







## 16. New Milk Recording Methods and Services

## **Title presentation**

Developing a new selection index for the Italian Mediterranean Buffalo (Bubalus bubalis)

# Author(s)

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#### **Abstract**

The breeding of the Mediteranean buffalo is a long-standing Italian tradition, being internationally recognized thanks to its iconic Mozzarella di Bufala Campana, a Protected Designation of Origin (PDO) certified mozzarella cheese.

Over a population of more than 419000 extant animals, the Italian National Association of Buffalo Breeders (ANASB) involved 121403 animals from 380 farms mainly widespread in central and southern areas of the country. In 2019, Official milk recording by certified recorders belonging to the Associazione Italiana Allevatori (AIA) and following the ICAR guidelines included 49932 buffalo cows in 215 herds.

In 1997 a first selection scheme was implemented. It was based on a traditional progeny testing and a BLUP genetic evaluation of milk productive traits. A first selection index, namely the PKM, was also developed. The breeding objective of the PKM was the mozzarella cheese yield using as selection criteria milk yield, fat and protein. Although a positive selection on milk yields was observed—from 1608 Kg in 1977 to 2169 Kg in 2018, PKM had an unfavorable effect on the genetic trend for fat and protein.

In order to recover the unfavorable trend of milk components as well as to include morphology, a new selection index named IBMI has been developed and applied since 2019. The IBMI breeding objectives are milk production and mozzarella yield. IBMI includes five selection criteria: feet and legs, udder morphology, milk kilograms, fat and protein percentage whose relative emphasis was 24, 20, 21, 15 and 20, respectively.

The expected genetic progress by generation using IBMI is +58 Kg for milk , +0.10 and 0.05 % respectively for fat and protein percentage

The next steps in the selective activity will be a) the development of a test day model for productive traits and b) the implementation of a single step genomic EBV evaluation.