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MICROSATELLITE DEVELOPMENT IN RHODOPHYTA

USING HIGH-THROUGHPUT SEQUENCE DATA

Lucia Couceiro^{1,2}, Isabel Maneiro¹, Stéphane Mauger², Myriam Valero², Jose Miguel Ruiz¹
and Rodolfo Barreiro¹

¹ Area de Ecoloxia, Facultade de Ciencias, Universidade da Coruna, Campus de A Zapateira s/n, 1571-A Coruna, Spain

² CNRS-UPMC, UMR 7144, Equipe BEDIM, Station Biologique de Roscoff, Place Georges Teissier, F-29682 Roscoff Cedex, France

Shotgun genome sequencing is rapidly emerging as the method of choice for the identification of microsatellite loci in nonmodel organisms. However, to the best of our knowledge, this approach has not been applied to marine algae so far. Herein, we report the results of using the 454 next-generation sequencing (NGS) platform to randomly sample 36.0 and 40.9 Mbp (139,786 and 139,795 reads, respectively) of the genome of two red algae from the northwest Iberian Peninsula [*Grateloupia lanceola* (J. Agardh) J. Agardh and a still undescribed new member of the family Cruoriaceae]. Using data mining tools, we identified 4,766 and 5,174 perfect microsatellite loci in 4,344 and 4,504 sequences / contigs from *G. lanceola* and the Cruoriaceae, respectively. After conservative removal of potentially problematic loci (redundant sequences, mobile elements), primer design was possible for 1,371 and 1,366 loci, respectively. A survey of the literature indicates that microsatellite density in our Rhodophyta is at the low end of the values reported for other organisms investigated with the same technology (land plants and animals). A limited number of loci were successfully tested for PCR amplification and polymorphism finding that they may be suitable for population genetic

studies. This study demonstrates that random genome sequencing is a rapid, effective alternative to develop useful microsatellite loci in previously unstudied red algae.

Key index words: 454 sequencing; conservation genetics; expressed sequence tags; microsatellite development; primer design; Rhodophyta; seaweed

Abbreviations: bp, base pairs; ESTs, expressed sequence tags; GS-FLX, Genome Sequencer FLX; Mbp, mega base pairs; MIDs, multiplex identifiers; NGS, next-generation sequencing; PAL, potentially amplifiable loci; TE, Tris-EDTA

Population genetics studies are an important tool for developing effective management strategies for endangered species (Frankham et al. 2004). However, obtaining appropriate molecular markers—a prerequisite for such studies—often becomes a limiting step. This is the case for microsatellites. Although they are often considered the marker of choice for population genetics analysis due to their high levels of polymorphism and codominant nature, their de novo development is a costly and time-consuming endeavor (Zane et al. 2002). These difficulties have acted in many cases as a deterrent for the utilization of these markers, particularly in poorly studied taxonomic groups (Squirrell et al. 2003).

The recent accessibility to NGS technologies is revolutionizing life sciences in several research fields (reviewed in Hudson 2008). Even though NGS is typically cited as a fast and cheap route to assemble genomes or transcriptomes, it also provides avenues to many broader purposes, including marker development (Thomson et al. 2010). In particular, high-throughput sequence data from the Roche 454 platform offer the potential for a rapid identification of microsatellite loci on nonmodel organisms, and several examples of this have been published already (Abdelkrim et al. 2009, Allentoft et al. 2009, Santana et al. 2009, Castoe et al. 2010, Csencsics et al. 2010). Briefly, the Genome Sequencer FLX System (GS-FLX) powered by 454 sequencing (454 Life Sciences, Branford, CT, USA) enables a random and extensive survey of

