ezRAD: A Simplified Method for Genomic Genotyping in Non-Model Organisms

Here, we introduce ezRAD, a novel strategy for restriction site–associated DNA (RAD) that requires little technical expertise or investment in laboratory equipment, and demonstrate its utility for ten non-model organisms across a wide taxonomic range. ezRAD differs from other RAD methods primarily through its use of standard Illumina TruSeq library preparation kits, which makes it possible for any laboratory to send out to a commercial genome analyses core facility for library preparation and next-generation sequencing with virtually no additional investment beyond the cost of the service itself. This simplification opens RADseq to any lab with the ability to extract DNA and perform a restriction digest. ezRAD also differs from others in its flexibility to use any restriction enzyme (or combination of enzymes) that cuts frequently enough to generate fragments of the desired size range, without requiring the purchase of separate adapters for each enzyme or a sonication step, which can further decrease the cost involved in choosing optimal enzymes for particular species and research questions. We apply this method across a wide taxonomic diversity of non-model organisms to demonstrate the utility and flexibility of our approach. The simplicity of ezRAD makes it particularly useful for the discovery of Single Nucleotide Polymorphisms and targeted amplicon sequencing in natural populations of non-model organisms that have been historically understudied because of lack of genomic information.
Robert J. Toonen\textsuperscript{1,2}, Jonathan B. Puritz\textsuperscript{1,3}, Zac H. Forsman\textsuperscript{1}, Jonathan L. Whitney\textsuperscript{1}, Iria Fernandez-Silva\textsuperscript{1,4}, Kimberly R. Andrews\textsuperscript{1,5}, Christopher E. Bird\textsuperscript{6}

\textsuperscript{1}Hawai‘i Institute of Marine Biology, School of Ocean & Earth Sciences & Technology, University of Hawai‘i at Mānoa, Coconut Island, 46-007 Lilipuna Road, Kāne‘ohe, HI 96744.

\textsuperscript{2}Email addresses: toonen@hawaii.edu, jpuritz@gmail.com, zac@hawaii.edu, jonathanlyonwhitney@gmail.com, iriafernandezsilva@gmail.com, kimandrews@gmail.com, chris.bird@tamucc.edu

\textsuperscript{3}Current Address: Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas 77843-2258

\textsuperscript{4}Current Address: Trans-disciplinary Organization for Subtropical Island Studies (TRO-SIS), University of the Ryukyus, 1 Senbaru, Nishihara, Okinawa 903-0213, Japan

\textsuperscript{5}Current Address: Durham University, School of Biological & Biomedical Sciences, South Road, Durham, DH1 3LE, UK.

\textsuperscript{6}Texas A&M University - Corpus Christi, Department of Life Sciences, 6300 Ocean Drive, Corpus Christi, TX 78412-5802
INTRODUCTION:

Next-generation sequencing (NGS) has provided unprecedented access to genomic information at ever-increasing speed and reduced cost (Mardis 2008). Until recently, profiling a large number of loci was only realistically possible for organisms with well-developed genomic resources, and the high cost of developing these resources has been a major impediment to studies for non-model organisms. Despite the rapid advances of sequencing technology, and dramatic reduction in cost associated with those advances, whole-genome sequencing remains a costly hurdle to undertake for marker development in non-model organisms, especially for species with large genomes. In the fields of phylogeography, phylogenetics, and population genetics, the majority of studies do not require whole-genome sequencing, but rather a spread of loci across the genome. As a result, there has been considerable interest in simple and more cost-effective approaches to using reduced representation genome sequencing, such as Restriction site Associated DNA Sequencing, or RADseq. RADseq effectively reduces genome complexity and size by resequencing only stretches of genomic DNA adjacent to restriction endonuclease sites, providing high coverage of homologous portions of the genome from multiple individuals for comparatively low cost and effort. A multitude of strategies have emerged for RAD sequencing, including the original method (Baird et al. 2008; Etter et al. 2011; Hohenlohe et al. 2010), genotype-by-sequencing, or GBS (Elshire et al. 2011; Sonah et al. 2013), 2-enzyme GBS (Poland et al. 2012), 2b-RAD (Wang et al. 2012), and ddRAD (Peterson et al. 2012). The RADseq approach provides a powerful tool for a wide range of genetic studies and is rapidly changing the field as a result (reviewed by Rowe et al. 2011).

