



NEWSLETTER



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ABOUT GENTORE

GenTORE – “GENomic management Tools to Optimize Resilience and Efficiency” - is a European Union funded project within the Research and Innovation Program H2020.

GenTORE will develop innovative genome-enabled selection and management tools to empower farmers to optimize cattle resilience and efficiency (R&E) in different and changing environments. The combined research and outreach program of GenTORE will make a contribution to addressing the challenges facing farming in a changing and volatile world.

ANNOUNCEMENTS

GenTORE Creative Christmas Contest

In GenTORE, important research is performed to grasp the definition and most important traits of the so called “Future Cow”. Although much insight has already been gained in scientific terms, we are still lacking a visual representation of what “The Future Cow” might look like. Therefore we encourage everyone with some creative bones to join us in making a visual that showcases their individual vision on “The Future Cow”. We award a gift card worth €25,- to the participant with the most creative project. Participation is open to all ages and professions! For more information visit our [website](#).

Join the stakeholder discussion on the outlook of the “Future Cow”

With the implementation of the results from the GenTORE project into breeding programmes, the genetic composition of cattle might change. If the results are implemented in an optimal way, it should lead to favorable genetic progress with a well-balanced change in resilience and efficiency. What do you think will be the genetic differences between cattle of today and of cattle in the future? We would like to hear your opinion on how breeding traits will improve in “The Future Cow” by 2040. Please join us in the discussion on our [Stakeholder Platform](#) and submit your thoughts by answering our polls. We will launch a different topic every week and encourage all stakeholders to share their opinion!

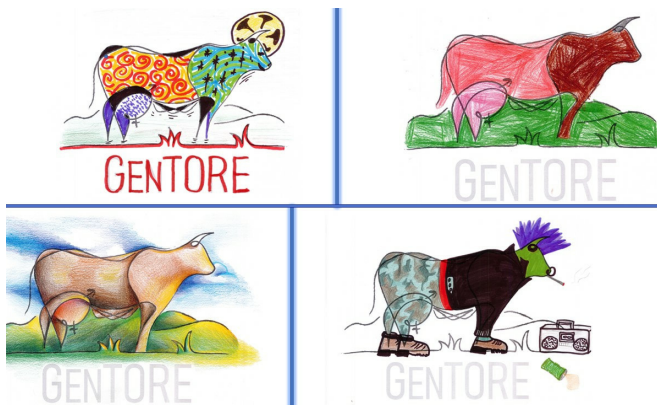




EDITORIAL

By: Nicolas Friggens (INRAE)

GenTORE is maturing, having gone through the conception and growth stages of the project we are now in the production phase. Even the GenTORE logo has evolved, picking up a plethora of different colours and customizations!! Indeed, we invite you to take this a step further and have fun re-looking our GenTORE cow for the future.

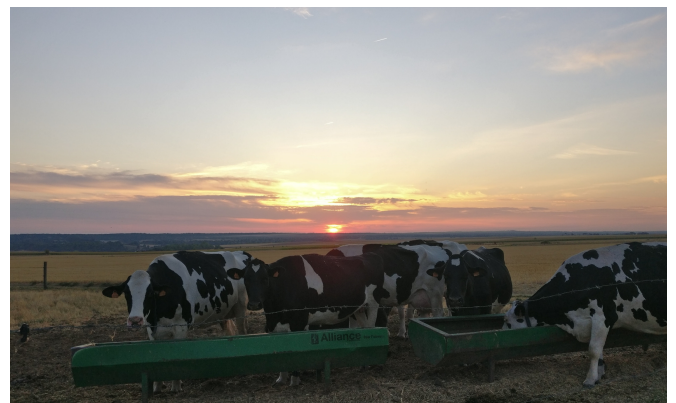


As the contents of this newsletter make amply evident, there are more and more exciting scientific results coming out the project, more and more presentations, more and more interaction with the various stakeholders, and all this despite the on-going Covid situation. The scientific papers that have been published are listed on the GenTORE website, this list includes the links to papers themselves as these are all freely available. Please help yourselves and spread the news.

As we go forwards into 2021, masks firmly fixed to our faces (at least at the beginning of the year), we are increasingly focussed on the integration tasks in the project. GenTORE like most European projects provides excellent opportunities for collaboration. Obviously, this occurs between countries and partners but more crucially we have the opportunity to build collaborations across disciplines. This is far from

being easy to achieve as we all have our own scientific perspectives and lingo so a good deal of effort, time, and goodwill is needed to break down the disciplinary barriers. My own experience is that this is a highly worthwhile endeavour, and some of the creative results that are coming to fruition in GenTORE demonstrate the synergies from cross-disciplinary collaboration. I guess you can understand why we are pushing the integration tasks, and why we are also increasing our stakeholder oriented activity. We strive to overcome the current constraints and get as much stakeholder interaction as we can. Please get in touch, if you have any ideas for events (virtual or otherwise) where you think we could usefully interact. Please, if you have any questions, issues, or experiences that you want to share with us, then again, do not hesitate to get in touch. [The Stakeholders Platform](#) makes this easy to do.

It is our aim in the last 18 months of the project to deliver a strong scientific basis for optimizing resilience and efficiency in genetic selection and in farm management. We will also work to make this basis applicable and accessible to the livestock sector going forwards. We sincerely hope that you will accompany us on this last phase of the project. And beyond!!





NEWS

GenTORE Fact Sheet

We are happy to announce that GenTORE's Fact Sheet is now available on the [GenTORE website](http://www.gentore.eu). The Fact Sheet describes how the GenTORE project can help farmers identify which animals to keep and breed as the best adapted to their farming conditions. This is of great importance with the increasing challenge of cattle farming, given climate change and ever-increasing demands for meat and milk. By providing farmers with decision support tools, incorporating the genetic and performance data of the herd (including sensor-based data), breeding and culling decisions can be aided by ranking cattle on resilience and efficiency across a full range of production systems.

