

## Letter

## Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application

Brittany A. Garner,<sup>1,2,‡</sup>  
 Brian K. Hand,<sup>1,‡,\*</sup>  
 Stephen J. Amish,<sup>1,2</sup>  
 Louis Bernatchez,<sup>3</sup>  
 Jeffrey T. Foster,<sup>4</sup>  
 Kristina M. Miller,<sup>5</sup>  
 Phillip A. Morin,<sup>6</sup>  
 Shawn R. Narum,<sup>7</sup>  
 Stephen J. O'Brien,<sup>8</sup>  
 Gretchen Roffler,<sup>9</sup>  
 William D. Temple,<sup>10</sup>  
 Paul Sunnucks,<sup>11</sup>  
 Jeffrey Strait,<sup>1,2</sup>  
 Kenneth I. Warheit,<sup>12</sup>  
 Todd R. Seamons,<sup>12</sup>  
 John Wenburg,<sup>13</sup>  
 Jeffrey Olsen,<sup>13</sup> and  
 Gordon Luikart<sup>1,2</sup>

We agree with Shafer *et al.* [1] that there is a need for well-documented case studies of the application of genomics in conservation and management as well as increased communication between academics and natural resource managers. However, we challenge Shafer *et al.*'s [1] relatively pessimistic assertion that 'conservation genomics is far from seeing regular application'. Here we illustrate by examples that conservation practitioners utilize more genomic research than is often apparent. In addition, we highlight the work of nonacademic laboratories [government and nongovernmental organizations (NGOs)], some of which are not always well represented in peer-reviewed literature. Finally, we suggest that increased agency-academic collaboration would enhance the application of

genomics to real-world conservation and help conserve biodiversity.

There is substantial controversy and confusion surrounding the definition of 'genomics' versus traditional genetic approaches. Here we address this by expanding Shafer *et al.*'s [1] definition to include a broad- and narrow-sense definition to better illuminate the different ways that genomics contributes to conservation practice. We define broad-sense conservation genomics as the use of new genomic techniques and genome-wide information to solve problems in conservation biology (as in Shafer *et al.* [1] and Allendorf *et al.* [2]). Our narrow-sense definition also requires the use of approaches that are conceptually and quantitatively different from traditional genetics to answer questions that would be impossible using genetic data alone (e.g., detecting genome-wide adaptation, use of transcriptomics, epigenetics, using annotated genomes). This narrow-sense definition includes using hundreds to thousands of mapped or gene-targeted marker loci in combination with recent computational and conceptual approaches such as mapping runs of homozygosity, comparing neutral versus adaptive patterns of population structure or gene flow, and testing for signals of selection to assess adaptation.

Narrow-sense genomic approaches have been used for diverse conservation applications including identifying conservation units, assessing gene flow, and detecting local adaptation (Table S1 in the supplementary material online). We agree with Shafer *et al.* [1] and others [2] about the general and serious concern of erroneous identification of adaptive loci and their subsequent use (or misuse) in conservation practice. However, we remain cautiously optimistic given the recent efforts to use putatively adaptive loci to inform management practices. For instance, genome-wide scans using diversity array technology (DArTseq) in gimlet trees (*Eucalyptus salubris*) generated 16 122 neutral and

putatively adaptive SNP markers used to uncover distinctive molecular lineages signaling adaptation to different environments. These genome-wide scans offered enhanced precision otherwise unavailable with traditional genetics or phenotypic traits alone [3] (Table S1). Such novel insights are important in seed choice for the ecological restoration of gimlet trees, a keystone species in the Great Western Woodlands of Australia, in the wake of wildfires [3].

In many broad-sense studies, next-generation sequencing (NGS) has enabled the discovery of management-informative markers that are subsequently screened in populations of conservation concern. For example, state management agencies in Washington and Idaho, USA used NGS to discover markers of introgression from hatchery broodstock into wild populations of salmonid fishes [4,5]. Other applications of broad-sense conservation genomics are evident (Table S1) and have been enabled by recent NGS and SNP genotyping technologies [6] (<http://biorxiv.org/content/early/2015/10/11/028837>). These approaches allow genome-wide discovery and genotyping of highly informative markers, making cost-effective monitoring feasible using relatively small marker sets (e.g., 100–500 markers) [7].

Decreases in costs (e.g., sequencing, library prep, bioinformatics) are sparking the application of NGS to a broader set of conservation questions and taxa where funding is relatively more limited. In addition to the examples above, genomic data are currently applied in conducting parentage analyses in Pacific lampreys (*Lamprologus tridentata*) and monitoring for disease in Tasmanian devils (*Sarcophilus harrisi*) [8,9] and fish (Table S1). Power analyses and cost-savings comparisons of using SNPs versus microsatellite markers in conservation genomics would be of great benefit, but such analysis is beyond the scope of this letter. However, using genomic approaches has been shown to provide more statistical power than

microsatellites and cost less for genotyping and are as low as 1% of the cost of traditional Sanger sequencing for marker discovery [3,6,7,10] (Table S1).