Despite rapidly gaining popularity, the application of RADseq has been limited to primarily model or emerging model species (Baird et al. 2008; Chutimanitsakun et al. 2011; Emerson et al. 2010; Hohenlohe et al. 2010), with only a single marine invertebrate species RADseq dataset (for the model organism Nematostella vectensis) published to date (Reitzel et al. 2013). Although it is debatable what the underlying cause of this delayed application is, applying existing protocols to non-model marine invertebrates can be challenging due to a variety of unknowns such as genome size and frequency of restriction sites. Additionally, many of the existing protocols require a significant initial investment for labs focused on Sanger sequencing and microsatellite typing. Thus, we sought to develop a simplified and general approach to RADseq that requires little to no optimization and would enable access to this powerful new approach among taxonomic groups across the tree of life. Here, we outline a novel RAD strategy that uses any restriction enzyme (or combination of enzymes) which cuts frequently enough to produce fragments suitable for sequencing, and then uses the standard Illumina TruSeq library preparation with agarose gel (or SPRI-bead) size-selection to target the fragments to be sequenced. The approach is flexible and scalable, making it possible for virtually any lab to send out restriction endonuclease digested DNA for RAD sequencing with no additional investment beyond the cost of the core lab costs for library preparation and sequencing itself. This simplification opens the door to RAD sequencing for any lab with the ability to extract DNA and perform a restriction digest, a very low technical bar for the application of NGS. Furthermore, this method is compatible with a wide range of restriction enzymes, and does not require the purchase of new adapters for each new enzyme.
Therefore, ezRAD provides flexibility for optimizing the number of unique fragments to be sequenced by simple modifications to the restriction enzyme and/or size selection range used. Here, we report and apply ezRAD across a wide taxonomic diversity of non-model organisms to demonstrate the utility of this approach. This generalized approach, using the standard Illumina TruSeq library preparation kit, will allow researchers to apply RADseq technology to a wide array of research questions.

METHODS:

DNA Extraction and Quantification

High molecular weight DNA was extracted from preserved tissue samples using a variety of methods. For *Patiria miniata*, *Porites compressa*, *Porites lobata*, and *Stenella longirostris*, the E.Z.N.A. MicroElute Genomic DNA extraction kit (Omega) was used according to the manufacturer protocol. DNA from *Cryptasterina hystera*, *Cryptasterina pentagona*, *Pocillopora damicornis*, and *Cellana talcosa* was extracted using the DNeasy tissue extraction kit (Qiagen), and DNA from *Paracirrhites arcatus* was extracted using a standard Phenol-Chloroform procedure with the addition of RNase. All extractions were inspected on 2% agarose gels for the presence of impurities and lower molecular weight DNA. Samples with “smear” gel patterns were subsequently purified with AmpureXP (Agentcourt) SPRI beads using a 2:1 template to bead volume ratio. Subsequently, all extractions were quantified using AccuBlue High Sensitivity fluorescence assay on a SpectraMax M2 plate reader, using the standard protocol for a 96 well assay (Application Note #22) with the adjustment of using the AccuBlue dye excitation and emission spectra. For all libraries, 1.5 μg of DNA was precipitated in 1/10 volume Sodium Acetate and two volumes 100% ethanol at -70°C for 30 minutes. DNA was pelleted by 15 min of centrifugation at 12,000 rpm. Pellets were resuspended in 24 μl of dI water with 0.1M Tris at 65°C.

Digestion

DNA was digested simultaneously with the isoschizomers MboI and Sau3AI (NEB) to minimize any potential impacts of methylation of DNA in digesting the genomic libraries. Each digestion was performed in 50 μl reactions: 5 μl NEB Buffer 4, 0.5 μl BSA, 2 μl MboI, 2.5 μl Sau3AI, 18 μl of DNA template (roughly 1.125μg) from above, and 22 μl of dI water. Digestions were incubated at 37°C for 3-6 hours and then cleaned using 80 μl of AmpureXP beads per reaction and eluted in 20 μl of water.

Illumina Library Preparation

Cleaned digestions were inserted directly into the Illumina TruSeq DNA kit following the Sample Preparation v2 Guide starting with the “Perform End Repair” step. Digestions can be inserted into any of the three available Illumina TruSeq DNA kits including the including the newest PCR-free and Nano kits. Due to the challenges of working with non-model marine invertebrates,
many of our libraries had less than 1μg of high molecular weight DNA with which to start the
library preparation, but the Nano kit was not yet available. Due to the low starting concentration,
we performed an initial PCR enrichment before gel extraction, but have had better success with
the Nano kit since its release, and would recommend that approach for low initial DNA
concentrations. We generally followed the TruSeq protocol, but attempted to save reagents and
further lower costs by performing nearly all reaction steps in 1/3 of the recommended volumes
(see detailed protocol - S1), although such modifications are not necessary for the protocol. In
brief, digested libraries were end repaired, 3’ ends were adenylated and TruSeq adapters were
ligated to the digested genomic DNA sample. Libraries were then size-selected following the
Illumina TruSeq protocol using a 2% low-melt agarose gel with 1X TAE buffer run at 120V for
120 minutes. The 400-500bp fragments (of which ~120bp are the ligated adapters) were cut out
with a sterile scalpel blade for each individual sample and DNA was recovered using the Qiagen
MinElute Gel Extraction Kit following manufacturer instructions. After gel extraction, libraries
were validated by visualization on an Agilent 2100 BioAnalyzer, quantified using qPCR, and
pooled (performed by the Hawaiʻi Institute of Marine Biology EPSCoR Core sequencing
facility). Pooled libraries were then sequenced as paired-end 100bp runs on the Illumina GAIIX
at HIMB.

