

Interbull Survey on Sequencing of Cattle

J.W. Dürr, F. Forabosco, J. Jakobsen and B. Zumbach

Interbull Centre, Department of Animal Breeding and Genetics, SLU, Box 7023

S-75007 Uppsala, Sweden, joao.durr@slu.se

Abstract

Given the increasing interest on bovine genome sequencing, Interbull decided to run a survey focused on describing how the individual organizations are establishing their own bovine genome sequencing program and in which stage of development they are, as well as investigating if Interbull has a role to play in organizing an international network on bovine genome sequencing. A total of 45 responses to the 22 questions included in the online form were sent back to the Interbull Centre during June 2011. Most investigation groups work with both *Bos taurus* and *Bos indicus*, although the main focus is on dairy cattle (especially the Holstein breed). Association studies and causative mutations are the main research objectives, and consequently the selection of individuals to be genotyped is mainly based on their influence on the genetic makeup of the population. Most institutions are dedicated to research and would engage to a network focused on data exchange and technical discussions, which could be facilitated by Interbull.

Key words: bovine, genome, network

Introduction

The completion of the bovine genome sequencing (The Bovine Genome Sequencing and Analysis Consortium *et al.*, 2009) represented an important milestone for all fields of research in ruminants. Additionally, the costs of sequencing techniques have decreased dramatically in the last decade, falling from US\$ 100 000 000 per genome in 2001 to less than US\$ 10 000 in 2011 (Wetterstrand, 2012), and the descending trend continues. For this reason, the interest of bovine genetics research and business on sequenced data has greatly increased, especially after genomic information have irreversibly become part of the animal breeding and selection routines. Following the experience of human genomics, there seems to be a consensus that advances on genome sequencing requires an effective collaboration among research groups and organizations, not only to avoid duplication of efforts, but mainly due to the size of the challenge ahead. In order

to assess the potential role of Interbull on providing network for a worldwide collaboration on bovine sequencing, the Interbull Steering Committee requested at the Interbull technical workshop in Guelph (February 2011), that the Interbull Centre should carry out a survey among all Interbull customers and other organizations working on bovine genomics worldwide. The aim of this article is to summarize the results of the survey.

Materials and Methods

The survey consisted of an online questionnaire with 22 questions, some of multiple choice and others with open answers. The link to the survey was sent to all Interbull customers and collaborators, as well as broadly distributed through discussion groups focused on animal genetics. The survey was open for contributions during the month of June 2011. A total of 45 responses were received, 41

expressing that the respondent does or plans to do research on the basis of bovine sequences, and 4 respondents declaring no interest to engage. The participants were from 31 countries: Argentina, Australia, Austria, Brazil (2), Cameroon, Canada, Colombia, Costa Rica, Croatia, Czech Republic, France, Germany (3), Hungary, India, Iran, Ireland, Israel, Italy (3), Jordan, Kyrgyz Republic, New Zealand, Nigeria, Norway, Pakistan, Poland, South Africa, Spain, Sudan, Switzerland, The Netherlands (2), United Kingdom (3) and United States (6).

The survey intended to draw conclusions about three main issues: a. how the individual organizations are establishing their own bovine genome sequencing program; b. in which stage of development they are; and c. how an international cooperation on bovine genome sequencing should be organized.

Results were presented during the Interbull business meeting in Stavanger, Norway, and interpretation is enhanced by the discussion carried out on that occasion.

Results & Discussion

The matter addressed by the survey extrapolates the current mandate of Interbull, and the expressive number of responses from both Interbull-related and other organizations showed that this is valued as an important theme and that Interbull is perceived as an adequate forum for this discussion.

Portrait of individual programs

An initial set of questions was proposed to investigate the focus of the respondents in their local or institutional programs. Figure 1 shows that 80% of the programs will sequence *Bos taurus*, but a significant number (56%) will

sequence *Bos indicus* and 37% will target both subspecies. Although all respondents will be sequencing either one of the above, four of them revealed interest on other species, namely yak (*Bos grunniens* or *Bos mutus*), Indian bison (*Bos gaurus*), American bison (*Bison bison*), African buffalo (*Syncerus caffer*) and water buffalo (*Bubalus bubalis*).

Asked if emphasis would be put on the zootechnical aptitude of the cattle (Figure 2), a clear preference for sequencing dairy cattle was declared, what is probably due to the survey being run by and associated with Interbull.

A total of 45 breeds were listed in response to the question "Are you interested in sequencing specific breeds?", some of them by several groups: Angus (4), Arsi, Blanco Orejinegro, Blonde d'Aquitaine, Bonsmara, Bradford, Brahman (2), Brangus, Brown Swiss (3), Bunaji, Butana, Charolais, Chianina (2), Criollo, Girolando, Grey cattle, Guzerat (2), Gyr (2), Harton del Valle, Hereford, Holstein (15), Holstein-Jersey crosses, Jersey (3), Jordanian cattle, Kenana, Keteku, Kuri, Limousin (2), Montbéliarde, Muturu (2), Namchi, N'dama, Nelore, Ngaoundere Gudali, Normande, Norwegian Red, Pakistani cattle, Rahaji, Red Fulani, Romagnola, Romosinuano, Simmental (3), Sindi, Sokoto Gudali and White Fulani.

