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A novel method of microsatellite genotyping-by-sequencing using individual combinatorial barcoding

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This study examines the potential of next-generation sequencing based 'genotyping-by-sequencing' (GBS) of microsatellite loci for rapid and cost-effective genotyping in large-scale population genetic studies. The recovery of individual genotypes from large sequence pools was achieved by PCR-incorporated combinatorial barcoding

using universal primers. Three experimental conditions were employed to explore the possibility of using this approach with existing and novel multiplex marker panels and weighted amplicon mixture. The GBS approach was validated against microsatellite data generated by capillary electrophoresis. GBS allows access to the underlying nucleotide sequences that can reveal homoplasy, even in large datasets and facilitates cross laboratory transfer. GBS of microsatellites, using individual combinatorial barcoding, is potentially faster and cheaper than current microsatellite approaches and offers better and more data.

1. Introduction

The advent of next-generation sequencing (NGS) technologies has fundamentally changed how genetic sequence data are generated [1]. While NGS was primarily introduced to substantially increase sequence yield for genome projects [2–4], it has in addition enabled high-throughput genotyping that can be used for genetic studies, including population genetics, by using a range of protocols (e.g. RAD [5], ddRAD [6], 2bRAD [7]). This is collectively known as 'genotyping-by-sequencing' (GBS) [8,9].

The primary advantage of GBS for population genetic studies is the generation of increased quantities of data that allows for improved statistical power and high genome representation [9]. The concurrent development of single-nucleotide polymorphism (SNP) genotyping platforms (e.g. SNP-chips [10,11], microfluidic TaqMAN assays [12]) and the persistent problems associated with microsatellite genotyping has led to a shift from using microsatellites to SNPs as the preferred marker for genetic studies [13]. The main problems with capillary and gel-based microsatellite studies include fragment size homoplasy, poor levels of inter-laboratory calibration, the genotype not including the underlying sequence information and inherently laborious genotyping [14,15]. However, there are also unresolved problems regarding SNPs, such as ascertainment bias, transferability among SNP genotyping platforms and the requirement for high template DNA quality [16–18]. While SNPs do not suffer many of the issues associated with microsatellite genotyping, the major advantage of microsatellites over SNP-based approaches for population analyses is the higher statistical power per locus [19–21]. Additionally, microsatellites are preferred to SNPs in forensic, parentage and kinship studies owing to their higher mutation rates and polyallelic nature [22–25].

Many of the issues associated with microsatellite-based population studies could be mitigated using a GBS approach. The effects of size-homoplasy [26] can be effectively eliminated because the genotype incorporates the underlying sequence information. The difficulties of inter-laboratory calibration would be significantly reduced, as GBS considers actual base-pair lengths of the alleles, and not the estimated allele size sequence length [15]. Additionally, the elimination of time consuming capillary or gel electrophoresis runs [27] can reduce genotyping time, thereby increasing efficiency. Further, GBS has the potential to use established microsatellite multiplex panels, enabling calibration with existing datasets and facilitating inter-laboratory collaboration. However, few GBS studies based on microsatellites have been published [28–30].

The current study aims to assess the potential of microsatellite GBS using Atlantic cod *Gadus morhua* (L.) as the study organism. The primary objective was to examine the potential of microsatellite GBS using *de novo* and existing capillary/gel electrophoresis-based multiplex marker panels. The secondary objective was to develop a rapid and cost-effective method for microsatellite GBS, that can take advantage of modern NGS platforms, using combinatorial barcoding for implementation in large-scale population genetics studies.

2. Material and methods

A total of 64 Atlantic cod were collected from the Celtic Sea ($n = 32$) and the West of Ireland ($n = 32$) in 2011. Tissue samples were preserved in molecular grade ethanol. DNA was extracted using a Chelex® protocol [31]. DNA was quantified using a NanoDrop 1000 Spectrophotometer (Thermo Scientific, Wilmington, DE, USA) and diluted to a concentration of 50 ng μl^{-1}. These samples had previously been genotyped in six original PCR multiplexes at 53 microsatellite loci using a conventional ABI capillary-based approach [32] thus providing a platform for direct comparison with the current study.

Six multiplex PCR panels comprising 53 microsatellite loci [32] were analysed to test the capability of microsatellite GBS on all individuals. Each of the six original multiplex panels included loci in

