Isolation and Characterization of Microsatellite Loci for the Isopod Crustacean Armadillidium vulgare and Transferability in Terrestrial Isopods

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Abstract

Armadillidium vulgare is a terrestrial isopod (Crustacea, Oniscidea) which harbors Wolbachia bacterial endosymbionts. A. vulgare is the major model for the study of Wolbachia-mediated feminization of genetic males in crustaceans. As a consequence of their impact on host sex determination mechanisms, Wolbachia endosymbionts are thought to significantly influence A. vulgare evolution on various grounds, including population genetic structure, diversity and reproduction strategies. To provide molecular tools for examining these questions, we isolated microsatellite loci through 454 pyrosequencing of a repeat-enriched A. vulgare genomic library. We selected 14 markers and developed three polymorphic microsatellite multiplex kits. We tested the kits on two A. vulgare natural populations and found high genetic variation, thereby making it possible to investigate the impact of Wolbachia endosymbionts on A. vulgare nuclear variation at unprecedented resolution. In addition, we tested the transferability of these kits by cross-species amplification in five other terrestrial isopod species harboring Wolbachia endosymbionts. The microsatellite loci showed good transferability in particular in Armadillidium nasatum and Chaetophiloscia elongata, for which these markers represent promising tools for future genetic studies.

Introduction

Armadillidium vulgare is a terrestrial isopod (Crustacea, Oniscidea) which exhibits a worldwide distribution. A. vulgare harbors alphaproteobacterial endosymbionts of the genus Wolbachia [1,2]. These maternally-inherited, intracytoplasmic bacteria are known to manipulate host reproduction to enhance their own transmission through four different mechanisms: cytoplasmic incompatibility, thelytokous parthenogenesis, male killing and feminization [3,4]. Wolbachia endosymbionts are prevalent in terrestrial isopods [5], and A. vulgare has emerged as a major model for studying Wolbachia-mediated feminization [3,6–8]. In A. vulgare, zygotes carrying Wolbachia develop a female phenotype, whatever their sex chromosome composition. In particular, genetic males harboring Wolbachia are converted into functional females. As a consequence, A. vulgare populations in which Wolbachia are present show sex ratio distortions towards females, thereby enhancing Wolbachia spread in infected populations. In addition, some A. vulgare individuals carry another feminizing factor, known as the f element, which may be a fragment of the Wolbachia genome carrying feminization information and transferred into the host nuclear genome [3,9]. Furthermore, the occurrence of multiple feminizing factors has generated genetic conflicts in this system, which resulted in the selection of A. vulgare nuclear genes resisting feminization [3,10,11]. Thus, sex determination mechanisms are very dynamic in A. vulgare, outlining the prime influence of Wolbachia. These endosymbionts are thought to impact A. vulgare evolution on various additional grounds, including population genetic structure, diversity and reproduction strategies [12].

Mitochondrial DNA markers have been used in several studies, indicating relatively high variability in A. vulgare [1,13–15] as compared to other terrestrial isopod species such as Porcellionides pruinosus [16]. A more elaborate understanding of A. vulgare/ Wolbachia interactions would benefit from information on A. vulgare nuclear variation. Recently, five microsatellite markers [17] were used to investigate nuclear variation in A. vulgare populations from western France, suggesting a genetic structure compatible with isolation by distance [14]. Although polymorphic, these markers may not be in sufficient number to offer the desired resolution for detecting a possibly subtle impact of Wolbachia on A. vulgare nuclear variation, population dynamics and evolution. To provide tools for examining these questions, we isolated microsatellite loci through 454 pyrosequencing of a repeat-enriched A. vulgare genomic library. We selected markers yielding clear amplification signals and showing appropriate polymorphism levels. Next, we used the candidate loci to develop three polymorphic microsatellite multiplex kits. The transferability of these kits was tested by cross-species amplification in other terrestrial isopod species harboring Wolbachia endosymbionts [5,18].
Materials and Methods

Ethics Statement

No ethics statement was required for the described study. No specific permission was required for sampling the two A. vulgare field populations (La Crèche and Beauvoir-sur-Niort, France) because they were located in public areas. Field populations of Armadillidium nasatum (Poitiers, France) and P. pruinosus (Buxerolles, France) were sampled on private lands after the land owners gave permission to conduct sampling on the sites. None of these species is an endangered or protected species.

