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REVIEW

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Genomic selection in pigs: state of the art and perspectives

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ABSTRACT

Genomic selection, that is based on the prediction of the breeding value (the genomic breeding value or GEBV) of the animals considering genomic information, is changing breeding strategies and approaches in dairy cattle and in several other livestock species. The starting points for the application of genomic selection in pigs were the development of a first commercial single-nucleotide polymorphism panel for high throughput genotyping, the sequencing of the pig genome and the application of statistical and methodological approaches first developed in dairy cattle and then adapted to the peculiarities of the pig breeding industry. In this review, we focused on the specific applications of the genomic selection in pigs, considering its limits, its advantages and its perspectives throughout an analysis of the simulation studies and field applications already available targeting many different traits (with high and low heritability). In addition, we presented an overview of the problems related to the implementation of genomic selection in crossbred and multi-breed pig populations and the potential solutions taking into account the economic aspects that should be faced in including genomic selection in pig breeding programmes.

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Introduction

Breeding and crossbreeding strategies based on quantitative genetics approaches have largely driven genetic progress in pigs during the last 40–50 years. Genetic progress increased its pace starting from the late 1980s of the last century with the introduction of BLUP Animal Models in the evaluation of boars and sows in selected nuclei (Figure 1a). Before then, the peculiarities of pig population structure and the limited use of artificial insemination had not prevented the use of progeny testing and BLUP technology based on Sire Models. In addition to the introduction of BLUP Animal Models, common to most species, pigs were the first livestock species to benefit from the introduction of molecular genetics in breeding programmes. The development of a DNA test to identify carries of the pale, soft and exudative (PSE) meat defect, causing also the porcine stress syndrome (PSS) was based on the analysis of the ryanodine receptor 1 (*RYR1*) c.1843C > T polymorphism (Fujii et al. 1991). This made it possible to manage or eliminate this mutation in most pig populations. In addition, a large number of other studies that identified candidate genes and quantitative trait loci (QTL) have provided a long list of other potentially interesting DNA markers associated with production traits, most of them in linkage disequilibrium with the unknown causative mutation(s) in the investigated populations (Ernst & Steibel 2013). Apart from a few interesting examples, in general, these markers explain a small fraction of the genetic variability of economically important traits and their effects should be verified in the populations that were not used for the primary discovery studies. For these reasons, most of these markers have not been fully exploited by the pig breeding industry mainly due to practical difficulties in integrating this information through the development of specific marker-assisted selection programmes for each potentially useful polymorphism.

These problems could be overcome by the introduction of the concept of genomic selection that can be considered an enhanced version of marker or gene-assisted selection (Dekkers & Hospital 2002). Genomic selection was first proposed by Meuwissen et al. (2001) to predict the genetic value of the animals based on the genotype at thousands of single-nucleotide polymorphisms (SNPs) covering the whole genome. When the concept of genomic selection was first defined, technologies and information needed to develop this

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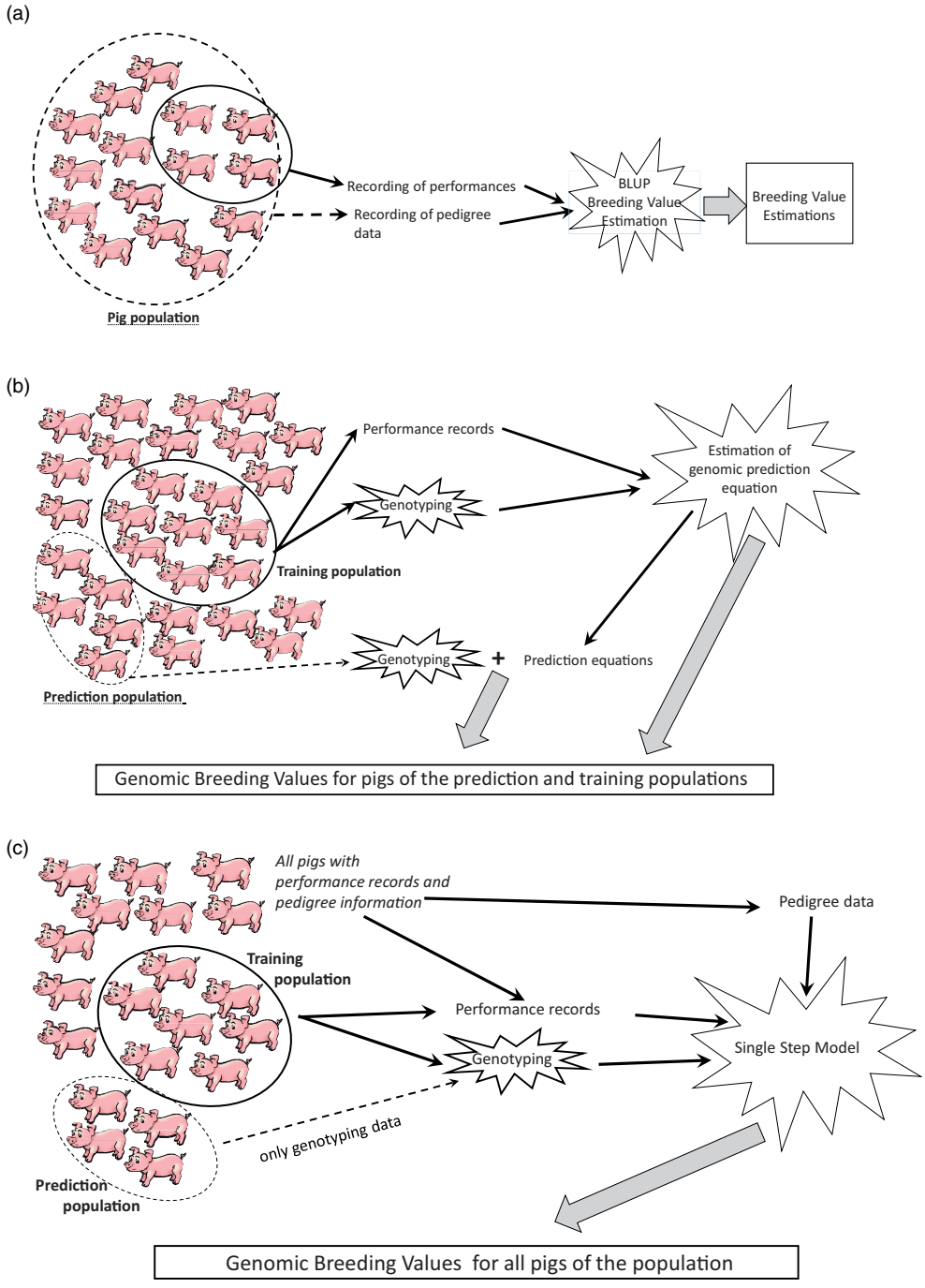

Figure 1. Pigs and data needed to estimate traditional breeding values (a), genomic breeding values (b), and genomic breeding values by using a single-step model strategy (c).

idea were not available yet. Three main subsequent advances have made it possible to implement genomic selection in the most relevant livestock species: i) the sequencing of their genome and the identification of thousands or even millions of polymorphisms (mainly SNPs); ii) the development of high throughput genotyping technologies that can genotype thousands of SNPs spread all over the genome in a cost-effective manner and iii) the development of statistical methods to estimate the allelic effects of thousands of markers in a data sets of limited number of animals.

These advances prompted the first practical and widespread implementation of genomic selection in 2009 with the evaluation of dairy cattle in the USA (VanRaden et al. 2009). Since then, most of dairy cattle organisations in the world have developed genomic selection programmes. Moreover genomic selection was also proposed and applied in several other

livestock species: beef cattle (Pollak et al. 2012), sheep (Duchemin et al. 2012), poultry (Preisinger 2012) and pigs (Ibáñez-Escriche et al. 2014). This review will focus on the state of the art and perspectives of the genomic selection in the pig breeding industry starting from the definition of the basic and general concepts of genomic selection and completing the overview with specific applications in pigs.

Principles of genomic selection

Genomic selection is based on the prediction of the breeding value (the genomic breeding value or GEBV) of each individual by summing up all SNP allele effects over the whole genome. Marker effects are estimated as a regression of the phenotype on the genotype in training data sets, i.e. the animals in the population with both phenotypic and genotypic (or genomic) information, and these estimates are used to predict GEBV for all individuals with genomic data without any phenotypic information (prediction population). Therefore, these animals are selected based on their genotype at thousands of SNPs, covering the whole genome, without the need of recording phenotype information on all animals under evaluation (Figure 1b).

Depending on prior distributions considered in SNP effects estimation, different procedures were already proposed by Meuwissen et al. (2001), including GBLUP, Bayes-A and Bayes-B, and later on additional Bayesian methods (e.g. Bayes Cπ, Bayesian-Lasso and others) were proposed by other authors (e.g. Yi & Xu 2008; Calus 2009; Gianola et al. 2009; Habier et al. 2011). The GBLUP method assumes that each SNP explains the same amount of variance with a similar approach to the infinitesimal model of classical quantitative genetics. The other methods fit different proportions of variance explained by different SNPs assuming that there are many loci across the genome with no genetic variance (VanRaden 2008; Yi & Xu 2008; de los Campos et al. 2009).

With a simulation study, VanRaden (2008) demonstrated the equivalence in genomic prediction computation between the GBLUP model that first estimates individual allelic effects and then sums those pertinent to each animal (as in Meuwissen et al. 2001) and the inclusion of genomic relationship matrix, in place of the traditional additive matrix, in the mixed model equations.

Other authors (Legarra et al. 2009; Mistzal et al. 2009; Aguilar et al. 2010) proposed an alternative approach, known as single-step method. This method incorporates marker information into the traditional pedigree models accounting also for all phenotypic and pedigree information available, including pedigree and performance records collected from non-genotyped individuals (Figure 1c).

