

Better Quality Beef and More Milk through Nuclear Research



P. Pavlicek/IAEA

Cattle breeders are now able to screen and select cattle for specific features, such as the ability to produce high-quality milk or resist specific diseases. After six years of work by more than 300 researchers from 25 countries and \$53 million in funding, in April scientists were finally able to reveal the genome of the cow - the first mapping of the genetic composition of a mammalian livestock animal ever completed, providing crucial information about the evolution and biology of cattle.

According to researchers at the Joint FAO/IAEA Division of Nuclear Applications in Food and Agriculture, who participated in the cattle genome study, this research is expected to provide breeders and farmers with the opportunity to address the issue of achieving efficient and sustainable food production for a rapidly increasing human population.

"This study is a first of its kind in the world," says Gerrit Viljoen, who heads the Animal Production and Health

(APH) Section of the Joint FAO/IAEA Division.

"By looking at the bovine genome we will be able to select for features that cattle breeders want in their cows, for example, better quality beef, more milk or disease tolerance/resistance and understand the genetic basis of the evolutionary success of ruminants which will provide opportunities to address some of the crucial issues of the present time — efficient and sustainable food production for a rapidly increasing human population."

The cow genome characterization study was conducted through two projects: the Bovine Sequencing Project and the Bovine HapMap Consortia Project — a HapMap is a map of genetic diversity among different populations of the same species. Funding for these projects was provided by an international group that included the IAEA through the Joint FAO/IAEA Division.

Nuclear techniques were also extensively used in the study and technical officers from the APHS contributed to data analysis and annotations.

"Radioactive isotopes were used for labelling and characterizing the genetic information of the cow genome, a process known as radiolabelling of DNA," explains Viljoen.

Specifically, the Joint Division's APH Section sponsored the study of Sheko breed, which is native to Ethiopia and is resistant to trypanosomiasis, a disease transmitted by the tsetse fly, and has the ability to achieve good productivity under difficult environmental conditions.

It is hoped that the information obtained from the study can be a first step in the greater utilization of the Sheko and other related indigenous breeds to improve livestock productivity and the livelihoods of farmers.

The results of the bovine genome sequencing and characterization studies were published in the journal "Science".

Genome Sequencing

By determining the order, or sequence, of the structural units in a DNA mol-

ecule, genome sequencing helps scientists study biological processes and identify key genetic characteristics in the animal or plant being examined.

The Bovine Genome Sequencing Project identified, or sequenced, the complete genome of a female Hereford cow. The Bovine HapMap Consortia, on the other hand, described genetic variation among different cattle varieties, starting with the major division between the humpless taurine cattle most commonly found in Europe, Africa and East and West Asia, and the *Bos indicus* cattle found in India, South and West Asia and East Africa.

The researchers used the complete sequence from a single Hereford cow and comparative genome sequences from six more breeds to look for variations in DNA molecules (known as single nucleotide polymorphisms, or SNP) in 497 cattle from 17 geographically and biologically diverse breeds and two related species, the Anoa and the Water Buffalo.

Their studies indicate the cattle have a diverse ancestral population that has

undergone a recent rapid decrease in effective population size, probably because of domestication, selection and the development of breeds.

The evolution of humans and cattle intertwined between 8,000 and 10,000 years ago, and today there are more than 800 cattle breeds selected for different economic, social and religious reasons.

The Bovine Haplotype Map is generating excitement because it offers the chance to select for features that cattle breeders want in their cows - in particular, high-quality milk. Until now, the only way to guarantee the best cow's milk was by taking a bull, inseminating cows with his semen, and then waiting for the female offspring to grow and produce calves and milk to feed them, at a cost of \$25,000 to \$50,000 per bull. (Most of the genetic improvements in the cattle industry come through males, because each male can produce tens of thousands of females.) Already, cattle breeders are eagerly mapping SNP in most of their bulls, with an eye toward identifying which SNP are linked with various desirable qualities.