Microsatellite isolation

For genomic library construction, we maximized genomic diversity by using eight A. vulgare female individuals selected from the following laboratory lines: BF (bac 377), BH (bac 366), CY (bac 291), CW (bac 49), POA (bac 42), WS (bac 43), WX (matricule 1288) and ZM (bac 47). Total genomic DNA was obtained for each individual by standard phenol-chloroform extraction [19] followed by RNase (10 mg/ml) treatment. DNA concentration was measured using a picogreen assay and equimolar amounts of the eight samples were pooled. The pooled sample was used by GenoScreen (Lille, France) to construct a microsatellite-enriched genomic library, as previously described [20]. The library was sequenced by GenoScreen in a partial 454 GS FLX sequencer run with Titanium chemistry, as previously described [20]. The resulting reads were analyzed with the QDD software [21] to identify reads containing microsatellite motifs and design primers for PCR amplification.

Locus validation and polymorphism tests

All microsatellite loci with PCR primers designed using QDD were initially tested using two A. vulgare female individuals from our laboratory line BF (matricule 2756). Total genomic DNA from the two samples was extracted as above and subjected to whole genome amplification using the illustra GenomiPhi V2 DNA Amplification Kit (GE Healthcare) to generate large enough amounts of template DNA for microsatellite testing. To reduce genotyping costs, each locus was amplified and fluorescently labeled using the M13(-21) primer genotyping protocol [22]. This PCR method uses three primers: a locus-specific forward primer with M13(-21) at its 5‘ end, a locus-specific reverse primer and a universal 6-FAM-labeled M13(-21) primer. PCR amplification was performed in 10 μL reactions, using 0.5 μM of both 6_FAM-M13(-21) and reverse primers, 0.125 μM forward primer, 0.25 U GoTaq DNA Polymerase (Promega), 1X PCR reaction buffer (Promega), 0.2 mM dNTPs (Promega) and 1 μL DNA template. PCR thermal conditions were as previously described [22]. Subsequently, 0.5 μL PCR products were added to 9 μL formamide and 0.35 μL ROX standard (Life Technologies), and resolved by electrophoresis on an ABI PRISM 3130 Genetic Analyzer. Product sizes were determined using the GeneMapper software (Applied Biosystems), followed by eye verification. Microsatellite loci amplifying in at least one of the two tested individuals and yielding unambiguous amplification signals were further evaluated for their informativeness. Amplification success rates and number of different alleles at each locus were assessed by genotyping a panel of 24 A. vulgare individuals (12 males and 12 females) from five laboratory lines: BF (n = 5), BFog (n = 4), WXa (n = 5), BG (n = 5) and ZM (n = 5). First, the 24 samples were subjected to whole genome amplification as described above. Next, microsatellite loci were genotyped using the M13 (-21) primer protocol described above.

Multiplexing and cross-species amplification

Based on the genotyping results of the 24-individual panel, we selected 14 microsatellite markers for which locus-specific forward primers (without M13(-21) tail) were ordered with labeled dyes (6_FAM, HEX or NED) [Table 1]. First, we verified amplification of the 14 markers in simplex PCR conditions on three individuals from each of two A. vulgare field populations (La Crèche and Beauvoir-sur-Niort, France) [Table 2]. Total genomic DNA was extracted as above. All PCR reactions were carried out using the QIAGEN multiplex PCR kit according to the manufacturer’s standard microsatellite amplification protocol in a final volume of 10 μL, with an annealing temperature of 58°C and a final concentration of 0.2 μM for each primer. DNA concentrations were adjusted for all individuals between 20 and 60 ng/μL. Next, 1 μL PCR product was added to 18 μL formamide and 0.5 μL ROX standard (Life Technologies). PCR products were resolved by electrophoresis and their size determined as described above.

