



PPS-jaarrapportage 2018

Algemene gegevens	
PPS-nummer	AF-16022
Titel	Breed4Food
Thema	Klimaatneutraal
Uitvoerende kennisinstelling(en)	Wageningen Livestock Research
Projectleider onderzoek (naam + emailadres)	Roel Veerkamp (Roel.Veerkamp@wur.nl)
Penvoerder (namens private partijen)	Erwin Koenen (Erwin.Koenen@Breed4Food.com)
Contactpersoon overheid	Françoise Divanach
Startdatum	01-01-2017
Einddatum	31-12-2021

Goedkeuring penvoerder / consortium

De jaarrapportage dient te worden besproken met de penvoerder/het consortium. De TKI's nemen graag kennis van evt. opmerkingen over de jaarrapportage.

De penvoerder heeft namens het consortium de jaarrapportage	<input checked="" type="checkbox"/> goedgekeurd <input type="checkbox"/> niet goedgekeurd
Evt. opmerkingen over de jaarrapportage:	

Planning en voortgang (indien er wijzigingen zijn t.o.v. het projectplan svp toelichten)

Loopt de PPS volgens planning?	Ja de PPS loopt volgens planning
Zijn er wijzigingen in het consortium/de projectpartners?	Nee
Is er sprake van vertraging en/of uitgestelde opleverdatum?	Nee
Is er sprake van inhoudelijke knelpunten, geef een korte beschrijving	In het eerste jaar was het lastig om te besluiten welke fenotypering kenmerken belangrijk waren over de diersoorten. Dat is nu ingehaald ne het loopt voorspoedig
Is er sprake van afwijkingen van het ingezette budget/de begroting?	Nee niet tov eerdere kasritme wijziging

Korte omschrijving inhoud/doel PPS

Sustainable production of high-quality animal protein for a growing world population is the key challenge for livestock industry in the future. The aim of Breed4Food is to develop and apply innovations that utilize the genetic potential of cattle, pigs and poultry to breed production animals that are suited to meet future needs. The Breed4Food activities focus on: (1) providing tools to enable efficient breeding for sustainability traits, and (2) efficient utilization of DNA information and different sources of phenotypic data in breeding programmes. The anticipated innovations will generate effective breeding programmes and broad breeding goals that capture traits related to resource efficiency, health and welfare.

Resultaten

New phenotype recording techniques, such as high-throughput robotic sensors, offer opportunities to collect complex and detailed animal data at a high or even real-time frequency. These data can be used to define and predict new phenotypes for sustainability traits, that were previously difficult and/or expensive to measure and analyse. Likewise, recent advances in genomics and molecular biology, such as massive sequencing and

genotyping technologies, offer unprecedented possibilities to create enormous genomic datasets. Simultaneously, novel data mining techniques facilitate the translation of Big Data into useful measures of animal performance by using combinations of observations or detection of specific patterns that yield accurate predictions for target traits. Practical examples include the utilization of longitudinal sensor data to collect information on individual and group behaviour to predict health, resilience and welfare. The utilization of new methods to collect and analyse phenotypic and genomic data will increase the efficiency of genetic improvement and herd management. Indeed, the unique combination of advanced techniques for recording and defining new phenotypes and genomics offers great opportunities to include traits in breeding goals that were unattainable with the classical approach.

Utilizing DNA information

Very good progress in this area. Projects teams with strong technical expertise work on issues that are relevant for all partners simultaneously. Great progress has especially been made regarding the development of algorithms and software for genomic evaluations. A test with a genomic breeding value estimation model using 1.2 million genotyped animals has successfully been completed, but further optimization is needed to reduce computing time. In terms of utilizing (additional) sources of genomic information, progress is being made in karyotyping from sequence data, deriving and characterizing copy number variants (CNV), using sequence data to boost genomic prediction for small breeds, and the contributions of de novo mutations to long term selection response in genomic breeding programs will be investigated in a new project. Finally, a project on genome editing with social sciences has started September 1st.

