Review. Promises, pitfalls and challenges of genomic selection in breeding programs

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Abstract

The aim of this work was to review the main challenges and pitfalls of the implementation of genomic selection in the breeding programs of different livestock species. Genomic selection is now one of the main challenges in animal breeding and genetics. Its application could considerably increase the genetic gain in traits of interest. However, the success of its practical implementation depends on the selection scheme characteristics, and these must be studied for each particular case. In dairy cattle, especially in Holsteins, genomic selection is a reality. However, in other livestock species (beef cattle, small ruminants, monogastrics and fish) genomic selection has mainly been used experimentally. The main limitation for its implementation in the mentioned livestock species is the high genotyping costs compared to the low selection value of the candidate. Nevertheless, nowadays the possibility of using single-nucleotide polymorphism (SNP) chips of low density to make genomic selection applications economically feasible is under study. Economic studies may optimize the benefits of genomic selection (GS) to include new traits in the breeding goals. It is evident that genomic selection offers great potential; however, a suitable genotyping strategy and recording system for each case is needed in order to properly exploit it.

Additional key words: breeding scheme; chip technology; genotyping; SNP.

Resumen

Revisión. Promesas, peligros y oportunidades de la selección genómica en los programas de mejora genética

El objetivo principal de este trabajo fue revisar las oportunidades y riesgos de la implementación de la selección genómica en las diferentes especies de producción animal. La selección genómica es actualmente uno de los principales retos en mejora genética animal. Su aplicación podría incrementar de forma considerable la tasa de ganancia genética en caracteres de interés. Sin embargo, el éxito de su implementación práctica depende de las particularidades de cada esquema de selección y por tanto debe ser estudiada para cada caso en concreto. En vacuno de leche, especialmente en Holstein, la selección genómica es una realidad. En el resto de especies de producción animal, vacuno carne, pequeños rumiantes, monogástricos y peces, la selección genómica, hasta ahora, se ha utilizado principalmente de manera experimental. El limitante principal para su implementación, común para todas las especies mencionadas, es el alto coste del genotipado en comparación con el bajo valor de los candidatos a la selección. No obstante, se está estudiando actualmente la posibilidad de utilizar chips de baja densidad, de manera que sea económicamente viable su aplicación. Serán necesarios estudios económicos para optimizar las ventajas de la selección genómica a la hora de incluir nuevos caracteres en los objetivos de selección. La selección genómica ofrece muchas posibilidades; sin embargo, para poder aprovecharlas es necesario adecuar la estrategia de genotipado y recolección de datos en cada caso.

Palabras clave adicionales: esquemas de selección; genotipado; SNP; tecnología de chip.

Abbreviations used: AI (artificial insemination), BLUP (best linear unbiased predictor), EBV (estimated breeding value), GEBV (genomic estimated breeding value), GS (genomic selection), HD-SNP (high-density single nucleotide polymorphism), IG (generation interval), LD-SNP (low-density single nucleotide polymorphism), QTL (quantitative trait locus), SNP (single nucleotide polymorphism), ΔG (genetic gain).

Introduction

Genomic selection (GS: Meuwissen *et al*., 2001) has become one of the main points of interest in the last few years in animal breeding and genetics. The genome sequencing and development of chips that are able to genotype thousands of single nucleotide polymorphisms (SNP) across the genome may be a breakthrough for breeders and scientists in animal breeding. The genetic gain (ΔG) in animal breeding programs depends on the intensity of selection (*i*), the accuracy of predictions (*r*), the genetic variance (σ^2_g) and the generation interval (*IG*):

$$\Delta G = i * r * \sigma^2_g / IG$$

There is great consensus on the benefits of GS for increasing genetic value prediction accuracies, shortening the generation interval, and therefore increasing the rate of genetic gain.

Genomic information may also assist the discovery of genomic regions that contribute to the underlying genetic variance of complex traits. So far, most efforts have been concentrated on the development of tools to incorporate the large amount of information into statistical analyses and genomic evaluations. However, so far, GS has been seldom implemented in the field. Some countries (*e.g.* United States, Canada, New Zealand) have started to deliver official genomic evaluations for dairy cattle or sheep. Some poultry companies have made some preliminary implementations, but without specific weights in their breeding programs (Avendaño *et al*., 2010). It is necessary to analyse and discuss the alternatives to implementing GS in different breeding programs. The difficulties and challenges must be evaluated for each breed or population in order to maximize the benefits of GS. For instance, the availability of a data recording scheme, the traits to be included, genotyping strategies, the role of the breeding companies and the associations and selection of genomic animals may differ between species and breeding programs. It is even possible that genomic selection might not be of interest in some species.