Although all respondents declared to work with animal genetics, 5 groups indicated also interest on human medical research. Figure 3 shows the focus of the investigations and association studies and quest for causative mutations represent the main interest of the respondents.

Regarding the part of the genome that will be (re)sequenced, 15 groups are focused on targeted re-sequencing and 22 on whole genome re-sequencing.

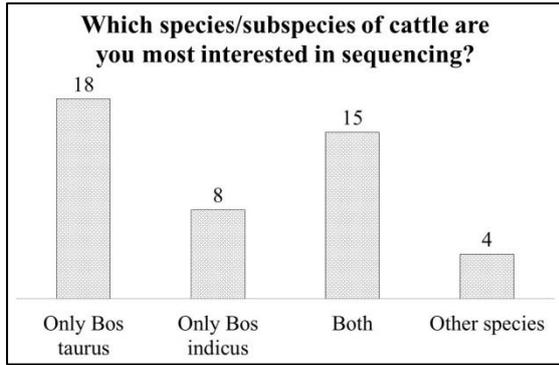


Figure 1. Target species or subspecies.

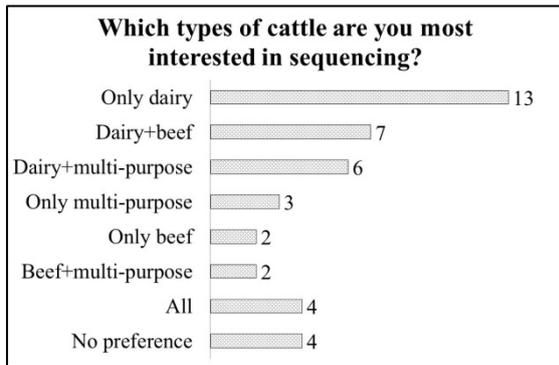


Figure 2. Target cattle types.

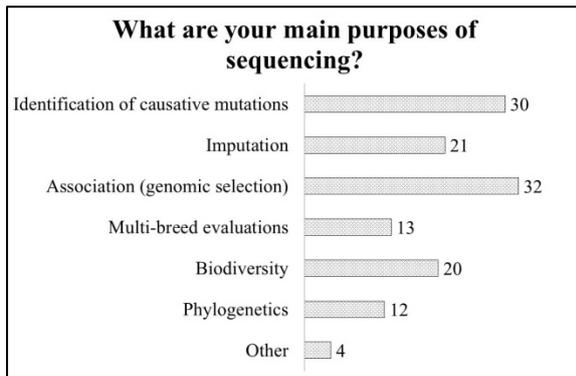


Figure 3. Focus of investigation.

Stage of development

A question was made to determine number of animals genotyped (whole genome) by May 2011, and 14 groups declared to have already sequenced individuals (10 only males, 2 only females, 2 both sexes), and 7 declared that have or intend to sequence pools of animals.

The number of genotyped individuals provided, however, seems exaggerated and it is probably due to the inclusion of target sequencing or other partial sequencing made by these groups. Given that there is no clear distinction between full and partial sequencing, the current number of sequenced individuals cannot be estimated based on this survey.

Figure 4 shows the sequencing methods currently applied by the respondents, and the Illumina Solexa system appears as the most popular.

Regarding the criteria adopted to choose the individuals that are being genotyped, 55% of the respondents considered the most important factor to be the individual’s contribution to the population genetic makeup, measured by number of relatives (founder animals, sires of sires, bulls with large number of progenies). Table 1 shows also a variety of other criteria considered by different groups.

Table 2 presents the types of organization that (will) own the genomes and in almost 60% of the cases the data belong to research institutions, which is a different situation if compared to the current ownership of SNP genotypes. This may be a facilitating factor for future data exchanges, given that commercial interests are not directly related to the genomic data generated.

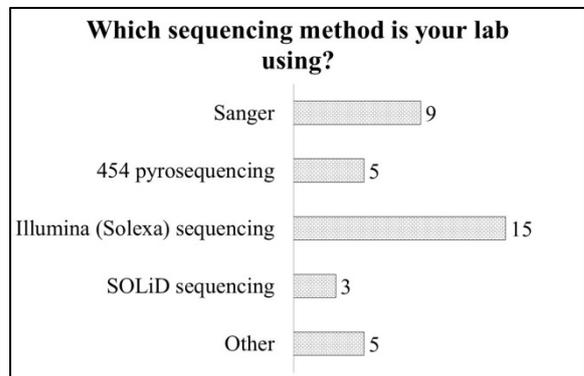


Figure 4. Sequencing methods.

Table 1. How do you choose the animals to be sequenced? What are your selection criteria?

