAD-Seq library were inspected for the eleven developed loci. (ii) The location of any recombination events with respect to the C-B supergene was inferred in each snail by comparison with the linkage map data. (iii) By inspection of the RAD-Seq segregation patterns of the remaining 33 loci, it was possible to estimate linkage to the established 11 loci and C-B. (iv) PCR primers were designed for the few markers that were suspected as being more closely linked. The locus-specific PCR products were then directly sequenced in the parents, as well as the single offspring individual that was identified as containing a chromosome that is recombinant between the tightest linked map markers and the supergene.

**Validation of RAD-derived markers**

Restriction site–associated DNA loci that were identified as being putatively linked to the supergene from

<table>
<thead>
<tr>
<th>Individual</th>
<th>Genotype</th>
<th>Library</th>
<th>Reads</th>
<th>RAD alleles</th>
<th>Coverage (fragments)</th>
<th>SD</th>
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<td>1</td>
<td>1379099</td>
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<td></td>
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<td></td>
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<td>2</td>
<td>693002</td>
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<td></td>
<td></td>
<td>3</td>
<td>1451806</td>
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<td></td>
<td></td>
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<td>46612</td>
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<td>3</td>
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<tr>
<td></td>
<td></td>
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<td>2064858</td>
<td>43053</td>
<td>6.6 (weighted)</td>
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<td></td>
<td>950895</td>
<td>3389</td>
<td>2.5 (weighted)</td>
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</table>

*Data for two individuals were excluded prior to searching for putative loci linked to C-B, due to them having lower allelic coverage.
the bioinformatic analysis (Table 3) were validated, by developing them into full markers for screening in a larger number of offspring from C100 × C101 and, in some cases, C118 × C119 (C119 being an F1 from C100 × C101; Table 1). Prior to developing these markers, paired-end contigs were assembled for all RAD alleles using VELVETOPTIMISER version 2.1.7, distributed with VELVET 1.1.04 (Etter et al. 2011; Davey et al. 2013). For each candidate RAD marker, the VELVETOPTIMISER-assembled paired-end contigs associated with each allele were manually checked and further minor edits made. From these high-quality contig assemblies, genotyping assays were designed, based either on length polymorphism or on cleaved amplified polymorphic sequence sites (CAPS) (Konieczny & Ausubel 1993; Thiel et al. 2004), using standard PCRs, GeneAmp PCR Gold according to manufacturer’s instructions and an annealing temperature of either 58 or 60 °C. For length polymorphism assays, the PCR product was visualized on an agarose gel for scoring. For CAPS assays, 7–10 μL of PCR product was digested in a 20 μL reaction with restriction enzyme and buffer and visualized on an agarose gel for scoring (see Table 3 for markers and their corresponding assays). The contig assemblies for the markers used to construct the linkage map are archived in DRYAD under doi:10.5061/dryad.560r4.

**Results**

_Cepaea crosses and recombination between the supergene loci_

Six crosses were generated (398 offspring; Table 1), of which five segregated for both the colour (pink C\(^9\) or yellow C\(^0\)) and banding (presence B\(^9\) or absence B\(^0\)) loci, with the other segregating only for colour. For the former, all crosses significantly deviated from expected Mendelian segregation ratios, as expected if the two loci are tightly linked (combined testcross repulsion populations: \(\chi^2 = 292.7, 3\) d.f., \(P \leq 0.001\); single testcross coupling population: \(\chi^2 = 14.2, 3\) d.f., \(P \leq 0.001\)). Zero recombinants were observed out of 323 individuals. Taking the probability of zero recombinants in \(n = 323\) meioses, given the recombination rate (θ) as \((1−0)\theta\), and a flat prior distribution for θ, the 95% upper confidence limit for θ was calculated from the posterior distributions as 0.5% between the colour (C) and banding (B) supergene loci.

