



<b>Algemene gegevens</b>	
PPS-nummer	TKI AF12018
Titel	Breed4Food
Roadmap/Koepel	Agri&Food, thema Duurzame Veehouderij
Uitvoerende kennisinstelling(en)	Wageningen Livestock Research
Projectleider onderzoek (naam en emailadres)	Lucia Kaal (lucia.kaal@wur.nl)
Penvoerder PPS (namens private partij)	Erwin Koenen Directeur Breed4Food, (Erwin.Koenen@Breed4Food.com)
Contactpersoon overheid	Suzanne Zwart
Werkelijke startdatum	1 januari 2013
Werkelijke einddatum	31 december 2016
Korte omschrijving inhoud (bij voorkeur 4 regels, max. half A4)	Het programma Breed4Food heeft zich gericht op de ontwikkeling van innovatieve onderzoeksprojecten in drie grote onderzoeksgebieden: i) exploiteren DNA informatie, ii) nieuwe fokdoelkenmerken en iii) toegevoegde waarde van fokkerij in de keten. In deze drie gebieden heeft Breed4Food nieuwe toegepaste kennis, specifieke en innovatieve methoden, software en tools opgeleverd. Dit heeft geresulteerd in wetenschappelijke doorbraken om genetische verbetering tot een rendabele veehouderij te realiseren, wat bijdraagt aan de duurzaamheid en het oplossen van maatschappelijke uitdagingen van de veehouderij

<b>Goedkeuring penvoerder / consortium</b>	
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:	Geen

<b>Planning en voortgang</b>	
Loopt de PPS volgens planning?	Ja
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	Nee
Is er sprake van afwijkingen van het ingezette budget/de begroting?	Nee
Verwacht u een octrooi-aanvraag vanuit deze PPS	Nee

<b>Resultaten en deliverables</b>	
1. Welke deliverables zijn	Als eerste stap in het project hebben de Breed4Food partners 4

<p>opgeleverd? (geef een korte beschrijving per deliverable uit het projectplan)</p>	<p>breakthroughs gedefinieerd:</p> <ol style="list-style-type: none"> <li>1. Genomische fokwaarden met een betrouwbaarheid van minimaal 85%.</li> <li>2. Genomische informatie kan als enige informatiebron gebruikt worden om prestatiegegevens van gekruiste dieren in de veehouderij te gebruiken voor selectie binnen een zuiverlijns fokpopulatie met minimale omvang en generatie-interval.</li> <li>3. Handvatten om duurzaamheid en weerbaarheid van landbouwhuisdieren te verbeteren zodat ze kunnen blijven produceren in een sector met verminderd antibioticagebruik en met meer aandacht voor dierwelzijn, humane gezondheid en maatschappelijke problemen.</li> <li>4. 20,000 ultra-gezonde dieren kunnen individueel gegenotypeerd worden en ontvangen precisie-management op basis van hun genetische aanleg; sommigen gericht op hoge vleeskwaliteit, anderen gericht op lage kosten.</li> </ol> <p>In Bijlage 1 staat de evaluatie ten aanzien van deze breakthroughs. Bijlage 2 betreft benchmarking aan de Breed4Food deliverables zoals gedefinieerd in het goedgekeurde Breed4Food TKI AF plan 2013-2016, bijlage 3 geeft het resultaat weer van het Breed4Food intern tevredenheidsonderzoek. In bijlage 4 staan de resultaten van het interne tevredenheidsonderzoek onder de stakeholders.</p>
<p><b>2.</b> Indien bepaalde deliverables niet gehaald zijn, wat was daarvoor de reden?</p>	<p>Het is in de afgelopen periode lastig gebleken om gemeenschappelijke projecten te identificeren met andere ketenpartijen, die tot doel hebben om nieuwe innovatieve producten en diensten te ontwikkelen voor de ketens op de thema's levensduur van dieren en de uniformiteit van koppels.</p>
<p><b>3.</b> Heeft het project onverwachte (neven)uitkomsten opgeleverd, die vooraf niet waren voorzien? Zo ja, benoem deze.</p>	<p>STW Partnership programm has been developed Bright Ideas see money projects have been initiated by project partners.</p>
<p><b>4a.</b> Binnen hoeveel jaar zullen de private partijen resultaten uit dit project gaan gebruiken in de praktijk?</p>	<p>Resultaten worden reeds gebruikt door de bedrijven in het consortium (met name modellen, algoritmes en software), of zijn nu in ontwikkeling om de komende jaren gebruikt te gaan worden</p>
<p><b>4b.</b> Kan het gebruik van de resultaten in de praktijk nog worden versneld, en zo ja, wat is daarvoor nodig?</p>	<p>Nee.</p>
<p><b>4c.</b> Op welke wijze is over het project en de resultaten gecommuniceerd naar de brede doelgroep (incl. niet-deelnemende bedrijven)?</p>	<ul style="list-style-type: none"> <li>- <a href="http://www.breed4food.com/">http://www.breed4food.com/</a></li> <li>- wetenschappelijke publicaties in diverse journals en presentaties op diverse internationale congressen</li> <li>- maandelijkse Breed4Food bijeenkomsten die ook op WURtv staan</li> </ul>
<p><b>5.</b> In hoeverre heeft het project bijgedragen aan de ontwikkeling van de betrokken kennisinstelling(en)? (bijv. wetenschappelijk track record, nieuwe technologie, nieuwe samenwerkingen)</p>	<p>Via een groot aantal wetenschappelijk publicaties en promoties (&gt;13 in de periode 2013-2017) heeft WUR een nog duidelijkere positie gekregen op het gebied van fokkerij.</p>
<p><b>6.</b> Krijgt het project een vervolg in de vorm van een nieuw project of een nieuwe samenwerking? Zo ja, geef een toelichting.</p>	<p>Ja het consortium heeft besloten om door te gaan, ondermeer door een nieuwe PPS</p>