the genome providing thousands of short reads (average length of 400 bp using GS-FLX Titanium Series Reagents). This huge data set of reads is then screened with simple bioinformatic tools to detect microsatellite motifs and to design PCR primers. Thus, this approach eliminates the prolonged, expensive, and laborious steps of constructing genomic libraries, including cloning, hybridization to detect positive clones, plasmid isolation, and Sanger sequencing. Herein, we report the results obtained by applying this approach to two Rhodophyta of conservation concern in Galicia (northwest Iberian Peninsula): *G. lanceola* and a still undescribed new member of the Cruoriaceae. Compared to other taxa, seaweeds have not been traditionally included in the debate about endangered species. However, there is a growing recognition that many seaweeds are restricted in their distribution and may thus be vulnerable to stochastic environmental and anthropogenic events (Brodie et al. 2009). The two species studied herein are candidates for inclusion in the regional catalog of endangered species (Xunta de Galicia 2007). In Galicia, *G. lanceola* occurs in only a few (<30) enclaves mostly concentrated in 30 km of coastline (Peez-Cirera et al. 1989, Ba'rbara and Cremades 2004). Besides their regional rarity, these populations possess biogeographic value derived from their marginality and isolation (Eckert et al. 2008) (Galician populations are located > 1,000 km north of the species' main range in the Atlantic coast of Africa). The conservation status of the second species also deserves attention. Its Galician populations were traditionally identified as *Furcellaria lumbricalis* (Huds.) J. V. Lamour., a common inhabitant of northern latitudes with a southern limit of distribution in the Iberian Peninsula (Pe' rez-Cirera 1975, Granja et al. 1993). However, some anatomical peculiarities led us to produce DNA sequence data to determine its taxonomic identity. Surprisingly, both plastid (*rbcl*) and nuclear (*rDNA* LSU) gene sequences have revealed that the plant found in Galicia is a still undescribed erect member of the Cruoriaceae family (unpublished results). Its limited presence in Galicia (it is known only from 12 enclaves, Barbara et al. 2006) renders this new species an interesting case to investigate its population structure and, eventually, to

determine its suitability for inclusion in the regional catalog of seaweeds of conservation concern. Previous experience with conventional protocols for microsatellite isolation suggests that seaweeds may display comparably low genomic frequencies of microsatellites (Wattier and Maggs 2001, Andreakis et al. 2007). Since we were particularly interested in discovering whether or not the use of NGS technology will still support this conventional wisdom, our results with the 454 technology are compared to those for other taxa obtained using comparable high-throughput approaches.

MATERIALS AND METHODS

DNA extraction and pyrosequencing. For each species, a single specimen was used as the sole source of tissue/DNA. Prior to DNA extraction, samples were frozen in liquid nitrogen and homogenized using a mechanical tissue disrupter (Mini-Bead-beater 1; Bio Spec Products Inc., Bartlesville, OK, USA) and steel beads. Total DNA was then extracted with the Wizard Magnetic DNA Plant System (Promega Corp., Madison, WI, USA) following manufacturer's recommendations. To achieve the required amount of DNA, multiple DNA isolations from each specimen were pooled, lyophilized, resuspended in Tris-EDTA (TE) buffer, and purified with QIAquick PCR Purification kit (Qiagen Sciences Inc., Germantown, MD, USA).

A total of 2–5 lg of DNA from each species was used to prepare their respective GS-FLX Titanium general libraries (454 Life Sciences) following manufacturer's protocols and quality control steps. Briefly, genomic DNA was fragmented by nebulization, small DNA fragments (<350 bp) were removed, short adaptors were ligated to the ends of each fragment, and, finally, only those fragments with adaptors in both 5' and 3' ends were retained. Each DNA sample was appropriately tagged using two different multiplex identifiers (MIDs) to enable pooling for simultaneous sequencing. DNA library fragments were then captured onto beads and clonally

amplified within individual emulsion droplets (emPCR). Finally, amplified fragments from both species were evenly mixed and sequenced on ¼ PicoTiterPlate regions using the Titanium GS-FLX chemistry (454 Life Sciences). Libraries preparation, amplification, and sequencing were carried out at the external facilities Centre de Recerca en Agrigenomica (Barcelona, Spain).

Data preprocessing and microsatellite discovery. Each read was automatically assigned to its correct library by GS-FLX software (454 Life Sciences) based on sample-specific MID sequence. In an initial attempt to remove redundancy, sequence reads from each species were analyzed using 454 GS De Novo Assembler v2.3 (454 Life Sciences) with default parameters. The assembled contigs and remaining singletons resulting from this analysis were clustered into a single fasta format file and used as input for the software QDD, a collection of freely available modules (ActivePerl, BLAST, CLUSTALw2 and Primer3) that proceeds in three successive stages (Meglec et al. 2010). Firstly, it selects sequences that are longer than a user-defined limit and have perfect microsatellites with a minimum number of repeats. Secondly, QDD automatically detects and removes redundancy as well as groups of sequences that potentially are part of a repetitive region of the genome and, consequently, might be problematic for microsatellite amplification (although QDD is not designed to describe mobile elements, this is a conservative method that eliminates many of these sequences). Finally, the software selects sequences that contain a target microsatellite and a flanking region free from nanosatellites and designs PCR primers to amplify these repeats when flanking regions enable it. All QDD parameters, including the parameters of the module Primer3, were set to default values.