**Searching for supergene-linked loci using RAD-Seq**

Twenty-six _Cepaea nemoralis_ snails were genotyped by RAD-Seq, all originating from a single mapping cross, C100 × C101 (Table 1; Fig. 2). This cross comprised 103 offspring that segregated for the colour (C) and banding (B) supergene loci. The cross was between a nonvirgin heterozygous pink-unbanded (C\(^9\)C\(^9\) B\(^0\)B\(^0\)) father and a double homozygous recessive yellow-banded (C\(^0\)C\(^0\) B\(^0\)B\(^0\)) mother. The resulting offspring phenotypes were pink-banded (C\(^9\)C\(^9\) B\(^0\)B\(^0\)) and yellow-unbanded (C\(^0\)C\(^0\) B\(^0\)B\(^0\)), implying zero recombination between the colour-banding element of the supergene. The dominant alleles were in repulsion (i.e. on separate chromosomes) in the heterozygous father and therefore segregated separately from one another in the nonrecombinant offspring (Fig. 2). Conveniently, this meant that RAD markers in phase with banding could be distinguished from markers in phase with the colour.

Three RAD-Seq libraries were generated, each comprising the same two parents and eight different offspring. Two libraries were sequenced across one flowcell of an Illumina GAIIx (Table 2; runs 1 and 3), with the
Table 3 Segregation patterns of assayed candidate-linked restriction site–associated DNA (RAD) markers. The binary segregation patterns are based on those used by RADTOOLS, where '1' indicates presence of a RAD allele in an individual and '0' indicates absence. The individuals are ordered: pink-unbanded father, yellow-banded mother, 12x pink-banded offspring, 9x yellow-unbanded offspring. The first two rows show the patterns expected for markers that fully cosegregate for either banding or colour across all individuals. An ‘x’ indicates where a RAD allele did not occur in an individual due to insufficient coverage, although the allele’s presence was subsequently confirmed by PCR. All candidate-linked RAD markers and explanations of the expected segregation patterns are given in Table S1, Supporting information.

<table>
<thead>
<tr>
<th>Marker</th>
<th>Allele</th>
<th>Segregation pattern</th>
<th>Assay Fragment sizes (bp)</th>
<th>Primer sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>Example</td>
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<td>Banded</td>
<td>Example</td>
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<tr>
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<td></td>
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<td>R3′</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>R3′</td>
<td>CACCTTCCCCATTCTTCAAA</td>
</tr>
</tbody>
</table>

CAPS, cleaved amplified polymorphic sequence sites. For marker Cne_RAD11, the polymorphism in the RAD-tag sequence is in phase with banding (see Table S1, Supporting Information). However, the SNP used to design the assay, which is derived from the associated paired-end contig assembly, is in phase with colour; this is the segregation pattern shown. The restriction digest produced up to 5 fragments (including an undigested 383-base pair fragment), although only the two fragments shown are diagnostic for linkage to the supergene. © 2013 John Wiley & Sons Ltd
other library sequenced on another two flowcells before concatenation (run 2). Across the three libraries, 61.9 million sequences with a recognized barcode and restriction site were generated, giving a mean number of reads per individual of >2 million (SD = 950,895; Table 2). These sequences are available via the NCBI SRA database under accession ID: SRA063152.

Using RADTOOLS, an initial 174,779 candidate alleles were found in more than one individual and clustered into 59,954 loci. After loci with >4 alleles were discarded (erroneously clustered loci, such as repeats), the resulting data set included 57,750 candidate loci, comprising 86,230 alleles, with a weighted mean fragment depth across all individuals of 6.6 (SD = 2.5).

The number of candidate RAD loci found corresponds well to a prediction of 52,520, assuming 6.6 Gb diploid genome (average of four helicid snails listed on http://www.genomesize.com/) and a 37% GC content (estimated from Biomphalaria glabrata; Adema et al. 2006). However, coverage was lower than was aimed for ~10×, due to a high proportion of presumed PCR duplicates—an average of 66.7% (SD = 16.1%) across all individuals (calculated from all putative RAD alleles found in an individual with a read depth >1).