**Highlights:**

De strategie voor Breed4Food, zoals gedefinieerd in 2012, was: afstemming en uitvoering van precompetitief genomics- en fokkerij-onderzoek op basis van de behoeften van de bij Breed4Food aangesloten fokkerijbedrijven, over diersoorten heen.

De waarde van de resultaten van het uitgevoerde onderzoek voor de Breed4Food partners is hoog vanwege de ontwikkeling en toepassing van genetische en genomische kennis en hulpmiddelen zoals betere en snellere algoritmen. Veel van deze kennis en hulpmiddelen zijn inmiddels in de R&D-activiteiten en de fokprogramma's van de Breed4Food partners geïmplementeerd. Daarnaast is de beschikbaarheid van deze kennis en hulpmiddelen de basis voor de succesvolle ontwikkeling van projecten in de andere Breed4Food onderzoeksthema's. Deze thema's winnen nu aan belang en omvang, mede door het succesvolle Breed4Food STW partnership programma en de projecten die voortvloeien uit de oproep van Breed4Food voor Bright Ideas.

Breed4Food is sterk gericht op de kwantitatieve genetica en genomica (thema's 1,2 en 3), disciplines die de kern vormen van de R&D-inspanningen van de Breed4Food partners. Het identificeren van eigenschappen die relevant zijn voor de fokkerij en het definiëren en meten van de daaraan verbonden fenotypes als voerefficiëntie, gezondheid en gedrag zijn vooral belegd in de Breed4Food onderzoeksthema's 4 en 5 en slaan een brug naar de toekomst van het fokkerij onderzoek. Daarbij wint het begrijpen en toepassen van de biologie achter deze eigenschappen en fenotypes terrein. De Breed4Food thema's 6 en 7 zijn diersoort-specifiek en ketengericht ingesteld. De projecten richten zich vooral op de bijdrage van fokkerij op de levensduur van dieren en de uniformiteit van koppels. Het is in de afgelopen periode lastig gebleken om gemeenschappelijke projecten te identificeren, die tot doel hebben om nieuwe innovatieve producten en diensten voor de ketens op deze thema's te ontwikkelen.

Het valoriseren van de Breed4Food innovaties zal leiden tot nieuwe generaties landbouwhuisdieren die gezond en robuust zijn, die efficiënt hun nutriënten omzetten in dierlijk eiwit met een verminderde uitstoot van broeikasgassen en mineralenverliers. Deze verbeteringen leiden tot een duurzame en maatschappelijk geaccepteerde productieketen, waarin fokkerij een wezenlijke bijdrage levert.

De bijlagen 1-4 (Annex 1-4) zijn, onder meer, ontleend aan de Breed4Food interne evaluatie die in het voorjaar van 2016 is afgerond. Deze evaluatie is georganiseerd door de Breed4Food partners als beslismoment voor de toekomst van Breed4Food. De Breed4Food partners hebben toen besloten om daadwerkelijk een plan voor de volgende fase van Breed4Food te gaan ontwikkelen, dit plan heeft de grondslag gevormd voor de verdere ontwikkeling en implementatie van het Breed4Food-programma voor de periode 1 januari 2017- 31 december 2017 en voor de periode 1 januari 2018- 31 december 2021.

