

Barley genome sequence emerges as a promising candidate in genetic research and breeding

Barley (*Hordeum vulgare* L.), domesticated since 8000 BC in western Asia and Northeast Africa (Fertile Crescent), is regarded as the founder crop of Old World agriculture¹. Cultivated barley is derived from its wild progenitor *Hordeum spontaneum* C. Koch, still inhabiting the Fertile Crescent from Israel and Jordan to South Turkey, Iraqi Kurdistan, and southwestern Iran². It possesses a distinct phenotype of broader leaves, shorter stem and awns, tough ear rachis, a shorter and thicker spike, and larger grains². Barley is the fourth largest cultivated cereal worldwide, both in terms of area harvested (1.9 m ha) and production (134 million tonnes; mt)³. Of its total production, 75% is used as animal feed, 20% processed into alcoholic and non-alcoholic beverages and 5% is used in the making of food products which contribute about 30% of the calories consumed worldwide⁴. With an added advantage of withstanding harsher environmental conditions, barley also serves as an important food crop in economically backward countries⁵. Collins *et al.*⁶ have reported that the abundance of soluble dietary fibre in barley has the potential to reduce severe human diseases, including type-II diabetes, disrupted immunity, colorectal cancers and other civilization diseases⁶. The US Food and Drug Administration authenticated the competent health claim relating barley to prevention of cardiovascular diseases (as a result of high content of cell wall polysaccharides)⁷. In addition,

barley is an exceptional source of other bioactive constituents, including vitamin E, B-complex vitamins, enzymes, minerals and phenolic compounds⁸. Hence considering its significance in human civilization, numerous attempts have been made to establish comprehensive genetic and genomic resources for accelerating crop improvement^{9,10}.

The recent release of barley genome sequence is the outcome of one such endeavour. Steered by Nils Stein, the International Barley Genome Sequencing Consortium (IBSC) constituted in 2006 executed the whole genome sequencing (WGS) using the next-generation sequencing (NGS) strategies and the sequence information was released on 29 November 2012 (ref. 4). Barley genome ($2n = 2x = 14$; 5.1 Gb) with highly repetitive sequence made the sequencing task more challenging, for instance, 90–95% of the genome sequence resulting from a whole genome shotgun sequencing will comprise almost the same sequence repeatedly, without any orientation. This hindrance was promptly tackled by IBSC, which constructed a complementary and heterogeneous sequence-enriched genome-wide physical map followed by the whole genome sequencing of *H. vulgare* cv. Morex, cv. Barke, cv. Bowman, cv. Igri, cv. Hauna Nijo and *H. spontaneum*. The genomic DNA was fragmented and used to construct paired-end and mate-pair libraries. The libraries of cultivars ‘Morex’, ‘Barke’, ‘Bowman’, ‘Igri’ and *H. spontaneum* were sequenced using

Illumina GAIIX and Hiseq 2000 platforms. Libraries of cultivar ‘Hauna Nijo’ were sequenced using Roche 454 GSFLX Titanium chemistry. The sequences are then assembled *de novo* and positioned into a linear order along each individual chromosome⁴.

The WGS data unveiled that ~84% of the barley genome encompasses mobile elements and other repeat structures. Unlike rice and *Brachypodium*, the barley genome has higher percentage of long terminal repeat (LTR)-*Gypsy* retrotransposon superfamily. RNAs from eight tissues of cultivar ‘Morex’ were also sequenced using Illumina transcriptome sequencing technology. The gene families were then compared against the gene complements of *Brachypodium distachyon*, *Sorghum bicolor*, *Oryza sativa* and *Arabidopsis thaliana*. The results showed a higher synteny of barley towards *A. thaliana*, with an estimate of 30,400 genes within its genome⁴. This also highlighted that some barley gene families showed barley-specific over-representation, which includes the immune genes such as (1,3)- β -glucan synthases, protease inhibitors, sugar-binding proteins, sugar transporters, NB-ARC (a nucleotide-binding adaptor shared by APAF-1, certain R gene products and CED-4) and NBS-LRR (nucleotide-binding site leucine-rich repeat). Moreover, the transcriptome analysis showed that about 36–55% of barley genes is differentially regulated, demonstrating the intrinsic dynamics of gene expression. The occurrence of extensive alternative splicing and presence of novel transcriptionally active regions in abundance highlighted the involvement of post-transcriptional processing as a key player in gene regulation⁴.