Bioinformatics

The HIMB Core facility runs a standard quality control filter and parses the Illumina reads into
FASTQ files sorted by index. Beyond that, a custom bash script (S2) was used to automate read
quality filtering, reference contig assembly, read mapping, SNP calling, and SNP filtering. A
brief description of each step of the analyses follows below:

Raw FASTQ files were trimmed using the program TRIM GALORE!
(http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) into two different read sets.
The first set of reads had only adapter sequences removed and were subsequently saved for
contig assembly. The second set of reads was trimmed for adapter sequences and also removed
any base that had a quality score of less than 10 (90% probability of being correct). These reads
were saved for mapping.

RAINBOW (Chong et al, 2012) clustered and assembled the first set of parsed FASTQ files into a
final assembly of reference contigs. RAINBOW is specifically designed to assemble contigs from
RAD sequencing. In short, it first clusters reads together that are less than 4 bp apart. These
clustered reads are then recursively divided into groups representing individual allele sequences.
Individual allele sequences are then assembled and merged into a final set of RAD contigs.

Quality trimmed reads were then mapped to the reference contigs using BWA (Li & Durbin 2009)
with the MEM algorithm and default parameters (with the exception of altering the number of
computational threads and restricting the output to only map scores of 10 and higher). SAM files
were converted to BAM files using SAMTOOLS (Li et al, 2009) and output was further restricted
to reads with mapping quality above 15. BAM files were then merged and realigned around
INDEL regions using the mpileup command of SAMTOOLS with default parameters and the additional command of outputting per-sample read depths.

SNP calling was performed using VARSCAN2 (Koboldt et al. 2009; Koboldt et al. 2012) using the mpileup2snp command with default settings. The strand filter was removed because overlapping forward and reverse reads are not expected for the insert size of this library, and the minimum variant frequency was raised from 1% to 10%, meaning that within one library the minimum allele frequency had to be above 10% to be called a SNP. Finally, the p-value for a significant variant was raised from 0.01 to 0.05. Genotypes failing any of these filters are reported as missing.

The raw SNP calls were then filtered using two instances of VCFtools (Danecek et al. 2011). The first instance filters out INDEL loci, sites that were fixed for the minor allele, and SNPs that were not genotyped in 99% of the samples. The second round of filtering removes sites with less than 10X coverage and outputs the final set of SNP genotypes in VCF format.

Reads from the four Patiria miniata libraries were used for validation of the ezRAD technique and bioinformatics pipeline. For the first test, contigs generated by RAINBOW (Chong et al. 2012) for the ezRAD P. miniata libraries were aligned using BWA (Li & Durbin 2009) with the MEM algorithm and default parameters to previously published P. miniata genomic contigs from GenBank (Assembly GCA_000285935.1). As a second test, genomic contigs were substituted for the ezRAD contigs in the analysis pipeline to directly compare the number of SNPs generated with different reference contigs from P. miniata.

RESULTS:

Taxonomic representation

We tested our generic protocol with no attempt at optimization across a range of taxonomic diversity including a marine mammal (Stenella longirostris), a coral reef fish (Paracirrhites arcatus), three echinoderms (Patiria miniata, Cryptasterina hystera & C. pentagona), a mollusk (Cellana talcosa), and three scleractinian corals (Porites compressa, P. lobata & Pocillopora damicornis). Across the range of metazoan diversity from cnidarians to vertebrates, the technique worked relatively well with no modifications or attempts at optimization (Table 1).

Sequencing results

All attempted libraries yielded thousands to tens of thousands of variable base calls. Results varied by taxon (Table 1), but as with other RAD protocols, the two factors most directly linked to the number of reads per library passing quality control were initial DNA fragment sizes and overall genome size, as opposed to taxonomic relatedness. When holding the size selection range constant, large genome sizes and low molecular weight DNA resulted in increased numbers of non-homologous DNA fragments with lesser coverage. For example, Acropora digitifera has ~420 megabase genome (Shinzato et al. 2011), but in combination with the suite of
dinoflagellate, prokaryotic and eukaryotic symbionts inextricably associated with the coral holobiont (reviewed by Ainsworth et al. 2010) this makes for an exceedingly large genomic pool from which to draw fragments for reduced representation genomic sequencing. Genome size is estimated from the amount of DNA (in picograms) contained in a haploid nucleus, taken from the Animal Genome Size Database (http://www.genomesize.com). The corals (1115 Mb for Siderastrea stellata, plus 1467 – 4694 Mb for Symbiodinium symbionts) have relatively lower coverage across each contig in comparison to species with smaller genome sizes, such as the limpets (421 Mb for Lottia gigantea) or the sea stars (743 Mb for Patiria miniata). The number of both fragments and putative SNPs identified for P. miniata may appear high, but the species is known to be extremely polymorphic - even by comparison to other sea stars in the Asterinidae (Keever et al. 2009; McGovern et al. 2010; Puritz & Toonen 2011). Further, we validate these variable bases as putative SNPs against published genomic contigs (see ezRAD Validation below).