According to the classical concepts of quantitative genetics, the introduction of genomic selection is expected to increase the genetic progress (ΔG) following the general formula defined by Falconer (1989):

$$\Delta G = \left(i * r * \sigma_g\right)/L$$

where i is the selection intensity, r is the accuracy, σ_g is the genetic variability and L is the generation interval.

The two terms that would be directly affected by the introduction of genomic selection are the generation interval (L) and the accuracy (r) of the predictions. In dairy cattle, a strong advantage derived by the genomic selection is the possibility to predict reliable evaluations of young bulls, well before the time needed to collect milk recording data from their daughters reducing, in turn, the generation interval (Schaeffer 2006). In pigs, the early use of young animals as reproducers, just after their puberty, might determine a very short generation interval (<2 years), with a rapid turnover of generations (Tribout et al. 2011). In this species, improvements by acting on this parameter are limited by the short interval that the current breeding plans can already reach and for practical difficulties in further reducing generation interval. Therefore, the largest impact of genomic selection in pig breeding can derive from the increased accuracy of genetic predictions and for the possibility to predict maternal traits in boars.

In the current pig genetic evaluations, accuracy is usually low, especially for traits with low heritability, like reproduction traits (e.g. fertility, litter size and piglets mortality), for traits recorded in a limited number of individuals (e.g. sex-limited traits and disease resistance), for traits recorded very late in life (e.g. longevity) or after death on the same animals or on carcasses of relatives, like meat quality parameters (i.e. Stock & Reents 2013; Van Eenennaam et al. 2014). On the other hand, accuracy of GEBV is influenced by other factors defined in the genomic selection approach. The precision of the estimation of the prediction equations is affected by the size of the training population on which the marker effects are estimated and its closeness to the prediction population (Habier et al. 2010; Akanno et al. 2014). A drop in accuracy due to loss of pedigree relationships is expected after the first generation by limiting the value of genomic predictions and in close breeding population a regular re-training is

Table 1. Different genomic data useful in genomic selection programmes.

Technological classification	Certainty in genotype calls	Proportion of the genome represented	Structure of missed genotype data
High coverage genome sequence data	Highly accurate genotype calls	High	No missed information
Low coverage genome sequence data	Reduced accuracy of genotype calls	Low or intermediate (depending on the coverage and costs of sequence data)	Random (missed loci, homozygotes called accurately, heterozygous called less accurately)
High-density SNP genotypes	Highly accurate genotype calls	Intermediate	Rigid structure (the same set of markers on each individual)
Low-density SNP genotypes	Highly accurate genotype calls	Low	Rigid structure (the same set of markers on each individual)
Pedigree data, inferred genotypes	Depends on imputation strategies and/or accuracy	None	Depends on imputation strategies and/or accuracies

recommended (Wolc et al. 2011). Meuwissen (2009) calculated the expected accuracy of GEBV for reference populations of different size and for different heritability levels. This simulation also reported, for example, that for traits with low heritability, an accuracy of 0.30 can be obtained with quite a large reference population (2000–5000 animals). In contrast, according to the simulation of Akanno et al. (2014), if resources are limited, also smaller sizes of the training population (of at least 1000 individuals) were considered appropriated but with multi-generational training populations and the re-estimation of marker effects after two generations of selection. Considering these aspects, genomic selection is expected to improve ΔG in pig populations, but the level of this improvement is strongly influenced by the population structure, by the trait (and its heritability) and by the phenotyping and genotyping strategies that can directly affect the accuracy of GEBV predictions.

Genomic selection in pig populations

The different types of genomic data relevant for applications in genomic selection programmes are summarised in Table 1. These types of data can be classified according to technological aspects related to their production, certainty in genotype calls, proportion of the genome represented and structure of the missing genotype data. Genotyping data can be ascertained to sequence data at high or low coverage, and high-density (HD) or low-density (LD) SNP panels. Sequencing data are costly (i.e. in the order of a thousand of euro) but might provide information for a very high proportion of the genome. Sequencing is performed by cutting the genome into small pieces, sequencing these pieces (i.e. determine the sequence of the nucleotides along these pieces: generate reads), and then reassemble reads by finding and analysing overlapping sequences, or identical DNA sequences at either ends of two or more different reads. Based on the number and the size of the produced reads, sequencing can be at high or low genome coverage and have proportional costs. Low genome coverage sequencing data have reduced accuracy on genotype calls as the sequencing covers a fraction or the whole genome only a few times. If we indicate with 'X' the average number of reads per each nucleotide of the reference genome, when we have a coverage of 1X, on average, all bases of the genome of an individual are covered by reads just once whereas with a coverage of 10× all nucleotides of the genome of an individual are read 10 times, on average.

At present, SNP genotyping panels are much cheaper solutions than sequencing. SNP chips were developed to include HD, medium density (MD) or LD representations of markers across the genome (Table 2). Differently from sequencing data, SNP genotyping panels have a high reliability of the called genotype. Nevertheless they have a rigid structure because they can analyse only what is already predetermined by the design of the chip, they miss a lot of potentially important information, and may present ascertainment bias: they are often selected to have intermediate allele frequencies to capture maximum variance and genetic diversity between and within breeds and lines, they may not have equal density on all chromosomes, and current arrays do not fully track structural genetic variation, e.g. insertions, deletions and copy number variants (Daetwyler et al. 2013).

The starting points for the application of genomic selection in pigs were the development of a first commercial SNP panel for high throughput genotyping (Ramos et al. 2009) and the sequencing of the pig genome (Groenen et al. 2012). This first SNP panel commercially available from Illumina (PorcineSNP60 BeadChip v2, at present available in the version 2; Illumina, San Diego, CA) contains about 60K SNPs that cover all autosomal and X chromosomes (Ramos et al. 2009; Table 2). In addition to this SNP panel, LD SNP panels has been simulated and proposed in several studies with the purpose of reducing genotyping costs that, at present, is one of the main obstacles reducing

Table 2. Commercially available SNP genotyping panels for the pig.

Chip name	No. of SNPs	Company	Technology	Other information
PorcineSNP60 BeadChip v2 array	61,565	Illumina	Illumina Infinium chemistry	This chip substitutes version 1 that included 62,163 SNPs
GeneSeek Genomic Profiler for Porcine LD (GGP-Porcine LD)	10,241	GeneSeek/Neogen[a]	Illumina Infinium chemistry	Possibility to customise including SNPs associated with production and reproduction traits and patented
GeneSeek Genomic Profiler for Porcine HD (GGP-Porcine HD)	68,528	GeneSeek/Neogen[a]	Illumina Infinium chemistry	Including about 43,000 most informative SNPs of the PorcineSNP60 v2 BeadChip array and additional 25,000 SNPs covering previous gaps and telomeres
Axiom® Genome-Wide Pig genotyping Array (high-density panel)	~650,000	Affymetrix	Axiom assay	Not yet commercially available (including the PorcineSNP60 v2 BeadChip SNPs)

[a]Patented or specific markers can be included in the chip. The list of markers that are routinely included are in the following genes or loci: *MC4R*, *HMGA*, *CCKAR*, *RN* (and other markers in the *PRKAG3* gene), *CAST*, dystrophin, *HAL* (*RYR1*), *ESR*, resistance markers to *E. coli*/F4 ab/ac), erythropoietin receptor; SNP WUR10000125 that has an impact on PRRS tolerance; commonly utilised SNPs for parentage at USDA.

the practical application of genomic selection in pigs (Habier et al. 2009; Dekkers et al. 2011; Wellmann et al. 2013). A commercial LD SNP chip was developed by GeneSeek/Neogen (Lincoln, NE) to face the need of the market (GeneSeek/Neogen GPP-Porcine LD Illumina Bead Chip panel). GeneSeek/Neogen prepared also a higher density SNP panel including about 70K SNPs. A HD SNP panel, containing ~650,000 SNPs and including all SNPs of the Illumina PorcineSNP60 BeadChip v2 array, has been recently released for testing by Affymetrix (Santa Clara, CA) that is also planning to release a LD panel. Features of all commercial SNP panels thus far developed in pigs are reported in Table 2. Batches of these panels can be manufactured including private SNPs that can be read only by the owner of this information or including patented markers and SNPs in a few genes associated with production traits (Table 2).

Other studies simulated the lower number of SNPs needed according to different scenarios of genotyping and imputation with higher density SNP chips to obtain sufficient predicting ability of GEBV (Wellmann et al. 2013; Stratz et al. 2014; Xiang et al. 2015). For example, based on simulations, a panel size of less than 1000 markers spread all over the pig genome (with the lower limit of 384 markers), if imputed to a higher density panel genotyped in at least one of the parents, could be used to obtain unbiased estimates of accuracy of genomic breeding values (Wellmann et al. 2013). This means that other LD and proprietary SNP panels may be developed in the future to reduce the genotyping costs.

The marker density to be used is directly determined by the extent of linkage disequilibrium captured by markers for the target trait across the genome. In case of high levels of linkage disequilibrium a low number of markers are needed to capture and explain the genetic variation in the tested population. The reliability of GEBV prediction depends on the level of linkage disequilibrium between markers and QTL in both within family or population-wise scenarios (Hayes et al. 2009). Increasing the density of markers would increase the level of linkage disequilibrium between markers and QTL that, in turn, would increase the accuracy of GEBV (Brito et al. 2011) till a maximum of accuracy that depend on the genetic architecture of the traits. The level of linkage disequilibrium is larger in livestock populations than in humans. This is due to the strong and recent selection and to the small effective population size in livestock (Khatkar et al. 2008). Several studies reported information on the extent of linkage disequilibrium in different pig populations (Table 3). In general, it appears that in pigs the level of linkage disequilibrium is larger than in cattle populations (Veroneze et al. 2013). Analyses, based on the use of the 60K Illumina chip, indicated that the averaged linkage disequilibrium levels (r^2) between two adjacent SNPs might range from 0.36 to 0.46 in different pig populations (Uimari & Tapio 2011; Badke et al. 2012; Veroneze et al. 2013). Actually this value exceeds the threshold of 0.2 that was simulated by Meuwissen et al. (2001) and that is considered the minimum level to reach an accuracy of GEBV prediction of about 0.85 that could make a genomic selection programme feasible.

