

# NDDDB scientists crack buffalo genome code

**Kalyan Ray**

**NEW DELHI, DHNS:** In what may improve India's milk production in the future, geneticists at the National Dairy Development Board in collaboration with US researchers have come out with a sophisticated tool to improve the water buffalo breed through genetic selection.

The scientists have successfully completed the "de novo genome assembly" of buffaloes that produces nearly 50% of India's milk yield.

"This will help identify the right type of bull (for breeding) through genetic

selection," said NDDDB scientist Sudhakar Anathasayanam, one of the leaders of the team comprising scholars from NDDDB and Johns Hopkins University. A Murrah buffalo was chosen for the study.

So what exactly is a "de novo genome assembly" and how is it different from sequencing the genome of a plant or animal?

Sequencing means mapping of an organism's complete genome. But in a genome assembly, a combination of short and long strands of the genome are sequenced separately to cover the maximum amount of genome mapped quickly.



**Murrah Buffalo**

A *de novo* assembly means doing the job from the scratch, without any reference point.

Once the fragmented genomes are mapped, they are put together to get a realistic sense of the complete genome. But the main challenge is to find out the right way of stitching the DNA strands together, explained

a senior geneticist who is not associated with the work.

The NDDDB team used a method called trio-binning for the task.

India has an estimated 113.3 million buffaloes, accounting for nearly 50% of the world buffalo population. They contribute more than 50% of India's milk yield and the milk they produce has a higher fat percentage compared to cow milk.

Since buffaloes are widely reared in the developing countries for milk production, creating a reference genome will help improve the breed faster.

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