After simplex PCR verification, we pooled the 14 markers in three multiplex kits (Table 1) according to amplified fragment sizes and dyes to maximize efficiency and minimize costs. The multiplex kits were tested with the same three individuals used for simplex PCR reactions, using the QIAGEN multiplex PCR kit as described above. Identical results were obtained for both simplex and multiplex PCR conditions, thereby validating the use of the three multiplex kits in subsequent analyses. Polymorphism of the 14 microsatellite loci in A. vulgare field populations was evaluated by genotyping 20 individuals from each of two populations (La Crèche and Beauvoir-sur-Niort, France) using the multiplex kits.

To investigate transferability of the 14 microsatellite markers, cross-species amplifications were performed in five terrestrial isopod species related to A. vulgare and known to harbor Wolbachia endosymbionts [5,18]: A. nasatum (n = 8) and P. pruinosus (n = 8), which were sampled in the field in 2012, and Chaetophiloscia elongata (n = 8), Poreello scaber (n = 8) and Oniscus asellus (n = 8) from laboratory populations (Table 3). Total genomic DNA was extracted as above. Genotyping was performed using the three multiplex kits.

Data analyses

To assess genetic variability and transferability of our microsatellite markers, we calculated number of alleles (Na), unbiased expected heterozygosity (He) [23], observed heterozygosity (Ho) and Fis [24] using Genetix version 4.05.2. We computed these genetic indices from two A. vulgare populations and from individuals of the five other aforementioned species. Departure from Hardy-Weinberg expectations was assessed for each microsatellite marker using exact tests (5000 permutations), as implemented in GENEPOL version 3.4 [25]. Linkage disequilibrium was assessed for each microsatellite marker using FSTAT version 2.9.3.2 [26] and with 1000 permutations. The level of significance was adjusted for multiple testing using a sequential Bonferroni correction technique [27].

Results and Discussion

Locus identification, validation and polymorphism

Sequencing of the microsatellite-enriched library yielded 18,511 reads. The sequence dataset is available in the Dryad database at http://doi.org/10.5061/dryad.md545. Of these, 5073 (27%) reads contained microsatellite motifs according to QDD analysis. Primer pairs were designed for all loci fulfilling our criteria for primer design [20]. The 146 resulting loci comprised 93 di- (n = 8) and Fis [24] using Genetix version 4.05.2. We computed these genetic indices from two A. vulgare populations and from individuals of the five other aforementioned species. Departure from Hardy-Weinberg expectations was assessed for each microsatellite marker using exact tests (5000 permutations), as implemented in GENEPOL version 3.4 [25]. Linkage disequilibrium was assessed for each microsatellite marker using FSTAT version 2.9.3.2 [26] and with 1000 permutations. The level of significance was adjusted for multiple testing using a sequential Bonferroni correction technique [27].

Microsatellite Loci for Armadillidium vulgare
5 to 22 repeat units (Table S1). Two *A. vulgare* individuals were genotyped for the 146 microsatellite loci and 41 loci were validated under our amplification conditions and criteria (Table S1). Out of the 41 loci, a first polymorphism analysis based on a 24-individual panel allowed us to identify 33 polymorphic loci (i.e. 80%) (Table S1). Among these 33 polymorphic loci, we selected 14 loci for inclusion in multiplex kits, according to the following criteria: (i) repeat type (larger motifs favored), (ii) number of different alleles