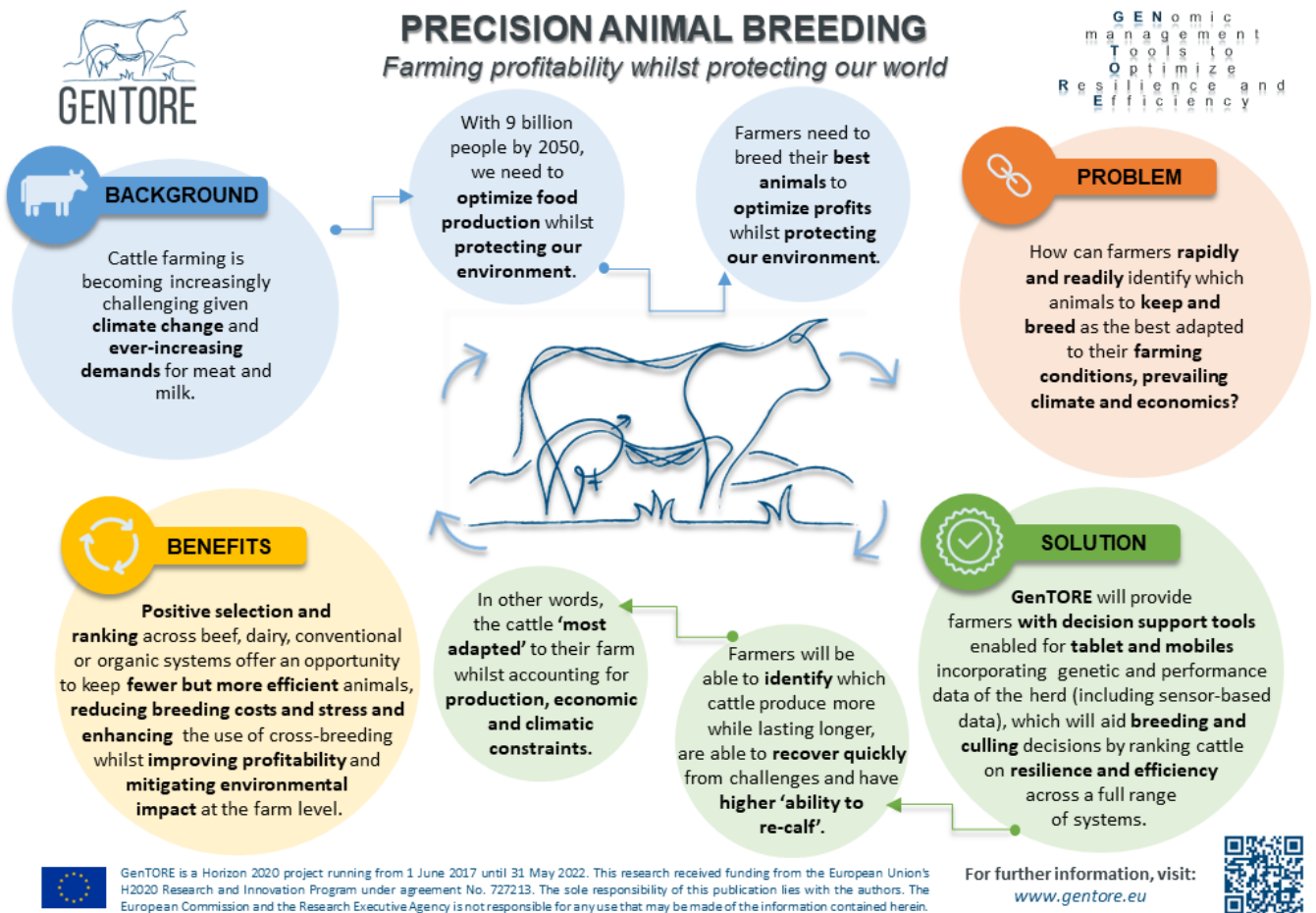


Figure 1. GenTORE Fact Sheet for farmers.





NEWS

GenTORE Midterm Online Meeting

On November 18 and 19, GenTORE organised an online midterm meeting focusing on "Genotype to phenotype: Precision Breeding Tools for the Best Cows". With an impressive number of 108 registered participants we look back at a fruitful meeting with project partners, stakeholders and external researchers and other interested participants. During the two day online meeting the achieved progress in all the different work packages was presented and discussed. The main topics that were discussed included: the interplay between R&E: combining proxies and linking to novel phenotypes for R&E; Modelling GxE: statistical and biological approaches; precise evaluations for R&E, and precision mating strategies, with genomics; building decision support tools: State of play, what's in the pipeline, what can be shared. With the use of break-out rooms, discussions with stakeholders were stimulated and resulted in a new way of looking at the projects objectives and the needs of farmers and breeders. We thank everyone who joined the meeting for their active participation!

GenTORE at EAAP Conference 2020

During the EAAP online conference, GenTORE presented its results during the session "Can you have your cake and eat it too - tools to get the most out of animal resilience and efficiency". The session started off with Donagh Berry presenting his research on "Decision support tools in cattle – from the cradle to the grave", where he showed that the developed indexes estimating the worth of both cows and bulls (C.O.W. and B.O.W.) assist in making supported decisions on both culling and breeding.

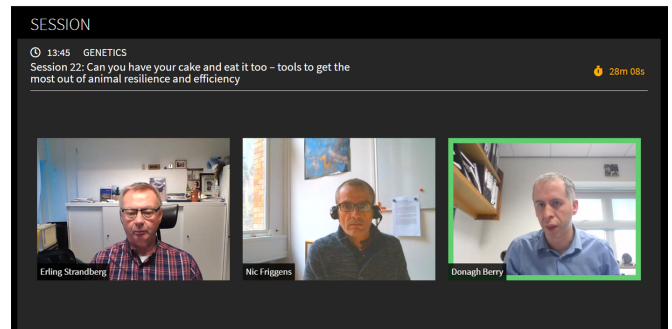
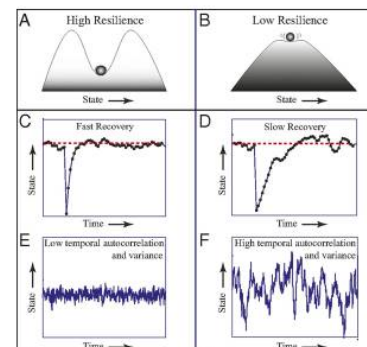


Figure 2. Q&A session during EEAP: Erling Strandberg and Nicolas Friggens moderate the session while Donagh Berry answers questions from the audience.

Yvette de Haas presented the results from WP3 on "Quantifying resilience of dairy cows from on-farm time-series measures", concluding that with improved sensor data, more advanced parameters and a clearer definition on resilience, it will be possible to predict resilience in dairy cattle using at-market sensor technologies.

Resilience



Resilience is the capacity of an animal to respond to environmental perturbations



12 From: <https://doi.org/10.1073/pnas.1810630115> This project has received funding from the European Union's Horizon 2020 research and innovation program under Grant Agreement No 101019713

Figure 3. Yvette de Haas explains resilience in regards to environmental perturbations during her presentation at EAAP.

Pauline Martin presented her work on "A new method to estimate RFI in dairy cattle using time-series data", where she indicated that we can use time-series data to follow biological changes over time, which can be used to infer residual feed intake in dairy cattle.





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What exactly is RFI ?



- Residual Feed Intake – a criterion of feed efficiency
- Difference between actual intake and intake predicted from performances
- The residual from a *linear regression*

$$\text{Intake} = a \cdot x_{\text{milk}} + b \cdot x_{\text{weight}} + c \cdot \text{body_condition} + \text{RFI}$$


- Linear regression = fixed coefficient (a, b, c)
- Lactation = dynamic process
- Li et al. (2017): lactation stage is important for RFI estimation

Figure 4. Pauline Martin explains residual feed intake during her presentation at EAAP.