Samples with low molecular weight DNA extractions and large genome size produced the lowest quality among all libraries in our tests. Further, genomic DNA samples characterized by low molecular weight fragments were also characterized by reduced adapter ligation efficiency that led to a large number of sequenced fragments consisting of only adapter dimers with low quality scores. For the sea star, C. pentagona a relatively large genome and the lowest molecular weight DNA in this study resulted in the lowest quality library (Table 1). However, despite only 18.02% of the sequence reads passing QC, we still discovered over 8,000 variable base sites which is more than sufficient for SNP discovery applications. Likewise, the fact that the arc-eye hawkfish (Paracirrhites arcatus) has a relatively large genome (714 Mb for Cirrhitichthys aureus) together with carryover of degraded DNA from the initial extraction, resulted in P. arcatus showing a relatively low percentage of reads that passed QC (Table 1).

ezRAD Validation with Published Reference Genomic Contigs

ezRAD derived genomic sequencing reads of P. miniata were mapped to reference consensus sequences generated from the publicly available genomic contig data from P. miniata on GenBank. Overall, 532,467 of the 635,376 P. miniata contigs generated from the ezRAD analysis pipeline mapped with high quality to publicly available genomic contigs (MAPQ mean =38.66; median 52.00; standard deviation 23.22). Approximately 15 million ezRAD reads mapped with high quality to the reference, versus ~21 million reads from the publicly available data set (Table 2). Most importantly, the number of variable sites, shared SNPs, and quality-controlled SNP datasets were similar between the reference contigs from each of the two approaches (Table 2).

SNP Discovery using Pooled and Unpooled Libraries

We compare results obtained by making a single library per individual for each of eight individuals of the reef fish P. arcatus relative to two pools of four individuals each (Table 1). After normalizing for lane use, we generated 2.4x more high quality mapped reads for the eight individual libraries (4.6 x 10^6/lane) than for two pooled samples containing eight individuals (1.9
x $10^6$/lane) and 2x more variable base calls ($2.6 \times 10^5$/lane vs. $1.2 \times 10^5$/lane). When accounting for cost however, the sample prep and sequencing was 4x more expensive for the 8 individuals versus two pools of four individuals, making the pooling strategy more cost effective per variable base identified. Furthermore, because of some variability among individual libraries, we identified 11.9x more shared SNPs with >10x coverage between the pooled libraries ($4.35 \times 10^4$/lane) than among the eight individual libraries ($3.67 \times 10^3$/lane). For example, 975 shared SNPs were genotyped (at >10x mean coverage) in all 8 individual libraries, and 635 of those (65%) were also genotyped in both pooled libraries. By comparison, of the 3344 SNPs that were genotyped (at >10x mean coverage) between the 2 pooled libraries, only 626 (19%) of those were also genotyped in all 8 individual libraries. Even without normalization for lane use, we identified more shared SNPs of higher quality for lower cost from the two pooled libraries relative to the individual libraries (Table 1; Suppl. S3).

DISCUSSION:

ezRAD, a novel approach to reduced representation genomic sequencing, differs from existing RADseq methods primarily in that it requires very little technical expertise or laboratory equipment to complete. These benefits are achieved through the use of the Illumina TruSeq library preparation kits, which also makes it possible to send digested DNA to any core lab that offers library preparation as part of their Illumina service package. This method now makes RADseq possible for any lab with the ability to perform DNA extraction and restriction digestion, an extremely low technical expertise and equipment bar to achieve NGS capability.

ezRAD is similar in concept to several other recently developed RAD methods, such as GBS, 2-enzyme GBS, ddRAD and 2b-RAD (Elshire et al. 2011; Peterson et al. 2012; Poland et al. 2012; Sonah et al. 2013; Wang et al. 2012) in that we use frequent-cutting enzymes to generate fragments of the appropriate length for sequencing (usually between 300-500bp), rather than using a sonication step to sheer DNA after digestion as in the original RADseq protocol (see Table 3 for a comparison among methods). ezRAD and ddRAD both use a size selection step to eliminate inappropriately-sized fragments generated by the restriction digest. In contrast, GBS relies on a PCR step to preferentially amplify shorter fragments over longer fragments; and 2b-RAD uses a special type of restriction enzyme (IIB enzymes) that cuts DNA into small, uniformly sized fragments (33-36bp) suitable for sequencing. As in GBS, ddRAD & 2b-RAD, the number of unique fragments generated by ezRAD can be optimized by altering the restriction enzyme/s used based on the frequency of cut sites in the genome (if known). ddRAD & ezRAD share the additional advantage that the number of fragments sequenced can be modified through the size selection step in the library preparation. However, ezRAD offers two advantages that simplify the process of choosing an appropriate restriction enzyme for a given organism and research question: 1) ezRAD generally targets just one restriction site (here both MboI and Sau3AI target GATC, but with different sensitivity to methylation). Assuming some knowledge of genome size and GC content, using a single cut site simplifies the calculations to predict the number of unique genomic regions within a given size range that will be generated through the
digest. In practice any restriction enzyme, or combination of enzymes, that result in appropriately sized fragments could be used. 2) The adapters are not custom-designed for the enzyme/s used, thereby allowing researchers to try many different restriction enzymes (or combinations of enzymes) without the costly investment of new adapters for each enzyme. The ability to quickly try multiple different enzymes may be particularly beneficial for recalcitrant genomes where no prior knowledge of genome content is available, as is the case in many non-model organisms. Regardless of such differences among techniques, for many applications optimization of restriction enzyme and size selection range are likely irrelevant for SNP discovery, because even without any attempt at optimization, and with as few as 18% of reads passing QC, we nevertheless discovered thousands of putative SNPs in each library here (Table 1).