Several works simulated genomic selection in pigs by using different assumptions, mimicking real population structures and data. Simulation studies made it possible to predict and evaluate the potential problems, advantages and drawbacks of genomic selection in different scenarios.

In particular, in simulation studies of pig breeding programmes in developing countries (Akanno et al. 2013, 2014), including indigenous and exotic, purebred and crossbred populations, the accuracy of GEBV decreased in the unselected indigenous population at

Table 3. Examples of linkage disequilibrium data reported by different studies in various pig breeds or lines.

References	Genotyped markers	Linkage disequilibrium between adjacent blocks/SNPs	Breeds/lines and no. of pigs
Nsengimana et al. (2004)	15 microsatellites on 2 chromosomes (4 and 7)	$D' = 0.21–0.46$	2872 pigs of 5 commercial pure lines
Harmegnes et al. (2007)	29 (SSC15) and 5 (SSC2) microsatellites	$r^2 = 0.15–0.50$	Two commercial populations (33 and 44 pigs)
Du et al. (2007)	Pairs of SNPs approximately 3 centiMorgan (cM) apart, 4500 SNPs on 18 autosomes	$r^2 = 0.1$ (pairwise linkage disequilibrium)	4300 pigs from 6 pure lines (600–750 per line): Pietrain, Duroc, Landrace and Large White-based lines
Huisman et al. (2010)	Illumina PorcineSNP60 beadchip: 3762 SNPs on chromosome 1	r^2 between 0.26 and 0.01 depending on distance in Mb	In 522 pigs of two lines derived from Pietrain and Landrace breeds
Uimari and Tapio (2011)	Illumina PorcineSNP60 beadchip	$r^2 = 0.43$ (Finnish Landrace), 0.46 (Finnish Yorkshire)	32 Finnish Yorkshire and 86 Finnish Landrace
Badke et al. (2012)	Illumina PorcineSNP60 beadchip	$r^2 = 0.46$ (Duroc), 0.44 (Hampshire), 0.36 (Landrace), 0.39 (Yorkshire)	351 pig from US breeds (Duroc, Hampshire, Landrace and Yorkshire)
Veroneze et al. (2013)	Illumina PorcineSNP60 beadchip: 62,163 markers on haplotypes blocks (number of blocks from 2640–3037)	$r^2 = 0.39–0.45$	3616 pigs from 6 commercial lines (from 169 to 1307 per line)
Sahana et al. (2013)	Illumina PorcineSNP60 beadchip: about 1420 SNPs on chromosome 14	$r^2 = 0.56$ between adjacent markers and 0.30 at 1000 kb distance.	3071 Duroc pig data (born from 1998 tp 2010)

a faster rate over generations, for the low initial linkage disequilibrium level and for the subsequent breakdown of the available linkage disequilibrium by recombination. In contrast, crossbred lines exploited the new linkage disequilibrium and maintained the accuracy of GEBV over generations (Akanno et al. 2013, 2014).

Since the availability of the 60K SNP Illumina panel, several breeding organisations and selection centres have started to genotype their populations on a regular basis generating data to build training populations with various strategies including the joint use of LD and HD panels in various groups of animals. Both the size and the pedigree closeness of the training sets (i.e. pigs having both genotypic and phenotypic data) to the prediction animals (i.e. pigs without phenotype records) directly influence the accuracy of GEBV (Habier et al. 2010) and the perspectives of adopting genomic selection in different population structures (Samorè et al. 2015). Nevertheless, the implementation of genomic selection on a routine level in pig populations has to face several practical logistic challenges (Figure 2) that include the collection of samples at a very early age (i.e. within few hours from birth), and the identification of the animals, the storage and transportation of the biological samples for genotyping (Ibáñez-Escriche et al. 2014).

Tables 4–6 report a list of published works describing studies on genomic selection in different pig populations, the characteristics of the field or simulated data and the main results. Several traits have been already targeted in genomic selection strategies in pigs, including production traits (i.e. loin depth, back fat thickness, carcass weight, average daily gain; e.g. Tribout et al. 2012; Akanno et al. 2014; Jiao et al. 2014), longevity aspects (i.e. leg score, health trait: e.g. Boddicker et al. 2014), meat quality parameters (i.e. pH, marbling, intramuscular fat: e.g. Miar et al. 2014) and maternal traits (i.e. total number of born, stillborn, preweaning mortality, piglet survival: e.g. Cleveland et al. 2010; Forni et al. 2011; Lillehammer et al. 2011; Tusell et al. 2013) with various results depending on the trait involved as well as on the adopted selection schemes and phenotyping strategies. This means that, before implementing genomic selection in pigs, particular attention should be paid to the population structure and the traits included in the evaluation. It is also clear that when genomic selection is applied in a population, all traits considered by the recording systems of that population would be included in the new evaluation process and optimisation of the whole genomic evaluation for all parameters would be sometimes difficult due to their different characteristics. Difficulties arise with multiple-trait genomic analyses, although application with single-step procedures was reported in literature in other species for a large number of traits (Tsuruta et al. 2011).

Maternal, performance and other traits in pig genomic selection

Maternal and performance traits are the two main groups of traits considered in pig genomic selection. Reproduction and functional traits in maternal lines are relevant in pig breeding for the commercial competitiveness of maternal genetic lines that should also guarantee efficient and sustainable productions of hog farms. However, due to the general low heritability, genetic progress for these traits is very slow and traditional BLUP predictions give a strong weight to records of relatives and a few emphases are assigned

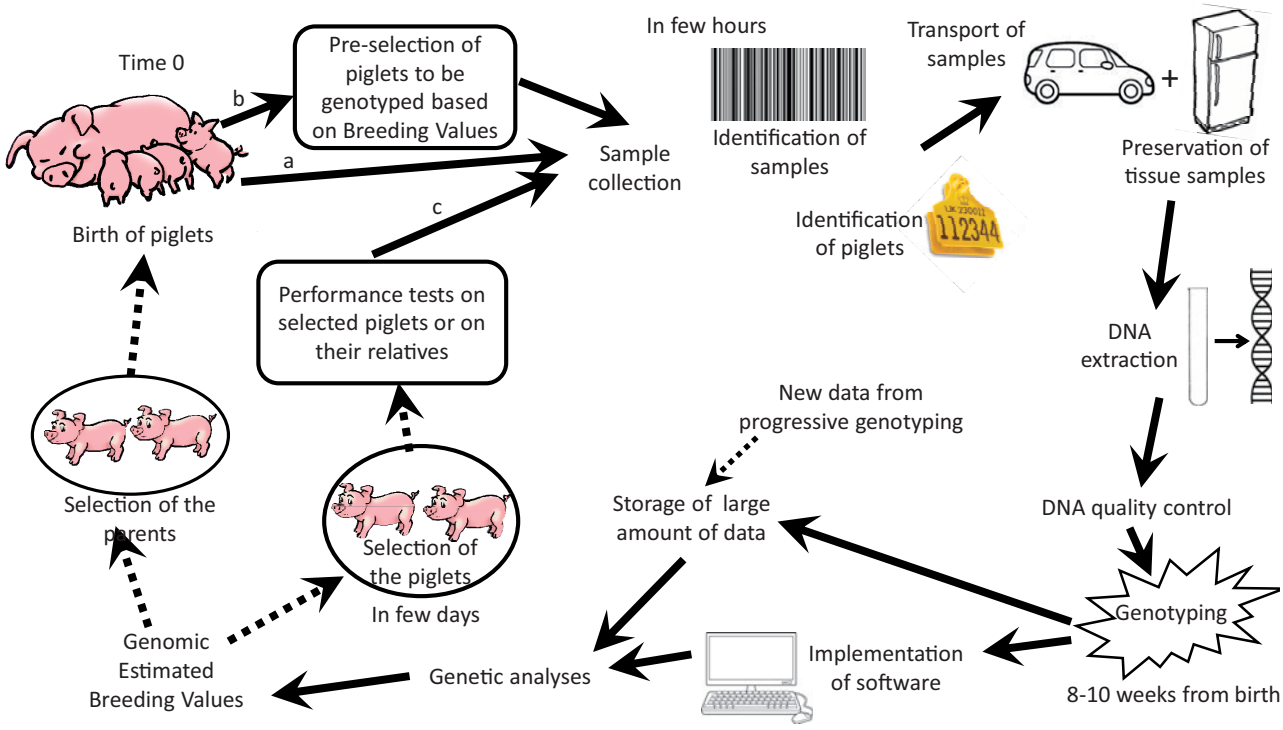

Figure 2. Practical aspects of the implementation of genomic selection programmes in pigs: (1) collection of samples on (a) just born piglets, (b) preselected piglets or (c) pigs in the performance test station; (2) identification of piglets and samples with bar coding systems; (3) transport and preservation of samples; (4) laboratory analyses including DNA extraction and quality controls; (5) genotyping; (6) storage of the large amount of genomic data envisaging the increasing amount of data derived by the continuous genotyping in the population during the time; (7) genomic analyses for genomic breeding value calculations; (8) use of genomic breeding value estimations for the selection of either parents and/or pigs for performance testing of the selected piglets or of their parents.

to the individual record by producing similar EBV among relatives and a preference to the selection of pedigree-related animals. Genomic selection, in contrast, can obtain a better exploitation of the genetic variation within families that can produce a more accurate selection of the candidates and a reduction of inbreeding level in the investigated populations (Sonesson et al. 2005), and it allows the accurate estimation of breeding values for selection candidates that have no phenotypic records (Meuwissen et al. 2001). Maternal traits include ovulation rate, embryonic survival, various measures of litter size (e.g. total number of piglets born, number of piglets born alive, number of weaned piglets, number of fully formed pigs, stillborn, pre-weaning mortality, piglet survival) and piglet birth weight. A list of genomic selection studies in pigs for maternal traits, on simulated or real data, is reported in Table 4. Summarising, genomic predictions usually outperform pedigree-based predictions for litter size and other maternal traits in pigs although the specificities of population structures, available datasets (i.e. training population size), as well as the model of analysis and the genomic relationships existing in each population can affect and limit the advantages of the genomic selection in different scenarios.