Data analysis. Tab-delimited files generated from QDD steps 1 (identified loci) and 3 (potentially amplifiable loci, PAL) were converted to spread-sheet files for use in Microsoft Office Excel 2003 (Microsoft Corporation, Redmond, WA, USA). Microsatellite frequency for each species was expressed as total number of identified microsatellites per mega base pair

(Mbp), and subsequent data analysis included sorting according to microsatellite category (i.e., di-, tri-, tetra-, penta-, and hexanucleotides), specific motifs and number of tandemly repeated units. Reverse-complement repeat motifs and translated or shifted motifs were grouped together so that there were four unique dinucleotides repeats and 10, 33, 102, and 350 unique tri-, tetra-, penta, and hexanucleotides repeats, respectively (Jin et al. 1994). To provide some comparison with other Rhodophyta, microsatellite frequency / attributes were also investigated using exactly the same procedure in seven species with >1,000 expressed sequence tag (EST) sequences available in the public database EST-GenBank: *Porphyra yezoensis*, *Furcellaria lumbricalis*, *Eucheuma denticulatum*, *Gracilaria changii*, *Porphyra haitanensis*, *Chondrus crispus*, and *Griffithsia okiensis*. Portions of this data set were screened for micro-satellite motifs by other authors (e.g., EST data for the two *Porphyra*; Liu et al. 2005, Sun et al. 2006, Wang et al. 2007, Xie et al. 2009), but they were reanalyzed here under common search criteria to facilitate comparison.

Microsatellite testing. A subset of the PAL for each species was tested for amplification (18 and 23 PAL for the *Cruoriaceae* and *G. lanceola*, respectively). To increase the chance of targeting polymorphic loci, we selected PAL with the highest number of repetitions. Markers producing clear electropherogram patterns were assessed for polymorphism using a number of individuals from various populations in the Iberian Peninsula (32 specimens from four populations in the case of the *Cruoriaceae*; 26–30 specimens from three populations in *G. lanceola*). DNA extractions were performed as described above, and PCR reactions (10 μ L) contained 10 ng of DNA, 200 nM of each primer (Life Technologies Corp., Carlsbad, CA, USA), 150 μ M of dNTPs (Fermentas Inc., Geln Burnie, MA, USA), 1.5 mM of MgCl₂ (Promega Corp.), 1 \times PCR Buffer (Promega Corp.), and 0.35 U Taq DNA polymerase (Promega Corp.). Amplifications were carried out separately for each locus on PTC-200 Thermo Cycler (GMI Inc., Ramsey, MI, USA) with initial denaturing at 94 $^{\circ}$ C for 5 min, followed by 30 cycles of 94 $^{\circ}$ C for 30 s, 57 $^{\circ}$ C–60 $^{\circ}$ C for 30 s, and 72 $^{\circ}$ C for 30 s with a final extension of 72 $^{\circ}$ C for 10 min.

DNA fragments were separated on an ABI 3730 Genetic Analyzer (Life Technologies Corp.) with GeneScan 600 LIZ as size standard (Life Technologies Corp.). Finally, electropherograms were analyzed with the software GeneMapper v4.0 (Life Technologies Corp.), and diversity estimates (number of alleles per locus, NA; observed heterozygosity, Ho; expected heterozygosity, He) were calculated with GenALEx 6 software (Peakall and Smouse 2006).