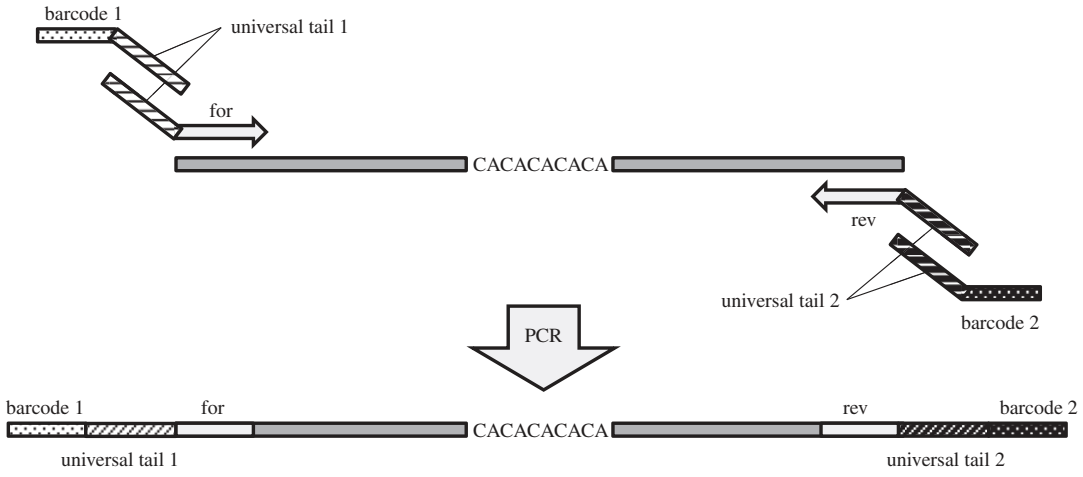

Figure 1. Diagram of the four-primer PCR and the structure of the resulting amplicon.

three different size classes (class I: 115–213 bp, class II: 203–320 bp and class III: 265–416 bp, see the electronic supplementary material, table S1). To assess the preferential amplification of shorter fragments during PCR and NGS sequencing [30,33], weighted ratio mixtures of fluorescently labelled amplicons were visualized on an ABI 3130xl Genetic Analyzer (Applied Biosystems; conditions according to [32] suggesting an optimal size-class amplicon-ratio of 1(I) : 1(II) : 8(III).

Three PCR size-class-combinations for GBS were evaluated (electronic supplementary material, table S1). The first *de novo* multiplex panels were weighted for amplicon size by combining all markers of the same size classes (3-PCR) from the six original multiplexes using a subset of 16 individuals from the Celtic Sea. The second size-class-combination consisted of the existing multiplexes (6-PCR) using the same subset of 16 individuals from the Celtic Sea (*sensu* [32]). The third PCR size-class-combination comprised the six existing multiplex panels, subdivided into three smaller multiplex panels according to the three size classes using all 64 individuals (18-PCR).

The three-primer PCR approach [32,34] was modified into a four-primer PCR to produce unique individual combinatorial barcoded amplicons suitable for pooled amplicon NGS in population genetics studies. Each barcode comprised 10 bp of synthesized DNA sequence [35]. The modified protocol consisted of locus-specific primers (forward and reverse) that were adapted to include universal primer sequence (figure 1; electronic supplementary material, table S2). Two barcoded universal primers were included to incorporate two barcodes into each of the resulting amplicons. In total, 12 forward and eight reverse DNA barcodes allowed for the recovery of 96 unique individual combinatorial barcodes (electronic supplementary material, table S3).

Multiplex PCRs (cycling condition as in [32]) were performed in 10 µl reactions (size classes I and II) and 20 µl reactions (size class III, in 3-PCR and 18-PCR size-class-combinations) with 1 µl template DNA, 1× Multiplex PCR Master Mix (Qiagen, Hilden, Germany), 2 pmol of each locus-specific primer and 8 pmol of each barcoded universal primer per locus-specific primer with the corresponding universal primer sequence. For each multiplex and PCR size-class-combination equal amounts of PCR product from each individual were pooled and separated by gel electrophoresis on a 2% agarose gel at 5 V cm^{-1}. PCR products were visualized using Safe Imager® (Invitrogen, Life Technologies, Carlsbad, CA, USA). Products corresponding to expected amplicon sizes were cut out from the gel and placed into 2 ml centrifuge tubes. DNA was extracted using the QIAquick® Gel Extraction Kit (Qiagen, Hilden, Germany). Amplicon DNA was quantified using Qubit® 2.0 Fluorometer with a dsDNA HS Assay kit (Life Technologies). Amplicons from the 3-PCR and 18-PCR size-class-combinations were normalized to the optimal size-class amplicons-ratio (1 : 1 : 8). The amplicons were concentrated using the Amicon® Ultra 30 K procedure (Merck Millipore Ltd., Merck KGaA, Darmstadt, Germany). An aliquot of the final library was diluted to a concentration of 500 ng in 16 µl for sequencing on a 454 Roche® platform ([36]; 454 Life Sciences Corp., a Roche Company, Branford, CT, USA).

Roche adaptors were added to the amplicon library using the Rapid Library Preparation Kit [37]. Amplicon concentrations were estimated using quantitative PCR to assess differential amplification success depending on amplicon size. Amplicons were sequenced on two 1/4 regions of a Pico TiterPlate using a 454 GS-FLX Sequencer with titanium reagents at Teagasc Food Research Centre, Moorepark,

Ireland. The Shotgun Data Processing Pipeline was used for signal processing to increase sequence yield [38].

A python script was developed to process raw sequence data by identifying sequence reads containing the forward and reverse (combinatorial) barcodes and the locus-specific primers and grouping them accordingly. The script was based on the Levenshtein distance metric which measures the distance between two sequences of characters. The error rate of Roche 454 GS-FLX amplicon sequences when including both sequencing and PCR errors has been estimated in *G. morhua* at 6% [39]. It was therefore necessary to allow for sequencing and PCR errors in the reads in order to avoid a significant loss of reads during the identification and grouping process. The python script allowed for up to two and three sequencing errors (both substitutions and indels) in the combinatorial barcodes and primers, respectively, to reflect a potential sequencing and PCR error rate of approximately 6%. All the scripts used are available on github (https://github.com/egenomics/micomba).