Searches for putative RAD markers that exhibited presence/absence patterns consistent with full cosegregation with the supergene were conducted based on the parents and 22 of the original 24 offspring (two were excluded due to lower coverage, which would result in many dropouts; Table 2). Stringent search criteria, not allowing for any loss of alleles in individuals, returned only a single candidate marker (identified by BLASTN), which was in phase with banding. Less stringent search criteria yielded a total of 17 markers in phase with colour, 23 markers in phase with banding (including the one above), and four markers for which phase with colour or banding was not known, giving 44 potential candidates to develop further (Table S1, Supporting information).

**Validation of RAD-Seq markers and creating the supergene linkage map**

We attempted to validate the 44 loci as being linked or not, primarily prioritizing further development of markers that were suspected to be most closely linked to the C-B supergene locus (Table S1, Supporting information). This strategy led us to develop full genotyping assays for 11 of the candidate RAD marker loci (Table 3). These loci were genotyped in the parents, the original 22 individuals from the C100 × C101 cross and 80 further offspring from the same cross (one individual not used). This data, in addition to phenotypic scoring of the genotypes of the colour and band presence supergene loci, were then used to construct a local linkage map. The eleven RAD markers and two supergene loci formed a 35.8 cM linkage group (Fig. 3). Three RAD markers (Cne_RAD08, Cne_RAD09 and Cne_RAD10) fall within ~1 cM (1 recombinant in 102) of the C-B supergene linkage group. Cne_RAD08 and Cne_RAD10 were also scored in an additional 66 individuals from another cross (C118 × C119; Table 1), placing them ~0.6 cM (1 recombinant in 168) from C-B.

Fig. 3 Linkage map of restriction site–associated DNA (RAD) markers flanking the *Cepaea nemoralis* colour (C) and banding presence (B) supergene loci. The 35.8 cM map was inferred from 11 bi-allelic RAD markers and the phenotypes of the ground colour (C) and banding presence (B) loci scored in 102 offspring from a single cross (C100 × C101; Table 1). Three markers (Cne_RAD08, Cne_RAD09 and Cne_RAD10) fall within ~1 cM (1 recombinant in 102) of the C-B supergene linkage group. Cne_RAD08 and Cne_RAD10 were also scored in an additional 66 individuals from another cross (C118 × C119; Table 1), placing them ~0.6 cM (1 recombinant in 168) from C-B.
Cne_RAD08/09/10. Although four loci were identified as being of high priority because the segregation patterns indicated likely strong linkage (including the single locus that showed perfect segregation, mentioned above), we were not able to develop a successful assay for them due to difficulty in alignment, designing primers and PCR. Three were discarded as erroneous or false positive unlinked loci because putative recombinants found in their segregation patterns did not correspond to the RAD offspring validated as recombinants in the linkage map. The remaining 26 loci were identified as being of limited interest at present, because the linkage of each RAD-Seq locus to C-B was estimated to be no closer than the existing tightest linked map markers (Cne_RAD08/09/10). Of these 26 loci, 10 were inferred to be orientated on the same side of C-B as Cne_RAD08/09/10 and 16 on the opposing side. Full validation details and linkage estimates are given for all 44 markers in Table S1, Supporting information.

Discussion

We used RAD-Seq to identify the first molecular markers that are closely linked to the *Cepaea* supergene and then derived a local genetic map for this region. The 11 markers assayed thus far form a 35.8 cM linkage group with the closest linked markers falling 0.6 cM away from the shell ground colour (C) and band presence (B) supergene loci. In addition, we found zero recombinants between the colour (C) and banding loci (B) in 323 individuals, giving an upper limit of 0.5% recombination. This figure is similar to previous estimates of between 0.02% and 2% (Cain et al. 1960; Cook & King 1966), consistent with tight physical linkage within the supergene. Together the linkage map and the crosses provide the basis for further research to fine map and, ultimately, to identify the supergene, as well as to understand the evolution and maintenance of the *Cepaea* polymorphism.