<b>Aantal opgeleverde producten in 2013-2016</b>			
Wetenschappelijke artikelen	Rapporten	Artikelen in vakbladen	Inleidingen/ workshops
Meer dan 110 wetenschappelijke publicaties	Meer dan 5	3	Meer dan 120 presentaties en posters op congressen, bij studieclubs voor veehouders, bij industriebijeenkomsten

**Wetenschappelijke artikelen**

Breed4Food heeft inmiddels meer dan 110 peer-reviewed, wetenschappelijke artikelen opgeleverd waarvan twee in Nature Genetics (Bijlage 5)

**Artikelen in vakbladen**

Breed4Food wordt regelmatig vermeld en aangehaald in vakbladen en publicaties van de Breed4Food partners.

### **Rapporten**

Breed4Food richt zich vooral op fundamenteel en industrieel onderzoek. Resultaten worden vastgelegd in wetenschappelijke publicaties. Rapportages in andere vormen worden niet officieel gepubliceerd. Desondanks wanneer rapportage wordt gevraagd door derden wordt hierop, in de regel, ingegaan.

### **Inleidingen/ workshops**

Presentaties en posters in (inter-nationale) congressen/invited lectures en in werkgroepen. Vertegenwoordigers van de Breed4Food partners nemen regelmatig deel aan internationale fokkerijcongressen, zoals de EAAP, WCGALP en PAG. Tijdens deze meetings worden vaak en regelmatig posters gepresenteerd en (invited) lectures gegeven over onderzoek dat uitgevoerd is binnen de PPS Breed4Food.

### **Spin off's**



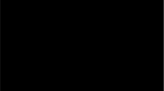






- MiXBLUP, een moderne zogenaamde Best Linear Unbiased Prediction software, en is ontwikkeld voor grote genetische evaluatie systemen.
- Breed4Food STW partnership programma Predicting Phenotypes (2014)
- Breed4Food call "project ideas" 2015
- Opzet en implementatie van het Wageningen High Performance Computing cluster Agronomics (2014)

## Bijlage 1: Titels van de producten of een link naar de producten op een openbare website

- Website: [www.Breed4Food.com](http://www.Breed4Food.com). Hier staan projectbeschrijvingen, gepubliceerde artikelen en nieuwsberichten, en er is de mogelijkheid om je in te schrijven voor de nieuwsbrief.
- Maandelijks zijn publieke Breed4Food bijeenkomsten georganiseerd, die uitgezonden zijn via WURtv:  
<http://wurtv.wur.nl/p2qplayer/Player.aspx?id=EazpN>

### 9 SEARCH RESULT FOR 'BREED4FOOD'

Show category

 <p><b>Breed4Food 8 december 2016</b> Dec 08, 2016</p> <p>7 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food 8 december 2016</b> Dec 08, 2016</p> <p>27 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food 3 november 2016</b> Nov 03, 2016</p> <p>35 views   Not Rated</p> <p><a href="#">more...</a></p>
 <p><b>Breed4Food 8 september 2016</b> Sep 08, 2016</p> <p>52 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food 7 juli 2016</b> Jul 07, 2016</p> <p>29 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food Thema 3 - 7 april 2016</b> Apr 07, 2016</p> <p>30 views   Not Rated</p> <p><a href="#">more...</a></p>
 <p><b>Breed4Food Thema 3 - 7 april 2016</b> Apr 07, 2016</p> <p>25 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food - On Land, at Sea and in the Air</b> Oct 01, 2015</p> <p>26 views   Not Rated</p> <p><a href="#">more...</a></p>	 <p><b>Breed4Food - Theme 3-ASG - 10 september 2015</b> Sep 10, 2015</p> <p>47 views   Not Rated</p> <p><a href="#">more...</a></p>

## **Bijlage 2 Deliverables of Breed4Food in relation to expected breakthroughs**

The general aims of the project plan became more specific in the B4F research breakthroughs defined to be realised in 2018:

1. Genomic breeding values have a reliability of at least 85%;
2. Genomics can be used as a sole carrier of breeding value information from crossbred field performance to a minimal size (non-pedigreed) nucleus breeding population with minimal generation interval;
3. Tools to improve sustainability and disease tolerance necessary to achieve performance in a world with reduced antibiotics use and more attention for welfare, human health and society;
4. 20,000 high health animals can be individually genotyped and pre-sorted and precision production handled based on individual genetic merit, some directed to high quality meat and others towards low cost production.