Grouped and classified sequences were imported into GENEIOUS® 7 as fasta files and organized into folders per locus per individual. Loci were manually genotyped by viewing all of the reads of a particular individual at a specific locus, as a read length histogram and verified by read alignment (GENEIOUS ALIGNMENT—default settings) and manually edited [40]. Only individuals with five or more reads for a given locus were genotyped.

Read alignments of a subset of 16 individuals, with 10 or more sequence reads, from the Celtic Sea dataset (six PCR size-class-combinations) were screened for homoplasy. The aligned sequences were scrutinized for the presence of SNPs and indels that were not part of the microsatellite repeat structure and would not change the amplicon size. The SNP or indel had to occur in at least 20% of the reads to be considered as homoplasy.

Correspondence between GBS and ABI capillary-based genotyping data [32] was fitted to a binomial model [41] (electronic supplementary material, equation S1). The impact of several factors on GBS–ABI correspondence was evaluated. These factors included microsatellite type (e.g. mono-, di-), PCR size-class-combination (3-, 6- or 18-PCR), and read depth used for genotyping (broken into 2 and 3 read depth categories). Model fit was compared using the finite-sample Akaike information criterion (AIC) [42–46] (electronic supplementary material, equations S3 and S4).

Binomial proportions of the correspondence data were modelled for a restricted subset of the data, 16 individuals from the Celtic Sea ('Celtic Sea' dataset), for which data existed across all PCR size-class-combinations. Differences in correspondence proportions among PCR size-class-combinations were evaluated using Bonferroni-corrected *z*-tests [47]. The effectiveness of PCR size-class-combinations on the total number of reads produced for the Celtic Sea data was then evaluated. Total reads were modelled as a function of PCR size-class-combination, locus-specific primer and universal primer type, in addition to potential intrinsic confounding variables, such as inter-locus or inter-individual variability. A multinomial probability likelihood model [41] (electronic supplementary material, equation S2) was employed to evaluate model support using AIC. Bonferroni-corrected Mann–Whitney tests [47] were performed on total, median and maximum number of reads per individual between the PCR size-class-combinations to assess significant differences in the performance of PCR size-class-combinations.

3. Results

Sequencing of the two 1/4 regions of a PicoTiterPlate resulted in 228 246 reads for region 1 and 226 848 for region 2. Read length ranged from 54 to 1200 bp with an average read length of 275 bp (s.d. 84 bp). A total of 95.5% of reads had a quality score higher than Q20 and the average quality score was Q35.9. The proportions of A, C, G and T nucleotides were 27.0%, 22.7%, 26.7% and 23.6%, respectively, with a GC content of 49.4%.

A total of 180 054 reads were successfully assigned to a specific individual and locus combinations (electronic supplementary material, table S4). The recovered reads per individual (combined across all loci) ranged from 57 to 9192 (median: 999) (electronic supplementary material, table S3), and the number of reads per locus (combined over all individuals) ranged from 33 to 11 197 (median: 2294). The numbers of reads per genotype ranged from 0 to 1097 (median: 12). Analyses of PCR size-class-combinations resulted in 3325 successful genotypes from 5088 possible calls, with 3196 genotypes used for correspondence checks with the ABI-capillary genotyping data. Of the 53 loci analysed, 10 loci had low numbers of sequence reads preventing genotyping in more than 50% of the individuals (electronic supplementary material, table S5).

Table 1. AICc model selection for the reduced ('Celtic Sea') dataset on the read yield. (Sample size is 90194. *K* is the number of parameters estimated for a given model structure, LogL is the log-likelihood of the model, AICc is the finite-sample AIC score for the model, dAICc is the difference in AICc score between the given model and the optimal model score, and Post. Prob is the model posterior probability.)

model description	*K*	LogL	AICc	dAICc	Post. Prob.
PCR	3	−87 627	175 260	0	1.000
tails	4	−123 574	247 157	71 896	0
forward	6	−143 882	287 776	112 516	0
reverse	8	−157 688	315 391	140 131	0
PCR × tails	12	−210 436	420 896	245 635	0
individuals	16	−216 345	432 722	257 461	0
forward × tails	24	−266 358	532 764	357 504	0
PCR × reverse	24	−245 065	490 177	314 917	0
reverse × tails	32	−281 170	562 403	387 143	0
locus	53	−318 574	637 253	461 993	0
PCR × reverse × tails	96	−367 637	735 467	560 206	0

In total, 529 genotypes were screened for homoplasy, which was detected in 32% of the genotypes and was present in 38 loci. SNPs represented 80% of the homoplasy with 20% represented by indels.