Emre Karamadan discussed his research on “Genomic prediction using data from multiple pure breeds and crossbreds”. According to Emre, combining data from admixed and pure breeds can improve genomic predictions, especially for small breedings populations. Emre’s study is also featured in this newsletter so continue reading if you are interested in his results.

Amanda R. de la Torre presented “Increasing duration of feed restriction: performance ranking and variability of beef cows’ response”. Amanda illustrated that short time feed restrictions highlight the dynamic responses in beef cows and have the potential to serve as proxy for animal robustness.

Objectives of the study



Short-term feed restriction (2 – 6 days)
 Bjerre-Harpoth, 2012, Friggens et al, 2016, Billa et al, 2019

↓ marked changes

- Production and metabolism
- Follow-up over time

Is Feed Restriction (FR) a relevant framework?

- ↔ Milk yield is low to moderate (<10 kg/d)
- ↔ Its measurement is difficult and prone to errors

Figure 5. Amanda R. de la Torre explains the objective of her study during her presentation at EAAP.

Roberta Rostellato discussed her research on “Identification of longevity predictors in French dairy cattle”. She concluded that insemination status, calving ease, udder depth, clinical mastitis, somatic cell count and displaced abomasum could all be used as indicators to predict true and functional longevity.

Marieke Poppe studied the effect of herd management on resilience in her presentation (“Between-herd variation in cow resilience and relations to management”). Her results indicate that a low average variance in milkyield deviations indicates good resilience and is related to somatic cell score, rumen acidosis and survival.

Generating phenotypes: from animal to population

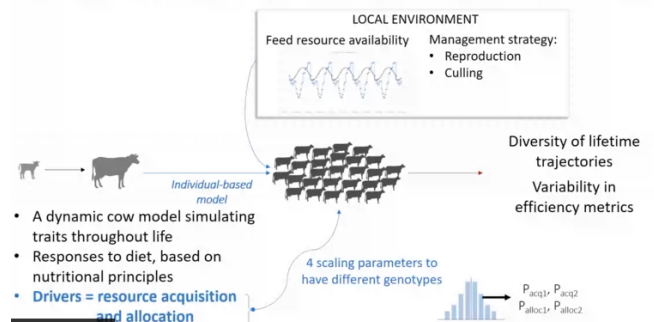


Figure 6. Laurence Puillet explains a dynamic way to generate phenotypes from animal to population during her presentation at EAAP.

Laurence Puillet presented “Simulation of genotype-environment interactions on short and long-term feed efficiency in dairy cows”. He looked at the effect of the environment on phenotypes in cattle. The genetic relationships emphasized the need for a balanced breeding goal, in line with GenTORE’s vision on breeding programs for “the Future Cow”.

Many thanks to everyone who presented in the EAAP conference for their excellent contributions!





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GenTORE Young Scientist Network

The [GenTORE Young Scientist Network](#) is aiming to create a network of PhD students and Young Scientists to share the interdisciplinary approach from the GenTORE project and related experiences and views with other early-career scientists. We encourage all early-career scientists to join the GenTORE Young Scientist Network on Facebook!

Operating with organic certification – Does it make economic sense for dairy farmers in Europe?

By: Christian Grovermann (FiBL)

Agroecology is increasingly recognized as a strategy for achieving more sustainable agricultural and food systems. To work for farmers, it needs to make economic sense. Organic certification plays a key role in this context, as it is crucial for managing compliance with agroecological farming requirements and also receiving price premiums. The dairy industry, both organic and conventional, is highly competitive and, in terms of output value, the second biggest agricultural activity in the EU. Organic cow milk

production in Europe has almost doubled between 2008 and 2017, with latest figures indicating an output of 4.7 million metric tons. The organic market share differs among countries in Europe, ranging from less than 1% to above 10%.

In the context of the GenTORE project a study was carried out to quantify the profitability and efficiency impacts of organic certification in dairy farming across Europe. The analysis is based on farm-level data from the Farm Accountancy Data Network (FADN) database, comprising more than 40,000 dairy enterprises across 25 countries in Europe. The novelty of the research is due to its scope and methodological approach, with similar studies being more location-specific and mostly focusing on farm incomes only, disregarding efficiency effects.

Through a class splitting model, the analysis accounts for heterogeneity in dairy farming across the continent. Four distinct classes with dairy farm enterprises operating under similar production conditions were identified in order to assess gross margin and efficiency differences among certified and non-certified farms. These are two key indicators for measuring the economic

Table 1. Certification impacts for profitability and efficiency outcomes across four classes.

	Class 1		Class 2		Class 3		Class 4	
	GM (€/cow)	EFF (0-1)	GM (€/cow)	EFF (0-1)	GM (€/cow)	EFF (0-1)	GM (€/cow)	EFF (0-1)
% change	43%	2%	38%	2%	50%	-1%	182%	7%
Sig.	**	***	***	ns	**	ns	***	***
Wald test	ns	ns	***	**	ns	ns	***	ns
Model	EB	EB	ET	ET	EB	EN	ET	EB
N	5,881		21,191		9,600		5,231	

GM = Gross Margin; EFF = Efficiency score; Sig. = Significance of effect; Wald test = Test to check need of accounting for unobservable confounders; ET = Endogenous Treatment as correction for selection bias; EB = Entropy Balancing as correction for selection bias; *** = 1% significance level; ** = 5% significance level; * = 10% significance level.





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performance of an enterprise. As farmers decide themselves whether to obtain certification, a simple comparison of certified versus non-certified farms is likely to be confounded by factors such as farm size, resource endowments and risk behavior, to name just a few examples. It is therefore necessary to control for observable and, in some instances for unobservable, farm characteristics in order to obtain an unbiased estimate of the certification effect. Depending on the nature of the bias, treatment effects were finally estimated either through an endogenous treatment model or through entropy balancing.

The results suggest that organic certification considerably increases profitability for organic dairy farm enterprises in Europe, while slightly increasing efficiency in two out of four instances. Significant certification effects range from 38% to 182% in terms of profitability gains, and from 2% to 7% in terms of efficiency gains. Overall, organic dairy production appears to be an economically sensible strategy for dairy farmers in Europe. It is important to note that organic dairy farming has been found to be more risky than conventional production, with organic farmers appearing to be generally less risk averse than conventional farmers. While certification might thus not be a viable option for all existing conventional dairy farms, the results point out that non-certified farms with characteristics that are similar to those of the certified farms may benefit from conversion.

