However, the reality of alarmingly high rates of irreversible, severe and sometimes fatal ADRs [3] confronts us with the fact that many practicing physicians are either not alert, lack the appropriate knowledge, or both. The latter is a strong argument for incorporating basic pharmacogenetics in the medical curriculum [4]. Even if physicians' general knowledge of genetics may be deficient [5] we should not give up seeking for improvement.

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International Rice Genome Sequencing Project
The map-based sequence of the rice genome
Nature 2005;436:793–800

DOI: 10.1159/000091491

Ninety-Five Percent of Rice Genome Sequenced

Rice (*Oryza sativa* L.) is one of the most important food crops worldwide and feeds over half of the global population. It has important synthetic¹ relationships with the other cereal species and is a model plant for the grasses. In 1998 the International Rice Genome Sequencing Project (IRGSP) started to sequence the genome of rice. It sequenced the temperate rice variety *O. sativa* L. subspecies *japonica* which is cultivated mainly in Japan, Korea and the USA. In *Nature* the authors presented a map-based, finished quality sequence that covers 95% of the 389-Mb genome. A total of 37,544 non-transposable-element-related protein-coding genes were identified.

The authors refer to other researchers who estimate that the world's rice production must increase by 30% over the next 20 years to meet projected demands from population increase and economic development. Rice grown on the most productive irrigated land has achieved nearly maximum production with current strains. Environmental degradation (including pollution, increase in night-time temperature due to global warming), reductions in suitable arable land, water, labour and energy-dependent fertilizer provide additional constraints.

In their publication the authors state that their findings will help to maximize rice productivity and quality by a combination of biotechnology and improved conventional breeding. Comparing genome organization, genes and intergenic regions between cereal species will permit identification of regions that are highly conserved or rapidly evolving. Such regions are expected to yield crucial insights into genome evolution, speciation and domestication.

Comments

The publication in *Nature* of the IRGSP has great value for the community. This genetic study provided a high potential to meet the world's growing demand on food. The authors state that the finished sequence of the rice genome can help to optimize rice production. With biotechnological and conventional breeding, new variations of rice can be developed which have higher yields and can grow in harsher conditions like extreme drought. Moreover, the disclosure of the rice genome can optimize community health by increasing the nutritional value of rice. For example, rice varieties that contain more vitamins can be developed.

On the 10th of August, 2005, the BBC News quoted Rod Wing from the University of Arizona who is a participant in the IRGSP. He said the map-based sequence had led to the identification of genes that confer important traits such as yield and demand for light during growth [1]. Although expectations run high, I would like to emphasize that we should not pitch our expectations too high. Much of the rice genome was known in 2002, and Robin Buell of the Institute for Genome Research already spoke of a milestone in rice research [2]. Many genes are located but the function of most of the genes needs to be unravelled further. In 2002 Robin Buell used the same terms for their results as in this *Nature* publication [1].

This is reminiscent of the fuss which was caused by the HUGO (Human Genome Project) project in 2003. The finished human genome sequence was said to have a great impact on health and the understanding of our genes. Today we see that these promises have only been partially fulfilled. Genes appear to be more complex than expected. And besides, rice is estimated to have 10,000–15,000 more genes than humans. By sequencing genomes, the mystery of life has not yet been revealed.

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- 1 <http://news.bbc.co.uk/1/hi/sci/tech/4138342.stm>.
- 2 http://www.tigr.org/news/pr_12_18_02.shtml.

¹ Genetic loci that lie in the same order on the same chromosome in different species.