AICc model selection for the Celtic Sea data demonstrated that PCR size-class-combination was the only important variable for predicting read yield. There was no support for other modelled variables (e.g. forward or reverse primers) or confounding variables (such as inter-individual and among-locus variation; table 1). Correspondence between the full GBS and ABI datasets was best explained by a model incorporating read depth and microsatellite motif type (table 2). PCR size-class-combination had an effect on the GBS–ABI correspondence in the Celtic Sea data (electronic supplementary material, table S6), with significantly higher correspondence for both 3-PCR and 6-PCR when either is compared with 18-PCR. However, there was no significant difference between 3- and 6-PCR (electronic supplementary material, table S6). In addition, significantly more reads per individual were observed for 3- and 6-PCR when compared with 18-PCR, although again, there was no significant difference between the two (electronic supplementary material, table S7). No significant differences were noted for median number of reads among size-class-combinations (electronic supplementary material, table S8). Maximum number of reads per individual showed a significant difference between 6-PCR and 18-PCR only (electronic supplementary material, table S9).

4. Discussion

This study demonstrates the potential for NGS-based GBS as a method for microsatellite genotyping using *de novo* and existing capillary/gel electrophoresis-based multiplex marker panels. It also illustrates the potential for a rapid and cost-effective method for microsatellite GBS, that can take advantage of modern NGS platforms, using combinatorial barcoding for implementation in large-scale population genetics studies. This method provides access to the underlying sequence data, providing an additional advantage over traditional fragment length genotyping by resolving issues of size homoplasy and revealing potentially hidden genetic variation in the amplicons.

Analysis of the Celtic Sea data indicates that size-class combination is the controlling factor for both sequence yield and GBS–ABI correspondence. Both the 3- and 6-PCR size class conditions outperformed 18-PCR, with no significant differences between the 3- and the 6-PCR conditions observed. It is possible that 6-PCR would not have performed as well as 3-PCR in the absence of pre-optimization [32]. However, the increased number of PCR reactions and DNA quantification steps in the 18-PCR method may have introduced quantification errors that were amplified at the pooling stage, lowering read yield, and hence correspondence. As such, it is proposed that future studies minimize the number of steps to reduce variability among PCRs.

Binladen *et al.* [48] reported biases in sequence recovery with 454 NGS as a result of different base pair composition of barcodes. In contrast to this, the current study found no bias in sequence

Table 2. Model selection using AICc on the correspondence between 454 microsatellites and ABI microsatellites, using the full dataset. (*K* is the number of parameters estimated for a given model structure, LogL is the log-likelihood of the model, AICc is the finite-sample AIC score for the model, dAICc is the difference in AICc score between the given model and the optimal model score, and Post. Prob is the model posterior probability.)

model	model comments	*K*	LogL	AICc	dAICc	Post. Prob.
no effects	average over all data	1	−1724.64	3451.28	131.96	2.22×10^{-29}
no. reads (2)	0–5 versus 5 + reads	2	−1693.93	3391.87	72.55	1.77×10^{-16}
no. reads (3)	0–5 versus 5–10 versus 10 + reads	3	−1676.04	3358.10	38.78	3.80×10^{-9}
MST type		5	−1693.54	3397.11	77.79	1.29×10^{-17}
reads (2) by MST type	0–5 versus 5 + reads	10	−1663.76	3347.59	28.27	7.26×10^{-7}
reads (3) by MST type	0–5 versus 5–10 versus 10 + reads	15	−1644.58	3319.32	0.00	0.999
PCR (3,6) v. 18		2	−1706.09	3416.18	96.86	9.27×10^{-22}
PCR 3,6,18		3	−1706.08	3418.16	98.84	3.45×10^{-22}
reads (2) by PCR 3,6,18	0–5 versus 5 + reads	6	−1675.28	3362.58	43.26	4.03×10^{-10}
reads (3) by PCR 3,6,18	0–5 versus 5–10 versus 10 + reads	9	−1658.37	3334.79	15.47	0.0004

recovery. Read depth had a significant effect on the genotyping correspondence between the GBS and ABI-based datasets, with correspondence rapidly increasing with sequence depth (figure 2). It is unlikely that complete agreement between these two approaches is achievable, owing to inherent errors in capillary electrophoresis, genotype calls and GBS platform-specific sequencing errors. ABI-based genotype calling from electropherograms can be obscured by spectral bleeding, cross-talk between capillaries and fluctuations in instrument parameters [30]. Similarly, for 454 sequence amplicon reads, error rates have been reported as high as 6% for our study species, *G. morhua* [39]. While the error rate for 454 sequencing can be relatively high, amplicon sequencing, as used here, will be further affected by PCR-induced errors. It is therefore important to allow for some errors in barcodes and primers. When employing other NGS platforms this requirement may be alleviated by the increased read yield of these platforms.