To evaluate the deliverable of the B4F research these breakthroughs have been discussed by the B4F partners in the context of the B4F achievements by the end of breed4food. The result of this discussion is elaborated upon in the next sections of this chapter:

### 1.1.1 Genomic breeding values have a reliability of at least 85%.

*Genetic trend depends on available genetic variation, on selection intensity ( $i$ ), generation interval ( $L$ ) and on reliability of the genetic evaluation. Genetic variation is a given (so far),  $i/L$  is a matter of investment in the breeding program. This leaves reliability as a trait to be improved with a maximum of 1, full and accurate knowledge of the genetic quality of an animal.*

Research within B4F sub program 'Exploiting DNA information' is carried out to combine pedigree, phenotypic and genomic data across lines. We tested denser genotyping and, although the results were not always promising, we gained more knowledge of when accuracy can increase for certain lines/individuals. In terms of the use of sequence data, within Breed4Food, we were able to impute all bulls in the Netherlands to full sequence, and GWAS and genomic predictions were developed and tested using such large datasets. The work on the use of sequence information in genomic prediction showed that simply including many SNP in prediction models does not increase reliability of prediction, and smarter ways are needed.

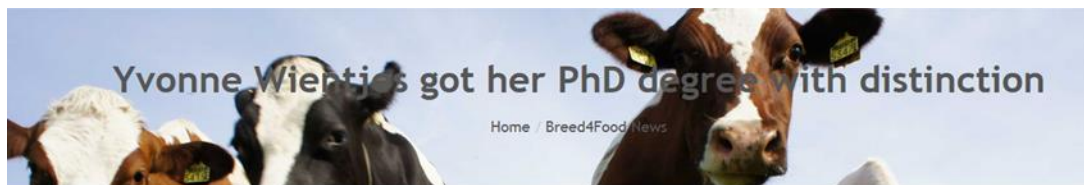
A second approach was to create genomic relation matrices and combine these with the classic pedigree with a continuously updated software package (CALC\_GRM). The resulting combined relationship matrix feeds into as MiXB LUP, creating "single step"-breeding values, where other approaches work with estimation of SNP effects in training populations. Regular updates of these tools are made available to keep up with the latest technology and insights. Within Hendrix Genetics (HG) the single-step procedure is implemented in layer breeding programs, within Topigs Norsvin (TN) in their pig breeding program. With the newly developed CALC\_GRM this method will

also allow the use of crossbred animals, which is challenging since population structure in general is more complicated and minor allele frequencies differ per purebred line.

Within Breed4Food we developed a vision on the next generation single-step methods and their requirements, considering that the number of available genotyped animals in the near future will exceed the capacity of the current methods. This method, first described by Misztal, is now being tested (also in collaboration with ICBF, who has >300,000 genotyped animals) and implemented in MiXBLUP. It is fascinating to experience that MiXBLUP can run more than 10 traits, with 10 million observations for the largest trait in a multi trait analysis combining data from different lines and crosses and using classic pedigree and genomic information (pig situation).

The High Performance Computing (HPC) facility strongly facilitates computational work. Pipelines, developed to filter raw sequence data and to run genome wide association analysis (GWAS), are used within the companies and in STW projects. This sequence data can be used as reference for imputation to full sequence from genotyped animals with 60k or 600k chips. This has improved GWAS studies considerably, which is key to start opening the black box, a strategic objective for most industrial partners. The research in this area, together with studying the effect of using full sequence on the accuracy of genomic prediction and GWAS, helps to come closer to achieving this example of the B4F breakthroughs. Progress is made in tracing back haplotypes of crossbreds to the line of origin which in future is promising in using client information for improving the parent lines. For both HG and TN, the HPC environment, the Breed4Food Bioinformatics Group (BIG), and the Technological Scouting Group are very relevant to High Performance Computing, scouting, implementation, operation and maintenance of IT hard- and software needed for their respective breeding programs.

The cum laude PhD of Yvonne Wientjes helps to understand the factors affecting the accuracy of genomic prediction, and also provided formulae for the prediction of the accuracy of genomic prediction. The failure of the sequence data to simply increase the accuracy, started the discussion on the design of the reference population, and biology inspired genomic prediction. Also, collaboration is sought with plant and human geneticists. In the STW partnership projects this line of research is now expanded by three PhD students, and talks by Hans Deatwyler, Mogens Lund and Theo Meuwissen during the Breed4Food seminar on 22 January 2016, showed that we are on top of this question scientifically, given the presentations of ongoing research in Melbourne, INRA, and Foulum.



Yvonne Wientjes, PhD candidate at the Animal Breeding and Genomics Centre, obtained her PhD degree with distinction (cum laude), based on her thesis 'Multi-population genomic prediction'. Yvonne did excellent research, under daily supervision of Dr. Mario Calus and promotor Prof. Roel Veerkamp. Her main conclusion is that genomic prediction can benefit from the use of another population, provided that the reference population is relatively small, both populations are closely related, and many individuals of the other population are being added.

