RÉPUBLIQUE FRANÇAISE
Liberté Égalité Fraternité

INRAE

Deep-Phenomic

EXPLORATORY PROJECT

2022-2024

Améliorer les performances de sélection chez les bovins laitiers grâce à la sélection phénomique

Coordination
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Key words
Phenomic selection
Genomic selection
Deep learning
Functional regression

INRAE units involved
GABI
MIA Paris Saclay
GQE-Le Moulon
AGAP Institut

Partnerships
Elliance

Context and challenges

In plant and animal genetics, selection programmes aim to identify individuals whose perfor-mance (yield, resistance to disease or environmental stress) meets previously defined criteria. This selection requires the acquisition of data, in the field or in breeding, which can be costly or time-consuming.

Since the 2000s, breeding programmes have used performance predictions to complement data on non-evaluated individuals. These predictions are based on information from the genome of the individuals: genotyping data. This strategy, known as genomic selection, has significantly increased the efficiency of breeding programmes for many animal and plant species and has become a ref-erence method in genetic improvement.

However, genomic selection has one drawback: the need to have genotyping data, which in some cases is too expensive to obtain (e.g. for field crop species for which thousands of candidates are produced each year, or for orphan species for which no efficient genotyping tool exists).

Phenomenal selection: a promising new alternative?

One alternative is to use phenomenal selection, recently introduced by Rincent et al. (2018), which consists of making performance predictions from phenomenal data obtained by spectroscopy, ra-ther than from genomic data. Spectroscopy has the advantage of being inexpensive, non-destructive, and already routinely implemented, both in breeding programmes for many plant species (to assess product quality) and in some animal species, notably in milk improvement pro-grammes.

The prediction performances obtained for different study cases are similar to those obtained with genomic prediction models. This very recent method has never yet been evaluated in an animal model and needs to be more widely tested and optimised.

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Métaprogramme
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Goals

The Deep-Phenomic project proposes a first application of phenomenal selection to an animal model: the method will be tested in dairy cattle, in a large-scale system (several tens of thousands of animals with mid-infrared spectra on milk, of which approximately 8,000 are genotyped).

The results of the phenomenal predictions will be compared with those of a classical genomic evaluation.

The project also plans to optimise the exploitation of spectral data with functional methods on the one hand and neural networks on the other:

- functional analysis will be specifically tested in a multi-environment context, where the prediction of unobserved spectra could increase the accuracy of phenomenal prediction.
- Neural networks will be used to test the interest of artificial intelligence methods in the context of phenomenal selection, thanks to the very broad scope of the experiment.

If successful, this work could have important implications for dairy cattle improvement, and would constitute a proof of concept for many other animal and plant species.

Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
Animal genetics	GABI	Genomic evaluation; bovine genetics
Mathematics, computer and data sciences, digital technologies	MIA Paris Saclay	Statistical learning, Artificial Intelligence
Plant biology and breeding	GQE-Le Moulon	Quantitative Genetics, Phenomic Selection, Cereals
	AGAP Institut	Quantitative Genetics, Phenomic Selection, perennial plants
External partners		**Expertises**
Elliance		Knowledge of bovine genomic evaluations

References

- **Rincent R, Charpentier J-P, Faivre-Rampant P, Paux E, Le Gouis J, Bastien C, Segura V (2018)** Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar. G3, 8(12), doi: https://doi.org/10.1534/g3.118.200760