In contrast with maternal traits, performance and carcass traits present moderate to high heritability and specific programmes have been established in pigs to collect relevant phenotypes (on the same alive animals or after their slaughtering or on relatives like in the sib testing programmes). Genomic selection is advantageous for performance traits as phenotypic information can be leveraged across all selection candidates and, potentially, generations (e.g. Stock & Reents 2013) and the collection of phenotypic data on a routine basis might be reduced with large flexibility possible concerning the pigs that should be phenotyped (Dekkers 2010). Nevertheless, as the accuracy of GEBV might decline rapidly over generations a continuous collection of phenotypes over generations, especially in animals related to selection candidates, is always needed to update the genomic selection prediction models (Muir 2007; Sonesson & Meuwissen 2009; Dekkers 2010). Table 5 reports major results on performance and carcass traits in pig genomic selection.

Examples of the implementation of the genomic selection in pigs in traits different than production and maternal ones are reported in Table 6. Similarly, to what has been already envisaged in other species, genomic selection would help in selecting pig disease

Table 4. Genomic selection studies on maternal traits in pigs.

	Traits	Data	Results as comparison with traditional BLUP or according to the aim of the paper
Cleveland et al. (2010)	DBV on number of piglet born ($h^2 = 0.16$) and percentage of stillborn ($h^2 = 0.16$)	Field data on PIC Landrace-based population of 3000 Landrace genotyped pigs (males and females) with SNP60 BeadChip, 2700 training pigs and 300 validation pigs	Mean accuracies (mean correlation between the GEBV calculated with a Bayes-A model and traditional BLUP EBV) in the validation sets of 0.82 and 0.83, but the accuracy decreased to 0.33–0.65 with age when a cross validation was performed mimicking the real selection (the oldest candidates in the training sets and pigs born on the last two years as the validation population).
Lillehammer et al. (2011)	Maternal trait measured after the first litter ($h^2 = 0.10$)	Simulation of pure bred line (300 females and 150 males) with 18 pairs of 100 cM chromosomes: in total 1800 QTL and 9000 SNP markers	The genetic gain increased by 23–91% and the rate of inbreeding was reduced with a GBLUP model if compared with traditional selection. Results depend on which and how many animals are genotyped. Genotyping dams, in addition to male candidates is more advantageous than genotyping more males.
Forni et al. (2011)	Litter size (total number born per litter)	Field data with 1919 sows and 70 sires genotyped with SNP60 BeadChip. Records on 338,346 sows	Average accuracies between 0.28 and 0.49 with single-step predictions versus 0.22 of traditional BLUP predictions for sows, no differences in sires.
Cleveland et al. (2012)	Phenotypes and de-regressed proofs of five traits (h^2 from 0.07 to 0.62)	Field data on 3534 pigs genotyped with SNP60 BeadChip from a single PIC nucleus pig line and pedigree for 6473 pigs	Comparison of alternative methods for genomic prediction (Bayes-B and single-step models). GEBV accuracy increased with the increased trait heritability and increased relationship between training and validation populations. Generally Bayes-B using de-regressed EBV outperform the use of other approaches.
Jafarikia et al. (2012)	Number of piglets born per litter	Field data on 542 genotyped pigs with the SNP60 BeadChip	Increased of 20% reliabilities of GEBV prediction compared to the parent average of official evaluations.
Akanno et al. (2013)	Number of born alive ($h^2 = 0.08$), average daily gain ($h^2 = 0.28$), back fat thickness ($h^2 = 0.63$)	Simulation data on 1275 training pigs and 1000 validation pigs. Genome of 5 chromosomes of 150 cM with a density of markers of 22 each, 50 segregating QTL per chromosomes	Estimation of higher genetic gain with genomic selection in pig breeding in developing countries by using the ridge regression method. Indigenous population, also with low linkage disequilibrium, may benefit of genomic selection but with the use of HD marker panels in genotyping.
Cleveland and Hickey (2013)	Total number born ($h^2 = 0.16$)	Field data on 4763 pigs from a single nucleus line genotyped with SNP60 BeadChip and three LD genotyping panels with SNP density of 450, 3071 and 5963	Evaluation of imputation strategies in a cost-effective genomic selection by using a single-step model. Alternative genotyping scenarios evaluated: GEBV may be calculated using imputed genotypes but the accuracy of GEBV depend on the level of genotyping in close relatives and the size of the dataset genotyped.
Tusell et al. (2013)	Litter size ($h^2 = 0.21$, 0.14 and 0.19 depending on lines)	Field data of three lines: about 2500 and 1600 sows for two Landrace purebred lines; 1900 sows for a commercial cross	Prediction ability (average correlation between observed and predicted phenotypes) always larger than that obtained with traditional plans both in crossbred (0.26) or in purebreds (0.15–0.22) with various pedigree and genomic prediction models.
Akanno et al. (2014)	Number of born alive ($h^2 = 0.08$), average daily gain ($h^2 = 0.28$), back fat thickness ($h^2 = 0.63$)	Simulated pig population (exotic or indigenous lines). Genome of 5 chromosomes of 150 cM with a density of markers of 22 each, 50 segregating QTL per chromosomes	The genomic selection improved the accuracy of breeding values if compared to pedigree-based models for traits with low heritability (number of born alive or average daily gain) and in pigs without performance data.
Andersen-Ranberg, Grindfleck (2014)	Total born, stillborn, piglet mortality, litter weight	Field data on 9745 genotyped Norsvin Landrace boars and Norsvin Landsvin sows	GEBV increase the selection difference for litter size and maternal ability traits between 26% and 67% IF compared to traditional EBV.
Tusell et al. (2014)	Adjusted litter size (total number of piglets born per litter)	Field data: two purebred Landrace lines (2598 and 1604 pigs) and commercial crosses (1829 pigs) genotyped with SNP60 BeadChip	It is one of the two data sets (pigs and wheat grain) used to evaluate various reproducing kernel Hilbert spaces regression models combing different number of Gaussian and t kernels.
Uimari et al. (2014)	Litter size and other maternal traits (total number of piglets born, number of still born piglets, pig mortality)	Field data on 723 genotyped Finnish Yorkshire AI-boars with SNP60 BeadChip	Reliability of genomic selection varied from 0.32 (total number of piglets born in the first parity) to 0.58 (pig mortality in later parities).

(*continued*)

Table 4. Continued

	Traits	Data	Results as comparison with traditional BLUP or according to the aim of the paper
Hidalgo et al. (2015b)	DBV for two female reproduction traits: gestation length and total number of piglets born	Field data. Genotypes with SNP60 BeadChip of 2078 Dutch Landrace-based, 2301 Large White-based, and 497 crossbreds pigs (F1 cross between the lines). More than 100,000 phenotypes in purebred and 85,000 in crossbred	Genomic value accuracies were equal or higher with training data based on phenotypes of purebred offspring versus phenotypes of crossbred offspring because purebred have high reliability (based on offspring phenotypes). When correcting for the reliability level, genomic values by using crossbred traits outperforms the usage of purebred traits by supporting the phenotyping on crossbred.
Guo et al. (2015)	Total number of piglets born, litter size, mortality rate	Field data on 1241 boars and 2131 sows genotyped with the SNP60 BeadChip. Pedigree on 778,095 litters from 309,362 Landrace sows and 472,001 litters from 190,760 Yorkshire sows	Comparison of genomic models and methods (single-step BLUP, GBLUP, selection index blending method, and traditional pedigree-based method-BLUP). Single step produced more accurate predictions in genotyped pigs (from 0.171 GBLUP to 0.209 single step) versus traditional BLUP (0.091). In non-genotyped pigs, reliability of 0.105 with single step versus 0.091 with traditional BLUP.
Park et al. (2015)	Litter size	Field data on 519 sows of Yorkshire pigs with genotyping and litter size data	Comparison of performance of three methods (LASSO, regularised LASSO, Fused LASSO and Elastic Net) to identify influencing SNPs for a trait in ultrahigh-dimensional data of GS. The Fused LASSO regression method was the best one for prediction errors and correlation coefficients between true litter value and predicted value.

GEBV: genomic estimated breeding values; DBV: deregressed breeding values; GS: genomic selection; EBV: estimated breeding values; LD: low density; SNP60 BeadChip: Illumina PorcineSNP60 BeadChip.

resistance, for example against the porcine reproductive and respiratory syndrome (PRRS; Jafarikia & Sullivan 2014). Genomic selection would make it possible to predict breeding values also for healthy pigs, distantly related to those with the phenotypes that could be collected in specific environments or only at occasionally disease outbreak (Bishop 2014). For example, PRRS seems largely controlled by many genomic regions with generally relatively small effects, but chromosome 4 might harbour an important QTL for PRRS resistance (Boddicker et al. 2012). Based on these findings, various strategies were proposed to predict GEBV by using both the QTL region on chromosome 4 or whole genome data (Boddicker et al. 2013, 2014), eventually integrated by a specific emphasis given on other chromosome regions following the progresses in QTL mapping for other important traits related to biological features of PRRS resistance (Lough et al. 2014; Orrett et al. 2014). Genomic selection for disease resistance is a hot topic and other studies including resistance to other pathogens will provide additional information to use this approach in pig breeding programmes to improve robustness of the animals.