## Recent news

Yvonne Wientjes got her PhD degree with distinction  
January 28, 2016

What are the possibilities to improve protein

**Quantification:** The goal of reliability of 85 % is still a nice goal, but typically most realistic for the cattle industry where very accurate “phenotypes” of bulls are being used. Current reliabilities of GEBVs of genomically tested animals in dairy cattle range from 35% (rate of maturity) to 80 % (milk yield). The reliability of the total index can be as high as 69%. The current goal of 85% seems not realistic for all traits by 2018. In cattle, the prediction is based on offspring of animals in the reference population and from the same families. Based on the current knowledge, more likely improvement of the accuracy can take place in the scenario where selection candidates are less related to the reference population or a different line or breed. This might be a further narrowing down of this breakthrough. Based on the insight of the current research, this is very hard to improve, given that most phenotypes are used. The goal is relevant, but probably 75% for total index is a more realistic (but still challenging) goal for 2018.

For pigs and poultry the goal of 85% is likely to be far too high because of the very different programs used compared to cattle breeding. However, we see very clearly an increase in accuracy when using genomic breeding values compared to traditional breeding values in cross validations. In poultry an improvement of 30-60% is seen. Implementation of the single-step genomic evaluations at TN generated an improvement of 37% in accuracy measured across 15 traits in pigs, using models implemented in CALC\_GRM and MiXBLUP. In the future reliabilities will further increase on the basis of the B4F sub program 'Exploiting DNA information'.

1.1.2 Genomics can be used as a sole carrier of breeding value information from crossbred field performance to a minimal size (non-pedigreed) nucleus breeding population with minimal generation interval;

*Until now breeding programs were dependent on collecting phenotypes and selecting animals in pure lines, mostly in high health high management systems; CCPS and Recurrent Selection systems tried to solve the genotype-environment (purebred-crossbred) interaction, but these approaches have severe limitations.*

Tracing back of haplotypes in crossbreds to the line of origin (without pedigree) helps to use field information in our selection programs. In the project Local Pork this 'line of origin' method is being developed. First tests in real crossbred data indicate that the method will indeed work pedigree free, and that it is able (already) to derive the line-of-origin for >90% of the alleles observed in



three-way crossbreds. This is an exciting and very promising result, and will allow to more closely model links between crossbreds and purebreds. Moreover, this type of work is not only relevant for poultry and pigs, but is also expected to improve current genetic evaluations in tropical dairy breeds such as Girolando pigs in Brazil.

In 2015 quite some work has been done on developing formulas to predict the accuracy of genomic selection, considering different numbers of animals genotyped in different environments or different populations, including crossbred versus purebred animals. These formulas, once properly validated in real data, will provide a valuable tool to the Breed4Food companies to advise them where money should be spent on genotyping efforts to obtain maximal returns in terms of genetic progress. The goal is approaching quietly, but rapidly.

A better understanding of the functional genetic variation underlying the observed phenotypic variation will further aid a more directed genomic selection and also contribute to the transfer of breeding value information from crossbred. For pigs progress in this area was achieved within the ERC funded project "SelSweep". The possibilities to use whole genome sequence information to identify such variants have been explored by Mirte Bosse, another Cum Laude PhD within Breed4Food.

1.1.3 Tools to improve sustainability and disease tolerance necessary to achieve performance in a world with reduced antibiotics use and more attention for welfare, human health and society

*Clients of the industrial partners are more and more large integrated organisations, aiming to follow the needs of the retailers and consumers. These integrated production companies combine genetics, nutrition, pharmaceutical interventions and management to realize their goals. Disease can be prevented by eradication, vaccination, medication or genetic selection. Welfare can be promoted by management and genetic selection for welfare traits. This goal is about optimization of all efforts, narrowed down to genetics.*

Within the subprogram 'Enabling new breeding goal traits', tools and understanding of sustainability and disease tolerance were studied. The projects "Nabs for Poultry" and "Social interactions" are of importance. The selection experiment for Nabs has delivered evidence for successful use of novel selection traits. The program "social interactions" was important to understand the genetics of direct and indirect effects. This helped building better models to be used in the layer program for selection on survival days. The follow-up STW project will deliver even more results because now whole pedigree of crossbred animals is reconstructed on basis of their 60k genotypes and parent genotypes. The data collected in this project is not only used in this project but is a basis for many other projects such as in the newly granted STW-partnership projects.

The impact of genotypic variation of two genetically diverse chicken lines on early life and microbial colonization of the gut and on functional development of intestinal tissue were investigated. The data indicate that the genetic background of chicken influences the early life microbial colonization

of gut as well as the functional development of intestinal mucosal tissue, probably also including the programming of the immune system.

As an extension of this experiment, Cobb has implemented an experimental sib-test challenge environment model that represents a potential expression of immune related phenotypes. This data will be used within the selection of pure lines as a potential trait for performance under immune challenge.