**Table 1.** Microsatellite multiplex kits developed for the terrestrial isopod *Armadillidium vulgare*.

| Locus name | Repeat motif | Forward primer (5’-3’) | Reverse primer (5’-3’) | Dye |
|------------|--------------|------------------------|------------------------|-----|
| Multiplex kit #1 |              |                        |                        |     |
| AV0023     | AG           | TGAATTTATGTTTGGAGAGGG   | GAGGTAAAGTCTGGGTCGG    | HEX |
| AV0056     | GTT          | TCCAAGGAGCGTTTGACCT     | AACCACAGCAACAACAGCA    | 6_FAM |
| AV0085     | GTA          | CAGCCGCTAGTCCTCTAGACA   | TGGTTATGTAAATACCTGAAGTT | NED |
| AV0086     | TTC          | CCGTGCTCCCGATATTCTT     | TGCCAAAGGCCAATGTA      | HEX |
| AV0096     | AAG          | TGGTGATTTGCTTAAACCAGGTG | TAGTTCTTTTCCCCCCTATT | 6_FAM |
| Multiplex kit #2 |              |                        |                        |     |
| AV0002     | ACTCCG       | CGACTCCGACTCCGAATG      | CTCCACGGTGTGATCTCT     | 6_FAM |
| AV0016     | TC           | GCTATTTTAGCTCTGTCGCG    | CTTGAAAGACTTAGACTG     | 6_FAM |
| AV0018     | CA           | GAAGAAATCAACTCACTCACTCA | CTTGGAACAGACTTGAATACATC | HEX |
| AV0032     | TC           | TTACACCTCTCTAAACAGCC    | TTGTATTATCCAGACATCC    | NED |
| AV0099     | TG            | CCCCCCTTGTGCTATGAGTG    | ACCCTCGCTTACATTACC     | HEX |
| Multiplex kit #3 |              |                        |                        |     |
| AV0061     | CT            | GTTTGTATGCATTTACCCCCTTC | GTATTGCAATGTACCTTG     | HEX |
| AV0063     | TACA          | CAAATCGACTGGATTCCCTCA   | GCAAACATATAAGTCTCGCT   | NED |
| AV0089     | CTA           | TTACACCTCTCACTCACTTGC   | TGCTCTATATGACATGAA     | HEX |
| AV0128     | GAT           | GTGCCTTGAGACAGCTAAGA    | CGTCCGATGGTATTTTGT     | 6_FAM |

doi:10.1371/journal.pone.0076639.t001

**Table 2.** Characterization of the 14 microsatellite loci used in multiplex kits in two Armadillidium vulgare populations.

| Populations | La Crèche (N = 20) | Beauvoir-Sur-Niort (N = 20) | Overall population (N = 40) |
|-------------|---------------------|-----------------------------|-----------------------------|
| Parameters  | Na | He/Ho | Fis | Na | He/Ho | Fis | Na | Size range (bp) | He/Ho | Fis |
| Multiplex kit #1 |     |       |    |     |       |    |     |                   |       |     |
| AV0023      | 1  | -    | -  | 1  | -    | -  | 1  | 193               | -    | -  |
| AV0056      | 4  | 0.57/0.70 | -0.23 | 5  | 0.46/0.50 | -0.09 | 6  | 198–219          | 0.52/0.60 | -0.15 |
| AV0085      | 2  | 0.10/0.10 | -0.03 | 4  | 0.28/0.30 | -0.09 | 4  | 175–190          | 0.19/0.20 | -0.06 |
| AV0086      | 3  | 0.10/0.10 | -0.01 | 3  | 0.23/0.25 | -0.09 | 3  | 113–122          | 0.17/0.18 | -0.06 |
| AV0096      | 2  | 0.51/1.00 | -1.00 | 3  | 0.55/1.00 | -0.87 | 3  | 83–107           | 0.52/1.00 | -0.94 |
| Multiplex kit #2 |     |       |    |     |       |    |     |                   |       |     |
| AV0002      | 5  | 0.51/0.45 | 0.12 | 5  | 0.54/0.61 | -0.15 | 5  | 260–308          | 0.52/0.53 | -0.02 |
| AV0016      | 3  | 0.34/0.30 | 0.11 | 2  | 0.14/0.15 | -0.06 | 3  | 114–126          | 0.24/0.23 | 0.08 |
| AV0018      | 4  | 0.71/0.70 | 0.02 | 5  | 0.77/0.85 | -0.10 | 5  | 97–136           | 0.74/0.78 | -0.04 |
| AV0032      | 4  | 0.43/0.45 | -0.04 | 3  | 0.38/0.35 | 0.07  | 4  | 89–105           | 0.40/0.40 | 0.00 |
| AV0099      | 5  | 0.49/0.20 | 0.60 | 6  | 0.71/0.58 | 0.19  | 6  | 160–198          | 0.60/0.39 | 0.36 |
| Multiplex kit #3 |     |       |    |     |       |    |     |                   |       |     |
| AV0061      | 1  | -    | -  | 1  | -    | -  | 1  | 138               | -    | -  |
| AV0063      | 3  | 0.45/0.50 | -0.12 | 3  | 0.50/0.40 | 0.20  | 3  | 129–137          | 0.48/0.45 | 0.05 |
| AV0089      | 2  | 0.10/0.10 | -0.03 | 1  | -    | -  | 2  | 85–88            | 0.05/0.05 | -0.01 |
| AV0128      | 2  | 0.51/0.95 | -0.90 | 3  | 0.45/0.61 | -0.37 | 3  | 120–129          | 0.49/0.79 | -0.61 |