This study represents an example of GBS using established microsatellite multiplex panels that were developed for analysis on conventional capillary/gel-based systems and contain loci with fragment sizes commonly reported in microsatellite studies (approx. 100–500 bp) [28,32,49,50]. Owing to the large size range of alleles in the established microsatellite multiplex panel, the choice of NGS platform was restricted to 454, as it produces up to 1 million reads of up to 700 bp [51]. While the 454 NGS platform has the capacity to produce long sequence reads, the sequence yield is significantly lower than in other platforms: for example, the Ion Torrent platform ([52]; Life Technologies) produces up to six million 400 bp reads on their 318® chip [53] and the Illumina® Miseq platform [54]; Illumina Inc. San Diego, CA, USA) currently produces 20–30 million paired end reads of 2 × 300 bp. The short read length of these platforms limits application to relatively short amplicons (including barcode, primers and repetitive sequence). However, this limitation may be mitigated by *de novo* development of microsatellite markers, the use of partial existing microsatellite panels (i.e. loci with amplicon sizes within the read length limitation of the chosen NGS platform), or the redesign of primers for existing microsatellite markers to produce shorter amplicons.

The current study was not optimized for population genetics scale genotyping as a larger number of loci and a lower number of individuals were analysed than is often used in population genetic studies (cf. [32]). However, in an effort to address multiple questions about the feasibility of GBS of microsatellites, it was judged advantageous to include a larger number of loci than needed for many population genetic studies. In addition, if this method was used on *de novo* developed loci, the success rate from microsatellite containing sequences to genotyped loci is only known *post hoc* and hence a larger number of initial loci would increase the likelihood of generating a sufficient number of informative loci. For deployment of the approach described here, in a population genetics setting, it may be more beneficial to interrogate fewer loci, but more individuals. This could be facilitated by increasing the number of forward and reverse combinatorial barcodes used to tag an increased number of individuals.

Manual scoring of conventional capillary and gel-based electrophoresis fragment length polymorphism is time consuming, and therefore carries a significant financial cost to genetic studies.

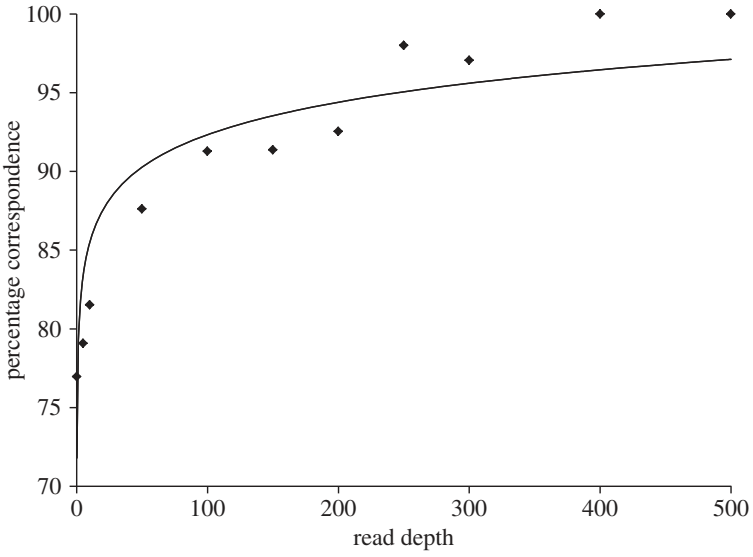

Figure 2. Correspondence of the GBS microsatellite data with ABI data for the full dataset. The *y*-axis represents the percentage of corresponding genotype calls of all genotype calls. The *x*-axis represents the increasing minimum threshold of read depth required for making a genotype call. The applied thresholds were 5, 10, 50, 100, 150, 200, 250, 300, 400 and 500 reads.

This study describes an approach that does not require manual correction of internal size standards or genotype calls owing to spectral bleed-through, thus reducing the genotyping time. In addition, the availability of the underlying sequence data lends itself to the development of automated genotyping [55]. The numbers of loci that can be multiplexed in capillary or gel-based electrophoresis in conventional studies are limited by the availability of fluorescent labels/detection channels and fragment size overlaps (rarely more than 12 loci per multiplex) [56]. The GBS approach described in this study using PCR-incorporated combinatorial barcoding has no limitations on the number of markers (other than number of sequences produced by the chosen NGS platform), as size overlap does not affect sequence yield.

The high proportion of homoplasy (32%) observed is in concordance with other studies addressing the prevalence of homoplasy [57–60]. This homoplasy would have been undetectable using traditional ABI-based microsatellite genotyping as the amplicon size would be unaffected. Previous detection methods include single-strand conformation polymorphism analysis and direct sequencing, with or without cloning, however, these detection methods can be laborious [57–60]. It should be noted that low read depth may prevent distinguishing homoplasy from true mutations and sequencing/PCR error. However, the purpose of the analysis in the current study was to explore the capacity to detect and quantify prevalence of homoplasy using GBS-based methods. The prevalence of homoplasy implies that allelic diversity in fragment size-based studies is probably substantially underestimated. Consequently, inferred population structures in these studies may also underestimate true levels of genetic variability. Aside from homoplasy, determining microsatellite repeat numbers could improve genetic diversity comparisons [61]. Essentially, accessing the molecular structure of the microsatellite markers will increase our understanding of the mutation model of the studied loci and thus improve the quality of the information retrieved from the data. In addition, access to actual sequence lengths and sequence information will greatly facilitate inter-laboratory calibration and data storage in repositories as sequence files offering a significant advantage.

