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NEWS AND COMMENTARY

Sequencing one sex or the other has to be justified

Gender genomics and equality

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Who gets to represent the genome? There is an ongoing debate with respect to the identity of the individuals whose genomes are the first to be sequenced in a worldwide effort to describe as much genetic code as possible in humans and in other evolutionarily and commercially relevant species (Brenner, 2007; Erren *et al*., 2008). But this debate seems to miss out on which sex should be sequenced at all or sequenced first. In addition to characterizing the genome of named and nameless human males (Brenner, 2007; News-in-Brief, 2008), molecular, evolutionary and behavioural biologists alike must be concerned with these trends, because, for instance, recent reports on the molecular basis of social complexity in honeybees (*Apis mellifera*) highlight a critical relevance of sex-specific genomics by exploring the biochemical mechanisms of the differences between the contribution of females (Vergoz *et al*., 2007) or males (Mattila and Seeley, 2007) to cooperative behaviour within the hive.

The honeybee genome had been sequenced with an explicit aim to provide a phylogenetic framework to understand behavioural evolution within complex animal societies (The Honeybee Genome Sequencing Consortium, 2006). A brief survey of already sequenced animal species shows that inconsistency in gender genomics derails this goal. For instance, the honeybee DNA was taken from several drones derived from a single queen, which resulted in the sequence of the haploid male genome. Yet, in the other five arthropod species also already sequenced, the genomes were derived from a mix of females and males, and only one species had its genome also sequenced using DNA extracted from the heterogametic sex (http://www.genomesonline.org/gold.cgi).

The picture is also unbalanced for 11 vertebrate species with their genome already sequenced; for example, in a fish species for which mechanism of sex determination remains unknown, two individuals of unspecified sex were sequenced. For humans, initially anonymous samples were taken from both sexes, but this has now changed to include a Nobel prize winner man (Brenner, 2007). Some other completed vertebrate genomes are dominated by data from the homogametic sex ($N=7$), with the Y chromosome being sequenced separately for two mammals so far. In contrast, individuals of only the heterogametic sex were sequenced in one fish, one bird and one primate.

Why does such gender genomics matter? Because our generalizations are only as good as the model systems on which they are based. For many years, the model for virtually all processes in humans and non-humans alike was the male, with females representing a special case; an exception to be studied after the representative subjects had been described. In medical research, this paradigm led to the disproportionate use of male subjects, whether rodents, monkeys or humans, in basic research on anatomy and physiology as well as studies of disease, an imbalance that has only been addressed in the last few decades (Zuk, 2002). In our human society, it has meant that women in atypical roles are often undervalued compared with their male counterparts, leading to relatively slower advancement for women with equal qualifications. Recently, this was aptly demonstrated by the lower publication rate of woman-first-authored papers in a behavioural journal that does not use a double-blind peer-review system (Budden *et al*., 2008). Such biases affecting decisions can occur in both decision-making men and women, and despite our belief that we are egalitarian.

There is an ongoing effort of 289+ programmes to sequence additional eukaryotic genomes, including 67 arthropods and 133 vertebrates, with $<20\%$ of taxa chosen explicitly as relevant for evolutionary studies. The recent description of a cephalochordate genome, for example, used the genome of a 'single gravid male' (Putnam *et al*., 2008). Genomics has only begun to scratch the surface in determining how interactions among genes and gene products influence the genotype, and it seems plausible that such interactions could differ between males and females. Ignoring the potential for biases in data collection at this crucial pioneering juncture could set the stage for regrettably limited data sets for years to come.

We urge genomics researchers to ensure that in these new data the diversity of genetic and environmental mechanisms (Quinn *et al*., 2007) that control gender-specific anatomy, physiology and behaviour will be fully represented.

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Brenner S (2007). *Nature* **449**: 783.
Budden AE *et al*. (2008). Trends in Ecology & Evolution **23**: 4.
Erren TC, Cullen P, Erren M (2008). *Nature* **452**: 151.
http://www.genomesonline.org/gold.cgi.
Mattila HR, Seeley TD (2007). *Science* **317**: 362.
News-in-Brief (2008). *Nature* **451**: 759.
Putnam NH *et al*. (2008). *Nature* **453**: 1064.
Quinn AE *et al*. (2007). *Science* **316**: 411.
The Honeybee Genome Sequencing Consortium (2006). *Nature* **443**: 931.
Vergoz V, Schreurs HA, Mercer AR (2007). *Science* **317**: 384.
Zuk M (2002). *Sexual Selections*. University of California Press: Berkeley, CA, USA.

Editor's suggested reading

Fairbairn DJ, Roff DA (2006). The quantitative genetics of sexual dimorphism: assessing the importance of sex-linkage. *Heredity* **97**: 319–328.
Fedorka KM, Winterhalter WE, Mousseau TA (2007). The evolutionary genetics of sexual size dimorphism in the cricket *Allonemobius socius*. *Heredity* **99**: 218–223.
Morgan TJ, Mackay TFC (2006). Quantitative trait loci for thermotolerance phenotypes in *Drosophila melanogaster*. *Heredity* **96**: 232–242.