Corrigendum to: Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA)

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(Vol. 31, Issue 1, pp. 1–7)

The authors wish to add the following author, who was inadvertently omitted, to The GIGA Community of Scientists (COS) on p. 7 in Appendix 1.

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Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA)

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Abstract. The Global Invertebrate Genomics Alliance (GIGA), a collaborative network of diverse scientists, marked its second anniversary with a workshop in Munich, Germany in 2015, where international attendees focused on discussing current progress, milestones and bioinformatics resources. The community determined the recruitment and training of talented researchers as one of the most pressing future needs and identified opportunities for network funding. GIGA also promotes future research efforts to prioritise taxonomic diversity and create new synergies. Here, we announce the generation of a central and simple data repository portal with a wide coverage of available sequence data, via the compagen platform, in parallel with more focused and specialised organism databases to globally advance invertebrate genomics. This article serves the objectives of GIGA by disseminating current progress and future prospects in the science of invertebrate genomics with the aim of promotion and facilitation of interdisciplinary and international research.

Additional keywords: biodiversity, evolution, genetics, Metazoa.

Received 11 August 2016, accepted 10 October 2016, published online 16 March 2017

Introduction

Genomic research will likely exhibit exponential growth for years to come (Stephens\textit{ et al.} 2015). In anticipation of this, the Global Invertebrate Genomics Alliance (GIGA) formed to address the multiple needs and opportunities of the expanding invertebrate genomics community (GIGA COS 2014). GIGA complements taxonomically similar but differently focused efforts, such as the arthropod-focused Genome 10K (Genome 10K COS 2009; Koepfl\textit{ i} \textit{ et al.} 2015) and the Arthropod Genomics Consortium (i5k) (Robinson\textit{ et al.} 2011), and interacts with other initiatives, such as the Genomic Observatories Network (Davies\textit{ et al.} 2014), the Global Genome Initiative (GGI, http://naturalhistory.si.edu/ggi/), and the Ocean Genome Legacy (OGL, http://www.northeastern.edu/cos/marinescience/ogl/). These latter initiatives were created to archive diverse arrays of specimens, tissues, nucleic acid samples, voucher material and supporting data in a global effort to help coordinate and disseminate these data and materials across the broader scientific community.

GIGA has adopted a ‘bottom up’ philosophy to advance its community goals, with voluntary and vigorous contributions of members building a consensus approach to avoiding duplication of research efforts through effective coordination within the community (see Fig. S1 for the distribution of member countries, available as Supplementary material). GIGA was launched with an initial workshop in 2013 and an inaugural white paper (GIGA COS 2014). The second GIGA workshop (March 2015 at the Ludwig-Maximilians-Universität, Munich, Germany) reviewed the progress of this growing initiative. More than 80 scientists from 23 countries participated in the 3-day event, which explored aspects of project implementation and comparative analyses across invertebrates as well as training and funding efforts and opportunities. We briefly report here on the major outcomes of these discussions.

Current status of invertebrate genome and transcriptome sequencing efforts

\textit{Genomes, transcriptomes and ‘priority species’}

The first GIGA white paper (GIGA COS 2014) and two workshops identified many major hurdles hindering large-scale
Distributed effort model and ambassador framework

The GIGA II workshop identified ‘divide-and-conquer’ as the best strategy for the distribution of efforts concerning the coordination of genome and transcriptome sequencing and knowledge exchange in different taxonomic and phylogenetic groups and scientific communities. For example, clade-specific ‘ambassadors’ (see http://giga-cos.org/index.php/members) were chosen to recruit within their own smaller communities and discuss candidate taxa for future genomics. The ambassador framework will also effectively distribute the efforts to provide a complete and comprehensive overview of current and future invertebrate genomic and transcriptomic resources, and GIGA members will have direct ‘go-to’ experts for the organisms of interest.

Developing online resources for sharing GIGA data

Sequence data archives

High-throughput sequencing technologies have boosted the field of comparative genomics (Green et al. 2015; Koepfl et al. 2015). The volume of sequence data available through public databases such as the International Nucleotide Sequence Database Collaboration (INSDC) portal and its members, GenBank (at the National Center for Biotechnology Information, NCBI), European Nucleotide Archive (ENA) (at European Bioinformatics Institute) and DNA Data Bank of Japan (DDBJ), has increased exponentially (Baxevanis 2011; Stephens et al. 2015). As overall sequencing costs continue to decrease, individual laboratories and community efforts can generate ever larger amounts of novel genomic and transcriptomic data from non-model organisms. Aggregative databases such as Compagen (http://compagen.org) (Hemmrich & Bosch 2008) or Reefgenomics (http://reefgenomics.org) (Liew et al. 2016) coordinate data presentation and analyses for particular species or ecosystem groups. While the development of a single database covering data from a wide variety of invertebrate species would likely have wide appeal, the programming, curatorial and funding burden of producing and maintaining a centralised resource goes beyond the reach of GIGA and similar consortia at present. Many researchers only need simple queries (e.g. BLAST-based sequence similarity searches), while a minority needs more complex, multivariate queries (e.g. synteny-based orthology inference).