The aim of this work was to review the main pitfalls and challenges of the implementation of GS in the breeding programs of different livestock species.

Genomic selection in ruminants

Dairy cattle

Genomic evaluations in dairy cattle have been a reality since 2008. The structure and data recording schemes, as well as the biological characteristics of these species, have made the implementation of GS possible in Holstein breeding programs worldwide. The United States, Canada, New Zealand, France, The Netherlands and the Nordic countries, among others, have already incorporated it, and the list will include other countries soon. As few examples, Van Raden *et al*. (2009) showed a large increase in the reliability of US genomic predictions in comparison to the traditional pedigree index, with a higher relevance for low heritability traits. Mastitis, body condition score, fertility and lameness are traits for which GS may increase the genetic gain. New Zealand has reduced the number of progeny-tested bulls by using a higher selection intensity of candidates selected based on genomic information (Spelman *et al*., 2010). The implementation of GS for other dairy breeds, such as the brown Swiss, is planned, although with some limitations due to smaller population sizes.

There is no straightforward manner for the implementation of GS in dairy breeding programs, and its application has been limited to sires and sire dams. Up to date, available genotypes are mainly from sires, which have been utilized to create a reference population of top male animals that is used to predict the genomic merit of other genotyped animals. Furthermore, daughter yield deviations are used as the response variable in genomic evaluations, which may lead to an underperformance of many statistical methods used in genomic evaluations (González-Recio *et al*., 2009). Other genotyping strategies are currently under evaluation in order to improve the potential benefits from GS. Strategies have to be developed to maximize the genetic gain obtained per euro spent on genotyping, as shown by Jiménez-Montero *et al*. (2010) and König *et al*. (2009). The cow population may be as informative or even more than the male population, and selective genotyping can be applied to certain population strata. Some preliminary studies have shown certain benefits to including females among the genotyped animals (Jiménez-Montero *et al*., 2010; Sorensen and Sorensen, 2010). The amount of genotyped animals depends on the heritability and on the marginal increase of genetic gain per genotyped animal. The best and worst animals for a given trait should be genotyped. If this criterion is used in several traits, a pseudo-random population may be selected as a reference population with average allele frequencies close to the whole population. Furthermore, once the reference population has been established, low density genotyping may also be considered to reduce future genotyping costs. It must be

pointed out that the reference population must be updated from generation to generation, otherwise the predictive ability will decrease over time (Meuwisen *et al.*, 2001; Muir, 2007). After obtaining their genotypes, the genomic value of cows and young sires may be predicted with higher accuracies, on average, than that from pedigree indices, which may assist in the decision process for selecting a sire dam or for selecting candidates for progeny testing. Decisions are made with a larger accuracy and earlier in life, increasing the genetic response. Nonetheless, the dairy industry is still reluctant to use sires with a low reliability, and the real genetic response may be even lower than theoretically expected; progeny testing will still be demanded by dairy producers in order to obtain a > 90% proof reliability. The optimal combination of sires and cows in the reference population should be studied in the future. Furthermore, the widespread genotyping of cows with phenotypes of their own will allow the investigation of non-additive genetic effects, such as dominance and epistasis, which cannot be analysed using the predicted transmission abilities of bulls in artificial insemination programs. The development of statistical models which deal with this problem and get accurate estimates must be also considered (Gianola *et al.*, 2006; González-Recio *et al.*, 2010; Toro and Varona, 2010; González-Recio and Forni, 2011).

Inbreeding is also a challenge dairy cattle, although it is not clear whether it can be reduced using GS. Some authors suggest that GS has lower increment of inbreeding than traditional best linear unbiased prediction (BLUP) because it estimates the mendelian sampling term of breeding values (Daetwyler *et al.*, 2007; Pedersen *et al.*, 2009). However, results from Pedersen *et al.* (2010) showed that true inbreeding rates could not be reduced regarding the traditional BLUP selection, in part due to the expected higher selection intensity placed on parents of sires. Inbreeding must be considered as a parameter of research when different genomic programs or methods are compared.

There are still some challenges that the dairy industry needs to face in order to exploit the full potential of GS. Among them, the completeness of the data recording scheme and genotyping strategies deserves attention first. Also, the combination of male and female genotypes and updating the reference populations (Lillehammer *et al.*, 2010) are further challenges to be considered.

Although the data recording scheme in dairy cattle is known to be quite complete, the genomic era demands important efforts towards the inclusion and recording of new information such as disease status, fertility, culling reasons, management practices, and hormonal levels, amongst others. This information must then be publicly available for institutions in the system in order to accomplish the objective as efficiently as possible (Kaye *et al.*, 2009). Data storing, management and transfer protocols have to be created, evaluated and followed to facilitate the use of GS in the dairy industry from breeding associations, research centres and back to the industry. The breeding associations have an important duty in making dairy producers aware of the importance of a quality data recording system.