In the era of global food insecurity, agriculture is threatened predominantly due to environmental stresses which include both biotic and abiotic factors. Engineering crop plants with durable tolerance towards these stresses along with an invariable yield is not feasible without the genome sequence information. Though the breeding and transgene-based approaches had assisted in overcoming the situation^{9,10}, the release of WGS data will impeccably accelerate the

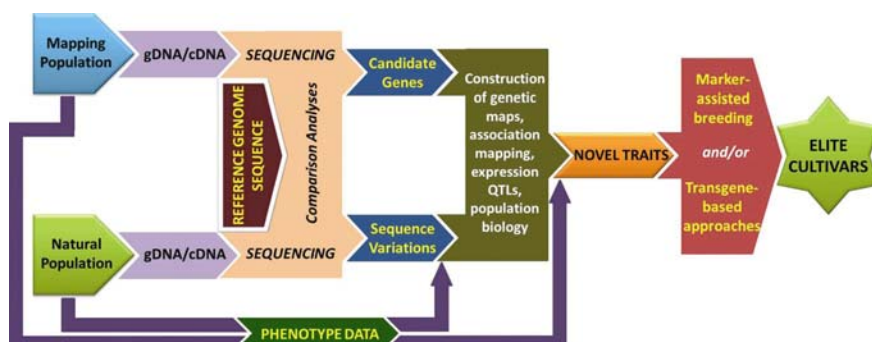


Figure 1. Summary of applications of barley whole genome sequencing information towards crop genetics and breeding. These applications include generation of genomic resources, quantitative trait loci mapping, wide crosses, expression analysis, association genetics and population biology, all of which accounts for generating elite barley cultivars.

forementioned research as summarized in Figure 1. As access to the genome sequence is crucial for resolving prime issues in crop biology and studying the molecular mechanisms fortifying trait formation, the barley WGS data will be essential for the advancement of true genomics-informed breeding strategies and for deciphering the full potential of natural genetic variation towards the improvement of agronomic traits. The over-represented gene families of the barley genome need to be further characterized through transgene-based over-expression and knockout studies under diverse environmental conditions in order to impart stress tolerance. Moreover, the occurrence of about 15 million non-redundant single-nucleotide polymorphisms would assist in instigating genome-wide marker technology for high-resolution genetics

and genome-assisted breeding for stress tolerance⁴. Thus the barley genome sequence not only hastens the analysis of complex traits and enables novel traditional and next-generation marker-assisted selection approaches, it also serves as an imperative and robust framework for the improvement of novel strategies in cereal breeding.

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MEETING REPORT

Goals towards healthy ageing*

Ageing is a universal feature affecting most organisms. It is a gradual process which may cause disability in individuals depriving them of leading a normal life. Gerontologists worldwide are interested in finding ways to address diseases related to old age and help the elderly population lead a disability-free life. Several studies in humans and animals indicate that eating healthy and nutritious food with regular exercise can minimize the process of ageing. It may also help in prolonging one's lifespan. A need is being felt to address issues pertaining to biological, medical and socio-psychological aspects of ageing, as the elderly population is on a rise.

An International Symposium on Ageing and the 16th Biennial Conference of the Association of Gerontology (India)

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(AGI) was organized to address the problems and prospects of the elderly in today's world. In his inaugural speech, Ramesh Sharma (President AGI and Chairman of the symposium) gave a brief on the theme of the symposium and paid tribute to the founder of AGI, Late M. S. Kanungo. A. N. Rai (Vice-Chancellor, North-Eastern Hill University, Shillong) presented the patron's remarks on issues related to ageing. Sataro Goto (Juntendo University Medical School, Tokyo, Japan) graced the occasion as the guest of honour.

Several papers pertaining to biological, medical and socio-psychological aspects of ageing were presented during many academic sessions. Poster presentations and panel discussions were also held during the meeting. Various issues related to ageing and problems of the aged were discussed. A few recommendations were also made: (i) studies on age-related diseases at cellular and molecular levels should be undertaken which may help in understanding the phenomenon of ageing; (ii) a financial and social

support system, like the Japanese model system should be followed for the welfare and maintenance of the elderly; (iii) the State and the Central Governments should support and advocate for the health of the elderly; (iv) greater emphasis should be given on research and use of nutraceutical or herbal and dietary therapies; (v) issues related to ageing must be incorporated in the curriculum or textbooks to sensitize the younger generation regarding the care of the elderly; (vi) ensure medical safety, including elderly-friendly gadgets; (vii) an urgent need was felt to set up a National Institute of Ageing to address and tackle age-related issues using a multi-disciplinary approach; (viii) the North East Council should establish a North East Regional Centre for Ageing Research for the welfare and management of the elderly in the NE states of India.

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