We propose an approach that will cater to both needs by providing: (1) a central sequence database that focuses on simple queries accessing a large range of data, in combination with (2) more focused, de-centralised species databases that satisfy complex queries and more specific requirements (Parkhill et al. 2010). The GIGA homepage will serve as a hub from which to access these platforms.

Compagen.org as a general data portal for GIGA transcriptomes and genomes

Compagen.org, originally designed to cater to the early branching (non-bilaterian) animal community, will be extended to serve as our central sequence database providing access to processed datasets such as assembled transcriptomes/genomes

Box 2. Criteria for sequencing candidacy – priority species for sequencing

Several detailed biological criteria for species selection were discussed previously (see GIGA COS 2014), including:

- species inhabiting extreme environments.
- species representing deep, isolated phylogenetic branches;
- species with contrasting life spans (particularly long or very short);
- species with specific physiological abilities such as regeneration or anhydrobiosis and
- species inhabiting ‘extreme’ environments.

Practical constraints include technological, technical, financial and cultural obstacles. Sample availability, individual researcher motivations, collaborations and availability of genome size estimates must also be considered.

Major technical criteria for taxon selection includes:

- the availability of appropriate sampling permits (following CITES, Rio Biodiversity and Nagoya Protocol guidelines (UNEP/CBD/COP 2002); https://www.cbd.int/abs/);
- availability of metadata;
- proper vouchering;
- the species being model and/or popular;
- availability of transcriptome data (or plans to generate them); and
- agreements for data sharing and access.

Box 1. The GIGA homepage as a community hub for invertebrate genomics data

The GIGA homepage (http://giga-cos.org) provides an informative, interactive and mobile-friendly portal to relevant invertebrate genomic research, data and news. A sign-up button welcomes new members to register, while another link invites members to upload current publications. Importantly, GIGA provides a landing page to relevant transcriptome and genome ‘links’ with the opportunity for users to add their own assembled sequence data. The GIGA website is not meant to be a database in itself. Rather, the community nature of this homepage is emphasised by its open access to data. GIGA strongly supports contributions from the community (bottom-up philosophy) to share their new publications, links to datasets and news items via web forms that can be filled without any prior knowledge on coding languages. Our anticipation is that the usefulness of the webpage will grow with the community.
Table 1. Proposed priority species for whole genome sequencing