RESULTS

Undescribed Cruoriaceae species. A total of 139,795 reads and 40,896,217 bp were obtained from the 454 shotgun library for the Cruoriaceae (mean read length 293 bp). When sequence reads were assembled using 454 GS De Novo Assembler v 2.3 with default parameters, the new data set consisted in 4,329 contigs plus 51,622 singletons. A total of 5,174 microsatellite loci (di-, tri-, tetra-, penta-, and hexanucleotides) with ≥ 4 repeats were identified in 4,504 of these sequences amounting to a yield of 0.037 microsatellites per initial read and 126.5 microsatellites per mega base pairs (Mbp). Most loci contained di- and trinucleotide repeats (4,309 and 699, respectively), followed far behind by hexa- (65), tetra- (64), and pentanucleotides (37) (Table 1). After a conservative removal of redundancy and potentially problematic sequences (e.g., those located in repetitive regions of the genome), PCR primers design was possible in 1,366 loci (26% of the loci identified). Again, these potentially PAL were dominated by di- and trinucleotide repeats (1,178 and 168 loci, respectively), while larger motifs lagged well behind (8 loci in each repeat category). A detailed description of these results including a unique accession for each PAL, GenBank accession number, repeat monomer sequence, number of perfect tandemly repeated units, and forward / reverse primer sequences is provided in Appendix S1 (see the supplementary material).

181 The relative numbers of perfect tandemly repeated units were fairly similar across the various
182 microsatellite categories (Table 1). In all five categories, there were many short repeats and
183 fewer long repeats although the relative abundance of loci with the lowest number of repeated
184 units (four) decreased with microsatellite complexity (from >70% for di- and tri- nucleotides to
185 <55% for larger motifs). Differences were even more pronounced in PAL where most loci
186 (>95%) only contained four to five repeat units. Since di- and trinucleotides were 97% of all
187 identified microsatellite loci and 99% of all PAL, differences in the relative abundance of
188 specific motifs were only investigated in these two categories (Fig. 1). For the dinucleotide
189 repeats, three of the four possible motifs were evenly represented and accounted 88% of the
190 identified loci, while AT was less frequent (12%). Among the trinucleotides, one of the 10
191 possible motifs (CCG) was clearly overrepresented and nearly doubled the frequency expected
192 simply by chance; the other nine motifs showed comparable frequencies except for two motifs
193 (ACT and AGT) with frequencies <5%. In general, the same pattern was applicable to PAL
194 data. Twelve of the 18 PAL tested for amplification (Table 1) yielded a product of the expected
195 size. Reliable scoring of allele sizes (one to two clear peaks, no multiband pattern) was possible
196 for seven of them, and they were used for subsequent polymorphism assessment. Among these
197 seven loci, five were polymorphic and heterozygous in at least one individual (Table S1 in the
198 supplementary material) with three to four (mean 3.4) alleles per locus. The observed and
199 expected heterozygosities ranged from 0.031 to 0.969 (mean 0.569) and from 0.254 to 0.656
200 (mean 0.515), respectively. The five polymorphic loci produced 28 distinct multilocus
201 genotypes in 32 individuals (88%). *Grateloupia lanceola*. The 454 shotgun library for *G.*
202 *lanceola* provided a number of reads very close to those obtained for the *Cruoriaceae* (139,786
203 reads) but a slightly lower number of base pairs (36,013,235 bp, mean length read 258 bp). The
204 preliminary assembling with the 454 GS De Novo Assembler v 2.3 resulted in 2,526 contigs
205 plus 67,005 singletons. A total of 4,766 microsatellite loci (di-, tri-, tetra-, penta-, and
206 hexanucleotides) with ≥ 4 repeats were identified in 4,344 of these sequences amounting to a

yield of 0.034 microsatellites per initial read or 132.3 microsatellites per Mbp (Table 1). As in the other species, most loci contained di- and trinucleotide repeats (3,959 and 686, respectively) followed far behind by tetra- (59), hexa- (33), and pentanucleotides (29). After removing redundancy in its widest sense, the proportion of loci for which PCR primers design was possible was again very similar to that obtained for the other red alga (1,371 loci, 29% of the identified loci). Likewise, PAL were dominated by di- and tri- nucleotide repeats (1,176 and 165, respectively), while more complex motifs lagged well behind (14 loci). A detailed description of these results including a unique accession of each PAL, GenBank accession number, repeat monomer sequence, number of perfect tandemly repeated units, and forward/reverse primers sequences is provided in Appendix S2 (see the supplementary material).