Novel culling decision-support tool for beef producers

By: Fiona Dunne (TEAGASC)

The Beef Female's Profit Potential (BFPP) tool

provides an exciting opportunity to offer bespoke decision-support to (Irish) beef farmers to facilitate data-driven culling decisions. As culling decisions are notoriously multifactorial and complex, the main objective when developing the BFPP in GenTORE was to capture as much information as possible when estimating the total merit of a beef female and, in doing so, provide the farmer with a single Euro value which represents the remaining lifetime profit potential of the beef female; this reflects the main goal of GenTORE's WP5 which strives to develop easy-to-understand decision-support tools for farmers. The BFPP was developed by Teagasc (Ireland), in collaboration with the Irish Cattle Breeding Federation (Ireland) and AbacusBio, New Zealand.

The Beef Female's Profit Potential (BFPP) decision-support tool

The BFPP encapsulates the beef female's profit potential based on four modules, namely:

- 1) the profit potential of the beef female when she is a heifer, provided she has not yet calved;
- 2) the profit potential of the beef female's current parity, provided she has calved at least once;
- 3) the expected profit potential of the beef female's remaining future parities; and,
- 4) the beef female's retention value, which represents the cost benefit of retaining the beef female within the herd and not voluntarily culling her. An assortment of 17 animal level traits underpin each of the four modules of the BFPP. Yet, unlike traditional breeding indexes whereby an animal's value for a trait is based solely on the genetic value that is transmitted to their offspring, the BFPP extends beyond just incorporating the additive genetic merit by also capturing her non-additive genetic merit (i.e., heterosis) as well as





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the non-genetic merit of the female such as her age, the environment she is performing in and both her current and expected calving dates; this ensures that an extensive estimation of the beef female's total merit is used in the estimation of her BFPP value. The progeny performance of the beef female is also considered within the BFPP as a proportion of her progeny will be slaughtered for beef production, whilst others will be retained, eventually graduating into the beef herd as cows. Transition matrices were also incorporated into the future parity module of the BFPP in order to estimate the probability of a beef female's subsequent calving date as well as her probability of survival.

Validation of the BFPP

The BFPP tool was validated on 21,102 Irish beef females and their progeny based on their calving in the year 2017. The beef females were then stratified into four groups based on their within-

herd BFPP value and the performance of both the females and their progeny followed. The beef females in the best 25% stratum, on average, calved 38.2 days earlier in the calendar year than the females within the bottom 25% stratum (Table 2). Despite calving earlier, the calving interval of the beef females within the best 25% stratum was, on average, 8 days longer than the calving interval of the females in the worst 25% stratum (Table 2). This is a reflection of the predominantly spring-based calving production system practiced in Ireland, whereby females with superior fertility tend to calve earlier in the season and are subsequently subjected to a longer voluntary waiting period and thus an extended calving interval. The beef females within the best 25% stratum were also 1.63 times more likely to survive to the next parity relative to the beef females in the bottom 25% stratum (Table 2). The progeny of the beef females within the best 25% stratum were, on average, not only harvested with

Table 2. Least squares means of the performance of beef cows and their progeny when ranked on their Beef Female Profit Potential value; standard errors in parenthesis.

Animal	Component	Best 25%	50% to 75%	25% to 50%	Worst 25%
	Calendar day at calving	April 6 th (1.14) ^a	April 17 th (1.10) ^b	April 29 th (1.07) ^c	May 15 th (1.12) ^d
Cow traits	CIV (days)	377.21 (0.55) ^a	372.38 (0.54) ^b	371.19 (0.53) ^b	368.88 (0.57) ^c
	Survival ¹ (0 to 1)	1.63 (1.52,1.72) ^a	1.49 (1.39,1.58) ^a	1.33 (1.23,1.42) ^a	1.00 ^b
Progeny traits	Carcass weight (kg)	398.46 (0.85) ^a	398.48 (0.82) ^a	396.61 (0.80) ^{ab}	394.29 (0.83) ^b
	Carcass conformation (EUROP scale) ²	7.19 (0.02) ^a	7.14 (0.02) ^{ab}	7.07 (0.02) ^b	6.94 (0.02) ^c
	Carcass fat (1 to 15 scale) ³	7.94 (0.02) ^a	7.99 (0.02) ^{ab}	8.04 (0.02) ^b	8.04 (0.02) ^b

Different superscripts within row indicate a significant difference of $P < 0.05$; 1 Odds of surviving to the next parity relative to the worst stratum; 2 Carcass conformation ranges from 1 (very poor) to 15 (excellent); 3 Carcass fat ranges from 1 (very low fat) to 15 (very high fat).



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heavier carcasses, but also had better conformed carcasses with lower fat grades relative to the progeny of the beef females within the worst 25% stratum (Table 2).

The difference in performance between the beef females in the best 25% stratum relative to those in the worst stratum was estimated to be worth an additional €32 per calving when considering their respective performance as well as the performance of their progeny. Therefore, the BFPP has huge potential in providing farmers with data-driven support to identify less profitable candidate females for culling. Moreover, as the BFPP contains a heifer sub-component, the BFPP can also be used to identify potential replacements who have the greatest lifetime profit potential. The BFPP tool itself is dynamic in nature and therefore, can be adjusted to include even more traits of interest should they become available.

Acknowledgements

Funding from the European Union's Horizon 2020 research and innovation programme – GenTORE – under grant agreement No. 727213 is greatly appreciated. We are also grateful for the contributions of Paul Crosson and Laurence Shalloo.

Influence of climate stress on technical efficiency and economic downside risk exposure of EU dairy farms

By Sylvain Quiédeville, Christian Grovermann, Florian Leiber, Simon Moakes (FiBL), Giulio Cozzi, Isabella Lora (UNIPD), Vera Eory (SRUC).

This paper aims to evaluate the influence of heat and drought stress on the annual performance of EU dairy cow systems. Performance was measured in terms of technical efficiency (TE) and economic downside risk (downside gross margin deviations). The analysis was undertaken by combining climatic data available from the Gridded Agro-Meteorological data in Europe (AGRI4CAST) and the farm accounting data available from the FADN database at a NUTS2 region spatial scale. Only farms with an economically relevant dairy enterprise were retained (economic output \geq 35% total farm economic output). The dataset used in this paper contained 30,884 observations, representing a sample of 4,412 farms (identical between years) in 22 EU countries over the period 2007-2013.

NUTS2 regions were grouped into classes representing similar climatic conditions (climatic regions). Latent Class Analysis (LCA) was used to identify the underlying structure of the data. This resulted in 5 lowland classes, whilst all upland farms were grouped into a single class. Therefore, 6 climatic classes were assessed, with the following geographically descriptive names: North Atlantic (NAT), West Atlantic (WAT), Boreal (BOR), Continental (CON), South (SOU) and Upland (UPL).

To account for heat stress, the number of occurrences when there were at least 3 consecutive days of exposure to high THI was calculated. Different THI thresholds were assigned to the classes: A threshold of 60 was selected for NAT and BOR (coolest western classes); 64 was the threshold for WAT; and 68 was the threshold for CON, SOU, and UPL.