Development of individual RAD markers was sometimes challenging. First, we found that additional screening was needed during marker development as, with one exception, we did not find RAD loci that fully cosegregated with colour or banding, across all the individuals that were sequenced. The main explanation is insufficient depth of coverage, due to a high proportion of PCR duplicates (Baxter et al. 2011; Davey et al. 2011; Etter et al. 2011), resulting in a relatively high number of allelic dropouts—even for the most closely linked of the eleven RAD markers. A second problem was difficulty in developing suitable assays for some markers, either because of a poor paired-end assembly (perhaps indicating the locus fell within a repeat region), or because of a lack of SNPs in suitable phase (a particular problem for tri-allelic loci). However, these issues were partly negated by the fact that we were focussing on finding a small number of candidate linked loci; this meant it was viable to compare PCR and RAD-Seq segregation data to determine whether absent alleles were real or sequencing artefacts.

**Future fine mapping of the supergene**

The genetic map is a preliminary, but important resource for leading the future direction of research on *Cepaea*. Fine mapping of the supergene is an obvious next step, which may be aided by taking a number of different approaches, such as mapping the other loci that comprise the polymorphism, creation of a whole-genome linkage map and association mapping in natural populations.

It is worth emphasizing that we have initially considered only the two most easily scored and intensively studied loci of the five *Cepaea* supergene loci (Fig. 1). However, given that observed recombination frequencies between the C-B linkage group and the pigmentation (P) and spread band (S) loci range between 3% and a maximum of 15% (Cain et al. 1960; Cook 1967), our closest linked RAD-Seq markers could already fall within the supergene. The creation of additional crosses that segregate for these other supergene loci is underway and will undoubtedly be important for understanding the context of our existing map as well as the structure of the supergene.

Development of a whole-genome linkage map will also be of great importance. The low and highly variable sequencing coverage of our current data set, as well as the limited number of included offspring, mean that a genome map was beyond the scope of the current work. However, future work will focus on using a lower number of PCR cycles, to reduce PCR duplicates, achieving high uniform coverage across individuals by synthesizing, and then pooling libraries, based on a few individuals (Baxter et al. 2011), and sequencing these to a greater depth using the latest Illumina Hi-Seq technology. Complexity reduction in the RAD libraries, either through the use of a less frequent cutting restriction enzyme or bioinformatically, could also be a route to generating a robust set of markers for a whole-genome map, although this would still need to be coupled with higher coverage than was achieved here.

Finally, of critical importance if we are to fine map the individual component loci of the supergene, is to identify recombinants within the supergene. This may be achieved using two complementary methods, first by detecting rare recombinants in further genetic crosses or, alternatively, by linkage disequilibrium or association mapping SNPs from natural populations.

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The latter method would rely upon the fact that different combinations of colour and banding alleles are frequent in linkage disequilibrium in separate populations, and so distinct populations are likely to represent independent cross-over events within the supergene.

**Evolution of the Cepaea polymorphism: a molecular perspective**

While our study represents only the initial steps towards a molecular genetics-led investigation of the *Cepaea* polymorphism, we already envision a number of novel avenues of research. These centre on trying to understand, both at molecular and population levels, the tension between directional selection and balancing selection (in addition to nonselective forces, such as migration), which have driven the evolution and maintenance of the supergene (Jones et al. 1977; Clarke et al. 1978; Cook 1998).

First, by what molecular mechanisms were coadapted colour and banding loci brought together into a supergene, and how have they been subsequently protected from recombination? Moreover, are these loci in tight physical linkage, or do they lie across a larger chromosomal region of suppressed recombination? In the case of the evolution and maintenance of a supergene for mimetic wing pattern variation in the butterfly *Heliconius numata*, a classic example of negative frequency-dependent balancing selection like *Cepaea*, recent targeted and whole-genome sequencing data have implicated both initial tight linkage of the supergene components (Jones et al. 2012) and local chromosomal inversions (Joron et al. 2011). In comparison, while the *Cepaea* supergene remains anonymous at present, it has been speculated that chromosomal rearrangements are involved; one of the 22 chromosome pairs in *Cepaea nemoralis* is much larger than the others, constituting ~15–20% of the genome. Certainly, in the first instance, it would be desirable to explore the use of physical mapping, via fluorescent in situ hybridization (FISH) (Adema et al. 2006), and whole-genome linkage mapping to see whether closely linked RAD-Seq markers map to this large pair of chromosomes.