In order to highlight the flexibility and broad applicability of this approach, we provide an example application of this approach in which we prepared 30 libraries across a wide taxonomic range. With no adjustments to the protocol, and no attempt at optimization of any step to accommodate the taxonomic or genomic differences among the taxa, we successfully RAD sequenced a marine mammal, a fish, a mollusk, several echinoderms, and scleractinian corals. While the protocol obviously did not work equally well on all samples in the run, sequencing of all libraries yielded sufficient data for most applications from every taxon attempted (Table 1).

Rather than a taxonomic bias in the success of the technique, the success of a library appears to be a direct result of the initial quality of DNA that went into the library preparation and the genome size. We find that starting with the highest possible molecular weight DNA and testing for the standard QC along the way makes the greatest difference in the amount of useable sequence data resulting from a run.

**Costs**

The total cost of preparing and sequencing our 30 libraries in two lanes of an Illumina GAIIx flow cell was $9,600. We were able to reduce the cost per dataset to ~$320 (start to finish) by buying all reagents and constructing the libraries in our laboratory and sequencing through our HIMB core facility, making the library preparation cost on the order of ~$60. Current prices for library preparation at academic institutions that offer the service in the USA are on the order of $200-300 for the TruSeq library preparation and approximately the same for 1/6th of MiSeq or 1/12th an Illumina GAIIx sequencing lane, making the total price of an ezRAD run on the order of $500-$600 USD if sent out. Some will note that this cost is substantially higher than the published library prep costs for other RAD methods which can be as low as $5/sample, but such estimates do not include the cost of sequencing, which is the majority of the cost of RADseq. However, it is also important to note that there is a trade-off between the ultimate cost per library and the initial investment to begin the process of library development. Initial investment for most RADseq methods would include, at the minimum, acquiring a Solid Phase Reversible Immobilization (SPRI) bead kit (~$1250), a 96-well magnet for the SPRI cleanups (~$620), restriction enzymes (~$2-300), a high accuracy DNA quantification kit (~$100, plus ~$2000 if an accurate fluorometer is not already available), plus the initial order of the custom oligo adapters with barcode sequences (which could also run into thousands of dollars depending on the number
of enzymes and barcodes desired for the protocol). If all of those reagents are used up fully in several hundred library preparations, the cost per library will be quite low, on the order of $5-10/sample, whereas the cost of sequencing (~$250 per sample) remains fixed. However, if only a few libraries are made before those reagents expire, the cost of the reagents alone may be greater than the total price for the 30 ezRAD libraries we ran here. Even using ezRAD, labs who plan to do only a few libraries are unlikely to want to invest in the Illumina TruSeq sample library preparation kit (~$2600), and are much better off sending out to a commercial service for their needs at a higher price per sample, but much lower overall cost. Ultimately, there are trade-offs for every method, and for labs that plan to prepare and run many RADseq libraries, there are more cost-effective options available (Table 3); however for labs that need only a few runs for SNP discovery or marker development for targeted amplicon sequencing, and have none of the required supplies listed above in hand, ezRAD is the least technically challenging and most cost-effective option currently available.