Important here is to come to cheap and fast genotyping. Other methods of genotyping (GBS=genotyping by sequencing) have been evaluated and tested by WUR in the "Technology scouting group". The results indicate that currently the available GBS approaches are not an alternative for assays based on SNP chips. The installation of a genotype/sequence database (BC platforms), should allow faster access to a high number of genotypes by the partners and in particular also by users with limited bioinformatics skills (Theme 2). Joint evaluation of genotyping options has been useful to significantly reduce cost of genotyping.

The new PPS Breed&Feed4Food (started May 2015) aims at the realization of methodological breakthroughs in the field of the interaction between the genotype, nutrients and intestinal microbiota. The program integrates research into the basic knowledge of preventive health and resource efficiency, which lead to commercial applications of genomic selection in combination with innovative feed strategies for the animal breeding and animal feed industry. It is anticipated that BF4F will improve collaboration between breeders and the feed industry. The approaches are new and challenging, results are anticipated in the upcoming years.

One of the deliverables within the 'Resource Efficiency' theme was the review of the main sustainability issues in livestock production from the perspective of animal breeding. After consulting Breed4Food partners and other stakeholders across the production chain and a desk study, a project team identified protein efficiency as the main trait of interest across species. Initially the analyses focused on protein efficiency in pigs, but this is extended to other species.

Maximizing genetic progress by combining phenotypic and genomic information has been shown by the implementation of a genomic evaluation for feed intake in dairy cattle. This breeding value now combines (1) the genomic predictions for feed intake based on a reference population of genotyped cows with individual feed intake records, and (2) milk and live weight as predictor traits of feed intake, which are based on the national population where milk production and milk content is recorded and where live weight is calculated based on nationally recorded conformation traits. The accuracy of the genomic prediction can probably be increased through international collaboration, as was shown by the consortium of the "global Dry Matter Initiative", where data on individual dry matter intake from 9 countries worldwide was combined. Breed4Food enabled ABGC and CRV to become key players in that international consortium. The breeding value has been implemented by CRV in December 2014 as part of the Better Life Efficiency index, that allows farmers to select better for efficient dairy cows.

To facilitate genetic selection for reduced methane production in dairy cattle, it is desirable to combine individual national datasets to produce a multi country database. Breed4Food enabled Wageningen UR to become a key player collected data and using different protocols and collaboration between scientists worldwide across a range of disciplines (network project Methagene).

In the **sub program 'Added value in the food chain'** sub-themes in uniformity, feet and legs and longevity, which are quite relevant for welfare and medication of animals. The B4F osteochondrosis project has come to an end, with a symposium on November 24th 2015. The sub-theme animal behaviour has shown, both in chickens and pigs, differences in behaviour between groups differing in merit for indirect genetic effects. Continuation of the behavioural part of the research within Theme 6 appears difficult, since it is not close enough to the core of B4F to be considered for funding. New tools and knowledge, however, might help to directly approach behaviour. The existing data set of seeking sociable swine is currently being genotyped and analysing metabolites in the blood is being considered.

In collaboration with VIT Germany new models are developed for the genetic evaluation of longevity in dairy cows. The aim is to implement these models in the genetic evaluation for the Netherlands & Flanders by CRV in 2017.

**1.1.4** 20,000 high health animals can be individually genotyped and pre-sorted and precision production handled based on individual genetic merit, some directed to high quality meat and others towards low cost production

*Genetics and genomics are mostly seen as tools for genetic improvement in pure lines. Knowledge of the genetic potential can help, however, in precision management. In dairy cattle this is a double goal, animals can be considered for selection and at the same time maximized in production in chickens and pigs a clearer difference between production and selection is observed.*

This is mainly work on uniformity in litter size, birth weight, and carcass weight, to identify lower problem families in pigs. This project starts from remarks and measurements of slaughter pigs (>50.000) trying to identify families with lower risks in terms of slaughter remarks and medication, linking this project to H2020 Feed-a-Gene, where first genomic relations of crossbred animals are linked to their pure bred animals and *then* predictions are made for new individuals. Although the approach is challenging, results are anticipated in the upcoming years. At present funding for projects on the theme 7 'New products and services for the production chain' is too low to be ambitious as there is little common ground for projects between the partners and is very relevant for TopigsNorsvin.

In Feed-a-Gene, breeding values for crossbred finishing pigs are used for sorting purposes, to maximize profit, given genetic potential and limitation. Part of the project is the use of mendelian

sampling where cost-price of genotyping becomes highly relevant. Goal is 5 euro genotyping, but even at that level probably not cost-efficient.

