

Scientists publish the water buffalo genome

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Credit: University of Adelaide

An international team of researchers led by the University of Adelaide has published the full genome of the water buffalo – opening the way for improved breeding and conservation of this economically important animal.

The consortium of partners in Australia, Italy, China, Brazil, and the USA, with additional contributors in other countries, say they have now created the tools needed to apply modern molecular breeding systems to water [buffalo](#).

"Water buffaloes were domesticated about 5000 years ago, and since then have been of economic importance for milk, meat and as a work animal around the world," says consortium leader Professor John Williams, Director of the University of Adelaide's Davies Research Centre at the Roseworthy campus.

"They are particularly important in developing countries and, in specialised markets, they provide milk for products such as mozzarella cheese in Italy. The water buffalo is a key agricultural animal because it is able to adapt to diverse environments, and is particularly tolerant of disease.

"In Australia, they were brought to Northern Territory in the early 19th century and today there are milking herds of buffalo in Northern Territory and in South Australia."

There are two subspecies of water buffalo. The researchers sequenced the genome of the River buffalo, which have been selected for milk production through organised breeding programs in Italy, India, the Philippines and Brazil.

Professor Williams says such advances in genomics have revolutionised dairy cattle breeding and now the same molecular tools will be available for water buffalo breeding. This project is another great example of the University of Adelaide's depth and expertise in research areas related to food innovation.

"The publication of the buffalo genome provides the essential reference

point for studies on the molecular genetics of the buffalo," Professor Williams says. "It will help breeders to enhance commercially desirable characteristics in the water buffalo, and researchers and conservationists to preserve the diversity of buffalo populations."

The buffalo genome has been published in the journal *GigaScience*.

Research collaborator and joint lead author Dr Daniela Iamartino, R&D Technical Manager at the AIA-LGS (Italian Breeder Association – Laboratory of Genetics and Services) in Italy, says: "It is also possible to compare the buffalo genome with that of other species to understand differences in the biology of buffalo and their ability to adapt to a wide variety of environments.

"The annotation of the genome identifies the genes present to explore their function and study the differences among species," she says.

The consortium led by Professor Williams has also published details of a specific molecular tool (called the Buffalo SNP chip) in the journal *PLOS ONE*. This SNP Chip will allow researchers and breeders to put the [genome](#) sequence information into practice. Genes that are involved in important traits related to production and disease can be located and used to estimate the breeding values of individual bulls and cows.

"This will offer buffalo breeders the same opportunities for accelerated genetics selection that is now used by cattle breeders," says Professor Williams.

Provided by University of Adelaide

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