We have included multiple case studies from salmonids because these species are of great conservation concern due to their ecological, commercial, and cultural importance in many Northern Pacific Rim river systems. For example, ~30% or more of salmonid populations in the Columbia River Basin (USA–Canada) have been extirpated and many remaining populations are listed as endangered or threatened under the Endangered Species Act (ESA) or the Species at Risk Act in Canada because of, for example, over-harvesting, habitat degradation, pollution, and hydrological dams [11]. Therefore, more money and time is being spent on these species than other taxa due to their multiple conservation concerns (e.g., climate change, hybridization, over-harvesting). There are ~12 nonacademic laboratories (e.g., federal, tribal, NGO, state agencies) using genomic data to work mostly or exclusively on salmonids in the Pacific Northwest of North America. Shafer *et al.* [1] insufficiently acknowledged one of the most significant contributions of genomics to conservation by not fully highlighting the work of these laboratories, particularly the Alaska Department of Fish and Game (ADFG), a leader in SNP and NGS tool development and application. ADFG genotypes approximately 100 000 fish annually for management using broad-sense conservation genomic approaches [12]. Such approaches are now feasible and being conducted in many other species thanks to declining costs of genomics, as mentioned above (Table S1).

We highlight recent applications of genomics in real-world management where some are published, but many similar studies are not published or widely disseminated. Some nonacademic laboratories have relatively limited incentive to

publish or are delayed due to urgent deadlines reinforced by political, legislative, or legal constraints. For example, some agency laboratories produce reports or declarations used in litigation or the planning of harvest regulations or introductions (e.g., hatchery fish management plans), which can delay scientific publication. Nonacademics could potentially publish more by collaborating with academic groups who have strong incentives to publish (e.g., to ‘publish or perish’). Academics could in turn achieve greater conservation impact by working closely with practitioners who can provide benefits such as large sample and data collections, funding and field staff, collection permits, and high-throughput, cutting-edge genomics platforms.

While research and publications from some nonacademic laboratories are often underappreciated or delayed, they can help the conservation biology community to understand the extent and feasibility of applying genomics to conservation. We hope by highlighting case studies we will expand discussions and applications of genomic techniques in conservation and encourage the closing of gaps between nonacademic laboratories and academia.

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### Supplementary Information

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<sup>1</sup>Flathead Lake Biological Station, Fish and Wildlife Genomic Group, Division of Biological Sciences, University of Montana, Polson, MT 59860, USA

<sup>2</sup>Wildlife Program, Fish and Wildlife Genomic Group, College of Forestry and Conservation, University of Montana, Missoula, MT 59812, USA

<sup>3</sup>Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, QC G1V 0A6, Canada

<sup>4</sup>Department of Molecular, Cellular, and Biomedical Sciences, University of New Hampshire, Durham, NH 03824, USA

<sup>5</sup>Molecular Genetics Laboratory, Pacific Biological Station, Nanaimo, BC V9T 6N7, Canada

<sup>6</sup>Southwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 8901 La Jolla Shores Drive, La Jolla, CA 92037, USA

<sup>7</sup>Columbia River Inter-Tribal Fish Commission, Hagerman Fish Culture Experiment Station, 3059-F National Fish Hatchery Road, Hagerman, ID 83332, USA

<sup>8</sup>Theodosius Dobzhansky Center for Genome Bioinformatics, St Petersburg State University, 41 Sredniy Prospect, St Petersburg, Russia

<sup>9</sup>Alaska Department of Fish and Game, Division of Wildlife Conservation, 802 3rd Street, Douglas, AK 99824, USA

<sup>10</sup>Gene Conservation Laboratory, Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, AK 99518, USA

<sup>11</sup>School of Biological Sciences, Monash University, Melbourne, VIC 3800 Australia

<sup>12</sup>Washington Department of Fish and Wildlife, Molecular Genetics Laboratory, 600 Capitol Way N., Olympia, WA 98501, USA

<sup>13</sup>Conservation Genetics Laboratory, 1011 East Tudor Road, MS 331, Anchorage, AK 99503, USA

<sup>†</sup>These authors contributed equally.

\*Correspondence: [brian.hand@umontana.edu](mailto:brian.hand@umontana.edu) (B.K. Hand), <http://dx.doi.org/10.1016/j.tree.2015.10.009>