doi:10.1371/journal.pone.0076639.t002

Sampled locations, GPS coordinates (longitude and latitude in World Geodetic System 1984) and number of sampled individuals (N) are shown. Number of alleles (Na), size range of alleles (bp), unbiased expected heterozygosity (He), observed heterozygosity (Ho), and Fis are shown. Significant values (P≤0.01) are shown in bold.

doi:10.1371/journal.pone.0076639.t002
### Table 3. Transferability of the 14 microsatellite loci used in multiplex kits in five terrestrial isopod species.

| Species                        | Armadillidium nasatum | Porcellionides pruinosus | Chaetophiloscia elongata | Oniscus asellus | Porcellio scaber |
|--------------------------------|-----------------------|---------------------------|--------------------------|----------------|-----------------|
| Populations                    | Poitiers              | Buxerolles                | Laboratory line          | Laboratory line | Laboratory line |
| GPS coordinates                | 46°35'3.77006"N, 00°22'16.07919"E | 46°36'50.3"N, 00°21'38.6"E |                                         |                       |                       |
| Parameters                     | Na | Size range | He/Ho | Fis | Na | Size range | He/Ho | Fis | Na | Size range | He/Ho | Fis | Na | Size range | He/Ho | Fis | Na | Size range | He/Ho | Fis |
| Multiplex kit #1               |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |
| AV0023                         | IN | -          | -    | -  | 1  | 193        | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0056                         | 3  | 198–209    | 0.24/0.13 | 0.5 | 2  | 209–219    | 0.13/0.13 | -  | IN | -          | -    | -  | 6  | 231–279    | 0.85/0.43 | 0.51 |
| AV0085                         | 4  | 169–178    | 0.74/0.38 | 0.51| 2  | 175–181    | 0.13/0.13 | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0086                         | 1  | 110        | -    | -  | 3  | 107–113    | 0.62/0.29 | 0.56| 2  | 110–113    | 0.48/0.67 | -0.43| 2  | 110–113    | 0.53/0.17 | 0.71| 2  | 110–113    | 0.13/0.13 | -  |
| AV0096                         | 4  | 77–89      | 0.70/0.71 | -0.02| 3  | 74–89      | 0.44/0.30 | -0.15| IN | -          | -    | -  | 2  | 74–83      | 0.53/0.50 | 0.06| 3  | 74–89      | 0.59/0.17 | 0.74|
| Multiplex kit #2               |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |
| AV0002                         | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0016                         | 2  | 94–116     | 0.36/0.14 | 0.63| 3  | 99–113     | 0.62/0.29 | 0.56| 2  | 110–113    | 0.48/0.67 | -0.43| 3  | 110–113    | 0.53/0.17 | 0.71| 2  | 110–113    | 0.13/0.13 | -  |
| AV0018                         | 3  | 100–106    | 0.54/0.38 | 0.32| 3  | 97–135     | 0.59/0.67 | -0.14| IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0032                         | 3  | 89–99      | 0.73/0.60 | 0.2 | 3  | 89–99      | 0.47/0.60 | -0.33| IN | -          | -    | -  | 3  | 95–99      | 0.32/0.33 | -0.05| 3  | 95–99      | 0.32/0.33 | -0.05|
| AV0099                         | 3  | 160–174    | 0.69/0.63 | 0.1 | 1  | 160        | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| Multiplex kit #3               |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |    |            |      |    |
| AV0061                         | 2  | 144–146    | 0.50/0.25 | 0.52| 2  | 138–146    | 0.13/0.13 | -  | IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0063                         | 2  | 133–137    | 0.20/0.20 | -  | 3  | 129–137    | 0.54/0.43 | 0.22| 3  | 129–137    | 0.67/0.67 | 0  | IN | -          | -    | -  | IN | -          | -    | -  |
| AV0089                         | IN | -          | -    | -  | 2  | 85–88      | 0.53/0.50 | 0.06| 2  | 85–88      | 0.33/0.38 | -0.17| 2  | 85–88      | 0.36/0.40 | -0.14| 2  | 85–88      | 0.17/0.17 | -  |
| AV0128                         | IN | -          | -    | -  | 2  | 126–129    | 0.53/0.80 | -0.6| IN | -          | -    | -  | IN | -          | -    | -  | IN | -          | -    | -  |