**Pooled versus Unpooled Libraries**

In comparing pooled and unpooled libraries, we find that SNP discovery is more cost effective in libraries constructed with DNA from pooled individuals in comparison to multiple runs of single individuals (Figure 1). For a substantial examination of pooled NGS sample strategies see Gautier et al. (2013). Here, our simple comparison of one library per individual on eight individuals of the reef fish Paracirrhites arcatus relative to two pools of four individuals each indicate pooled libraries are more cost-effective for SNP discovery (Figure 1, Suppl. S3). Comparing our individual libraries illustrates that there is some variability among libraries in the markers recovered, likely due to imprecision in the gel size selection step; ultimately, the proportion of SNPs that were shared among all individuals drops as we compare across more of the individual libraries (Suppl. S3). Still, the highest coverage SNPs tend to be those shared among libraries, and the slope of loss asymptotes after about 5 individuals for reasonable levels of coverage (Suppl. S3). Even without normalization for lane use, we identified 3x more shared SNPs from the pooled libraries than from the individual libraries (Table 1, Suppl. S3). Although we used only eight individuals in this simple comparison of pooled and unpooled libraries, the best results for SNP discovery were in pooled libraries in which we had 20 or more individuals and other genomic resources against which to compare our variable base calls (e.g., P. miniata or C. talcosa, Table 1). Based on our findings here, our future efforts for SNP discovery would likely use two pooled libraries of many individuals (>20) each as the most cost-effective strategy to identify hundreds to thousands of high quality shared SNPs or loci for targeted amplicon sequencing (e.g., Puritz et al. 2012) that could be reliably used for genotyping from these libraries (Suppl. S3).

**Benefits and trade-offs of ezRAD**

Ultimately, there are tradeoffs to consider for each of the various approaches to reduced representation genomic sequencing strategies (reviewed by Wang et al. 2012). Although ezRAD is simple, works without optimization across a broad diversity of metazoan taxa, and requires little initial investment beyond the direct cost of NGS, it is important to consider that this
approach, like many others, will not survey all restriction cut sites in the entire genome. Likewise, for labs in which a large number of libraries will be generated, another approach may prove more cost-effective (Table 3). However, for many population genomics applications, this limitation is unlikely to be of consequence, especially if the RAD sequencing is used to identify variable markers used in SNP analyses or for targeted amplicon sequencing (e.g., Puritz et al. 2012). Our approach provides a greatly simplified and standardized approach that can be used to obtain RADseq libraries from a wide range of species, especially those for which little or no genomic information exists to guide restriction enzyme selection. Another potential concern often raised with reduced representation approaches is that of ascertainment bias – the systematic deviations from theoretical expectations that result from the sampling processes used to discover and measure their population-specific allele frequencies. The only RADseq study published for a marine invertebrate to date, Nematostella vectensis, has an available genome against which to compare results from the reduced representation genomic sequencing. While always a concern for such studies, Reitzel et al. (2013) tested for ascertainment bias among RAD loci using the available reference genome for N. vectensis and found no evidence of it for this species. They also compare results from their RADseq library with and without use of the reference genome to demonstrate that the lack of an available genome would have had no substantial impact on the results they obtained in terms of the number of SNP loci, detection of population genetic structuring or detection of loci under selection (Reitzel et al. 2013). Thus, particularly in the realm of marine invertebrates, for which species with available genomes are particularly sparse, RAD approaches hold considerable promise to access genomic information. The various methodologies of RADseq are rapidly becoming the standard approach for a wide range of studies, and ezRAD adds to the growing suite of methods available for sequencing reduced representation genomic libraries to access genomic information in non-model organisms.

ACKNOWLEDGEMENTS:

We are grateful to Amy Eggers of the Hawai’i Institute of Marine Biology EPSCoR Evolutionary Genetics Core Facility for her assistance in the preparation of the libraries and sequencing. We also thank Brian Bowen, Steve Karl, Mahdi Belcaid, Dan Barshis, Matt Iacchei, Mareike Sudek, and Ingrid Knapp, as well as all the other members of the ToBo lab for their discussion, advice and support of this work, and putting up with us taking over the lab to try out this crazy idea. We also thank Rick Grosberg and Brenda Cameron for generously allowing C. Bird to work on early RADseq attempts in their laboratory. This is contribution #### from the Hawai’i Institute of Marine Biology and SOEST ####.
REFERENCES

Ainsworth TD, Thurber RV, and Gates RD. 2010. The future of coral reefs: a microbial perspective. *Trends in Ecology & Evolution* 25:233-240.

Baird NA, Etter PD, Atwood TS, Currey MC, Shiver AL, Lewis ZA, Selker EU, Cresko WA, and Johnson EA. 2008. Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS One* 3:e3376.

Chong Z, Ruan J, and Wu C-I. 2012. Rainbow: an integrated tool for efficient clustering and assembling RAD-seq reads. *Bioinformatics* 28:2732-2737.

Chutimanitsakun Y, Nipper RW, Cuesta-Marcos A, Cistué L, Corey A, Filichkina T, Johnson EA, and Hayes PM. 2011. Construction and application for QTL analysis of a Restriction Site Associated DNA (RAD) linkage map in barley. *Bmc Genomics* 12:4.

Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, and Sherry ST. 2011. The variant call format and VCFtools. *Bioinformatics* 27:2156-2158.

Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, and Mitchell SE. 2011. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS One* 6:e19379.

Emerson KJ, Merz CR, Catchen JM, Hohenlohe PA, Cresko WA, Bradshaw WE, and Holzapfel CM. 2010. Resolving postglacial phylogeography using high-throughput sequencing. *Proceedings of the National Academy of Sciences* 107:16196-16200.

