Walloon strategies targeting new traits for efficiency, mitigation, adaptation and resilience in dairy cattle

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Abstract

The transition towards sustainable dairy production requires the development and implementation of novel traits addressing environmental impact, resource efficiency, animal welfare, adaptation, and resilience. In the Walloon Region of Belgium, these developments are supported by long-term investments in milk mid-infrared (MIR) phenotyping, routine milk recording, genomic evaluation infrastructure, and digital data integration. The objective of this paper is to present a unified framework enabling rapid implementation of novel traits into routine genomic evaluations. The proposed framework relies on predicting novel phenotypes from routinely collected MIR milk spectra, followed by genomic evaluation using existing random regression single-step genomic BLUP (RR-ssGBLUP) procedures originally developed for production traits. Methane emissions predicted from MIR spectra (PCH4) represent the first trait already implemented in routine evaluations. The methane evaluation currently includes more than 4.5 million test-day records from over 328,000 Holstein cows and 9,631 genotyped animals. Genomic breeding values and methane efficiency indexes are routinely generated. The same framework is currently being expanded towards adaptation and resilience traits. A recent example is Heat Stress Response (HSR), developed from MIR-based phenotypes generated from data collected during periods of thermal challenge. Genomic evaluations resulted in heritability estimates of approximately 0.10 and generated more than 6,700 genomic breeding values with moderate to high reliabilities. Preliminary analyses indicate favorable opportunities for selection aimed at improving heat tolerance while maintaining productive performance. Additional developments include welfare-related traits, feed efficiency indicators, nitrogen use efficiency, and the integration of sensor-derived information through the WALLeSmart digital platform. These developments demonstrate that routine phenotyping infrastructures can support rapid deployment of novel sustainability traits. The presented strategy illustrates how a common genomic evaluation architecture can accelerate implementation of emerging traits and facilitate future international collaborations and genomic exchange.

Key words: genomic evaluation, methane emissions, heat stress, mid-infrared spectra, resilience, sustainability

Introduction

The dairy sector faces increasing societal, environmental, and economic pressures requiring breeding objectives that go beyond traditional production traits. Sustainable dairy production requires simultaneous improvement of efficiency, mitigation of greenhouse gas emissions, adaptation to changing climatic conditions, welfare, and resilience.

The Walloon breeding program has invested for more than fifteen years in the development of milk MIR-based phenotypes through the Futurospectre consortium (the Walloon Breeders Association - Elevéo, the Milk Committee - CdL, the Walloon Agricultural Research Center - CRA-W and ULiège-Gembloux Agro-Bio Tech). This infrastructure provides access to routine MIR spectra for nearly all milk-recorded cows and offers a

unique opportunity to derive large-scale phenotypes for novel traits. This regional organization of dairy recording in Wallonia further facilitates interactions among breeders, breed organizations and research institutions. Through long-term collaborations not only standardized MIR spectral information (Grelet et al., 2015) is routinely available for virtually all milk-recorded cows but also numerous MIR prediction equations, including fatty acid profiles, methane emissions and heat stress related traits, thereby creating a favorable environment for rapid implementation of novel phenotypes into breeding programs.

The objective of this paper is to describe a unified genomic evaluation strategy for MIR-based novel traits and to illustrate its implementation using methane emissions as a routine application and heat stress response as an advanced prototype. Perspectives for welfare, efficiency, and resilience traits are also discussed.

Materials and Methods

Walloon Phenotyping Infrastructure and Common Genomic Evaluation Pipeline

The Walloon phenotyping infrastructure is built on the routine collection of milk samples through dairy herd improvement and milk payment schemes, providing MIR spectra for the vast majority of dairy cows in Wallonia. Spectra are standardized following CRA-W procedures (Grelet et al., 2015), and novel phenotypes are generated through prediction equations linking MIR spectra with directly measured biological traits (Grelet et al., 2021) but also physiological status as heat stress (Lemal et., al 2026). This cost-effective approach enables large-scale phenotyping while avoiding the expense and logistical constraints of direct measurements.