Parameters are as described in the legend to Table 2. IN indicates inconsistent amplification of the locus in one species.

doi:10.1371/journal.pone.0076639.t003
expected heterozygosity ranged from 0.40 to 0.53. Results from *A. nasatum* are not really surprising given the close phylogenetic relationship with *A. vulgare*. The important rate of successful cross-amplification found in *Celongata* is more surprising but microsatellite loci show a reduced number of alleles and low heterozygosity indices in *C. elongata* relative to *A. vulgare*. We detected no linkage disequilibrium whereas departure from Hardy-Weinberg expectations was detected for loci AV0056 and AV0059 in *P. scaber* and for loci AV0032 and AV0005 in *A. nasatum*. The deficit in heterozygotes observed for these loci could be explained by the quite small sampling.

Conclusions

In sum, our work highlights a large set of microsatellite markers useful for studies on *A. vulgare* and other terrestrial isopod species. The polymorphism of these markers now makes it possible to analyze genetic diversity, population structure and reproduction strategies of *A. vulgare* at unprecedented resolution. A study based on these markers is now underway to analyze the impact of *Wolbachia* bacterial endosymbionts on *A. vulgare* nuclear variation. Moreover, these microsatellite markers showed good transferability in five other terrestrial isopod species, in particular in *A. nasatum* and *C. elongata*, for which these microsatellite markers represent promising tools for future genetic studies.

Supporting Information

Table S1 Information on the 146 microsatellite loci from *Armadillidium vulgare* tested for inclusion in multiplex kits. For each locus the following information is provided: locus name, repeat motif, repeat number, reference sequence, forward primer, reverse primer, PCR product size in reference sequence, and results of experimental tests leading to final selection for three multiplex kits. (XLSX)

Author Contributions

Conceived and designed the experiments: RC FG NB. Performed the experiments: IG VV. Analyzed the data: IG VV RC FG NB. Contributed reagents/materials/analysis tools: VV FG RC. Wrote the paper: RC. Coordinated the study: RC. Revised the manuscript: VV FG NB.

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