Etter PD, Bassham S, Hohenlohe PA, Johnson EA, and Cresko WA. 2011. SNP discovery and genotyping for evolutionary genetics using RAD sequencing. *Molecular methods for evolutionary genetics*: Springer, 157-178.

Hohenlohe PA, Bassham S, Etter PD, Stiffler N, Johnson EA, and Cresko WA. 2010. Population genomics of parallel adaptation in threespine stickleback using sequenced RAD tags. *PLoS Genet* 6:e1000862.

Keever CC, Sunday J, Puritz JB, Addison JA, Toonen RJ, Grosberg RK, and Hart MW. 2009. Discordant distribution of populations and genetic variation in a sea star with high dispersal potential. *Evolution* 63:3214-3227.

Koboldt DC, Chen K, Wylie T, Larson DE, McLellan MD, Mardis ER, Weinstock GM, Wilson RK, and Ding L. 2009. VarScan: variant detection in massively parallel sequencing of individual and pooled samples. *Bioinformatics* 25:2283-2285.

Koboldt DC, Zhang Q, Larson DE, Shen D, McLellan MD, Lin L, Miller CA, Mardis ER, Ding L, and Wilson RK. 2012. VarScan 2: somatic mutation and copy number alteration discovery in cancer by exome sequencing. *Genome Research* 22:568-576.

Li H, and Durbin R. 2009. Fast and accurate short read alignment with Burrows–Wheeler transform. *Bioinformatics* 25:1754-1760.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, and Durbin R. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics* 25:2078-2079.

Mardis ER. 2008. The impact of next-generation sequencing technology on genetics. *Trends in Genetics* 24:133.
McGovern TM, Keever CC, Saski CA, Hart MW, and Marko PB. 2010. Divergence genetics analysis reveals historical population genetic processes leading to contrasting phylogeographic patterns in co-distributed species. *Molecular Ecology* 19:5043-5060.

Peterson BK, Weber JN, Kay EH, Fisher HS, and 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:e37135.

Poland JA, Brown PJ, Sorrells ME, and Jannink J-L. 2012. Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *PLoS One* 7:e32253.

Puritz JB, Addison JA, and Toonen RJ. 2012. Next-generation phylogeography: a targeted approach for multilocus sequencing of non-model organisms. *PLoS One* 7:e34241.

Puritz JB, and Toonen RJ. 2011. Coastal pollution limits pelagic larval dispersal. *Nature Communications* 2:226.

Reitzel A, Herrera S, Layden M, Martindale M, and Shank T. 2013. Going where traditional markers have not gone before: utility of and promise for RAD sequencing in marine invertebrate phylogeography and population genomics. *Molecular Ecology*.

Rowe H, Renaut S, and Guggisberg A. 2011. RAD in the realm of next-generation sequencing technologies. *Molecular Ecology* 20:3499-3502.

Shinzato C, Shoguchi E, Kawashima T, Hamada M, Hisata K, Tanaka M, Fujie M, Fujiwara M, Koyanagi R, and Ikuta T. 2011. Using the *Acropora digitifera* genome to understand coral responses to environmental change. *Nature* 476:320-323.

Sonah H, Bastien M, Iquira E, Tardivel A, Légaré G, Boyle B, Normandeau É, Laroche J, Larose S, and Jean M. 2013. An improved genotyping by sequencing (GBS) approach offering increased versatility and efficiency of SNP discovery and genotyping. *PLoS One* 8:e54603.

Wang S, Meyer E, McKay JK, and Matz MV. 2012. 2b-RAD: a simple and flexible method for genome-wide genotyping. *Nature Methods* 9:808-810.
Figure 1

Bar graph comparing pooled and unpooled libraries.

Relative proportion of high quality mapped reads, total SNPs, shared SNPs with greater than 10x coverage, and cost when employing one of two strategies: 1) preparing one library for every individual (8 individuals here), or 2) preparing two libraries of four pooled individuals. For all categories except Cost, taller bars represent better performance.
Table 1 (on next page)

Summary of ezRAD results from 2 lanes of Illumina GAIIx sequencing across a range of taxonomic diversity.