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To account for heat stress, the number of occurrences when there were at least 3 consecutive days of exposure to high THI was calculated. Different THI thresholds were assigned to the classes: A threshold of 60 was selected for NAT and BOR (coolest western classes); 64 was the threshold for WAT; and 68 was the threshold for CON, SOU, and UPL.

To account for drought stress, a threshold of 40 consecutive dry days was selected in most of the classes apart from NAT (30 days), and SOU (60 days). As the drought might induce a delayed effect on the following feeding periods due to decreased forage supplies, a time-lagged drought variable, based on the same thresholds, was also created.

Technical efficiency characterises farm performance and reflects the ability of a farm to generate output units given the inputs and the state of technology at its disposal. Technical efficiency was estimated using a 'true-fixed' effect

stochastic frontier model and by using the annual production of milk (kg) per dairy cow as a dependent variable. Inputs were also expressed per dairy cow. Economic downside risk was based on downside gross margin deviations. It was calculated as the difference between the gross margin in year t and the average gross margin over the seven year period.

Results show very high efficiency scores across the 6 climatic classes, ranging from 0.88 (out of 1) in SOU to 0.96 in NAT. In the WAT, BOR, SOU and UPL classes, drought is significantly and negatively associated with efficiency in a given year t (table 4). Otherwise, drought has no significant effect in CON, while it has a delayed negative significant effect in NAT for year $t+1$ (but positive in year t). Heat also is significantly and negatively associated with efficiency in most of the classes.

Furthermore, we found that drought consistently had a significant negative effect on economic

Table 3. Climatic classes across Europe.

Climatic class	North Atlantic (NAT)	West Atlantic (WAT)	Boreal (BOR)	Continental (CON)	Southern (SOU)	Mountain / Upland (UPL)
Description	Cool and wet, with low temperature variation (IE, UK)	Moderate temperature, with warmer summers and cooler winters (BE, DE, ES, FR, LU, NL, PT, UK)	Very cold winters, moderate temperature in summers, dry (FI, SE)	Warm summers, cold winters (AT, CZ, DE, EE, FR, LT, LV, PL, SE)	Hot summers, cool winters (AT, CY, EL, ES, FR, HU, IT, MT, PT, SI)	Quite warm summers and cool winters, (AT, CZ, DE, ES, FR, IT, PL, PT, SE, SI)
Production (kg/cow)	5,809	7,259	8,628	5,946	6,984	6,425
Dairy cows (#)	87	67	41	33	61	29



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downside risk in BOR, CON, SOU, and UPL directly in year t and also a delayed effect on the year $t+1$ for CON (table 5). The effect of drought is more ambiguous in NA and WA as in the current year it appears to lessen the economic downside risk whilst it has a negative effect in the year $t+1$. Heat is significantly and negatively associated with economic downside risk across all classes.

Table 4. Drought and heat effect on technical efficiency across climatic classes.

Climatic class	NAT	WAT	BOR	CON	SOU	UPL
Drought effect	+	-	-	(not sign.) ¹	-	-
Delayed drought effect	-	(not sign.)		(not sign.)		
Heat effect	-	-	-	(not sign.)	-	(not sign.)

1 Not significant.

Table 5. Drought and heat effect on economic downside risk across climatic classes

Climatic class	NAT	WAT	BOR	CON	SOU	UPL
Drought effect	+	-	-	(not sign.) ¹	-	-
Delayed drought effect	-	(not sign.)		(not sign.)		
Heat effect	-	-	-	(not sign.)	-	(not sign.)

To conclude, this study confirms that European dairy farms are technically highly efficient. A significant effect of drought stress on efficiency was shown in most of the classes. The delayed effect of drought observed in the NAT class could be due to a shortage of forage stock in the subsequent year, potentially causing an increase in feed costs per cow. A shortage of forage may lead to a reduced proportion of forage in the diet, which may affect production levels. In terms of the heat stress, a significant effect was observed on

efficiency across four out of six climatic classes. The lack of a significant heat effect on efficiency for UPL was somehow expected as this class grouped upland farms, located above 600 m of altitude, where heat waves are less frequent and intense compared to lowland classes.

The downside economic risk was also clearly affected by drought and heat stress across classes. However, an unexpected significant positive effect of drought was found in NAT and WAT. This finding may indicate a negative role played by excessive rainfall, as NAT and WAT are two of the three most humid classes present in the analysis, with an average daily precipitation level of 2.99 and 2.27 mm over 2007-2013, respectively.

Ruminal microbiota is associated with feed efficiency phenotype of fattening bulls fed high-concentrate diets

By: Sandra Costa-Roura; Daniel Villalba (UDL), Mireia Blanco; Isabel Casasús (CITA), Joaquim Balcells; Ahmad Reza Seradj (UDL).

Improving feed efficiency in livestock production is of great importance to cut down on nutrition costs. Our assay aimed to examine the relationship between ruminal microbiota and variation in feed efficiency in beef cattle fed concentrate-based diets.

Residual feed intake of 389 fattening bulls, supplied with corn-based concentrate and forage ad libitum, was used to estimate animals' feed efficiency. Bulls' concentrate intake was recorded on a daily basis, and their body weight (BW) was





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measured at least once a week. Feces and ruminal fluid samples were collected, at mid-growing (159 d of age and 225 kg BW) and mid-finishing periods (266 d of age and 434 kg BW), from 48 bulls chosen at random to estimate their forage intake and to characterize their apparent digestibility, ruminal fermentation and microbiota.

Within the 48 sampled bulls, only those animals with extreme values of feed efficiency (high-efficiency [HE, n=12] and low-efficiency [LE, n=13]) were subjected to further comparisons. No differences in dry matter intake were found between the two categories of feed efficiency (P=0.699); however, HE animals had higher