<table>
<thead>
<tr>
<th>Species</th>
<th>Common name</th>
<th>Phylum/Class</th>
<th>Genome size (Gb)</th>
<th>Significance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alitta (Nereis) virens</td>
<td>King ragworm or sandworm</td>
<td>Annelida/Polychaeta</td>
<td>TBD</td>
<td>Ecological model</td>
</tr>
<tr>
<td>Montipora digitata</td>
<td>Finger coral</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Cubitella annulata</td>
<td>Boulder star coral</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research, taxonomy</td>
</tr>
<tr>
<td>Ricordea florida</td>
<td>Florida false coral</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Tubipora musica</td>
<td>Organ pipe coral</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Millepora dichotoma</td>
<td>Net fire coral</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Cassiopea frondosa</td>
<td>Upside-down jellyfish</td>
<td>Porifera/Demospongiae</td>
<td>0.3</td>
<td>Research</td>
</tr>
<tr>
<td>Gephyrocrinus messingii</td>
<td>Sea lily</td>
<td>Echinodermata/Crinoidea</td>
<td>TBD</td>
<td>Sister to remaining echinoderms</td>
</tr>
<tr>
<td>Himerometra robustipinna</td>
<td>Feather star</td>
<td>Echinodermata/Crinoidea</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Pontiometra andersoni</td>
<td>Feather star</td>
<td>Echinodermata/Crinoidea</td>
<td>TBD</td>
<td>Research, taxonomy</td>
</tr>
<tr>
<td>Bankia setacea</td>
<td>Feather shipworm</td>
<td>Mollusca/Bivalvia</td>
<td>1.5</td>
<td>Physiology, invasive</td>
</tr>
<tr>
<td>Bathymodiolus azoricus</td>
<td>N/A</td>
<td>Mollusca/Bivalvia</td>
<td>Deep sea ecology</td>
<td></td>
</tr>
<tr>
<td>Corbula fluminea</td>
<td>Asian clam or golden clam</td>
<td>Mollusca/Bivalvia</td>
<td>1.5</td>
<td>Physiology, invasive</td>
</tr>
<tr>
<td>Dreissenia polymorpha</td>
<td>Zebra mussel</td>
<td>Mollusca/Bivalvia</td>
<td>1.7</td>
<td>Invasive, pest</td>
</tr>
<tr>
<td>Limnoperna fortunei</td>
<td>Golden mussel</td>
<td>Mollusca/Bivalvia</td>
<td>TBD</td>
<td>Invasive</td>
</tr>
<tr>
<td>Mya arenaria</td>
<td>Soft-shell clam</td>
<td>Mollusca/Bivalvia</td>
<td>1.4</td>
<td>Invasive, commercial</td>
</tr>
<tr>
<td>Ruditapes decussatus</td>
<td>Grooved carpet shell</td>
<td>Mollusca/Bivalvia</td>
<td>1.8</td>
<td>Commercial, ecological</td>
</tr>
<tr>
<td>Ruditapes philippinarum</td>
<td>Manila clam</td>
<td>Mollusca/Bivalvia</td>
<td>1.9</td>
<td>Commercial, invasive, model for adaptation (cold)</td>
</tr>
<tr>
<td>Chaconia scabra</td>
<td>Glass squid</td>
<td>Mollusca/Cephalopoda</td>
<td>TBD</td>
<td>Deep sea ecology</td>
</tr>
<tr>
<td>Graneledone verrucosa</td>
<td>Atlantic longarm octopus</td>
<td>Mollusca/Cephalopoda</td>
<td>TBD</td>
<td>Benthic deep sea species</td>
</tr>
<tr>
<td>Japetella diaphana</td>
<td>Pelagic holotrichid octopod</td>
<td>Mollusca/Cephalopoda</td>
<td>TBD</td>
<td>Pelagic deep sea species</td>
</tr>
<tr>
<td>Loligo pealeii</td>
<td>Longfin inshore squid</td>
<td>Mollusca/Cephalopoda</td>
<td>2.7</td>
<td>Cellular neurobiology, fishery</td>
</tr>
<tr>
<td>Macrotropis defilippi</td>
<td>N/A</td>
<td>Mollusca/Cephalopoda</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Conus bullocki</td>
<td>Bubble cone</td>
<td>Mollusca/Gastropoda</td>
<td>2.7</td>
<td>Natural products</td>
</tr>
<tr>
<td>Pomacea maculata</td>
<td>Apple snail</td>
<td>Mollusca/Gastropoda</td>
<td>0.6</td>
<td>Invasive species, biomedical research</td>
</tr>
<tr>
<td>Cellana sandwicensis</td>
<td>Hawaiian limpet</td>
<td>Mollusca/Gastropoda</td>
<td>TBD</td>
<td>Model for sympatric diversification</td>
</tr>
<tr>
<td>Aplysia californica</td>
<td>Row pore rope sponge</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Cinachyrella alloclada</td>
<td>Golfball sponge</td>
<td>Porifera/Demospongiae</td>
<td>TBD</td>
<td>Research</td>
</tr>
<tr>
<td>Halicola oculata</td>
<td>N/A</td>
<td>Porifera/Demospongiae</td>
<td>0.1–0.2</td>
<td>Research</td>
</tr>
<tr>
<td>Tedania ignis</td>
<td>Fire sponge</td>
<td>Porifera/Demospongiae</td>
<td>0.6</td>
<td>Early diverging bilaterian clade</td>
</tr>
<tr>
<td>Themistella lageniformis</td>
<td>Peanut worm</td>
<td>Sipuncula/Sipunculidea</td>
<td>0.5</td>
<td>Taxonomy, developmental biology</td>
</tr>
<tr>
<td>Milnesium tardigradum</td>
<td>Limno-terrestrial tardigrade</td>
<td>Tardigrada/Eutardigrada</td>
<td>TBD</td>
<td>Taxonomy</td>
</tr>
<tr>
<td>Xenoturbella profunda</td>
<td>N/A</td>
<td>Xenacoelomorpha/Xenoturbellida</td>
<td>TBD</td>
<td>Early diverging bilaterian clade</td>
</tr>
</tbody>
</table>
and predicted peptides, thereby complementing sequence datasets available from public domains (e.g. NCBI Sequence Read Archive (SRA), NCBI dbEST (GenBank’s sequence data on cDNA sequences or expressed sequence tags) and ENA trace archives). Compagen.org provides a critical extension to public databases due to the disconnect between what is submitted in the form of primary sequence data and what is available in the form of assembled and annotated data (Fig. 1). Having compagen.org as a central repository will clearly facilitate provision of assembled invertebrate sequence data as well as retrieval of data for analyses. This present choice does not preclude the additional development of other (taxon or feature specific) portals to GIGA-related sequences in the future.