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## Letter

### Reply to Garner *et al.*

Aaron B.A. Shafer,<sup>1,\*</sup>  
 Jochen B.W. Wolf,<sup>1,\*</sup>  
 Paulo C. Alves,<sup>2</sup>  
 Linnea Bergström,<sup>1</sup>  
 Guy Colling,<sup>3</sup> Love Dalén,<sup>4</sup>  
 Luc De Meester,<sup>5</sup>  
 Robert Ekblom,<sup>1</sup>  
 Simone Fior,<sup>6</sup>  
 Mehrdad Hajibabaei,<sup>7</sup>  
 A. Rus Hoesel,<sup>8</sup>  
 Jacob Hoglund,<sup>1</sup>  
 Evelyn L. Jensen,<sup>9</sup>  
 Michael Krützen,<sup>10</sup>  
 Anita J. Norman,<sup>11</sup>  
 E. Martin Österling,<sup>12</sup>  
 N. Joop Ouborg,<sup>13</sup>  
 John Piccolo,<sup>12</sup>  
 Craig R. Primmer,<sup>14</sup>  
 Floyd A. Reed,<sup>15</sup>  
 Marie Roumet,<sup>6</sup>  
 Jordi Salmons,<sup>16</sup>  
 Michael K. Schwartz,<sup>17</sup>  
 Gernot Segelbacher,<sup>18</sup>  
 Jens Thaulow,<sup>19</sup>  
 Mia Valtonen,<sup>20</sup>  
 Philippine Vergeer,<sup>21</sup>  
 Matthias Weissensteiner,<sup>1</sup>

Christopher W. Wheat,<sup>22</sup>  
 Carlese Vilà,<sup>23</sup>  
 and Piotr Zielinski<sup>24</sup>

The letter by Garner *et al.* [1] continued an important discussion regarding the role genomics might play in conservation biology. In general, we do not see a dichotomy between our point of view [2] and that put forth by Garner *et al.* [1]. At the heart of the issue is how to define an actual impact of genomics on applied conservation and find suitable ways to remove existing barriers limiting the use of genomics for managing wild populations. The promised gains of identifying adaptive loci and the genes underlying phenotypes [3,4] have in most systems not yet been realized and recent empirical work further highlights the challenges [5,6]. Thus, our take-home message boiled down to the application of genomics in wild populations being at an early developmental stage that is far from straightforward and far from regularly applied [2].

Garner *et al.* [1] extended the list of examples where genomics has aided the conservation and management of wild species. It is promising to see that examples are beginning to emerge and we are pleased that the authors repeated the call for increased agency–academic collaboration to enhance the application of genomics to real-world conservation issues. However, the list of case studies provided (Table S1 in [1]) underscores the absence of genomic work effectively impacting the conservation of a broad array of organisms. The majority of examples involve commercially important species in North America, most often salmonid fish populations. Other featured examples, such as the Tasmanian devil, are interesting genomic studies, but the key conservation strategy revolves around maintaining an insurance (disease-free) population, with genomic applications labeled as ongoing research [7]. The lack of taxonomic and geographic breadth and applied impact on noncommercial entities suggest that genomics has as yet not been as influential

on conservation biology as initially promised [3] or implied [1]. Examples with high commercial potential might in the best case reflect a starting point for testing the applicability of genomics more broadly.

Cooperation across the academic and practical realms is an integral part of applied conservation and increased attention in published literature does have a beneficial corollary for conservation. In that regard, we agree that reports from the grey literature are valuable and play an important role of disseminating valuable information. However, we must not lose sight of the main incentive of conservation research, which is conserving biodiversity. To truly bridge the conservation genomics gap, alternative ways to measure impact [8] and fund conservation science [2] need to be considered. We therefore echo our original call for the need to develop research-to-application frameworks that will accelerate the crossing of the conservation genomics gap that is still present for the very large number of species not commercially harvested and with limited resources.

<sup>1</sup>Uppsala University, Ecology and Genetics, Evolutionary Biology Centre, Uppsala 75236, Sweden

<sup>2</sup>University of Porto, Centro de Investigação em Biodiversidade e Recursos Genéticos and Faculdade de Ciências, Porto 4485-661, Portugal

<sup>3</sup>Musée National d'Histoire Naturelle Luxembourg, Population Biology, 2160 Luxembourg, Luxembourg

<sup>4</sup>Swedish Museum of Natural History, Bioinformatics, and Genetics, 104 05 Stockholm, Sweden

<sup>5</sup>KU Leuven – University of Leuven, Aquatic Ecology, Evolution, and Conservation, 3000 Leuven, Belgium

<sup>6</sup>ETH Zurich, Integrative Biology, 8092 Zurich, Switzerland

<sup>7</sup>University of Guelph, Integrative Biology, Guelph, ON N1G 2W1, Canada

<sup>8</sup>Durham University, Biological and Biomedical Sciences, Durham DH1 3LE, UK

<sup>9</sup>University of British Columbia Okanagan, Biology, Kelowna, BC V1V 1V7, Canada

<sup>10</sup>University of Zurich, Anthropological Institute and Museum, 8057 Zurich, Switzerland

<sup>11</sup>Swedish University of Agricultural Sciences, Wildlife, Fish and Environmental Studies, 901 83 Umeå, Sweden

<sup>12</sup>Karlstad University, Biology, 651 88 Karlstad, Sweden

<sup>13</sup>Radboud University Nijmegen, Experimental Plant Ecology, Nijmegen, GL 6500 The Netherlands

<sup>14</sup>University of Turku, Biology, 20014 Turku, Finland

<sup>15</sup>University of Hawai'i at Manoa, Biology, Honolulu, HI 96822, USA

<sup>16</sup>Instituto Gulbenkian de Ciência, Population and Conservation Genetics Group, 2780-156 Oeiras, Portugal