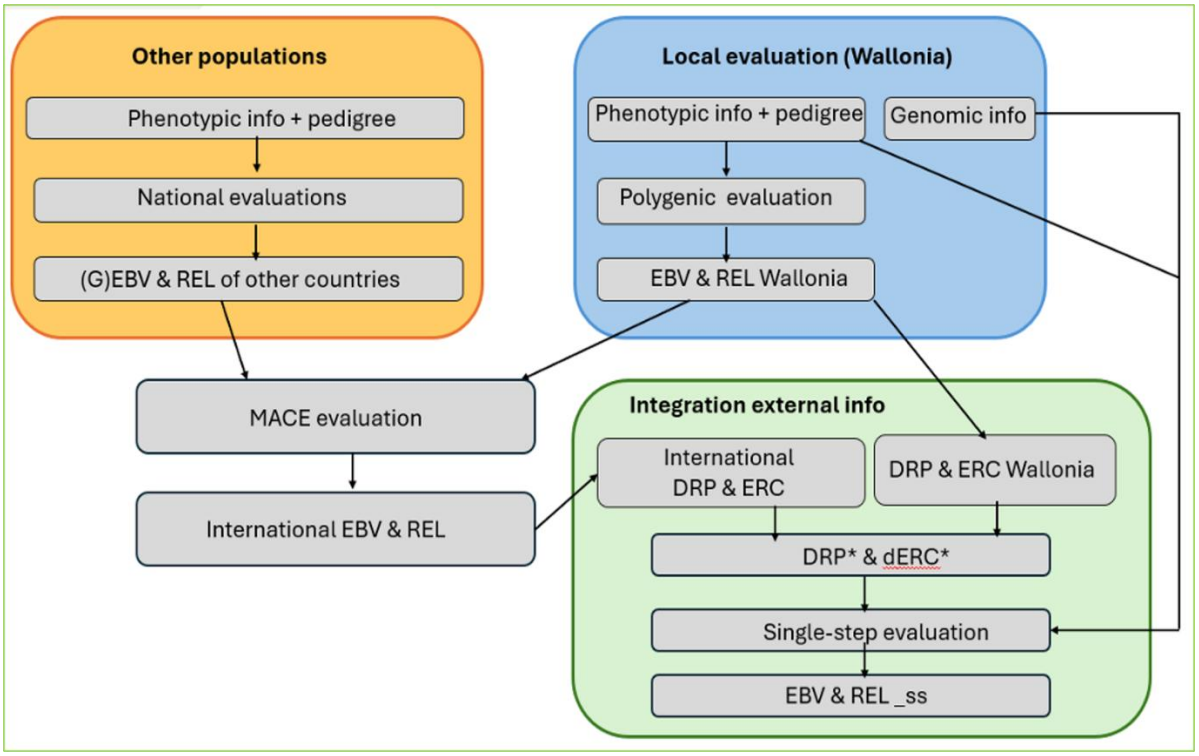


Figure 1. Generic ssGBLUP framework used in Wallonia showing the general evaluation pipeline, here illustrated for a trait which has a MACE evaluation (Vanderick et al., 2025).

All MIR-derived traits can be integrated into a common genomic evaluation pipeline (Figure 1.) based on (i) derivation of phenotypes from MIR spectra, (ii) test-day random regression modelling, (iii) integration of pedigree and genomic information through single-step GBLUP (ssGBLUP), (iv) estimation of genomic breeding values and reliabilities, and (v) dissemination of breeding values and derived indexes.

In practice, conventional milk, fat, and protein traits are replaced in the genetic evaluation framework by MIR-predicted traits while maintaining the same statistical evaluation framework, allowing new traits to be implemented with minimal modifications once a sufficiently robust prediction equation is available.

An alternative to replacement of milk, fat and protein is outlined by Chen et al. (2026) where a highly correlated trait is added as a trait to the system. In this specific application somatic cell score was added.

The entire system is supported by the WALLeSmart platform, which integrates phenotypic, genomic, management, and sensor-derived information, facilitates collaboration among breeders, breed organizations, and scientists, and accelerates the validation, deployment, and routine use of innovative phenotypes and precision breeding tools.

Methane Emissions

An already implemented trait is methane emissions. More details are reported by Chen et al. (2025). Methane emission were predicted using an MIR calibration equation developed from 1,089 reference observations collected on 299 cows originating from Belgium, Ireland, Switzerland, the United Kingdom, France, Denmark and Germany. The published calibration achieved a cross-validation coefficient of determination of approximately 0.68 with a prediction error of approximately 57 g CH4/day (Vanlierde et al., 2021).