Linked to the previous, precision production is an interesting challenge which requires cost-effective large-scale genotyping methods and methods to predict phenotypes from these genotypes. Breed4Food initiatives have not yet contributed to reduced genotyping costs. However, the Breed4Food consortium has resulted in the development of high density SNP chips (Affymetrix 600K), thereby promoting the impact of large scale genotyping. For both pigs and turkey, the design of these HD SNP chips was coordinated by the Breed4Food Wageningen UR partner.

### Bijlage 3 Deliverables of Breed4Food in relation to project deliverables

For the PPS Breed4Food, deliverables were defined for each projects. Below these deliverables are benchmarked by the theme leaders (and their counterparts). For the benchmark ☺, ☹ or ☹ are used as an overall score about the deliverable.

Research Theme	Deliverables (Starting in 2013)	Benchmark
1	Optimal use of sequence information	1.1 Genotyping strategies to make optimal use of genomic information in breeding programs ☹ especially related to sequence information, imputation accuracy, and design reference population. In terms of genotyping there are very close links to 3.1
		1.2 sequenced strategic or founder animals and animals with particular attributes. ☹ In cattle access to >1700 bovine sequences through the 1000 bulls consortium, In cattle, pigs and poultry generated >900 whole genome sequences.
		1.3 SNPs, indels and CNV in populations related to particular phenotypic attributes. ☹ Remains difficult to find causal mutations. But some found in all species
		1.4 Tools, methods and strategies that capture the genomic data explosion to enable more accurate selection for (new) breeding goal traits. ☹ (see also 3.4) fruitful discussions on future direction of one-step approach leading to testing and even implementation of Fernando and Garrick model. Improvement in calc-GRM, mixblup and BSSVS.
		1.5 MiXBLUP 2.0 – Breeding value estimation software that allows for the incorporation of genomic information ☹ current one-step implemented and many other improvements
2	A common ICT infrastructure	2.1 A document that describes the requirements of breeding companies and possible architecture for joint bioinformatics and ICT infrastructure Joint bioinformatics and ICT infrastructure ☹ BC Platforms is installed and training is given to the partners. Not fully functioning yet due to hardware issues
		2.2 Operational plan, management plan and implementation plan for joint ICT and bioinformatics infrastructure ☹ High Performance Cluster is operational. Bio-informatics infrastructure is under review
3	(A)cross breed genomic selection	3.1 Models for across-breed and across-line genomic prediction, and insight in the accuracy of direct genomic breeding values of a multi-breed or multi-line reference population ☹ Multi-breed genomic prediction is proven to hardly increase accuracy. General equations are developed to predict the accuracy of, amongst others, multi-population genomic prediction.
		3.2 Optimal strategies and genomic prediction models to improve cross-bred performance. ☹ First studies have been performed to include crossbred performance in genomic prediction. A strategy is developed to derive line-origin of alleles in crossbreds.
		3.3 Insight in the importance of non-additive variance (in particular dominance and ☹ For some traits, dominance is important in terms of genetic variance and accuracy to predict phenotypes.

		imprinting) in crossbred performance, and optimal models to use this non-additive variance in breeding programs.	Levels of heterosis mainly depend on choice of lines, and much less so on mating within lines.
		3.4 Algorithms that enable using SNP data with very large dimensions in genomic prediction, either by efficiently estimating all effects simultaneously or by clever ways of pre-selecting SNP that are most informative	☺ (see 1.4)
		3.5 Insight in differences in genetic architecture of traits in different species, breeds, lines, and populations	
4	Improving resource efficiency	4.1 Evaluation of the effect of breeding on environmental efficiency using Life Cycle Analyses	☺ Studies on the effect of breeding in LCA have been performed for several species; laying hens, turkeys, dairy cows. Also when looking at the full chain, improvements by breeding contribute to sustainability.  Also an improvement of the LCA models by including land-use has been investigated intensively
		4.2 Identified and collected environmental phenotypes	☺ For cattle, the focus was on feed efficiency and methane emissions. Breeding value for feed intake in cattle released in Dec '14. International consortia are built and synergies are established with increased accuracies of predictions.  In pigs a focus was on Total Feed Efficiency, taking into account the full chain.
5	Disease resistance and intestinal health	5.1 Biomarkers of immune competence & natural antibodies, its impact on robustness and other (production) traits	☺ Study on the effect of NAb levels on health and performance of poultry & Weerbaar Vee & PRRS SNP's to improve health by genomic selection implementation
		5.2 Insight into immune development and immune competence, definition of associated traits resulting in candidate or validated biomarkers of immune competence and development	☺ Several studies in poultry and pigs performed to explore the functioning of immune competence systems in the gut.
		5.3 Insights into the biological variation of immune competence within / between breeding line(s)	☺ Early-life gut microbial colonization and intestinal development differences in 2 broiler lines
		5.4 Technology to evaluate the predictive value of biomarkers for robustness, and tools to select for improved robustness of animals	☹ No tools available yet
		5.5 Defined data requirements for robustness traits, including specifications for challenge trials	☹ Defined data requirement; Not yet started ☺ Specifications for challenge trails are defined and used in broiler