Addressing the population genetics of the *Cepaea* polymorphism using the supergene-linked markers will also be vital for understanding the historical and contemporary evolution of the polymorphism. While past studies, using allozymes (Johnson 1976; Ochman et al. 1983), mitochondrial DNA and microsatellites (Davison 2000; Davison & Clarke 2000), have attempted to address the local history of polymorphism, they are limited by the imperfect resolution they provide and the fact that they may share a different history to the supergene. In contrast, RAD markers that are in linkage disequilibrium with the supergene will probably share the same phylogeny as the supergene, so when used in combination with neutral loci, are likely to be more informative for inferring the adaptive history of the polymorphism, both at regional and local scales (Wilding et al. 2001; Hines et al. 2011).

In conjunction with population genetic data, looking at patterns of linkage disequilibrium in the region within and surrounding the supergene may tell us something about the strength and type of selection operating, the length of time variation has been maintained in populations and in turn may shed light on the population processes that have contributed to its maintenance (Charlesworth 2006). For example, sequence diversity within and surrounding the *H. numata* supergene (Joron et al. 2011) may be indicative of balancing selection acting within populations having a more important role in maintaining polymorphism than local adaptation and migration between populations (Charlesworth & Charlesworth 2011).

Finally, a future line of research will be to use the molecular data generated from *C. nemoralis* to study the degree of sympathy with its sister species *Cepaea hortensis*. Given that the polymorphism is phenotypically and genetically (Murray 1975) similar, if not identical, between the two, it is likely that the supergene existed prior to their divergence into separate species, suggesting that we may find trans-specific polymorphism, or else introgression (Jones et al. 1977; Heliconius Genome Consortium 2012). Moreover, across the pulmonates as a whole, it is likely that shell polymorphisms and even supergenes have independently evolved multiple times (Clarke et al. 1978), raising the question of whether the same loci have been co-opted.

High-throughput sequencing has clearly revolutionized what can be achieved in all of the different fields of molecular ecology (Tautz et al. 2010), particularly for nonmodel organisms (Ekblom & Galindo 2011). It is understandable that RAD-Seq is rapidly becoming the method of choice for generating ‘reduced representation’ genomic data in nonmodel systems (Rowe et al. 2011), be it for genetic mapping (Amores et al. 2011; Baxter et al. 2011; Gagnaire et al. 2013; Hecht et al. 2013; Takahashi et al. 2013), generating markers for population studies (Emerson et al. 2010; Corander et al. 2013; Hess et al. 2013; Keller et al. 2013) or aiding both the assembly and inferences that can be made from whole-genome sequencing (Heliconius Genome Consortium 2012). In our case, we have been able to take a classic polymorphism for which no molecular genetic data existed and rapidly generate a set of linked markers, which will form the foundations of future work to re-establish *Cepaea* as a prominent model of molecular ecology.
Acknowledgements

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P.M.R., M.L. and A.D. conceived and designed the experiment. P.M.R., M.L., N.L. and A.D. performed the laboratory work. P.M.R., M.L., J.W.D. and M.L.B. involved in RAD-seq and bioinformatics. P.M.R. and A.D. wrote the manuscript. M.L. and J.W.D. critically reviewed the manuscript.

Data accessibility

1 The Illumina 100-bp RAD-tag and paired-end sequences for each individual are available via the NCBI SRA database under accession ID: SRA063152.

2 The RAD-tag sequences and segregation patterns of all 44 RAD loci that were found to putatively cosegregate with shell colour or banding are supplied as online supporting information (Table S1, Supporting information).

3 Assemblies of RAD-tag and associated paired-end sequences for each of the linkage map markers, the data set of genotypes used to construct the linkage map, and the shell colour and banding phenotype data for all individuals from the six crosses (Table 1) are archived in DRYAD under doi:10.5061/dryad.5604.

Supporting information

Additional supporting information may be found in the online version of this article.

Table S1 All candidate supergene-linked RAD loci and details of their validation, grouped by the different co-segregation patterns expected for supergene-linked markers.