Methane emissions were represented by MIR-predicted methane output (PCH4). The current evaluation includes

- approximately 4.5 million test-day records,
- 328,000 Holstein cows,
- 1,520 herds,
- 9,631 genotyped animals.

Routine genomic evaluations generate breeding values for expected methane emissions together with alternative methane-efficiency indexes.

Heat Stress Response

Heat Stress Response (HSR) was developed using an MIR-based prediction equation derived from 399 Holstein cows recorded during 2024 (Lemal et al., 2026). The approach was designed to characterize the biological response of cows to thermal challenges independently of direct THI measurements. The resulting equation was subsequently applied to more than one million MIR spectra collected from Holstein cows between 2020 and 2022 to generate large-scale phenotypes for genomic evaluation.

The genomic evaluation dataset included approximately:

- 64,000 cows with phenotypes,
- 146,000 pedigree animals,
- 7,170 genotyped animals.

Genomic breeding values were estimated using the same ssGBLUP framework as used for methane emissions.

Future Trait Developments

Additional developments currently under investigation include:

- Welfare-related traits;
- Feed efficiency indicators;
- Nitrogen-use efficiency;
- Traits derived from automatic milking systems;
- Sensor-based resilience indicators.

They will not be described in detail except welfare-related traits (Chen et al., 2026)

Results & Discussion

Generic Implementation of MIR-Based Genomic Evaluations

The principal advantage of the proposed framework is that once an acceptable MIR prediction equation becomes available, implementation within the genomic evaluation system requires only minimal modifications to existing procedures. This substantially reduces development costs and facilitates rapid deployment of novel traits.

Routine Methane Evaluation

Methane emission evaluations represent the first routine implementation of this strategy (Chen et al., 2025). Therefore, Methane emissions provided the first operational example of how MIR-based phenotyping can be translated into routine genomic selection. Rather than directly measuring methane emissions on each cow, methane output is predicted from routinely collected milk mid-infrared (MIR) spectra using a previously validated calibration equation. This approach transforms MIR information already generated through milk recording into repeated predicted methane phenotypes (PCH4) at the test-day level, which can subsequently enter the same random regression genomic evaluation framework used for other dairy traits.

The current Walloon evaluation includes more than 4.5 million test-day records from approximately 328,000 Holstein cows, illustrating how routine MIR recording can provide the phenotypic depth required for genomic evaluation of a trait that would otherwise be difficult and costly to measure directly at population scale.

As illustrated in Figure 1 and 2, the Walloon methane evaluation combines MIR-predicted methane records with pedigree and genomic information to generate genomic breeding values for methane emissions. In parallel, existing genomic evaluations for milk production and composition provide information on the methane emissions expected from an animal's production potential. Contrasting these two components allows methane efficiency to be evaluated while accounting for productive performance, rather