6	Data from the production chain for sustainable animal production	6.1	Methods to record and understand social interactions, insight in genomic architecture of social interactions	experiments (2015) ☹
		6.2	Improved statistical model for longevity in dairy cattle to combining phenotypic and genomic information;  tools to reduce OC in pigs and improve longevity	☺ PhD student is now validating new model for longevity of dairy cattle and planned to implement in the Netherlands in 2017/2018
		6.3	Models to identify genomic regions affecting uniformity and for prediction of genome-wide breeding values; improved quantitative genetic models for analysis of uniformity	☺
		6.4	Prototype for a breeding program for non-cage layers	☹ Not started
7	Differentiation and adding value in the production chain	7.1	An overview of opportunities and risk profiles of application of tracking, tracing and securing as a breeding company service product	☹ Not started
		7.2	Inventory of potential genomic products not being conventional increased genetic trend	☺ Genomic selection for boar taint compounds
		7.3	Two examples of new products (meat or milk) based on genetic extremes	☹ Not started
		7.4	New business products/solutions at the end of the pre-competitive phase	☹ Not started

## Bijlage 4 Questionnaire among stakeholders

In 2015 an internal questionnaire was sent to Breed4Food stakeholders. The evaluations of the Breed4Food partners evaluations are averaged in the table below, where most of the partners had an internal evaluation by several persons to come to one average score.

<b>A. Quality Expertise and Research</b>	
<b>How do you rate?</b>	<b>Average</b>
1. The overall quality of the performed research?	7,8
2. The expertise of the research team(s)?	8,0
3. The awareness of the project team(s) of developments at the science and technology level?	7,7
4. The quality of the project proposals/ideas/design of experiments?	7,8
<b>B. Operational</b>	
1. The organisation of the B4F consortium?	7,4
2. The internal communication in the B4F consortium?	7,1
3. The external communication of the B4F consortium?	6,4
4. The Breed4Food meetings?	7,4
5. Identification and solving of bottlenecks?	6,9
6. Whether deliverables are met in time and in budget?	7,4
<b>C. Culture</b>	
1. The transparency and openness between partners?	7,9
2. The taking of initiatives of the partners?	7,1
3. The involvedness of the partners?	7,2
4. The responsibility of team members/partners?	7,5
5. Your pride to be part of B4F?	7,9
<b>D. Overall opinion</b>	
1. The scientific relevance of the performed research?	8
2. The business relevance (in terms of R&D) of the research?	8
3. The societal relevance of the research?	7,1
4. Your overall rating of the Breed4Food consortium?	7,7

These Scores were discussed in a combined board and working group meeting leading to the following Tips & Tops for the breed4food consortium:

### A Quality expertise and research

-HPC helps innovation and **decreases risks of investment**

-Science aspects of B4F very much appreciated

-Time to move to application in terms of traits

-**Ensure continuity in innovation**

-More focus on results/deliverables

-More involvement of University staff

### B Operational

-**Linking pin** between stakeholders

-Positive in **communication with clients**

-Organisation structure is OK and works, working group central to activities, works well

-**Be ambitious in communication:** make a bid to organise WCGALP



**-Business far away from B4F**

-Attention to B4F Thursdays is decreasing.

-**External communication to be improved**, B4F too much seen as owned by partners

-Improve financial planning/increase financial transparency

-**What is B4F, and not?**

-**Relationship with Dept. Economics Affairs (Agriculture)/TKI AF to be improved**

C Culture

-University too much influenced by "dept. Agriculture" thinking

-**Distance to business too big**

-**B4F restricted to people involved**, not broadly embedded within B4F partner organisations

-**Trust** between partners is clear and visible

-Too many changes in B4F board

-Success of projects and theme's very dependent on people

D Overall opinion

-**Efficiency gains** by joint research

-B4F **no standard PPS**, real consortium that builds on each expertise etc

-B4F is an excellent **platform** to stay abreast of new developments

-Important to **balance science and application**

-B4F close to application, **less attention to fundamental research**

-More emphasis within B4F on **strategic research** (medium/long term),

-**Critical mass at Wageningen** is crucial, sets stage to future, focus!

-Financial expectations as stated at start not realised

**Bijlage 5: References: refereed publications Breed4Food program.**

[1-114]

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