This study presents a novel method for microsatellite GBS using individual combinatorial barcoding that can be faster and cheaper than current approaches while offering better and more data.

Ethics. The fish were caught during a Ryan Institute/Marine Institute (Ireland) Fisheries Science Services survey or recreational sea angling. The fish were killed immediately to avoid suffering. Tissue samples were taken from dead fish. All procedures were conducted according to Irish law.

Data accessibility. The genotype datasets supporting this article are provided as part of the electronic supplementary material, table S10). All the scripts used are available on github (https://github.com/egenomics/micomba).

Authors' contributions. S.V. carried out the molecular laboratory work, carried out the genotyping, participated in data analysis, participated in the design of the study and drafted the manuscript; J.L.V.-C. lead the bioinformatics with the assistance of G.M.H.; J.A.F. carried out the statistical analyses; L.M. collected samples and helped to draft the manuscript; E.F. and P.C.C. helped to structure and draft the manuscript; R.F. provided reagents and samples; P.D.C.

and F.C. provided expertise in the sequencing library design and F.C. carried out the sequencing; J.C. conceived the study, designed the study and helped draft the manuscript. All authors participated in writing of the manuscript and gave final approval for publication.

Competing interests. We declare we have no competing interests.

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References

1. Mardis ER. 2013 Next-generation sequencing platforms. *Annu. Rev. Anal. Chem.* (*Palo Alto. Calif*). **6**, 287–303. (doi:10.1146/annurev-anchem-062012-092628)
2. Hofreuter D *et al*. 2006 Unique features of a highly pathogenic *Campylobacter jejuni* strain. *Infect. Immun.* **74**, 4694–4707. (doi:10.1128/IAI.00210-06)
3. Oh JD *et al*. 2006 The complete genome sequence of a chronic atrophic gastritis *Helicobacter pylori* strain: evolution during disease progression. *Proc. Natl Acad. Sci. USA* **103**, 9999–10 004. (doi:10.1073/pnas.0603784103)
4. Wheeler DA *et al*. 2008 The complete genome of an individual by massively parallel DNA sequencing. *Nature* **452**, 872–876. (doi:10.1038/nature06884)
5. Baird NA, Etter PD, Atwood TS, Currey MC, Shiver AL, Lewis ZA, Selker EU, Cresko WA, Johnson EA. 2008 Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS ONE* **3**, e3376. (doi:10.1371/journal.pone.0003376)
6. Peterson BK, Weber JN, Kay EH, Fisher HS, Hoekstra HE. 2012 Double digest RADseq: an inexpensive method for *de novo* SNP discovery and genotyping in model and non-model species. *PLoS ONE* **7**, e0037135. (doi:10.1371/journal.pone.0037135)
7. Wang S, Meyer E, McKay JK, Matz MV. 2012 2b-RAD: a simple and flexible method for genome-wide genotyping. *Nat. Methods* **9**, 808–810. (doi:10.1038/nmeth.2023)
8. Davey JW, Hohenlohe PA, Etter PD, Boone JQ, Catchen JM, Blaxter ML. 2011 Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nat. Rev. Genet.* **12**, 499–510. (doi:10.1038/nrg3012)
9. Narum SR, Buerkle CA, Davey JW, Miller MR, Hohenlohe PA. 2013 Genotyping-by-sequencing in ecological and conservation genomics. *Mol. Ecol.* **22**, 2841–2847. (doi:10.1111/mec.12350)
10. LaFramboise T. 2009 Single nucleotide polymorphism arrays: a decade of biological, computational and technological advances. *Nucleic Acids Res.* **37**, 4181–4193. (doi:10.1093/nar/gkp552)
11. Ha N-T, Freytag S, Bickeboeller H. 2014 Coverage and efficiency in current SNP chips. *Eur. J. Hum. Genet.* **22**, 1124–1130. (doi:10.1038/ejhg.2013.304)
12. Chowdhury J *et al*. 2007 Microfluidic platform for single nucleotide polymorphism genotyping of the thiopurine S-methyltransferase gene to evaluate risk for adverse drug events. *J. Mol. Diagn.* **9**, 521–529. (doi:10.2353/jmoldx.2007.070014)
13. Seeb JE, Carvalho G, Hauser L, Naish K, Roberts S, Seeb LW. 2011 Single-nucleotide polymorphism (SNP) discovery and applications of SNP genotyping in nonmodel organisms. *Mol. Ecol. Resour.* **11**, 1–8. (doi:10.1111/j.1755-0998.2010.02979.x)
