

Barley Genome Sequencing expected to complete by 2012

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Alexandria, Alexandria, EGY, 2008-04-09 17:39:58 (IndiaPRwire.com)

Scientists working on barley genome sequencing are aiming to complete it by 2012.

Prof Andreas Graner, Acting Director of the Leibniz Institute of Plant Genetics and Crop Plant Research in Germany, said that the International Barley Sequencing Consortium (IBSC) consisting of eight member laboratories in Australia, Japan, Finland, Germany, United Kingdom and the United States is currently working on sequencing the barley genome.

The consortium was set up in 2006 with the **objective** to physically map and sequence the barley gene space, with the near-term need being the identification of the remainder of about 30,000 genes, including the 5' and 3' regulatory regions, and the longer-term goal an ordered physical map linked to the genetic map to accelerate crop improvement.

"Partners are providing active contribution toward sequencing the barley genome, which is aimed to be completed by 2012," said Prof Graner, who is attending the 10th International Barley Genetics Symposium, organized by the International Center for Agricultural Research in the Dry Areas (ICARDA) and Bibilotheca Alexandrina.

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Prof Graner said sequencing the barley genome is important to understand the genetic architecture of the plant. "The better we have deciphered the genome of the plant, the better will be our understanding of its ability to produce more and its resistance to biotic and abiotic stresses.

Barley is cultivated in over 56 million hectares of land the world over and is the fourth most planted cereal crop. Over the last few years there has been a steady increase in barley and scientists believe that with the increasing global temperatures and the challenges posed by climate change, barley cultivation would expand even more, as this crop grows in harsh climatic conditions.

Besides being the staple food for the poor in parts of North Africa, Central and South Asia, Barley is grown as a cash crop in many developing countries and is used for malt production all over the world.

"There is a demand for further increase in food, feed and renewable energy sources. Our abilities to meet this demand depend on how best we can make use of our biodiversity, which is locked up in

the genes. In this way genebanks like the one at ICARDA will be able to further improve their contribution to the world-wide utilization of the genetic resources by both scientists and farmers," said Prof Graner.

Prof Graner said that sequencing the barley genome would enhance the use of biodiversity to meet the future needs of mankind. "Farmers will benefit by having improved varieties that can produce more yield. It would also help reduce input of fertilizers and chemical plant protection to facilitate more sustainable agriculture," he added. Dr Udda Lundqvist of the Nordic Genetic Resource Center in Alnarp, Sweden, and has been working on barley for nearly 59 years said that sequencing the genome would help develop varieties that will have more resistance to salinity, drought and diseases.

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Established in 1977, ICARDA (www.icarda.org) is one of the 15 international research centers supported by the Consultative Group on International Agricultural Research (CGIAR). ICARDA serves the entire developing world for the improvement of barley, lentil, and faba bean; and dry-area developing countries for the on-farm management of water, improvement of nutrition and productivity of small ruminants (sheep and goats), and rehabilitation and management of rangelands. In the Central and West Asia and North Africa (CWANA) region, ICARDA is responsible for the improvement of durum and bread wheats, chickpea, pasture and forage legumes and farming systems; and for the protection and enhancement of the natural resource base of water, land, and biodiversity.

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