Growing phase: 159 d of age and 225 kg

Finishing phase: 266 d of age and 434 kg

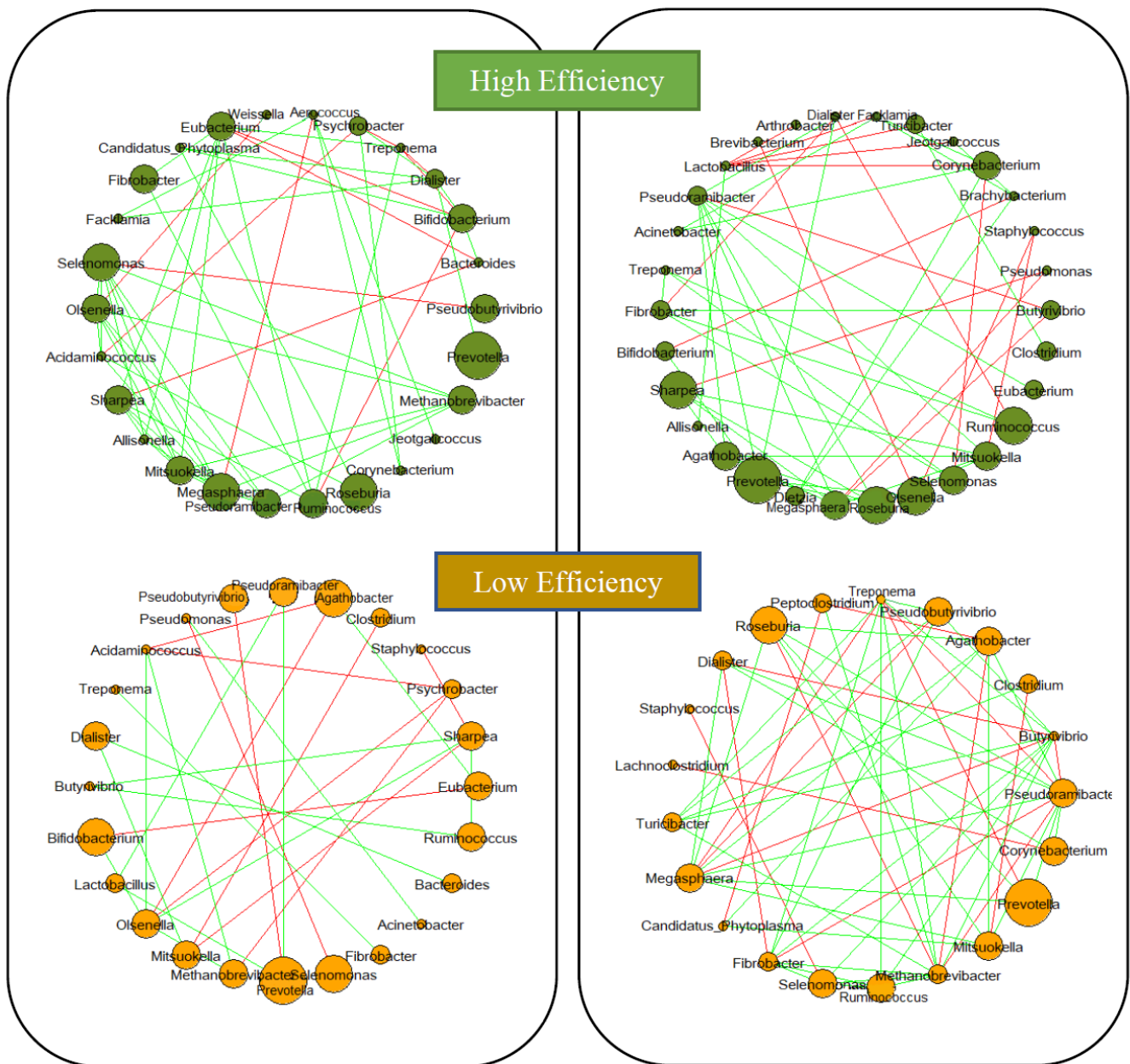


Figure 7. Microbial genera network in the rumen high-efficiency and low-efficiency. Networks were generated based on those genera establishing significant correlations ($r > 0.60$ and $P < 0.05$). Green and red edges indicate positive and negative correlations, respectively. Node size is proportional to genus abundance in ruminal fluid.





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apparent digestibility of dry matter ($P=0.002$), organic matter ($P=0.003$) and crude protein ($P=0.043$). Volatile fatty acids concentration remained unaffected by feed efficiency ($P=0.676$) but butyrate proportion increased with time in LE animals ($P=0.047$).

Ruminal microbiota was different between HE and LE animals ($P=0.022$): both alpha biodiversity ($P=0.005$ for Shannon index and $P=0.020$ for Simpson index) and genera network connectance (Figure 7) increased with time in LE bulls; which suggests that LE animals hosted a more robust ruminal microbiota. Methanobrevinacter, Roseburia, Agathobacter, Butyrivibrio, Pseudobutyrvibrio, Ruminococcus and Selenomonas genera are usually related to high energy loss through methane production and were found to establish more connections with other genera in LE animals' rumen than in HE ones (Figure 7). Microbiota function capability suggested that methane metabolism was decreased in HE finishing bulls. In conclusion, rumen microbiota was found to be associated with feed efficiency phenotypes in fattening bulls fed concentrate-based diets. Our results also highlighted a possible trade-off between animal feed efficiency and ruminal microbiota robustness that should be taken into account for the optimization of cattle production, especially in systems with intrinsic characteristics that may constitute a disturbance to rumen microbial community.

Acknowledgements

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article has been accepted for publication in Animal Production Science

Genomic prediction using purebred and crossbred individuals

By: Emre Karaman; Guosheng Su (QGG AU), Iola Croue (ALLICE), Mogens S. Lund (QGG AU)

Crossbreeding is an efficient strategy in dairy cattle breeding, to achieve better productivity and robustness at the animal and herd level. Crossbreeding systems, e.g. ProCROSS system (<https://www.procross.info>) yield crossbred animals with different proportions of genome segments coming from the pure breeds included in the system. Genomic evaluations in dairy cattle are generally carried out separately for each pure breed, and neither crossbred data is used, nor do they get evaluations. Genetic evaluation for crossbreds requires methods which can efficiently handle data from purebred and crossbred individuals. In WP4 (Task 4.1) of the GenTORE project, we provided and tested a model which can handle data from purebred and crossbred individuals, allowing for simultaneous evaluation of purebred and crossbred animals. The proposed model includes a genomic component for each pure breed in the gene pool. It relies on the accurate determination of breed origin of each genome segment. Models using breed origin of alleles (BOA) are generally referred to as BOA models.

Accuracies for within-, across- and multi-breed predictions using standard genomic prediction models were compared with BOA models, using simulated data sets. Genotypic data (~13K SNPs, 5 chromosomes) from real dairy populations, i.e. Danish Holstein (H), Swedish Red (R) and Danish





SPOTLIGHT NOTABLE RESULTS

Jersey (J), were used as base populations to start genotype simulations for each of the pure breeds and a population of crossbred animals (C) for nine generations, mimicking a rotational crossbreeding system. Simulations started with mating J males and H females to generate first generation of C, and continued such that crossbred dams were mated with purebred sires from R, H and J in turn, until nine generations were reached. At each generation, there were 1,050 animals in H, R and C, and 220 animals in J. Phenotypes were also simulated considering 250 QTL with different levels of QTL effect correlations (1.00, 0.50 or 0.25) between the breeds.

Table 6. Summary of data and approaches used.