14. Delmotte F, Leterme N, Simon J. 2001 Microsatellite allele sizing: difference between automated capillary electrophoresis and manual technique. *Biotechniques* **31**, 810–818.
15. Pasqualotto AC, Denning DW, Anderson MJ. 2007 A cautionary tale: lack of consistency in allele sizes between two laboratories for a published multilocus microsatellite typing system. *J. Clin. Microbiol.* **45**, 522–528. (doi:10.1128/JCM.02136-06)
16. Kuhner MK, Beerli P, Yamato J, Felsenstein J. 2000 Usefulness of single nucleotide polymorphism data for estimating population parameters. *Genetics* **156**, 439–447.
17. Nielsen R. 2000 Estimation of population parameters and recombination rates from single nucleotide polymorphisms. *Genetics* **154**, 931–942.
18. Helyar SJ *et al*. 2011 Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. *Mol. Ecol. Resour.* **11**, 123–136. (doi:10.1111/j.1755-0998.2010.02943.x)
19. Anderson EC, Garza JC. 2006 The power of single-nucleotide polymorphisms for large-scale parentage inference. *Genetics* **172**, 2567–2582. (doi:10.1534/genetics.105.048074)
20. Morin PA, Martien KK, Taylor BL. 2009 Assessing statistical power of SNPs for population structure and conservation studies. *Mol. Ecol. Resour.* **9**, 66–73. (doi:10.1111/j.1755-0998.2008.02392.x)
21. Haasl RJ, Payseur BA. 2011 Multi-locus inference of population structure: a comparison between single nucleotide polymorphisms and microsatellites. *Heredity (Edinb)*. **106**, 158–171. (doi:10.1038/hdy.2010.21)
22. Clayton TM, Whitaker JP, Sparkes R, Gill P. 1998 Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci. Int.* **91**, 55–70. (doi:10.1016/S0379-0738(97)00175-8)
23. Gill P. 2001 An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensic purposes. *Int. J. Legal Med.* **114**, 204–210. (doi:10.1007/s004149900117)
24. Glaubitz JC, Rhodes OE, Dewoody JA. 2003 Prospects for inferring pairwise relationships with single nucleotide polymorphisms. *Mol. Ecol.* **12**, 1039–1047. (doi:10.1046/j.1365-294X.2003.01790.x)
25. Morin PA, Luikart G, Wayne RK. 2004 SNPs in ecology, evolution and conservation. *Trends Ecol. Evol.* **19**, 208–216. (doi:10.1016/j.tree.2004.01.009)
26. Estoup A, Jarne P, Cornuet JM. 2002 Homoplasy and mutation model at microsatellite loci and their consequences for population genetics analysis. *Mol. Ecol.* **11**, 1591–1604. (doi:10.1046/j.1365-294X.2002.01576.x)
27. Kan CW, Fredlake CP, Doherty EAS, Barron A. 2004 DNA sequencing genotyping in miniaturized electrophoresis systems. *Electrophoresis* **25**, 3564–3588. (doi:10.1002/elps.200406161)
28. Fordyce SL *et al*. 2011 High-throughput sequencing of core STR loci for forensic genetic investigations using the Roche Genome Sequencer FLX platform. *Biotechniques* **51**, 127–133. (doi:10.2144/000113721)
29. Scheible M, Loreille O, Just R, Irwin J. 2011 Short tandem repeat sequencing on the 454 platform. *Forensic Sci. Int. Genet. Suppl. Ser.* **3**, e357–e358. (doi:10.1016/j.fsigss.2011.09.041)
30. Van Neste C, Van Nieuwerburgh F, Van Hoofstat D, Deforce D. 2012 Forensic STR analysis using massive parallel sequencing. *Forensic Sci. Int. Genet.* **6**, 810–818. (doi:10.1016/j.fsigen.2012.03.004)
31. Mirimin L, O'Keeffe D, Ruggiero A, Bolton-Warberg M, Vartia S, Fitzgerald R. 2011 A quick, least-invasive, inexpensive and reliable method for sampling *Gadus morhua* postlarvae for genetic analysis. *J. Fish Biol.* **79**, 801–805. (doi:10.1111/j.1095-8649.2011.03049.x)
32. Vartia S, Collins PC, Cross TF, Fitzgerald RD, Gauthier DT, McGinnity P, Mirimin L, Carlsson J. 2014 Multiplexing with three-primer PCR for rapid and economical microsatellite validation. *Hereditas* **151**, 43–54. (doi:10.1111/hrd2.00044)
33. Wattier R, Engel CR, Saumitou-Laprade P, Valero M. 1998 Short allele dominance as a source of heterozygote deficiency at microsatellite loci: Experimental evidence at the dinucleotide locus Gv1CT in *Gracilaria gracilis* (Rhodophyta). *Mol. Ecol.*

7, 1569–1573. (doi:10.1046/j.1365-294x.1998.00477.x)