**Databases for GIGA-relevant taxa with a larger research community**

For taxon groups studied by larger research communities, it is realistic (and tractable) to develop or coordinate independent, researcher or laboratory-curated, taxon-specific databases, such as http://www.spongebase.net for sponges or http://reefgenomics.org for coral reef invertebrates. These databases can accommodate the needs of the specific research groups focusing on specific taxa or groups of taxa, emphasising genomics, transcriptomics, variation or multi-species interaction as required. In connection with those, several single-species databases already exist, including the Aiptasia genome platform (http://aiptasia.reefgenomics.org/) (Baumgarten et al. 2015) and the Hypsibius dujardini genome server (http://www.tardigrades.org) (Koutsovoulos et al. 2016). From these efforts, cross-species databases can arise, such as http://comparative.reefgenomics.org, which provides a comparative platform for coral transcriptomes focusing on orthologous genes that can be used to interrogate coral species-specific genes (Bhattacharya et al. 2016). Community-managed data repositories should be extended to link genomic efforts to physical specimens deposited in natural history collections or to genetic resources deposited in genetic repositories in natural history museums or in other institutions. Overall, the accessibility of novel sequence data enhanced with metadata will open multiple doors to new hypotheses and cross collaborations, thereby propelling broad scientific, technological and societal advances (i5K Consortium 2013; Dubilier et al. 2015; Green et al. 2015; Koepfli et al. 2015).

**Community opportunities**

**Collaboration**

The GIGA II workshop highlighted the common goals shared among i5k and GIGA initiatives, primarily with regards to help in structuring and advising the community for handling large genome project initiatives. Other key shared goals include funding, expert genome annotation and dissemination of results. There will be additional opportunities for collaboration between research groups involved in these and other large invertebrate genomics and transcriptomics consortia (such as 1Kite or the nematode.net) due to the shared methodological and bioinformatic approaches and training opportunities.

**Training**

Achieving the broad goals of GIGA will require new commitment and investment in training and educating the next generation of genome scientists (Fig. 2). Computational biology skills are needed to allow students to navigate, customise and populate increasingly complex databases, but additionally, training in aspects of organismal and evolutionary biology, ecology and biodiversity legislation that regulates the exchange of genetic resources across national boundaries needs to be provided. Besides a sweeping view and comparison of various Big Data issues, recent reviews provide a compelling argument for the genomics community to prepare an educational foundation to handle the deluge of genomic data and its associated metadata (Stephens et al. 2015; Dougherty et al. 2016). In general, current genomics and bioinformatics curricula appear relatively staid, while independent bioinformatics workshops (e.g. evomics.org, and those listed at http://meetings.cshl.edu/courseshome.aspx) can provide cutting edge approaches and showcase innovation; however, scheduling may be more uncertain and irregular for the latter and those specialist courses do not cover all aspects needed for the holistic training needed to cater for future job markets in (invertebrate and/or biomedical) genomics.

**Funding agencies for invertebrate genomes**

Currently, targeted funding for invertebrate genomes pales in comparison to the investments being made in vertebrate genomics (Couzin-Frankel 2012; AAAS 2015), so we compiled a limited selection of some of the agencies that we thought might contribute funding to further GIGA efforts (Table 2). Realising these will eventually expire, individual scientists, small collaborative cohorts or larger groups will have to forge imagination, fortitude...
and the scientific foundations and infrastructure discussed herein to persuade funding entities on the values of each particular project. However, during GIGA II the current dearth of international, multilateral funding programs that allow researchers in different continents (e.g. EU, Asia and Americas) to collaborate became strikingly obvious.

Concluding statement

Many benefits derived from single or multi-species genome sequencing projects have been described, realised and projected in recent years (GIGA COS 2014). Discoveries will continue to accrue with further innovations. Efforts will be further enhanced through the GIGA framework, which coordinates and promotes the concerted contributions of diverse experts. In the words of Immanuel Kant by way of Durant (1938), ‘Science is organized knowledge; wisdom is organized life’. In a similar spirit, GIGA will facilitate scientific organisation, and consequently the collective progress (wisdom) of humanity.

Acknowledgements

The GIGA Community of Scientists gives special thanks to the German Research Foundation (DFG, project Wo896/16-1 to G. Wörheide) for substantially supporting the GIGAII workshop in Munich (Germany) in March 2015.

References


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Appendix 1. The GIGA Community of Scientists (COS)

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