Criteria	Number of responses
Contribution to population	18
Phenotypic information	4
Haplotype information	3
Number of progeny with SNP information	3
Specific genotypes	2
Random	2
Highly inbred	1
Unrelated animals	1
Not decided	3

Table 2. Nature of the organizations that are the proprietary of the bovine whole sequencing data.

Type of organization	Number of responses
Research Institution	20
Breeders	7
Breeding company	2
Governmental body	5
Undefined	2

Networking

The main objective of the survey was to examine the opportunities for cooperation among the surveyed organizations. Figure 5 shows a promising willingness to share genomic information with other organizations. One simple way of cooperation which seems particularly strategic to organizations dedicated to selection and breeding is to establish an open list of the sequenced animals' identification, in order to avoid duplication and foster collaboration to maximize the number of influential animals being genotyped.

A very similar conclusion can be inferred from Figure 6. Among all potential benefits associated with the establishment of a network, sharing of genomic information was the most common answer. Comparison of results and protocols was also considered important by a good number of respondents.

Regarding the possible obstacles for having a network around bovine sequencing, corporate interests/intellectual property/legal agreements seem to be the biggest concerns of the participating groups (Figure 7).

Finally, when asked who should facilitate the establishment of such a network, 26 respondents (76%) would prefer that Interbull takes the initiative and 8 (24%) would rather let the working groups organize themselves without the participation of Interbull. Some indicated that the working groups had already started organizing themselves, sparing Interbull from this commitment. One alternative organization was suggested as the possible facilitator: the International Society of Animal Genetics (ISAG).

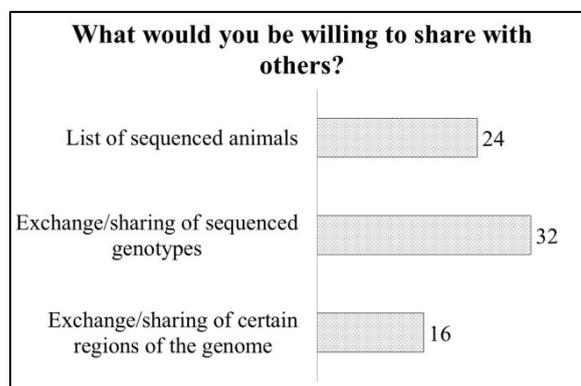


Figure 5. Willingness to share.

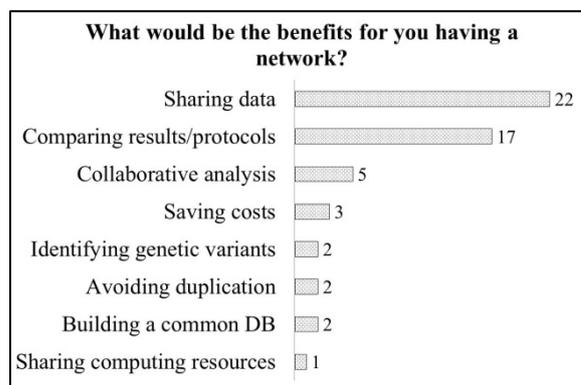


Figure 6. Benefits of networking.

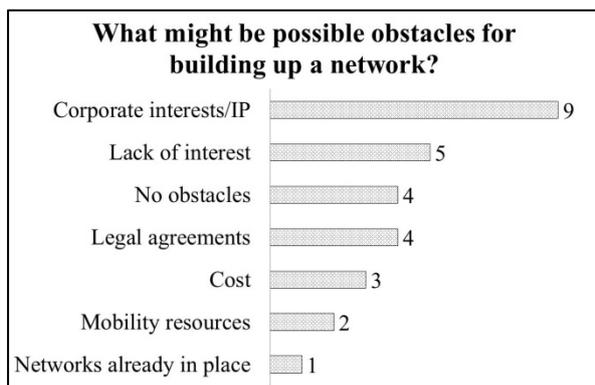


Figure 7. Obstacles for establishing network.

Spontaneous remarks

The survey allowed comments from the respondents and the ones not covered by the questions are summarized below:

- A web list of sequenced and genotyped animals was already under development at Iowa State University
- Interbull contribution should be limited to organize a list of sequenced animals
- No more overriding bureaucracy is needed (meaning that no Interbull involvement is preferred)
- Some questions were considered commercially sensitive
- Interbull could organize a workshop to bring parties together
- Interbull could provide infrastructure for the network but let the parties to set the rules

Conclusions

Most of the organizations working on bovine genome sequencing by June 2011 investigate both *Bos taurus* and *Bos indicus*, although the main focus is on dairy cattle (especially the Holstein breed). Association studies and causative mutations are the main objectives of most groups, and therefore the main criterion for selecting the individuals that are genotyped is their influence on the genetic makeup of the population. The majority of the institutions is dedicated to research and declare willingness to establish a network among working groups for exchanging data and knowledge, which could be facilitated by Interbull according to most respondents.

References

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