As already observed in the Cruoriaceae, the relative abundance of perfect tandemly repeated units was fairly similar across microsatellite categories (Table 1) with abundant short repeats and fewer long repeats. However, the relative abundance of loci with the lowest number of repeated units (four) decreased with microsatellite complexity (86, 75, 69, 62, and 60% for di-, tri-, tetra-, penta-, and hexanucleotides, respectively). The higher relative abundance of loci with a small number of repeated units was even more marked in PAL as >95% loci only contained four to five repeats.

Both di- and trinucleotide loci revealed notable changes in the relative abundance of specific motifs and, more interestingly, substantial differences with the other species (Fig. 1). For the dinucleotide repeats, one of the four possible motifs (AG) accounted for 50% of the identified loci, while AC showed a frequency similar to that expected by chance (31%) and the other two motifs (AT and CG) were <15%. Among the trinucleotides, one of the 10 possible motifs (AAG) doubled the frequency expected by chance; the other nine motifs exhibited comparable frequencies (10%) except for AGC and CCG with frequencies <7%. PAL showed the same general pattern of motif frequencies.

A large proportion of the PAL tested for this species showed good, size-expected amplification products (20 of 23 tested PAL, 87%) and easily scorable profiles (19 of 23 tested PAL, 83%) (Table 1). Twelve of these loci were monomorphic, and the seven remaining ones were polymorphic; however, six were heterozygous in at least one individual, while the last one was homozygous across all samples. The mean number of different alleles per locus was lower than in the Cruoriaceae (2.4 vs. 3.4, two to four alleles per locus), and the observed and expected heterozygosities ranged from 0 to 0.933 (mean 0.196) and from 0.034 to 0.531 (mean 0.204), respectively (Table S1). Likewise, the seven loci produced 13 distinct multilocus genotypes in 30 individuals (43%). The low levels of polymorphism detected in *G. lanceola* are consistent with the low genetic diversity found in this species using AFLP markers (unpublished results).

Microsatellite frequency / attributes in other Rhodophyta. A total of 60,444 public EST sequences (27 Mbp) from the other seven red algae were screened for perfect tandemly repeated units with QDD using the same criteria applied to our shotgun sequencing data (Table S2 in the supplementary material). Microsatellite frequency oscillated from 261.8 counts \pm Mbp⁻¹ in *E. denticulatum* to 860.89 counts \pm Mbp⁻¹ in *G. changii*. As in our Cruoriaceae and *G. lanceola*, most of the microsatellite loci (>95%) contained di- and trinucleotide repeats. Relative abundances of perfect tandemly repeated units were also similar to our results with genome sequencing data. More than 65% of the detected loci contained just four repeats, while the percentage of microsatellites with >10 repeats was <1% in three species (*E. denticulatum*, *F. lumbricalis*, and *G. changii*), ranged 1%–5% in *C. crispus* and *G. okiensis*, and was >5% in the two *Porphyra*. The relative abundance of specific motifs also showed considerable variation. AG was the most abundant dinucleotide motif in three species (*E. denticulatum*, *P. haitanensis*, and *G. changii*; 34.4%–44.9%), AC dominated in *F. lumbricalis* (49.2%) as well as in *G. okiensis* (39.4%), and CG was the most common motif in *C. crispus* (44.4%) and *P. yezoensis* (48.2%). Among the trinucleotides, CCG prevailed in all species except *F. lumbricalis*, but its relative abundance was variable.

258

259 **DISCUSSION**

260

261 Population genetics studies are still comparatively scarce in seaweeds (Valero et al. 2001) and
262 have mostly focused on a limited number of genera / species (Andreakis et al. 2007). This
263 shortage of intraspecific studies has been attributed, at least in part, to a lack of appropriate
264 molecular markers. In particular, the detection of useful microsatellite loci has been
265 challenging, and it has been suggested that their genomic frequency in this group might be low
266 (Olsen et al. 2002, Andreakis et al. 2007). Our relatively extensive and random survey of the
267 genome of two Rhodophyta should allow some test- ing of this conventional wisdom.