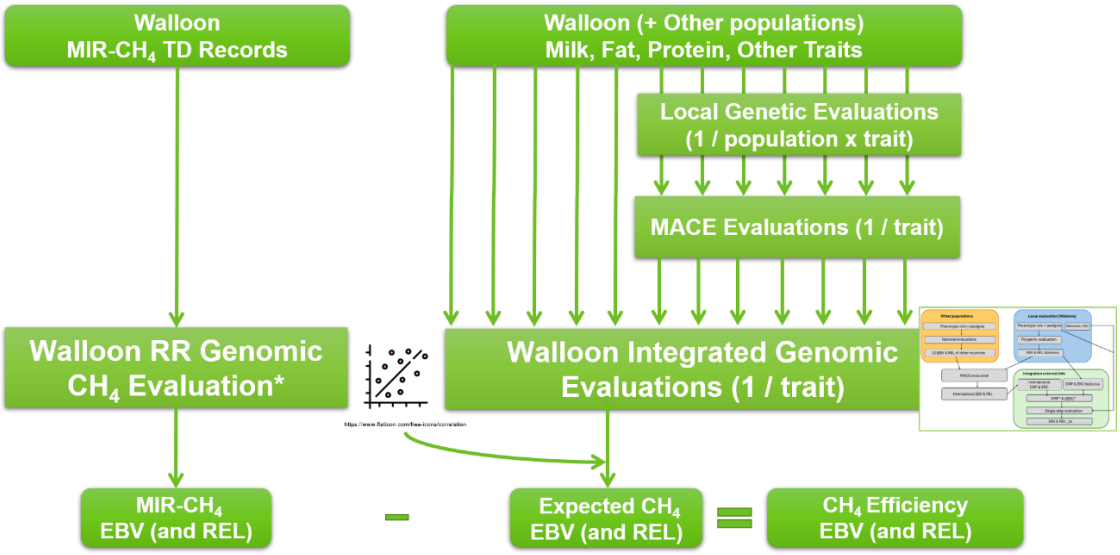


Figure 2. Walloon genomic evaluation framework for methane emissions and methane efficiency. MIR-predicted methane test-day records are used in a random regression genomic evaluation to derive methane breeding values. Information from routine genomic evaluations for production traits is used to derive expected methane emissions, and the contrast between MIR-predicted and expected methane breeding values provides an indicator of methane efficiency.

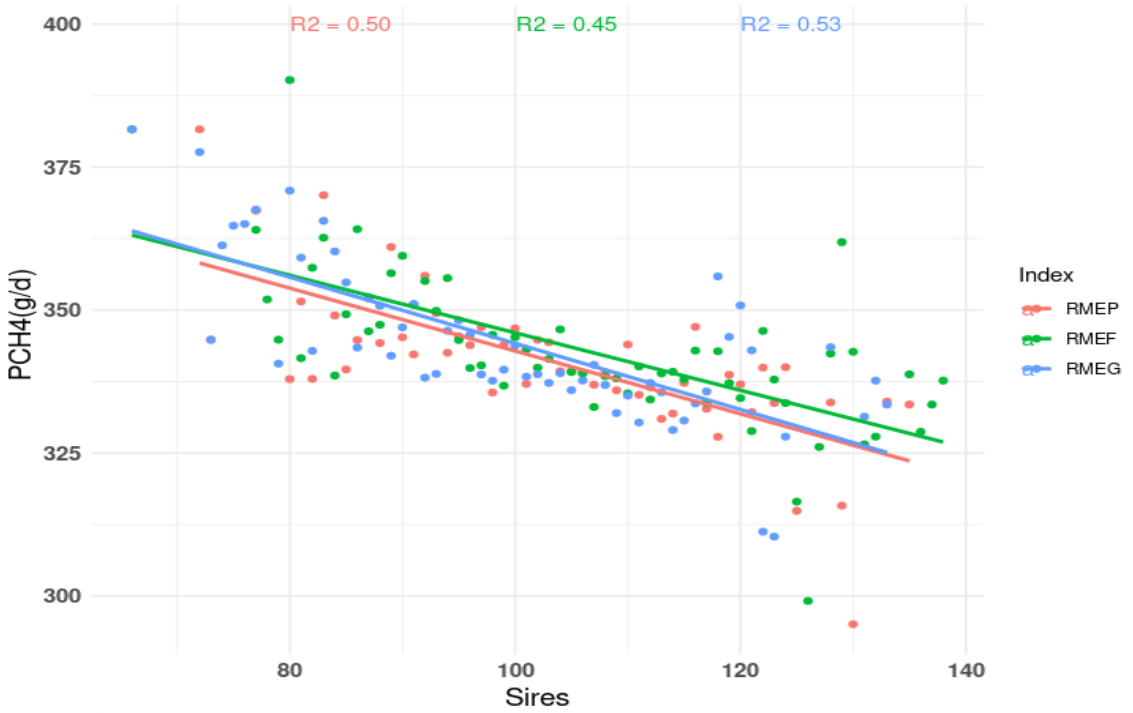


Figure 3. Relationship between sire methane-efficiency indexes and MIR-predicted methane emissions (PCH4) pf daughter groups. Lines represent linear regressions for the three alternative methane-efficiency indexes; corresponding coefficients of determination (R^2) are shown above the graph (Chen et al., 2025).

than simply favoring animals with lower methane output because of lower production.

Alternative definitions of methane efficiency can therefore lead to somewhat different sire rankings. Their relationship with observed PCH4 of daughter groups is shown in Figure 3.