Boar taint is the undesirable smell and taste of pork meat derived from uncastrated male pigs that is usually associated to androsterone and skatole compounds. These two components were considered both in GWAS studies (be e.g. in Duijvesteijn et al. 2010) and more recently in GEBV prediction analyses (Azevedo et al. 2014; de Campos et al. 2015). In detail, de Campos et al. (2015) reported GEBV accuracy values of 0.65 for androstenone and 0.58 for skatole levels. Boar taint is another trait that the pig breeding industry is trying to deal with due to the new proposed regulation about pig castration in Europe.

Meat quality traits have been considered in genomic selection by a few studies. Meat quality parameters have generally low heritability and they are expensive and difficult to be recorded, especially because often measured *post mortem*. The potentials of genomic selection in the genetic improvement of these traits were evaluated, for example, for meat pH. For this trait, Miar et al. (2014) based on information on about 2000 commercial crossbred pigs obtained accuracy of 0.25 of GEBV predictions by using GBLUP models. With the aim of comparing heteroskedastic versus homoscedastic error in various genomic models, Ou et al. (2015) predicted genomic values on 45-min *post mortem* carcass temperature and loin muscle pH, recorded in a swine F2 population. No significant advantages, evaluated in terms of prediction accuracy, resulted when accounting for heteroskedastic error variance. Nevertheless the results of this study suffered from the selection design that aimed to evaluate and select crossbred lines through the use of phenotypes recorded in purebred animals. Another study included a total of 16 meat quality traits that were predicted with GBLUP and Bayes B models in about 1200

Table 5. Genomic selection studies on performance and carcass traits.

	Traits	Data	Results as comparison with traditional BLUP or according to the aim of the study
Ostersen et al. (2011)	DBV for 1375 pigs on daily gain (h^2 = 0.27) and 898 pigs on feed conversion ratio (h^2 = 0.21)	Field data on Duroc pigs: 1911 genotyped with SNP60 BeadChip, pedigree records of 52,537 pigs	The use of DBV in GEBV predictions yielded to 18 to 39% higher reliabilities of GEBV and the choice of statistical method (GBLUP, Bayesian Lasso, and mixture models) was less critical in purebred pigs predictions.
Tribout et al. (2012)	Two traits with: one easy and cheap to collect (i.e. growth rate or ultrasonic back fat thickness) and a second one difficult or expensive to measure (i.e. meat quality, feed efficiency or intramuscular fat). h^2 of 0.20 or 0.40	Simulated data on 1050 breeding females and 50 breeding males for a purebred pig male line. Genome simulated: 10 pairs of 100 cM chromosomes, each with 3600 biallelic loci (alternatively being SNP or QTL)	Various results on average accuracy of GEBV of young candidates depending the heritability of the traits and the phenotyping (if on candidates or on relatives) and training population size. Usually the GBLUP model increases genetic gain and reduce inbreeding. A GBLUP model with large training population including selection candidates produced 27% to 33% of extra genetic improvement in the global breeding goal. With training that did not include selection candidates, but only phenotypes on relatives, advantages with the genomic selection were small.
Christensen et al. (2012)	Average daily gain and feed conversion rate (feed intake/weight gain between 30 and 100 kg)	Field data of 1500–2700 pigs genotyped (for the two traits) with SNP60 BeadChip and 25,000 or 330,000 pigs èphenotyped	Various prediction models (pedigree-based, original single step, adjusted single step, and GBLUP methods). Predictions were more accurate with genomic models, with single-step predictions were more accurate in non-genotyped pigs. Adjusted single-step methods (adjustment in the genomic relationship matrix) produced more accurate predictions than with other methods.
Su et al. (2012)	DBV on daily gain (h^2 between 0.36 and 0.39)	Field data on 1911 Danish Duroc genotyped with SNP60 BeadChip and 339,393 pig records	GBLUP model including additive and non-additive genetic effects increase the prediction accuracy and improve unbiasedness of genomic predictions.
Akanno et al. (2013)	Number of born alive (h^2 = 0.08), average daily gain (h^2 = 0.28), back fat thickness (h^2 = 0.63)	Simulation data on 1275 training pigs and 1000 validation pigs. Genome of 5 chromosomes each one of 150 cM, with 22 markers and 50 segregating QTL	Estimation of higher genetic gain with genomic selection in pig breeding in developing countries by using the ridge regression method. Indigenous population, also with low linkage disequilibrium, may benefit of genomic selection but with the use of HD marker panels in genotyping.
Tribout et al. (2013)	A fattening trait (inexpensive and easy to measure) and a trait difficult or expensive to record (e.g. feed efficiency) or that cannot be measured on selection candidates. h^2 = 0.20 or 0.40	Simulated data on 1050 breeding females and 50 breeding males. Genome simulated: 10 pairs of 100 cM chromosomes, each with 3600 biallelic loci (alternatively being SNP or QTL)	Genomic selection can increase genetic gain in a purebred male population based on the combined phenotyping of candidates and relatives for lowly to moderate heritable traits while significantly reducing the annual increase in inbreeding. Direct phenotyping is usually the choice to prefer. Genotyping of a limited number of pre-selected candidates reduce extra costs associated to the genomic approach while preserving both the increase in genetic gain and the reduction in inbreeding.
Akanno et al. (2014)	Number of born alive (h^2 = 0.08), average daily gain (h^2 = 0.28), back fat thickness (h^2 = 0.63)	Simulated pig population of exotic or indigenous lines (high- or low-linkage disequilibrium). Genome of	The genomic selection improved the accuracy of breeding values if compared to pedigree-based models

(*continued*)

Table 5. Continued

	Traits	Data	Results as comparison with traditional BLUP or according to the aim of the study
		5 chromosomes of 150 cM, each with 22 markers and 50 segregating QTL	for traits with low heritability (number of born alive or average daily gain) and in pigs without performance data.
Andersen-Ranberg and Grindfleck (2014)	Maternal and production traits (age at 40 kg, days from 40 kg to 120 kg, feed from 40 kg to 120 kg, lean meat %, carcass %)	Field data on 9745 genotyped Norsvin Landrace boars and Norsvin Landsvin sows	Genomic selection increased the selection differences for production traits between 8% and 34%, if compared to the use of traditional EBV's.
Badke et al. (2014)	DBV for backfat thickness ($h^2 = 0.45$), number of days to 250 lb ($h^2 = 0.26$) and loin muscle area ($h^2 = 0.47$)	Field data on 983 Yorkshire sires genotyped with SNP60 BeadChip	A feasible method for a cost-efficient design of genomic selection in swine is the use of HD genotypes for selection candidates but when LD panels are imputed with high accuracy. The addition of supplementary animals genotyped at LD to a large number of pigs genotyped at HD is a promising solution in genomic selection.
Jiao et al. (2014)	Feed intake ($h^2 = 0.44$), average daily gain ($h^2 = 0.44$), and real-time ultrasound traits: back fat thickness ($h^2 = 0.58$), muscle depth ($h^2 = 0.39$), intramuscular fat content ($h^2 = 0.54$)	Field population of about 1047 Duroc boars (training population) and 516 boars (validation population). Genotyping with SNP60 BeadChip	Low GEBV accuracies for several traits genotyped with LD or HD SNP chips. Bayes-A prediction model.
Samorè et al. (2015)	Traits recorded both on living animals (i.e. growth traits, $h^2 = 0.40$) and after slaughtering (i.e. carcass traits, $h^2 = 0.10$)	Simulated population with a training population constituted only by relatives of boars in a sib-testing programme and phenotypes recorded only on sibs of candidate boars	With this specific selection structure (sib test of boars), population structure and genotyping strategies, no advantages are expected for traits with high or medium heritability and only small advantages are expected for traits with low heritability.
Do et al. (2015)	Daily feed intake, average daily gain, back fat	Field data on 1272 Duroc pigs (training dataset: 968 pigs, validation dataset: 304 pigs)	Predictive accuracy of different annotated genomic classes for the traits ranged from 0.508 to 0.531(daily feed intake), 0.506 to 0.532 (residual feed intake), 0.276 to 0.357 (average daily gain), and 0.308 to 0.362 (back fat).
Ou et al. (2015)	45-min post-mortem carcass temperature (921) and loin muscle pH (908) F2 phenotypes	Field data on 3 generations swine population: 19 F0, 55 F1 and 928 F2 in the pedigree. All F0, F1 and 336 F2 pigs genotyped with SNP60 BeadChip	Whole-genome prediction models (RR-BLUP, BayesA, BayesB and BayesCπ) were fitted to predict GEBV. Heteroskedastic error of whole-genome prediction models showed improved model fit and enhanced prediction accuracy if compared to homoscedastic error models although the magnitude of the improvement was small (less than two points % net gain in prediction accuracy).
Azevedo et al. (2015)	Carcass traits: bacon depth ($h^2 = 0.34$), and 4 measures of backfat thickness: midline lower ($h^2 = 0.33$); midline after the last rib ($h^2 = 0.35$); midline on the last lumbar vertebrae ($h^2 = 0.36$), and after last rib ($h^2 = 0.42$)	Field data. F1 population of 106 sows and 134 boars (from 2 native Piau Brazilian boars and 18 commercial sows), and F2 population of 840 offsprings	Application of various methods of dimensionality reduction (i.e. number of markers larger than number of genotyped individuals, and such markers are highly correlated) to genome wide selection in F2 pig population. Principal component regression and independent component regression had the highest predictive ability values and the most efficient prediction of phenotypic values. Partial principal components method had the highest predictive ability value for midline lower backfat thickness, and it was biased for remaining traits.