34. Schuelke M. 2000 An economic method for the fluorescent labeling of PCR fragments: a poor man's approach to genotyping for research and high-throughput diagnostics. **18**, 233–234. (doi:10.1038/72708)
35. 2009 Using Multiplex Identifier (MID) adaptors for the GS FLX titanium chemistry - extended MID set. 454 Sequencing Technical Bulletin No. 005–2009, 454 Life Sciences Corp., a Roche Company, Branford, CT, USA.
36. Margulies M *et al*. 2005 Genome sequencing in microfabricated high-density picolitre reactors. *Nature* **437**, 376–380. (doi:10.1038/nature03959)
37. 2011 *Rapid library preparation method manual*: Branford, CT, 454 Life Sciences Corp., a Roche Company.
38. 2012 454 *Sequencing system guidelines for amplicon experimental design*: Branford, CT, 454 Life Sciences Corp., a Roche Company.
39. Balzer S, Malde K, Jonassen I. 2011 Systematic exploration of error sources in pyrosequencing flowgram data. *Bioinformatics* **27**, 304–i309. (doi:10.1093/bioinformatics/btr251)
40. Kearse M *et al*. 2012 Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**, 1647–1649. (doi:10.1093/bioinformatics/bts199)
41. Edwards AWF. 1992 *Likelihood: expanded edition*. Baltimore, MA: The Johns Hopkins University Press.
42. Akaike H. 1973 Information theory as an extension of the maximum likelihood principle. In *Second Int. Symp. on Information Theory* (eds BN Petrov, F Csaki), pp. 267–281. Budapest, Hungary: Akademiai Kiado.
43. Akaike H. 1974 A new look at the statistical model identification. *Inst. Electr. Electron. Eng. Trans. Autom. Control AC* **19**, 716–723.
44. Hurvich CM, Tsai C-L. 1989 Regression and time series model selection in small samples. *Biometrika* **76**, 297–307. (doi:10.1093/biomet/76.2.297)
45. Burnham KP, Anderson DR. 2002 *Model selection and multimodel inference: a practical information-theoretic approach*. New York, NY: Springer.
46. Burnham KP, Anderson DR. 2004 Multimodel inference: understanding AIC and BIC in model selection. *Sociol. Methods Res.* **33**, 261–304. (doi:10.1177/0049124104268644)
47. Sokal RR, Rohlf FJ. 1995 *Biometry*, 3rd edn. New York, NY: W.H. Freeman.
48. Binladen J, Gilbert MTP, Bollback JP, Panitz F, Bendixen C, Nielsen R, Willerslev E. 2007 The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing. *PLoS ONE* **2**, e197. (doi:10.1371/journal.pone.0000197)
49. Skirnisdottir S, Pampoulie C, Hauksdottir S, Schulte I, Olafsson K, Hreggvidsson GO, Hjorleifsdottir S. 2008 Characterization of 18 new microsatellite loci in Atlantic cod (*Gadus morhua* L.). *Mol. Ecol. Resour.* **8**, 1503–1505. (doi:10.1111/j.1755-0998.2008.02327.x)
50. Higgins B, Hubert S, Simpson G, Stone C, Bowman S. 2009 Characterization of 155 EST-derived microsatellites from Atlantic cod (*Gadus morhua*) and validation for linkage mapping. *Mol. Ecol. Resour.* **9**, 733–737. (doi:10.1111/j.1755-0998.2008.02475.x)
51. 454.com.2015 Products—GS FLX+ System: 454 Life Sciences, a Roche Company. Accessed 4 June 2015. Life Sciences Corp., a Roche Company, Branford, CT, USA. See http://454.com/products/gs-flx-system/index.asp.
52. Rothberg JM *et al*. 2011 An integrated semiconductor device enabling non-optical genome sequencing. *Nature* **475**, 348–352. (doi:10.1038/nature10242)
53. 2013 The Ion PGM™ System, with 400-base read length chemistry, enables routine high-quality de novo assembly of small genomes. Life Technologies Corporation.
54. Bentley DR *et al*. 2008 Accurate whole human genome sequencing using reversible terminator chemistry. *Nature* **456**, 53–59. (doi:10.1038/nature07517)
55. Suez M, Behdenna A, Brouillet S, Graça P, Higet D, Achaz G. In press. MicNeSs: genotyping microsatellite loci from a collection of (NGS) reads. *Mol. Ecol. Resour*. (doi:10.1111/1755-0998.12467)
56. Guichoux E *et al*. 2011 Current trends in microsatellite genotyping. *Mol. Ecol. Resour.* **11**, 591–611. (doi:10.1111/j.1755-0998.2011.03014.x)
57. Garza JC, Freimer NB. 1996 Homoplasy for size at microsatellite loci in humans and chimpanzees. *Genome Res.* **6**, 211–217. (doi:10.1101/gr.6.3.211)
58. Angers B, Estoup A, Jarne P. 2000 Microsatellite size homoplasy, SSCP, and population structure: a case study in the freshwater snail *Bulinus truncatus*. *Mol. Biol. Evol.* **17**, 1926–1932. (doi:10.1093/oxfordjournals.molbev.a026294)
59. Anmarkrud JA, Kleven O, Bachmann L, Lifjeld JT. 2008 Microsatellite evolution: mutations, sequence variation, and homoplasy in the hypervariable avian microsatellite locus HrU10. *BMC Evol. Biol.* **8**, 138. (doi:10.1186/1471-2148-8-138)
60. Barkley NA, Krueger RR, Federici CT, Roose ML. 2009 What phylogeny and gene genealogy analyses reveal about homoplasy in citrus microsatellite alleles. *Plant Syst. Evol.* **282**, 71–86. (doi:0.1007/s00606-009-0208-2)
61. Petit RJ, Deguilloux MF, Chat J, Grivet D, Garnier-Géré P, Vendramin GG. 2005 Standardizing for microsatellite length in comparisons of genetic diversity. *Mol. Ecol.* **14**, 885–890. (doi:10.1111/j.1365-294X.2005.02446.x)