268 Microsatellite frequency is known to vary to a con- siderable extent among eukaryotes. Even
269 when complete genomes are screened for microsatellite occurrence with consistent procedures,
270 among-taxa differences can be as high as three orders of magni- tude (Sharma et al. 2007). A
271 review of the literature reveals that microsatellite frequency is likewise variable in taxa
272 investigated with a genome sequencing approach comparable to ours (Table S3 in the sup-
273plementary material). Estimates for a number of plants and animals range from 11.7
274 microsatellite counts per Mbp to 544.0 counts \pm Mbp)¹ (mean 148.4 counts \pm Mbp)¹). In this
275 context, our results may seem comparable to those obtained for various animals and higher than
276 the estimates reported for some plants. However, our review also shows that search parameters
277 vary between studies, and, consequently, caution must be exercised in doing this comparison.
278 In particular, the minimum number of repeats for microsatellite detection can be especially
279 influential. Most studies used cutoff values slightly larger than ours, especially for the smaller
280 motifs that often constitute a major fraction of the detected loci. When our estimates were
281 recalculated for a higher cutoff (five for every category), the new microsatellite frequencies
282 (21.9 and 28.8 counts \pm Mbp)¹) placed our two red algae in the lower end of the values reported
283 in the literature (Table S3).

284 As our study is the first case where 454 shotgun genome sequencing was used to detect
285 microsatellite motifs in algae, it is difficult to assess to what extent our estimates may be
286 relevant for other taxa. However, it is worth mentioning that our two taxa yielded very similar
287 microsatellite frequencies despite the fact that they belong to different orders and show obvious
288 differences in other microsatellite attributes. Thus, the genome of the Cruoriaceae was
289 particularly enriched in CG motifs, while *G. lanceola* was dominated by AG motifs. This
290 variation is consistent with the great differences in di- and trinucleotide motifs reported in
291 other photosynthetic organisms (Von Stackelberg et al. 2006). It also suggests that
292 microsatellite attributes are species specific rather than group specific, an observation with
293 obvious implications for the enrichment protocols often used for isolating microsatellite loci
294 (Zane et al. 2002) as inappropriate a priori choices about repeat size and motif sequence may
295 lower the efficacy of obtaining useful microsatellite loci.

296 In contrast with the absence of random genomic sequencing data for Rhodophyta, the growing
297 body of publicly available DNA sequences—including vast collections of ESTs—can be used
298 to explore the density/attributes of repeat motifs in the genome of other red algae. Our analyses
299 of EST data for seven species of Rhodophyta (covering four orders and six families) reveal that
300 microsatellite density is 2- to 7-fold higher in EST sequences than in our 454 sequencing data,
301 suggesting that EST collections may be a more effective source for microsatellite mining. As
302 in our random sequencing, EST-derived loci were dominated (>95%) by di- and trinucleotide
303 repeats (Table S2); also, dinucleotides were three to five times more abundant than trinucleo-
304 tides in all taxa except the two Porphyra. This prevalence of dimer repeats is in agreement
305 with the higher density of dinucleotides found in nine of the 25 photosynthetic organisms
306 investigated by Von Stackelberg et al. (2006), and contrasts with the notion that EST-derived
307 microsatellites may be prone to trinucleotides (Varshney et al. 2002, Rota et al. 2005, Wang et
308 al. 2006). However, the particulars of our search criteria may have had some influence on our

estimates, and alternative estimates for the two *Porphyra* can be found in the literature (Liu et al. 2005, Sun et al. 2006, Wang et al. 2007, Xie et al. 2009).

A survey of service providers indicates that many companies guarantee the development of 10 polymorphic microsatellite loci in 1–3 months with a cost of \$5,000–10,000 (Abdelkrim et al. 2009). Using shotgun sequencing, we were able to develop 12 polymorphic microsatellite loci in a similar period of time with a final cost of €7,000. Polymorphism (as number of alleles) in our loci was comparable to values reported for other red algae (Guillemin et al. 2005, Andreakis et al. 2007). In this regard, previous analysis with dominant AFLPs markers has revealed very low levels of genetic diversity in one of the species included in this study (*G. lanceola*; I. Maneiro, L. Couceiro, I. Ba'rbara, J. Cremades, J. M. Ruiz, and R. Barreiro, unpublished), and the slightly lower number of alleles found for this species, as well as the high proportion of monomorphic loci (12/19), seems consistent with these previous results. Therefore, our approach shows a time- and cost-effectiveness comparable to those of traditional methods of microsatellite development. However, the genome sequencing approach still offers a number of alternatives that may enhance its effectiveness. Using microsatellite-enriched DNA before pyrosequencing, Santana et al. (2009) reported that 25%–97% of their initial reads contained microsatellite motifs (estimates vary depending on the species and enrichment protocol used), values that clearly surpass the <10% found in our two red algae. Likewise, our microsatellite search was restricted to perfect motifs, but there is some evidence that complex repeated core motifs (i.e., multiple or interrupted repeats) dominate in other red algae (Wattier et al. 1997, Luo et al. 1999, Guillemin et al. 2005, Andreakis et al. 2007). The possibility that complex patterns may be more abundant in red algae surely warrants further investigation and suggests that the development of polymorphic loci from NGS data could benefit from less stringent screening criteria. Although interrupted repeats are expected to have lower mutation rates compared to pure ones (Buschiazzo and Gemmell 2006), empirical data from red algae reveal