Reference data	SNP effects	BOA for "C" (reference/validation)
H	Breed specific	na/-
R		na/-
J		na/-
H/R/J		na/+
H+R+J	Identical	na/-
H+R+J+C		-/-
H+R+J+C	Breed specific (uncorrelated)	+/+
H+R+J+C	Breed specific (correlated)	+/+

*na: not applicable

Data from a full rotation cycle (generations 6-8) was used as reference to estimate SNP effects, and data from generation nine to validate prediction accuracy. In within-breed predictions, reference and validation populations were from the same breed, whereas in across-breed predictions, they were from different breeds ("C" as a separate breed). We also considered a scenario (H/R/J), where SNP effects were estimated for each pure breed separately, and BOA was considered for the candidates of C. For multi-breed predictions we either combined data of all purebred populations (H+R+J) or purebred populations and crossbred animals (H+R+J+C), to

estimate breeding values for validation animals. It should be noted that analysis using a combined reference reference data assume that SNP effects are identical across the breeds, unless a BOA model is used. The SNP effects were breed specific, and also assumed to be either uncorrelated or correlated when using BOA approach. A summary of data and approaches used in predictions were given in Table 6.

For demonstration, we focus on the results for a high heritability trait ($h^2=0.4$) and from an extension of the well-known genomic prediction method, BayesA, where each SNP is assumed to have its own (co)variances. The results are shown in Figures 8-10. Across-breed prediction accuracies were low for pure breeds, in some cases close to zero (Figures 8 and 9). Multi-breed genomic prediction using reference population of pure breeds generally led to lower accuracies, more profound for small breed (J vs H; Figure 8 vs 9), than within-breed prediction. Including data from crossbred animals, C, in a multi-breed reference population generally improved accuracies over within-breed prediction for J. The benefit of BOA models was more apparent when the correlation of QTL effects was lower than one, and in those cases BOA models yielded higher accuracies than simply pooling all available data to form a reference population (H+R+J+C). The results for R were not given due to space limitations, but the pattern in accuracies from different scenarios was similar to that for H.

Accuracies for C using SNP effects from pure breeds reflected the recent relationships of C to the pure breeds (Figure 10). Using the SNP effects estimated from pure breeds, but accounting for breed origin of alleles for validation





SPOTLIGHT NOTABLE RESULTS

individuals increased accuracies for C. As expected, multi-breed genomic prediction without including data of C was not efficient, as it reflects a situation where the target population is not represented in the multi-breed reference population. Together with data of crossbred individuals, BOA models were able to yield accuracies higher up to 10 percentage points than multi-breed genomic prediction for C. Accounting for correlation of SNP effects between the breeds

was not beneficial. In conclusion, the use of crossbred data together with purebred data in genomic prediction has two main advantages: (i) it increases the data size for all pure breeds, particularly for the breeds with a small population size, allowing more accurate estimation of breeding values in small breeds, (ii) it increases the prediction accuracy for crossbred animals.

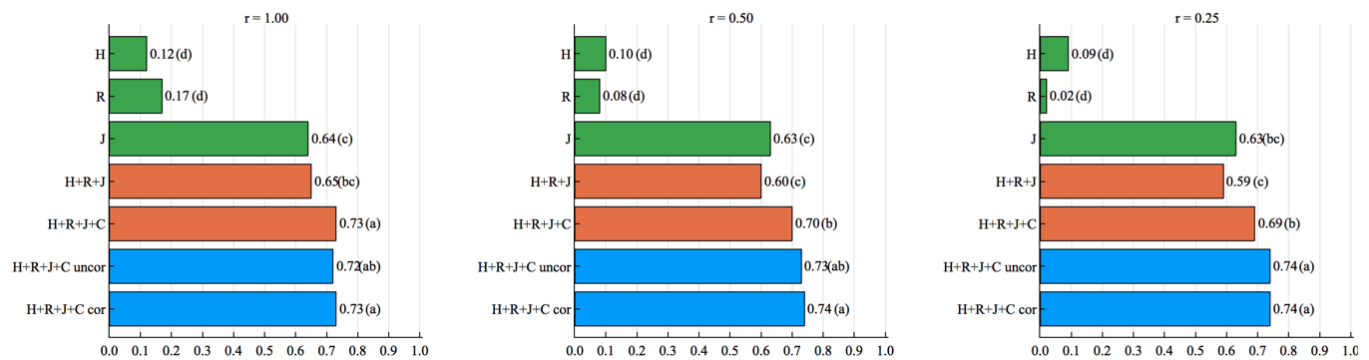


Figure 8. Accuracy for validation animals of Jersey (J). Green bars represent predictions using SNP effects from a single breed (H,J or R). Orange bars represent predictions using SNP effects from a combined population of pure breeds (H+R+J) or pure breeds and crossbred animals (H+R+J+C). Blue bars represent predictions using SNP effects (uncor and cor: uncorrelated and correlated SNP effects between the breeds) from analysis considering BOA.

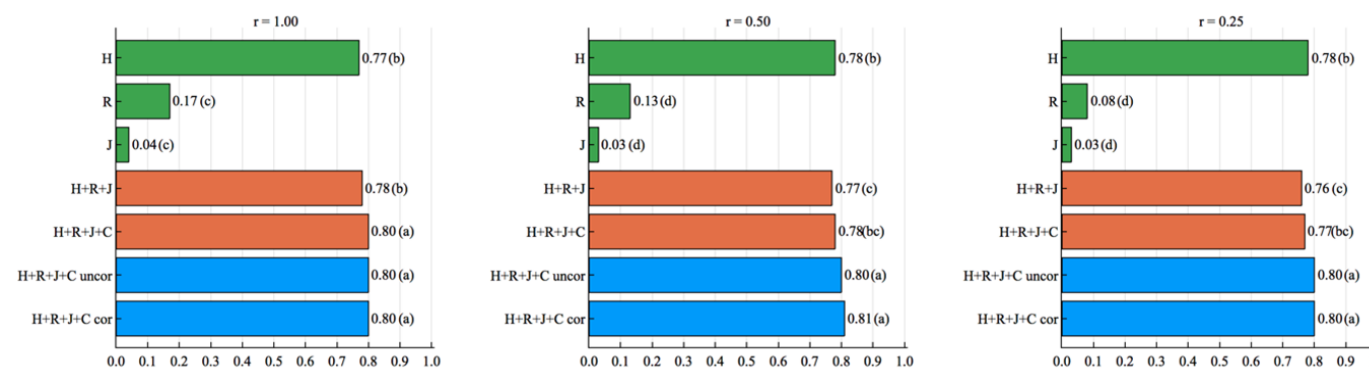


Figure 9. Accuracy for validation animals of Holstein (H) breed. Green bars represent predictions using SNP effects from a single breed (H,J or R). Orange bars represent predictions using SNP effects from a combined population of pure breeds (H+R+J) or pure breeds and crossbred animals (H+R+J+C). Blue bars represent predictions using SNP effects (uncor and cor: uncorrelated and correlated SNP effects between the breeds) from analysis considering BOA.