GEBV: genomic estimated breeding values; EBV: estimated breeding values; DBV: deregressed breeding values; RR-BLUP: ridge-regression best linear unbiased prediction; SNP60 BeadChip: Illumina PorcineSNP60 BeadChip; LD: low density; HD: high density.

Table 6. Genomic selection studies on traits other than production or maternal traits or with joint selection for more types of traits in pigs.

References	Traits	Data	Results as comparison with traditional BLUP or based on the aim of the study
Lillehammer et al. (2013)	Joint selection with equal weight to maternal and performance traits	Simulation study with a large and continuously updated training population with the genotyping of boars at the test station or also of female sibs	Increase in genetic gain of 13% and better with the genotyping of female sibs.
Wellmann et al. (2013)	DBV of 14 growth, carcass and meat quality traits recorded with progeny testing	Field data of 895 German Piétrain boars genotyped with SNP60 BeadChip, LD panels used for selection candidates	When using LD SNP panels in a sire pig line, with GBLUP models, to limit the reduction in GEBV accuracies, it is useful to genotype at HD at least one parent of selection candidates.
Azevedo et al. (2014)	Precorrected phenotypes. Boar taint: androsterone ($h^2 = 0.44$), skatole ($h^2 = 0.38$); carcass traits: back fat thickness ($h^2 = 0.36$) and loin depth ($h^2 = 0.24$).	Field data on 622 boars with phenotypes, genotyped with a panel of 2500 SNPs (average of 131 SNPs per chromosome)	Comparative analyses among various methods for the estimation of GEBV.
Baby et al. (2014)	A total of 16 carcass and meat quality traits (h^2 from 0.11 to 0.46)	Field data on a Berkshire population with 1205 genotyped pigs with SNP60 BeadChip. Missing genotypes imputed	GEBV accuracy depends on the size of training data and heritability of traits.
Boddicker et al. (2014)	Porcine reproductive and respiratory syndrome resistance measured post-virus infection: viral load ($h^2 = 0.44$) and weight gain ($h^2 = 0.29$)	Field data on 8 trials of about 200 pigs experimentally infected genotyped with the SNP60 BeadChip	Accuracies of GEBV predictions based on significant markers on Sus Scrofa chromosome 4 were higher than those of GEBV calculated on the whole genome.
Bishop (2014)	Resistance to infectious diseases		Discussion on genetic and genomic studies on the resistance to infectious diseases. Main challenge is the obtaining of suitable phenotypes especially from epidemics and to understand the biology and epidemiology of the disease.
Jafarikia and Sullivan (2014)	Health indicator traits and performance traits		Overview of the status of genomic evaluation research in pigs with special concern to health traits.
Miar et al. (2014)	Pork pH and meat quality traits	Field data on 2384 pigs genotyped with SNP60 Beadchip: 1948 commercial crossbred pigs from 139 sires of two Duroc lines bred to 429 F1 hybrid Landrace × Large White sows	Genomic selection in purebred pigs for crossbred performances with imputation of missing genotypes and a GBLUP model. Prediction model of the parental pure lines had accuracy of prediction (correlation between EBV-GEBV) of 0.21 and crossbred animals of 0.25.
Stratz et al. (2014)	Conventional EBV for 14 traits: growth, carcass and meat quality	Field data: 895 German Piétrain boars genotyped with SNP60 BeadChip and LD panels	Study to evaluate possibilities of genomic selection with a single-step method using very LD markers.
de Campos et al. (2015)	Boar taint: concentration of androsterone, skatole; carcass: back fat thickness, loin depth	622 boars genotyped with SNP60 BeadChip and a panel of 2500 SNP (about 131 SNPs per chromosome)	Genomic selection for boar taint compounds and carcass traits by using Ridge regression and Bayesian Lasso methods to predict GEBV.

DBV: deregreesed breeding values; SNP60 BeadChip: Illumina PorcineSNP60 BeadChip; LD: low density; HD: high density.

Berkshire pigs genotyped with the 60K Illumina SNP panel (Baby et al. 2014). The accuracy of GEBV, calculated on the standard errors of GEBV, mainly depended on the heritability of the traits and the size of the training dataset that was different for each trait. Larger training sets were envisaged to increase the accuracy of GEBV to efficiently implement genomic selection in that population (Baby et al. 2014).

Finally, implementation of genomic selection is also expected for several other traits that might indirectly affect production efficiency, like pig welfare-related-parameters such as sow longevity and behaviour. However, at present, as far as we know, there is no report in the scientific literature on these traits or aspects, with the only exception of few studies on health indicator traits (e.g. Boddicker et al. 2014).

Genomic selection in crossbred and multi-breed populations

Selection in pig populations is generally based on a pyramidal structure with three levels: selection, multiplication and production (Dekkers et al. 2011; Tribout et al. 2011) to exploit the effects of both heterosis and

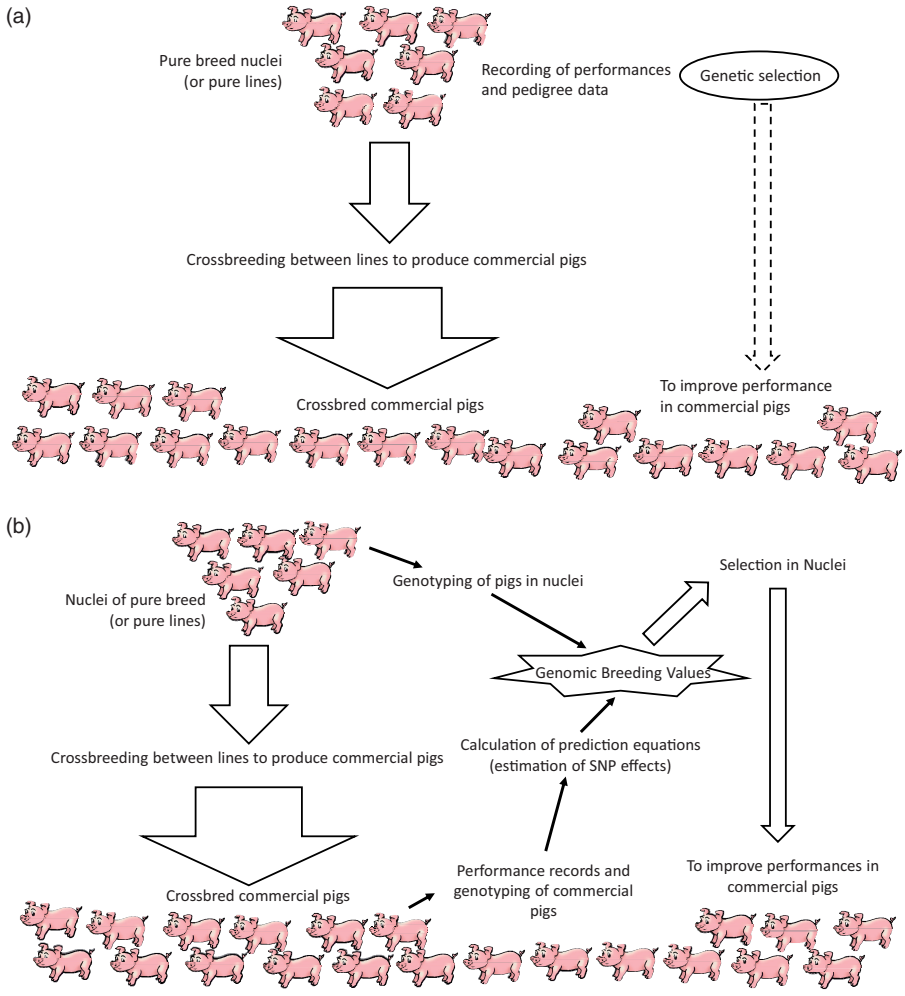

Figure 3. Selection for crossbreeding performances. (a) Traditional genetic selection in pig crossbreeding with selection in the nuclei of purebred (or pureline) pigs to improve the performance of commercial crossbred pigs. (b) Perspectives of the selection in crossbred pigs with the genomic selection: selection in the nuclei of purebred (or pureline) pigs based on prediction equations calculated in crossbred commercial pigs.

line complementarity by the practice of crossbreeding. Most of the genetic progress is realised at the first level of pure breed, or pure lines, with the assumption that the realised genetic progress is transmitted to the following levels (Figure 3a). However, the general breeding goal is the improvement of crossbred performances at the commercial herds (the final slaughtered products) but phenotypic data are collected on purebred animals in high-health environments with optimised managements (Dekkers 2012). The distance between this level and the bottom level of the pyramidal structure produces a reduced genetic improvement at the bottom (Tribout et al. 2011). Notwithstanding the success of current breeding schemes, genetic differences between purebred and crossbred animals, together with the environmental differences between nucleus and field conditions, make the performances of purebred animals poor predictors of the performance of their crossbred descendants (Dekkers 2007). Moreover, some important traits, like disease resistance, cannot be measured in nucleus lines (Ibáñez-Escriche et al. 2009). By simulating a population structure organised in three tiers (nucleus, multiplier and production tiers), Lillehammer et al. (2015) evaluated that the increase in the genetic gain of a trait not measured in the nucleus strongly depends on the economic weight assigned to it and that the most effective strategy, for the enlargement and update of the reference population, is the genotyping of animals of the production progeny of genotyped nucleus sires, other than the only genotyping nucleus sires.