Precision Phenotyping

Good progress in all Precision Phenotyping projects. A trial was run by Hendrix Genetics on objective scoring of locomotion of turkeys with the use of video imaging, IMU's and a force plate. To analyse the video images a collaboration with experts in Agrofood Robotics has been set up. The recorded data during this trial have also been used in the Big Data project to learn lessons on a data lake stack. These lessons learned included: setting up a data lake stack is possible with limited investment in additional software, filling the data lake with data from animal experiments is possible, but a metadata framework is essential to structure and link data collected during an animal experiment automatically and afterwards (in contrast to think about how to record things and link them beforehand and doing the linking by hand). Another way of objectively tracking and monitoring animals housed in groups is investigated in broilers, with ultra wide bands and with RFIDs. The UWB data showed that it is possible to track animals and monitor their activity during the day over a couple of days. Two genetic lines were compared and differences were observed.

Longitudinal data on milk yield of dairy and feed intake of turkeys have been analysed in the Health project, with the aim to link deviations in patterns to resilience of the animals. First results show that there are differences between animals, and that genetic parameters of these indicators of the deviations show differences in the genetic abilities of the animals.

A novel approach on recording feed efficiency in livestock with organoids was developed further, and showed that, even though numbers were small, differences could be detected between organoids of pigs that were selected as high and low efficient, based on phenotypic performances during life. Now that this methods shows promises, the next steps are (1) to explore how informative tissues can be collected during life, and (2) to investigate how the number of animals with organoids can be scaled up.

Aantal opgeleverde producten in 2018 (geef in een bijlage de titels en/of omschrijving van de producten of een link naar de producten op openbare websites)			
Wetenschappelijke artikelen	Rapporten	Artikelen in vakbladen	Inleidingen/ workshops
22	8	0	>20

Bijlage: Titels van de producten of een link naar de producten op een openbare website

- Aldridge, M. N., J. Vandenplas, and M. P. L. Calus. 2018. Efficient and accurate computation of base generation allele frequencies. *J. Dairy Sci.* In press.
- Calus, M. P. L., and J. Vandenplas. 2018. SNPPrune: an efficient algorithm to prune large SNP array and sequence datasets based on high linkage disequilibrium. *Genet. Sel. Evol.* 50:34.
- Calus, M. P. L., M. E. Goddard, Y. C. J. Wientjes, P. J. Bowman, and B. J. Hayes. 2018. Multibreed genomic prediction using multitrait genomic residual maximum likelihood and multitask Bayesian variable selection. *J. Dairy Sci.* 101:4279-4294.
- Vandenplas, J., M. P. L. Calus, and G. Gorjanc. 2018. Genomic prediction using individual-level data and summary statistics from multiple populations. *Genetics.* 210:53-69.
- Vandenplas, J., M. P. L. Calus, and J. ten Napel. 2018. Sparse single-step genomic BLUP in crossbreeding schemes. *J. Anim. Sci.* 96:2060-2073.
- Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. (2018) Bouwman, et al. *Nature genetics* 50 (3), 362
- Vandenplas, Eding, Calus, and Vuik. 2018. Deflated preconditioned conjugate gradient method for solving single-step BLUP models efficiently. *Genet. Sel. Evol.* 50:51.
- EAAP: Ten Napel et al. 2018. One million animals genotyped Vandenplas et al. 2018. Efficient computational strategies for multivariate single-step SNPBLUP. EAAP, Dubrovnik, Croatia
- Groß C, de Ridder D and Reinders M (2018) Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. *BMC Bioinformatics*201819:373
- Derks MFL, Megens HJ, Bosse M, Visscher J, Peeters K, Bink MCAM, Vereijken A, Gross C, de Ridder D, Reinders MJT, Groenen MAM. (2018) A survey of functional genomic variation in domesticated chickens. *Genet Sel Evol.* 50:17.
- Derks MFL, Herrero-Medrano JM, Crooijmans RPMA, Vereijken A, Long JA, Megens HJ, Groenen MAM. (2018) Early and late feathering in turkey and chicken: same gene but different mutations. *Genet Sel Evol.* 50:7.
- Derks MFL, Lopes MS, Bosse M, Madsen O, Dibbits B, Harlizius B, Groenen MAM, Megens HJ. 2018. Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. *PLoS genetics* 14(9): e1007661.
- Wu Z, Derks MFL, Dibbits B, Megens HJ, Groenen MAM, Crooijmans R. 2018. A Novel Loss-of-Function Variant in Transmembrane Protein 263 (TMEM263) of Autosomal Dwarfism in Chicken. *Frontiers in genetics* 9: 193.
- Bosse M, Megens H-J, Derks MFL, de Cara ÁMR, Groenen MAM. Deleterious alleles in the context of domestication, inbreeding, and selection. *Evol Appl.* 2018;00:1-12. <https://doi.org/10.1111/eva.12691>
- Duenk, P., M.P.L. Calus, Y.C.J. Wientjes, V.P. Breen, J.M. Henshall, R.J. Hawken, and P. Bijma. 2017. Estimating the purebred-crossbred genetic correlation of body weight in broiler chicken with pedigree or genomic relationships. *GSE* - under review.
- Duenk, P., M. P. L. Calus, Y. C. J. Wientjes, V. P. Breen, J. M. Henshall, R. J. Hawken, and P. Bijma. Genomic prediction of body weight in broilers using crossbred information and considering breed-origin of alleles. *GSE* - submitted.
- Wientjes, Y. C. J., M. P. L. Calus, P. Duenk, and P. Bijma. Required marker properties for unbiased estimates of the genetic correlation between populations. *GSE* - under review.
- Raymond et al., Utility of whole genome sequence data for across breed genomic prediction *GSE* (published, May 2018).
- Raymond et al. Genomic prediction for numerically small breeds, using models with pre-selected and differentially weighted markers. *GSE* (published, October, 2018)
- Raymond et al., A deterministic equation to predict the accuracy of multi-breed genomic prediction with multiple genomic relationship matrices (Draft, to be submitted to *GSE*)
- EAAP presentation: The effect of using sequence data instead of a lower density SNP chip on a GWAS (Van den Berg et al.).
- Comparison WGS and SNPs for GWAS detection is being finalized to be resubmitted to *GSE* (Van den Berg).
- Poster presentation at WIAS science day - February 2018 (Malou)
- Oral presentation at precision livestock workshop - May 2018 (Malou)
- Oral presentations at measuring behavior conference - June 2018 (Malou & Esther)
- Oral presentation at GroupHouseNet training school - November 2018 (Malou)
- Paper "Sensor technologies in animal breeding: phenotyping behaviours of laying hens to select for less damaging behaviour" (aim: January 2019)
- seminar presentation: Upscaling locomotion phenotyping for animal breeding and management purposes (Aniek, 13-06-2018)
- EAAP abstract presented (turkey locomotion) (Aniek, 30-08-2018)
- Report pilot study "using organoids from colon tissue to study feed efficiency in pigs"
- Report "protein efficiency in livestock"
- Paper "Animal Management Board Invited Review: Livestock breeding for adaptation to new diets using feed components without competition with human edible protein sources" (aim: November 2018)
- Report "Literature review organoids"
- Paper "review organoids" (aim January 2019)
- Report "Digestibility in livestock"
- Oral presentation EAAP - pilot study organoids - August 2018 (Esther)
- ECPLF abstract "using a data lake stack in animal sciences" (August 2019, Cork, Ireland)