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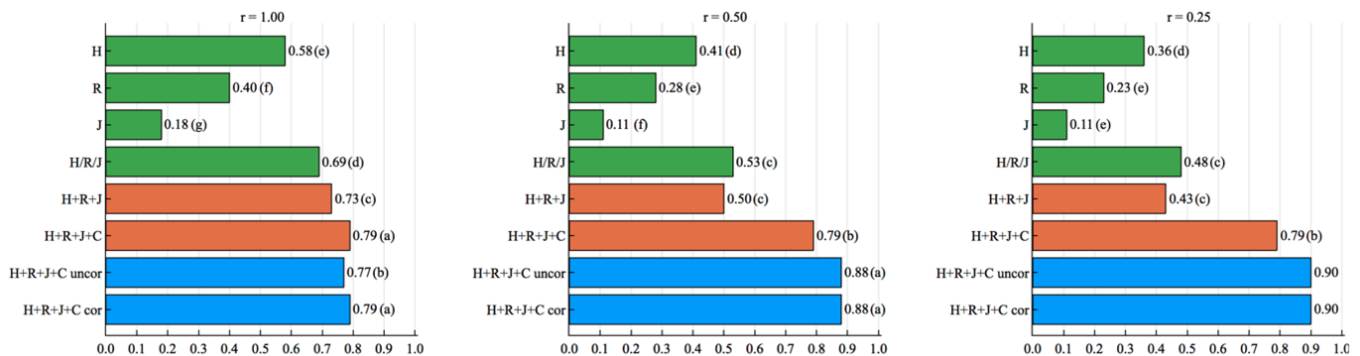


Figure 10. Accuracy for crossbred (C) animals. Green bars represent predictions using SNP effects from a single breed without (H,J or R) or with (H/R/J) considering BOA for the validation animals. Orange bars represent predictions using SNP effects from a combined population of pure breeds (H+R+J) or pure breeds and crossbred animals (H+R+J+C). Blue bars represent predictions using SNP effects (uncor and cor: uncorrelated and correlated SNP effects between the breeds) from analysis considering BOA both for reference and validation animals.

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MEET GENTORE



Claudia Kamphuis (Wageningen Research)

WP3 Associate Leader – Proxies for Resilience and Efficiency

claudia.kamphuis@wur.nl

When I was nine years of age I wanted, as any little girl, to ride horses. But because we had no farm, and because my parents found horse riding to be too expensive, I had to find a solution. So, stubborn me, I took my pushbike to knock on the door from a random farmer that had horses in the paddock. That farmer happened to be a dairy farmer, and that is where my dairy cow fever started. Their continuous search for improving health of their animals got my interest too. After finishing my MSc in Animal Health and Welfare, I started a PhD at Utrecht University. During my PhD, I applied machine learning on sensor data from automatic milking systems to improve the automated detection of mastitis. Since then, my research focuses on improving animal health through technology and data science. Within GenTORE, I am associate leader of a work package that uses national data, on-farm data, and data from new technologies (drones) to develop proxies for resilience and efficiency. This brings the challenge to work with large volumes of high-frequency data and how to retrieve the relevant information from these incomplete and noisy data. To face this challenge with the consortium is really nice. Today, I still like horses, but replaced the 1 horsepower with riding a motorbike with 135 horsepower. Besides that, I enjoy outdoor sports and the reading a good book.



Simon Moakes (FiBL)

WP1 Associate leader - Production system metrics: Assessing the systems context

simon.moakes@fibl.org


Simon qualified as an agronomist in 1996 and after some years developing a dairy goat business, returned to science in 2006 at Aberystwyth University in Wales, UK, conducting research into livestock system sustainability and organic farming. Since 2015 he has worked at FiBL (Research Institute of Organic Agriculture) and is currently a thematic leader in the area of farm systems, economics and policy. His main research and development aim is to enable more sustainable agricultural systems, with a special focus on the use of LCA and quantitative systems modelling to assess and identify promising innovations in pastoral livestock and mixed farming systems. Simon has worked in many EU projects such as SOLID and Cantotogether, as is currently a WP leader in the new MIXED project. Within GenTORE Simon supports Floian Leiber as the WP1 leader, and is focused on the top down approach of identifying cattle systems characteristics from high level, e.g. FADN data, with the aim of being able to use this data to explain environmental characteristics within phenotypic data, the so-called G x E relationship. He is also working in WP6 to support animal and herd level modelling of the impacts of environment on animal longevity and productivity.





GENTORE TV

[GenTORE TV](#) continues to publish informative videos about the GenTORE project and its work packages. We would like to highlight the Future Cow Workshop that took place on May 13, 2020, the workshop including the discussions and reporting sessions are now available on [our channel](#). Subscribe to GenTORE H2020 on YouTube to see all videos. The videos are also accessible from the GenTORE website under [Media](#).

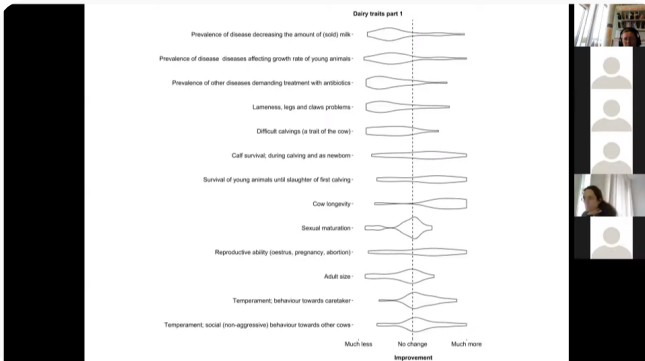


"GENomic management Tools to Optimize Resilience and Efficiency"

Assume a well-balanced genetic change in resilience *and* efficiency
There may be some goal conflicts

In the questionnaire
Beef: genetic potential for growth rate as today
Dairy: genetic potential for milk yield as today

Characteristics of future animals according to your answers in the questionnaire



Dairy traits part 1

- Prevalence of disease decreasing the amount of (total) milk
- Prevalence of disease diseases affecting growth rate of young animals
- Prevalence of other diseases demanding treatment with antibiotics
- Lameness, legs and claws problems
- Difficult calvings (a trait of the cow)
- Calf survival: during calving and as newborn
- Survival of young animals until slaughter of first calving
- Cow longevity
- Sexual maturation
- Reproductive ability (oestrus, pregnancy, abortion)
- Adult size
- Temperament behaviour towards caretaker
- Temperament, social (non-aggressive) behaviour towards other cows

Much less No change Much more
 improvement

CONTACT

Nicolas Friggens

Project Coordinator, INRA
nicolas.friggens@agroparistech.fr

Agathe Renard

Project Manager, IT
agathe.renard@inra.fr

Cagla Kaya

Outreach & Dissemination, EFFAB
cagla.kaya@effab.info

For more information visit our website: www.gentore.eu



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