Finally, genomic prediction is calculated by using realised relationships instead of the expected genetic relationships as it happens in traditional models. This has the main advantage of allowing the calculation of individual genomic prediction based on the effective relationships and without the need of recording the

relationship data, something that it might be difficult especially in commercial hogs.

To reduce the gap between purebred and crossbred animals, the collection of phenotypic data on crossbred offspring was proposed as a possible solution to estimate breeding values of purebred animals. This design requires expensive programmes due to the need of recording both phenotypes and pedigree data at the commercial level that are usually difficult to obtain (Tribout et al. 2011; Dekkers 2012). Genomic selection would overcome these limitations by selecting purebred animals from crossbred performances. By incorporating information from crossbred pigs, the SNP effects would be estimated by using phenotypes and SNP genotypes of crossbred animals and the selection of purebred pigs based on purebred genotyping data and prediction equations from crossbred pigs (Dekkers 2007). This design would take advantages from the collection of performances on crossbred pigs (the final products) overcoming the difficulties of recording pedigree information in crossbred animals (Toosi et al. 2009). This scenario (Figure 3b) was evaluated with promising results in pigs, through simulations analyses (Ibáñez-Escriche et al. 2009; Toosi et al. 2009). Ibáñez-Escriche et al. (2009), using phenotypes on crossbreds and a genomic model with breed of origin specific allele substitution effects, reported that accuracies based on crossbred data were a little bit lower than accuracies based on pure breed data. This difference was almost null, when the crossed breeds were closely related breeds, depending on the models, genotyping density and assumptions that were included in the simulations. This was nevertheless evaluated under additive models and differences might arise with the inclusion of non-additive effects in the models. Similar results were obtained by Toosi et al. (2009) who reported that accuracy of genomic selection for predicting candidate breeding values of purebred animals based on estimates of marker effects in a crossbred population was slightly lower (from 0.66 to 0.74) than what was obtained in a pure breed training population (from 0.79 to 0.85). In another study, genomic selection in purebred pigs for crossbred performances was evaluated on muscle pH using field data showing that genomic selection might be of great utility for traits difficult to measure and with low heritability (Miar et al. 2014). In contrast, experiences of genomic selection programmes in crossbred animals that replaced purebred animals with crossbred pigs in the reference population did not produce any advantage except for the cases of low correlation between purebred and crossbred performances (<0.70) or where purebred performances were not included in the breeding goal (van Grevenhof & van der Werf 2015). Recently, by using field data, Veroneze et al. (2015) reported accuracy of 0.25–0.29 in crossbreds by using purebred data, and Hidalgo et al. (2015b) reported that the use of crossbred training data would outperform those of purebred training data in the prediction of crossbred merits. Several methodological aspects related to the use of pure breed and crossbreeding information were further developed by Christensen et al. (2014) who presented a single-step method for genomic evaluation of both purebred and crossbred performances in a two-breed crossbreeding system by extending a model proposed by Wei and van der Werf (1994). The method included two partial relationship matrices for the two breeds and constructed marker-based partial relationship matrices that were adjusted to be compatible to pedigree-based partial relationship matrices to combine marker and pedigree-based source of information. This single-step method provided a coherent approach for genomic evaluation in a scenario in which all animals cannot be genotyped (e.g. Guo et al. 2015).

Another important issue that should be considered when genomic selection is applied in crossbreds is that genomic predictions are usually carried out using models that ignores non-additive effects. This is a problem because final performances of crossbred animals are only in part determined by additive genetic effects (that are considered in GEBV predictions), with an important contribution of non-additive dominance and epistatic genetic effects that are generally not considered in prediction calculations. Therefore, it would be expected that a model including non-additive genetic effect would increase the prediction accuracy and reduce estimation-based biases. Su et al. (2012) described an approach to estimate additive and non-additive genetic variations and predict genetic values for complex traits using models integrating additive and non-additive genomic relationship matrices. The method was used to investigate the variance components of additive and non-additive genetic effects and the accuracy of genomic predictions for daily gain in a Danish Duroc population. The models including non-additive genetic effects predicted breeding values more accurately and unbiasedly, compared with a model ignoring non-additive genetic effects. However, in a real genetic evaluation system, there are two main limiting factors for using a model with both additive and non-additive genetic effects for genomic prediction (Su et al. 2012). The first problem is due to the high computational demand for models with both additive and non-additive genetic effects requiring more powerful computers and/or more efficient algorithms. The second problem is derived by the fact that

animals in a population under selection are conventionally evaluated by genomic model using estimated breeding value (EBV), de-regressed EBV or mean of corrected progenies' performances which are more informative than individual observation but are appropriate descriptors for an additive genetic model. These pseudo observations are not appropriate for a model that includes non-additive genetics effects (Su et al. 2012).

In another simulation study, Esfandyari et al. (2015) reported a more efficient genomic selection on crossbreeding performances than on purebred phenotypes when, in addition to additive effects, only dominant effects were considered. Costa et al. (2015) suggested to integrate pedigree and genomic data to better estimate additive and dominance variance for growth rate and carcass traits in an F2 pig population and Toro and Varona (2010) evaluated the possibilities of genomic selection approaches with non-additive effects in mating design.

Another critical aspect that genomic selection programmes have to face is the reduced training population. With the aim of enlarging the training population on which the marker effects were estimated, and increasing therefore the accuracy of GEBV, multi-breed genomic evaluations were proposed in dairy cattle as an alternative to the organisation of large consortia of breeding companies or associations for the same breed (Hayes et al. 2009; VanRaden et al. 2009). The inclusion of data from more breeds in the training set would improve the accuracy of GEBV only if the linkage phase between markers and traits, and the genetic architecture of the trait involved, was comparable in the different populations. In pigs, Toosi et al. (2009) evaluated genomic selection in an admixture population, i.e. with multiple genetically distinct subgroups within a population (Wang et al. 2005), and found that given that genes from the target pure breed were included in the admixed or crossbred population; the accuracy was not greatly reduced with the admixed training population. This was true, even without specifically designed populations by accounting for breed composition or breed origin of marker alleles. In contrast, other studies (i.e. Hidalgo et al. 2014, 2015a) suggested that multi-breeds training populations would not result in advantages in genomic selection implementations, as the across-breeds GEBV prediction yielded to null or low accuracies.

Economic aspects of genomic selection

Although the economic aspects associated to the introduction of genomic selection in pig populations might represent the main limits to extensive field applications, few researches evaluated this problem in detail. Actually, unlike in dairy cattle, where genomic selection is a reality nowadays, in pigs no great economic changes are expected with the introduction of genomic selection and the advantages should cover the extra financial costs associated to its implementation in pig breeding programmes (Tribout et al. 2013). The primary expected benefit from incorporating genomic information into pig breeding value estimation is the improved accuracy and this increase should be large enough to recover the genotyping costs (Abell et al. 2014). Differently from other species, as i.e. dairy cattle, no great advantages are expected in terms of reduction of phenotyping costs because phenotypic measures recorded in the field are, in general, not very expensive (i.e. female reproduction traits are routinely recorded by the farmers). For other traits, that, for their high cost are recorded in testing stations, or that can only be recorded after slaughtering, the need of obtaining data and updating them for the training population (to make the training set closely related to the population under selection to obtain a more accurate GEBV prediction) might not produce a reduction in the number of animals to be phenotyped (Muir 2007; Sonesson & Meuwissen 2009).

The genotyping cost seems larger than the increase in expenses of additional infrastructure, as i.e. ancillary expenses associated to genotyping, costs due to the additional time needed to develop and calculate EBV, and to the increased computer power necessary to predict GEBV (Abell et al. 2014).

For the current price of genotyping of about 100 euro per animal (even if the price is expected to decline, in particular with the development of LD SNP chips), costs might still be too high, considering also that a large number of selection candidates should be evaluated (Dekkers et al. 2011). To overcome this problem, various approaches were proposed as by e.g. the pre-selection of animals to be genotyped (Stock & Reents 2013) or the recording of phenotypic data only in a limited part of the selection candidates (Okeno et al. 2014). Henryon et al. (2012) evaluated the amount of marginal returns derived by the introduction of genomic selection in a population with increasing proportion of selection candidates with genotyping data and in which the selection candidates to be genotyped were defined based on their breeding value calculated on a priori information. In that population, if compared to the situation in which all candidates were genotyped, only 5–20% of selection candidates could be genotyped to produce most of the benefits associated to the introduction of genomic

selection programmes. Okeno et al. (2014) evaluated the marginal return from genomic selection when the proportion of selection candidates with phenotypic information changed and reported that the phenotyping of only the 80% of top breeding value ranking selection candidates would produce the maximum genetic gain in the breeding programme with a subsequent reduction in costs. Larger number of candidates with phenotypic data is necessary when the choice was at random and not based on prior information as i.e. breeding value rankings.

Another scenario to reduce routine costs of genomic selection is the genotyping with a SNP panel of reduced density, to impute missing SNP genotypes from a HD panel (Habier et al. 2009; Dekkers et al. 2011). Imputation techniques were recently reviewed by Calus et al. (2014) by giving a complete overview of features and techniques associated to this strategy. Summarising, imputation can be done on a within family base (Daetwyler et al. 2010), or based on linkage disequilibrium information (Sheet & Stephens 2006), or on a combination of both information (Druet & Georges 2010) from the individuals in the reference population. After the imputation process, values of GEBV can be predicted for all candidates, genotyped with LD or HD, and by using the complete set of SNPs of the HD panel.