Furthermore, comparisons with foreign methane evaluations based on sniffer and GreenFeed technologies showed positive indications of consistency between breeding values despite substantial differences in phenotyping approaches. These results provide indirect evidence that MIR-predicted methane phenotypes capture biologically meaningful variation associated with methane production and may serve as a useful proxy phenotype for large-scale genetic evaluation (Chen et al, 2025).

Heat Stress Response as an Advanced Prototype

Heat stress response illustrates the extension of the framework beyond environmental mitigation towards climate adaptation. We present here the ongoing developments as reported by Lemal et al. (2024, 2026). Figure 4. illustrates the ability of the developed HSR indicator to detect that animals are in heat stress generating conditions.

Preliminary analyses indicate that genetic variability exists for HSR and that genomic evaluations can be produced with practical

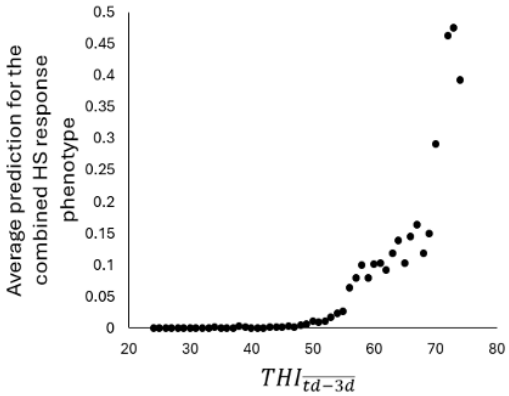


Figure 4. MIR-predicted combined heat stress response compared to observed THI 3 days before test-day (Lemal et al., 2026).

reliability levels. Approximate correlations derived from genomic breeding values suggest modest associations with production traits (0.15 for milk, 0.04 for fat and −0.14 for protein) and more pronounced relationships with functional traits such as longevity (−0.33) and fertility (−0.39). Although preliminary, these results support further investigation of HSR within future breeding objectives.

The growing availability of sensor-derived data may further improve the definition and validation of heat stress phenotypes. Sensor-derived behavioral and activity data are expected to play a particularly important role in both validating reference heat stress phenotypes and improving the timeliness of detecting responses to thermal challenges (Lemal et al., 2024).

Towards Integrated Sustainability Breeding Goals

Methane emissions, feed efficiency, welfare indicators, adaptation, and resilience should not be viewed as independent objectives.

The unified Walloon framework aims to create a portfolio of compatible genomic evaluations that can ultimately be combined through selection indexes according to future economic, environmental, and societal priorities.

In this context several very innovative local research efforts are ongoing. As an example, we can cite here Chen et al. (2026).

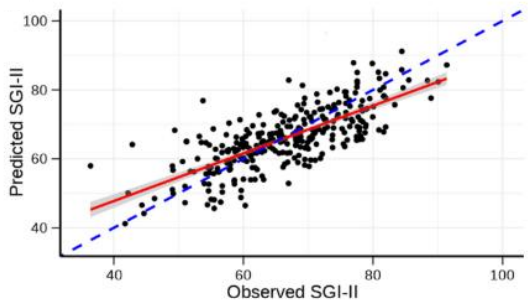


Figure 5. Random regression test-day model (RR-TDM) predicted versus observed "individual welfare score". The shaded area represents the 95% CI. (Chen et al., 2026).

Current general developments include the estimation of SNP effects and the derivation of direct genomic values for selected traits. These technical advancements directly facilitate data exchanges with external partners, thereby supporting collaborative genomic evaluations beyond regional populations. Consequently, this approach opens new pathways for international collaboration through common trait definitions and genomic exchanges, establishing a solid framework for future contributions to Interbull activities focused on emerging traits.

Conclusions

The Walloon breeding program has established a unified framework for implementing MIR-based novel traits in routine genomic evaluations. While methane emissions represent the first fully operational application, heat stress response has reached an advanced prototype stage, with further developments underway for welfare, efficiency, and resilience indicators. By combining routine MIR phenotyping, ssGBLUP evaluations, and digital data integration, this methodology provides a highly effective pathway to accelerate the deployment of sustainability traits in dairy cattle. Ultimately, this proposed framework can serve as a scalable bases for future international strategies aiming to seamlessly integrate mitigation, adaptation, and resilience into modern genomic selection programs.

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