

An ontology approach for the collection and management of genetic traits and milk protein data

C. Franzoni Migliorati^{1*}, J.B.C.H.M. van Kaam¹, R. Finocchiaro¹, C.A. Lombardi¹, M. Marusi¹, M. Cassandro^{1,2} Associazione Nazionale Allevatori della Razza Frisona, Bruna e Jersey Italiana (ANAFIBJ), Via Bergamo 192, 26100 Cremona (CR), Italy; ² Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy. * Corresponding author: chiarafranzonimigliorati@anafi.it



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The aim of this study is to propose a new approach for the collection of data from genetic traits and milk proteins and to manage this information in a ontology database

All input data are recorded in the database with a **priority** that is defined by **the database update algorithm**. Priority levels have been designed to represent the reliability of the data, based on the type of genetic test and the source of the data.

TYPE OF GENETIC TESTS'
 PRIORITY LEVEL:

Direct analysis (marker-based tests) > Indirect tests (haplotypes) > Imputation

SOURCE OF DATA'S PRIORITY LEVEL:

Test by Accredited laboratories > Genomic test files > Official documents by foreign herdbooks > Old genetic traits management system > Unofficial documents

In this way, the **most reliable information is considered official** herd book data, according to the established priorities.

INPUT GENETIC TRAITS' DATA	UPLOADING D	ATA FOR THE FIRST RELEASE ON 14 JULY 2022
Source of DATA'S PRIORITY LEVEL TYPE OF GENETIC TESTS' PRIORITY LEVEL DATABASE UPDATE ALGORITHM	0 MARKER-BASED TESTS OLD GENETIC TRAITS MANAGEMENT SYSTEM HAPLOTYPES	3.000.000 6.000.000 9.000.000 12.000.000 no. of data entered 4.873.098 125.522 8.779.924
PRIORITY = RELIABILITY OF THE DATA		
RELATIONAL DATABASE	 Conclusion Key elements of the ontological system of genetic traits: Data reliability Reduction of human errors International harmonization and data exchange Flexibility and future interaction with Interbull This study was supported by "Latteco2 project, sottomisura 10.2 of the PSRNBiodiver 	

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