that many useful microsatellite loci have complex patterns (Wattier et al. 1997, Luo et al. 1999, Guillemin et al. 2005, Andreakis et al. 2007).

Microsatellite detection with genome sequencing data has other additional benefits. The access to a large volume of sequences allows the detection of putative mobile elements by spotting sequence similarity groups (Meglecz et al. 2010). Using the package QDD (Meglecz et al. 2010), we removed 25.8%–26.2% of the sequences with potential loci, possibly saving time and money in primer design and laboratory testing for useless loci since PCR amplification can be seriously affected by microsatellite and mobile element associations. On the other hand, genome sequencing produces a large number of novel genomic resources that may be useful for both related and unrelated research such as gene content, gene functions, or even the association of PAL with coding regions (Sharma et al. 2007, Tangphatsornruang et al. 2009). In summary, we have reported the cost- and labor-effective development of microsatellite markers in two red algae using shotgun sequencing data (454 technology). To our knowledge, this is the first time that random genome sequencing is used for microsatellite identification in seaweeds. Our results suggest that microsatellite density in our two red algae is below the levels reported for other taxa studied with shotgun technology. However, and despite the use of a stringent filtering procedure to avoid redundancy, we still obtained a substantial number of PAL. A limited number of these PAL were successfully tested for PCR amplification and polymorphism finding that they may be suitable for population genetic studies. Shotgun sequencing appears as an efficient alternative for the fast development of microsatellite loci in difficult and/or poorly studied red algae species.

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TABLE 1. Counts of loci for each combination of microsatellite category (di-, tri-, tetra-, penta-, and hexanucleotides) and number of perfect tandemly repeat units in each species. Within each cell, values are given for identified/potentially amplifiable microsatellite loci.

	Cruoriaceae species					<i>Grateloupia lanceola</i>				
	di-	tri-	tetra-	penta-	hexa-	di-	tri-	tetra-	penta-	hexa-
4	3,409/1,019	515/131	27/5	20/4*	25/4	3,385/1,052	513/124	41/8	18/3	20/7
5	536/118	85/18	11/1*	5/0	9/3*	385/92	107/31	11/5*	8/1	6/3*
6	134/21	38/8	3/1*	4/0	4/0	77/16	35/5	3/0	0/1	4/0
7	69/5	12/6*	7/0	0/0	0/0	30/7	4/0	2/1*	3/0	0/0
8	37/7	14/2*	4/1*	1/0	2/0	11/4*	6/2*	1/0	0/0	2/1*
9	23/5*	9/0	2/0	2/0	4/0	15/2*	5/2*	0/0	0/0	0/0
≥10	73/3*	21/3*	8/0	3/0	17/0	54/3*	16/1*	1/0	0/0	1/0
≥25	17/0	3/0	1/0	2/0	4/1*	2/0	0/0	0/0	0/0	0/0
≥50	11/0	2/0	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Total	4,309/1,178	699/168	64/8	37/4	65/8	3,959/1,176	686/165	59/14	29/5	33/11

*, Denotes categories of potentially amplifiable loci that were tested for amplification and polymorphism.