- FAIR symposium abstract "using a data lake stack in animal sciences (December 2018, Wageningen, the Netherlands)
- Scientific paper "Machine Learning to further fine-tune differentiation of sub-fertile boar semen" submitted to Animal Science
- Oral on "Developing resilience indicator traits based on longitudinal data: opportunities and challenges" at EAAP (Han)
- Oral on "Development of resilience indicators using deviations in milk yield from the lactation curve" at EAAP (Marieke)
- FAIR symposium abstract on "Development of resilience indicators using deviations in milk yield from the lactation curve" (Marieke)
- Report by Tette van der Lende entitled "Regulation and modification of appetite in broilers"
- Review paper entitled: "Regulating appetite in broilers for improving body and muscle development - A review" (Marinus te Pas 1st author). Submitted in November 2018.
- Poster on "Sources of variation in fecal nutrient digestibility in individual pigs" by Verschuren *et al* at 14th International Symposium on Digestive Physiology of Pigs.
- Poster on "The relationship between fecal nutrient digestibility and microbiota composition in grower-finisher pigs at slaughter weight" by Verschuren *et al* at 14th International Symposium on Digestive Physiology of Pigs.
- Oral on "Faecal microbiome profiles can predict complex traits in pigs" by Dirkjan at EAAP 2018.
- Alsahaf et al. (2018): Prediction of slaughter age in pigs and assessment of the predictive value of phenotypic and genetic information using random forest. JAS.
- Van der Heide et al. (2018) Early prediction of survival to 2nd lactation in Holstein cows using genomic and phenotypic data. JDS under review