

Axiom Buffalo Genotyping Array

Highest-density array for genotyping water buffalo across multiple species and breeds

The Applied Biosystems™ Axiom™ Buffalo Genotyping Array provides the highest genome-wide coverage of polymorphic SNPs across multiple species and breeds of water buffalo (*Bubalus bubalis bubalis* and *Bubalus bubalis carabanensis*), one of the most important beef and dairy animals in Italy, Brazil, and South Asia.

This array is the only commercially available high-density buffalo-genotyping tool.

Highlights

- **Comprehensive content**—90,000 common and rare markers selected from sequencing initiatives for water buffalo (*B. bubalis bubalis*)
- **Multiple breeds represented**—Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi
- **Robust assay performance**—SNPs demonstrate a ≥99% call rate and ≥85% conversion rate on Murrah and Mediterranean samples

Applications

Molecular breeding

- Genomic biomarker discovery
- Marker-assisted selection
- Routine screening
- DNA fingerprinting for animal tracking

Complex trait research

- High-resolution mapping of genetic loci for complex traits such as milk production, percentage of milk fat, and feed-conversion efficiency
- Discovery of genes and pathways underlying simple and complex traits

Conservation and biodiversity

- Population diversity studies of river and swamp buffalo

- Genomic marker–assisted conservation strategies

Array design

The Axiom Buffalo Genotyping Array was designed through our Expert Design Program in collaboration with the International Buffalo Genome Consortium, including Fondazione Parco Tecnologico Padano in Italy, Iowa State University, and the Agricultural Research Service (ARS) of the United States Department of Agriculture (USDA).

SNP discovery

1. The genome of one Mediterranean female water buffalo (*B. bubalis bubalis*) was assembled at >100x genome sequence coverage.
2. Sequence contigs and paired-end reads were aligned from 86 other buffaloes representing 8 breeds (Italian Mediterranean, Murrah, Nili-Ravi, Jaffarabadi, Kundhi, Aza-Kheli, Egyptiana, and Swamp type from Philippines) [1] and 2 subspecies, including river and swamp types.
3. The sequence reads were aligned to the *Bos taurus* reference genome (UMD3.1).

4. Starting with a list of 16.7 million SNPs and indels, markers that did not have another SNP within 10 bases and had a base pair quality score of >10 were included for calculation of minor allele frequency (MAF).
5. A total of 5.8 million SNPs that were polymorphic in at least one breed were selected as candidate SNPs.

Marker selection

1. SNPs that met the threshold criteria for predicting reproducibility of SNPs based on our *in silico* design scores were included.
2. Sequences that were highly repetitive in the genome and contained ambiguities were removed.
3. The resulting SNPs were selected for uniform spacing across the genome.

The array contains 90,000 SNPs, 7,583 probes for sample QC, and 6,853 gender-calling probes. The Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi water buffalo breeds are represented in the ratio 30:30:20:20.

Results

A total of 1,056 samples representing two different river buffalo breeds (Mediterranea Italiana and Murrah) were genotyped on the array.

Data analysis and clustering was automated using the Applied Biosystems™ Genotyping Console™ Software and SNPolisher™ package. The SNPs were filtered according to the Best Practice Supplement to Axiom Genotyping Solution Data Analysis User Guide (P/N 703083). Today, the Applied Biosystems™ Axiom™ Analysis Suite should be used for analysis following the Best Practices Workflow as described in the Axiom Genotyping Solution Data Analysis Guide (P/N 702961).

Ordering information

Product	Description	Cat. No.
Axiom Buffalo Genotyping Array	Contains one 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550431
Axiom GeneTitan Consumables Kit	Contains all GeneTitan Multi-Channel Instrument consumables required to process one 96-array plate	901606
Axiom 2.0 Reagent Kit	Includes all reagents (except isopropanol) for processing one 96-array plate	901758

References

1. Iamartino D, Williams JL, Sonstegard T et al. (2013) The buffalo genome and the application of genomics in animal management and improvement. *Buffalo Bulletin* 32 (Special Issue 1):151-158.

Find out more at thermofisher.com/microarrays

Array performance was measured in 89,988 SNPs across 1,036 samples that passed the sample QC thresholds. A total of 12 Y chromosome SNPs were excluded. The SNPolisher package refined the clustering based on six genotype cluster classifications (Table 1).

The PolyHighResolution category has a sample call rate of 99.75% and average sample reproducibility of 99.96%.

Cluster plots representative of two of the classification categories from the Axiom Buffalo Genotyping Array analysis are shown in Figure 1.

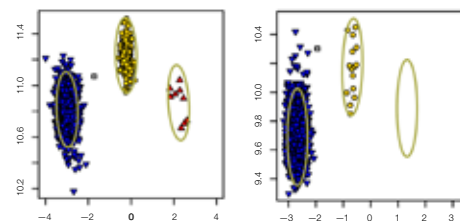


Figure 1. Representative cluster plots. (Left) Example of a marker in the “PolyHighResolution” category that demonstrates good cluster resolution and at least two examples of the minor allele. **(Right)** Example of a marker in the “NoMinorHomozygous” category, which represents markers with two clusters with no representation of the minor allele.

Table 1. Genotyping performance on commercial samples.

Genotype cluster category	Percentage of markers	No. of markers
PolyHighResolution	74.8	67,330
MonoHighResolution	10.3	9,229
NoMinorHomozygous	1.7	1,494
OffTargetVariant	0.1	83
CallRateBelowThreshold	4.1	3,668
Other	9.1	8,184
All markers	100.0	89,988