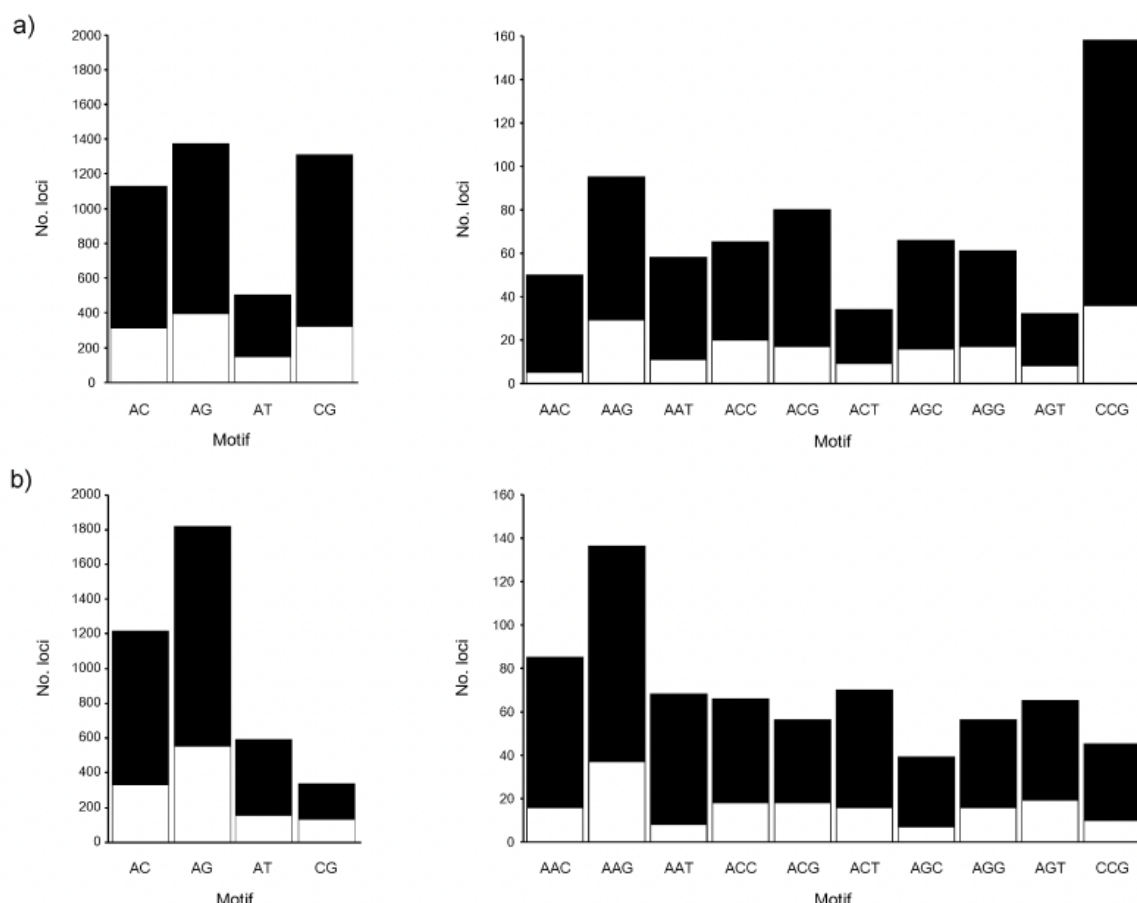


FIG. 1. Motif frequency in di- and trinucleotide repeats. Number of identified microsatellite loci (black) and subset for which PCR primers could be designed (potentially amplifiable loci, PAL; white) for different repeat sequence motifs in (a) undescribed Cruoriaceae and (b) *Grateloupia lanceola*.

Supplementary Material

The following supplementary material is available for this article:

Appendix S1. Details of Cruoriaceae PAL (GenBank accession, number of perfect tandemly repeated units, repeat monomer sequence) and designed primers (forward and reverse sequences, melting temperatures).

Appendix S2. Details of *Grateloupia lanceola* PAL (GenBank accession, number of perfect tandemly repeated units, repeat monomer sequence) and designed primers (forward and reverse sequences, melting temperatures).

Table S1. Characteristics of five and seven polymorphic microsatellite loci in the undescribed Cruoriaceae and *Grateloupia lanceola*, respectively (attributes/primer sequences for monomorphic loci are available from authors upon request). N : sample size; N_A : number of alleles; H_o : observed heterozygosity; H_e : expected heterozygosity.

Table S2. Frequency/attributes of EST-derived microsatellites for seven Rhodophyta species.

Table S3. Microsatellite frequencies (microsatellite counts per Mbp) reported for genome sequencing approaches in this (as shaded data) and other studies.

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