The use of imputation of LD genotypes with high accuracy was supported in pigs GEBV predictions (Cleveland & Hickey 2013). The accuracy obtained with the imputation depends on several factors, such as the number of markers in the LD panel, the markers informativeness and their distribution across the genome, the relationship between the genotyped animals, the effective population size and the used method of imputation (Wellmann et al. 2013). The reduction in the accuracy of direct GEBV is ranging only between 0.02 and 0.05, depending on the reference base, and the average reliability increased with large training populations (Dassonneville et al. 2011). For example, the imputation error rate was very low, and the reduction in selection efficiency was small when selection candidates were genotyped for at least 5000 markers, with both parents mapped with porcineSNP60 beadchip (Hickey et al. 2012). Genotyping with LD panels represents low-cost genotyping possibilities and therefore a chance of genotyping large number of animals in a species like pigs where the economic value of individual animals would be low as compared to individual genotyping cost (Huang et al. 2012). Bouquet et al. (2015) assessed that imputation of LD to HD genotyping of crossbred pigs would result in a similar precision of imputation than those on purebred animals when both the parental lines are genotyped at HD and with similar values of precision than in the imputation of purebred lines when sufficient dense genotyping (at least 10K).

Abell et al. (2014) predicted the expenses associated to the incorporation of genomic selection into traditional pig breeding schemes while using two different types of genotyping densities (LD and HD chips). With the selection candidates genotyped at LD and all animals used for breeding genotyped at HD, costs resulted in US$0.164 (in a 1000 sow maternal line nucleus herd) or US$0.21 (in a 600 sow terminal sire line) per weaned piglets. The decrease in GEBV accuracy due to imputation was estimated in a maximum of 3% in a scenario with a panel of only 384 markers if at least one parent of the selection candidates were genotyped at HD (Wellmann et al. 2013). In another study (Jiao et al. 2014), the accuracy of the prediction of GEBV was considered low in a population with 1047 boars genotyped at HD (e.g. 60K SNP chip) and 516 pigs genotyped at LD with a 9K SNP chip. The accuracy of GEBV with highly accurate imputed data was large (correlation of 0.95 between GEBV of imputed data and the estimated breeding value) whereas it significantly decreased when genotypes were imputed with low accuracy in training and prediction animals (Badke et al. 2014).

Perspectives of the genomic selection in pigs and concluding remarks

Genomic selection is already a routine practice in dairy cattle and is becoming a reality in other livestock species. Field applications of genomic selection are opening new opportunities also in pig breeding.

Specific strategies and solutions were proposed and envisaged to overcome the main limits associated to the introduction of genomic selection in pigs. These limits and associated problems but also new opportunities are related to (i) the high cost of genotyping, compared to the individual animal value, (ii) the peculiarities of pig selection schemes, i.e. pyramidal population structures with selection mainly on pure lines, affecting how many animals should be genotyped and phenotyped, the use of data from performance stations, further limiting the amount of available phenotype data and the accuracy of GEBV estimation, (iii) the short time available for the genetic evaluation (compared to dairy cattle), (iv) the possibility to better control inbreeding, (v) the possibility to perform selection among full sibs and vi) the overall implementation of the logistics aspects, including storage of DNA or other biological materials from the animals, computation

power, storage and handling data and personnel training.

The definition of two main questions (that are not completely independent) may at present represent the starting point for the introduction of a genomic selection programme in a pig breeding scheme: (i) the preselection of pigs for genotyping and phenotyping and the (ii) combined use of HD and LD SNP panels. That means which and how many animals should be genotyped with one or the other panel.

However, quite soon SNP genotyping technologies are expected to be substituted by sequencing-based approaches also in genomic selection, as sequencing costs should decrease with the introduction of new sequencing approaches and technologies (Table 1). Whole genome sequence data are expected to increase GEBV accuracy by enabling a large proportion of the genetic variance to be finely mapped to causal variants that would make it possible to generate prediction equations more stable over populations and over time (Meuwissen & Goddard 2010; Meuwissen et al. 2013; Hickey et al. 2014) although the accounting for genetic interactions, such as dominance or epistatic effects, might represent serious limitations in prediction calculations. Computational problems associated to the use of sequence data could be a potential bottleneck at present should the shift in technologies (from SNP genotyping platform to sequencing platforms) be complete (for all animals). However, despite the decrease in costs, sequencing might still be too expensive for implementation on a large number of animals. For this reason, the identification of which animals should be first sequenced and at what fold coverage to correctly infer haplotype information of the descendant animals from sequencing data is also necessary (Kemp 2014). Continuing on what could be envisaged in the feature, improvements in sequencing data analysis and management would derive (i) by the application of low coverage sequencing strategies to reduce costs, (ii) by the improvement of imputation techniques and (iii) by the functional annotation of all variants contributing to better clarify genetic variance (Hickey et al. 2014).

Finally, perspectives and applications of genomic selection in pigs were generally evaluated within the context of existing selection programmes with already established phenotype recording procedures. Although perspectives of introducing genomic selection were generally promising for traits at low heritability or recorded only in a part of the population, i.e. on litter size recorded only for females or health traits; in contrast, small advantages were expected for performance traits with moderate to high heritability or for traits recorded through the use of some of the peculiar pigs testing programmes. Dekkers (2010) suggested that to fully capitalise the benefits of genomic selection, existing breeding programmes should be eventually redesigned. The implementation of genomic selection actually removes some limitation factors of current phenotype-based breeding programmes with regard to when and on which individuals phenotypes should be recorded and might lead to the re-organisation of both the selection schemes and the population structure.

Crossbreeding is a common practice in commercial pig populations while selection is generally performed on pure bred lines only, with scarce or no information on crossbred performances. Using genomic models, it is possible to evaluate pure bred lines with genomic information, by using marker effects estimated on crossbred animals with both phenotypic and genotypic data. That would allow a new contribution coming from field phenotypes in real production environments (crossbred), through the selection of pure line breeds at the top level of the pyramid of pig breeding structure. Furthermore, the genetic improvement of crossbreeding performances implies that non-additive genetic variance could be taken into consideration. Accounting for non-additive effects in GEBV predictions may be theoretically and computationally complicated and additional studies are needed to dissect and take advantages from these genetic components (Boysen et al. 2013). Their correct estimation would likely require the use of raw data as dependent variable (Su et al. 2012) and their practical use would be probably limited to planned mating. Another potential interesting factor, that should be considered in this context even if it could be complicated to disentangle, is the imprinting parent-of-origin effects. Imprinted gene expression can have an important effect on crossbreeding performances. In order to effectively capture imprinting genomic models should weigh imprinted gene-associated SNPs according to the expected effects on gene products when those effects are relevant (during a specific developmental phase or across the whole lifespan of the animals) (O'Doherty et al. 2015) and more recently, Nishio and Satoh (2015) presented two statistical GBLUP models that included imprinting effects on the basis of genotypic or gametic values.

It could also be important to consider that, when genomic selection is running in a population, particular attention should be paid to monitoring the inbreeding level as an increased could be expected (Sonesson & Meuwissen 2009; Lillehammer et al. 2011; Tribout et al. 2011, 2013). However, this is more an issue in dairy

cattle selection where production is usually by pure-bred, than in swine, where production is by crosses.

Traits considered for pig genomic selection span from traditionally selected traits, i.e. performance or reproduction traits, to new traits, as boar taint trait, longevity and health trait parameters or diseases outbreaks. For several of these complex traits and new traits (i.e. longevity) one of the main problems to be solved is the definition of a reliable dependent variable. Lucot et al. (2015) calculated the genomic predictions for the trait of 'age at puberty in gilts' as an early indicator of reproductive longevity by using various subsets of the most informative SNPs from PorcineSNP60 BeadChip and calculated the expected genetic gain. With a selection also on males, as it is possible with genetic tools by exploiting the genomic selection features with sex-limited traits, the genetic gain resulted in an extra value of 20.5% if compared to those on females alone. With a different approach, Santos et al. (2015) evaluated the measure of slaughter age to measure longevity by using a genomic selection model for longevity based on the Cox frailty model.

The emerging fields of metabolomics and phenomics in pigs (Fontanesi et al. 2014) might represent a rich potential source of new interesting traits associated to production level and quality, health status and well-being of pigs. The prediction of GEBV might therefore be envisaged for the most significant parameters, both in terms of selection for the trait in itself or as indicator of the status of the pigs, considering that most novel phenotypes are expensive to measure and can be collected on a limited number of animals. Finally, a GEBV multi-trait setting would be the logical frame for setting up selection indexes for the overall selection objective by accounting for GEBV variance–covariance structure (Dekkers & van der Werf 2014). This is a key issue for the implementation of genomic selection in specific breeding programmes, i.e. in Italian heavy pigs in which the simultaneous selection for productivity and seasoning meat quality traits require the simultaneous selection of antagonistic traits.

Several models and tools to predict GEBV have been presented and others will certainly be developed in the next future for genomic selection in pigs. Among them, single-step strategies to predict GEBV opened new scenarios with the possibility of using a large amount of phenotypic records collected on genotyped or non-genotyped individuals, and of pedigree data, precisely recorded in selected parental lines (Christensen & Lund 2010; Christensen 2012). That would be of significant value for traits recorded on field over a large part of the population and few animals being genotyped (Forni et al. 2011; Christensen et al. 2012), but with less advantages for traits needing a sib performance test programme with phenotypic data collected in a small part of the population (Samorè et al. 2015). An interesting approach to reduce the deepness of pedigree in a single-step GEBV prediction is the attempt to limit to the last few years of historical data in the pig data set, (i.e. about two generations) without any reduction of accuracy of predictions in large populations (Lourenco et al. 2014). In conclusion, accounting for all these aspects outlined here, genomic selection might represent the strategy of choice in pig breeding. Caution should be taken for its implementation, considering their current limits and problems but new developments might be expected to overcome the most important critical points. Several aspects relevant in pigs could be also interesting models for other species (i.e. fish, poultry and rabbits) with analogous selection programmes, especially in terms of crossbreeding, presence of different lines and breeds and family structures.

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