Organisms run with ezRAD include: the limpet Cellana talcosa; sea stars Cryptasterina hystera, C. pentagona & Patiria miniata; reef fish Paracirrhites arcatus; corals Porites lobata, P. compressa & Pocillopora damicornis; and the spinner dolphin Stenella longirostris. Lane use indicates the proportion of a single lane of PE100bp sequencing on the GAIIx flow cell. Library prep specifies what those libraries contained. Paired reads are the number of reads in each index parsed file returned after initial quality control (QC) filter from the sequencer. Reads and % Pass QC are the number of sequence reads remaining after excluding all sequences for which Phred scores were < 20, contained adapter sequences, or were less than 20bp long after adapters were cut. Mapped reads and High quality mapped reads are the number of reads overall and the number reads that passed quality control, respectively, that were assembled de novo into contigs. Contig statistics and polymorphic SNP counts reported here come from the bash script pipeline described in Supplement S2.
| Species               | Lane Use | Library Prep | Paired Reads | Reads Passing QC | % Pass QC | No. Contigs | Mapped Reads | High Quality Mapped | Variable Sites | Shared SNPs | >10X SNPs shared | >30X SNPs shared | SNPs Per Contig |
|-----------------------|----------|--------------|--------------|------------------|-----------|-------------|--------------|---------------------|----------------|-------------|------------------|------------------|-----------------|
| Cellana talcosa       | 1/3      | 2 pools of 24 individ | 8,109,327 | 4,472,365 | 55.15 | 189,444 | 8,389,669 | 3,483,833 | 127,609 | 73,014 | 49,761 | 9,997 | 0.26 |
| Cryptasterina hyster a | 1/12     | 1 pool of 10 individ | 6,441,832 | 3,880,080 | 60.23 | 27,007 | 2,242,589 | 655,509 | 36,666 | 36,666 | 31,127 | 12,827 | 1.15 |
| Cryptasterina pentagona | 1/12    | 1 pool of 10 individ | 1,804,165 | 325,137 | 18.02 | 4,354 | 1,452,171 | 148,580 | 9,501 | 9,501 | 8,058 | 3,538 | 1.85 |
| Patiria miniata       | 3/4      | 4 pools of 20 individ | 15,632,982 | 13,132,267 | 84.00 | 635,137 | 47,718,931 | 14,987,372 | 1,167,981 | 187,597 | 143,254 | 21,914 | 0.23 |
| Paracirrhites arcatus | 2/3      | 8 tagged individ | 13,586,625 | 5,261,386 | 38.72 | 205,360 | 22,892,817 | 3,088,806 | 171,712 | 2,705 | 2,447 | 366 | 0.01 |
| Paracirrhites arcatus | 1/6      | 2 pools of 2 individ | 2,733,965 | 995,543 | 36.41 | 13,340 | 2,980,976 | 324,331 | 20,512 | 10,221 | 7,249 | 2,082 | 0.54 |
| Pocillopora damicornis | 1/6      | 2 tagged individ | 3,289,007 | 2,929,932 | 89.08 | 164,553 | 5,710,298 | 2,956,701 | 232,734 | 110,454 | 80,221 | 21,658 | 0.49 |
| Porites compressa     | 1/4      | 3 tagged individ | 5,512,212 | 3,852,694 | 69.89 | 123,874 | 7,011,801 | 2,338,160 | 297,648 | 77,346 | 60,149 | 13,040 | 0.49 |
| Porites lobata        | 1/4      | 3 tagged individ | 7,131,427 | 3,926,250 | 55.06 | 95,887 | 7,587,534 | 2,689,310 | 275,769 | 65,731 | 47,617 | 9,419 | 0.50 |
| Stenella longirostris | 1/3      | 4 pools of 2 individ | 7,660,053 | 2,563,007 | 33.46 | 43,427 | 9,910,871 | 1,022,661 | 69,208 | 7,502 | 7,280 | 3,828 | 0.17 |
Table 2 (on next page)

Validation of ezRAD data against genomic contigs.

Comparison of ezRAD results using two different sets of reference contigs, the original ezRAD analysis pipeline contigs and published genomic contigs for the seastar Patiria miniata.
| Reference Type          | ezRAD       | Genomic Contigs |
|-------------------------|-------------|-----------------|
| Number of Contigs       | 635,376     | 179,756         |
| Mapped Reads            | 47,718,931  | 26,130,869      |
| High Quality Mapped     | 14,987,372  | 21,997,385      |
| Variable Sites          | 1,167,981   | 1,156,633       |
| Shared SNPs             | 187,597     | 151,742         |
| >10X Shared SNPs        | 143,254     | 114,620         |
Table 3 (on next page)

Comparison of most commonly used RAD sequencing methodologies and associated costs.
| Method     | No. of enzymes | Cut frequency | Shearing required | Size selection | Library prep time & required expertise | Initial outlay cost | Subsequent library cost per sample | Scalability to reduce overall cost per sample |
|------------|----------------|---------------|-------------------|---------------|----------------------------------------|--------------------|-----------------------------------|-----------------------------------------------|
| ezRAD      | 1 or more      | Frequent      | No                | Yes           | Low                                    | Very Low           | Moderate                          | Low                                           |
| RAD tags   | 1              | Rare          | Yes               | Yes           | High                                   | High               | Low                              | Low                                           |
| GBS        | 1              | Rare or frequent | No              | No            | Moderate                               | High               | Moderate to Very Low             | Low                                           |
| 2-enzyme GBS | 2            | Rare + frequent | No              | No            | Moderate                               | High               | Moderate to Very Low             | Low                                           |
| ddRAD      | 2              | Frequent      | No                | Yes           | Moderate                               | High               | Very Low                         | Moderate                                      |
| 2b-RAD     | 1              | Frequent      | No                | No            | Moderate                               | High               | Low                              | Moderate                                      |