Imputation techniques for selective genotyping strategies are promising. These techniques infer high-density genotypes from low-density genotypes with a high accuracy (Weigel *et al.*, 2010a).

Finally the use of GS by farmers and AI stud farms may have many different strategies depending on the breeding goals, population size or available budget, among others. Some common aspects to be considered are:

— Combined genomics with sexed semen.

— Genomic mating programs can now combine certain genomic regions in the parental animals to increase the probability of inheriting certain favourable gene combinations.

— Dairy producers can make breeding decisions on calf females earlier in life according to their genomic merit for yield, functionality or disease resistance.

— Cow candidates for sire dams may be found in a larger variety of herds, and bias due to preferential treatment will be less important.

— An independent organization such as Interbull is still necessary for comparing genomic proofs from different countries (Van Raden and Sullivan, 2010). Preliminary studies have already been done at the Interbull centre in August and November 2010, without official results but information is available at the Interbull webpage (www.interbull.org; accessed on January 3rd, 2010). New methods for international evaluations may be developed in the future.

Beef cattle

The biological characteristics of beef cattle are similar to dairy cattle, with a large generation interval, small prolificacy and similar heritabilities for traits of interest. However, GS has not been applied in this field yet. The main reasons are probably due to the different

sorts of organization in the breeding programs, the lack of systematic recording of phenotypic information, different breeding goals between populations and a smaller population size. Genomic selection may improve the genetic gain of traits that are difficult to record in beef cattle, such as behaviour, reproductive ability, longevity or meat quality (Garrick, 2010). Efforts have focused on creating a reference population from different breeds and countries; however, so far the results have not been satisfactory for genetically distant populations (Hayes *et al.*, 2009; Garrick, 2010; Kizilkaya *et al.*, 2010). A few studies have shown some advantages to pooling different populations and these populations had a small number of individual genotypes and were from the same Norwegian Red breed (Brøndum *et al.*, 2010). Dominance and epistasis scenarios may bring further complications to multi-breed analyses (Garrick, 2010). This drawback might be solved in the future with the development of methods and proper data treatment. As in any breed or species, the quality and quantity of the recording scheme is necessary for implementing GS. Breeding organizations should invest most of their efforts into determining which traits are economically profitable in each breed and phenotyping populations for these traits of interest, placing higher emphasis on traits like fertility (Fernández-Perea and Alenda, 2004). Furthermore, the breeding goals and phenotype recording criteria between populations should be homogenized in order to work in a multi-population scenario; otherwise the implementation of GS may be hampered when using a multi-breed reference population. Also, genotyping strategies must be developed, as in dairy cattle, in order to maximize the investment per genetic gain rate.

Last but not least, the industrial cross between dairy cows and beef sires may be genomically exploited using non-additive effects. The GS of industrial crosses also requires the definition of breeding goals and data recording organization.

The genomic era may be a favourable time for motivating the development of new organization procedures in beef breeding programs considering the aspects commented above: economic studies, record and selection of new traits, reference population, cross-breeding and accounting for dominance and epistatic effects.

Small ruminants

Genomic selection has not yet been implemented in small ruminants, although a few studies have used sheep genomic data, and pilot genomic evaluations have been implemented in New Zealand. The sheep SNP chip has recently become available (www.sheephapmap.org), although this technology is not yet available for goats.

The data recording scheme for these species is limited, and therefore the genetic gain using current GS strategies may be worse than that obtained with traditional selection (Van der Werf, 2009). Genomic selection could offer new opportunities for small ruminants if an adapted version of the dairy cattle organization is followed, but there are also some threats as some commercial interests may be leading species towards a pyramidal structure, with close selection nucleus genetic management (Banks and Van der Werf, 2009). An experimental nucleus flock has been created in Australia to obtain data and information on new traits for genome-wide association studies (Van der Werf and Banks, 2010) and New Zealand has implemented a genomic evaluation for sheep meat traits, although the practical implementation is still limited. As for other species, economic studies of the benefits of GS in small ruminants should be carried out.

Genomic selection in monogastrics

Pigs

Nowadays, although GS is a reality in the dairy cattle breeding industry, in pig breeding it is still under research and its application remains mainly restricted to experimental studies. The SNP chip technology has only recently become available for pigs, and therefore the implementation of GS in commercial pig breeding programs has been delayed in comparison to dairy cattle. However, there are other factors (*e.g.* genotyping cost) that could also limit the implementation of GS in pigs.

As mentioned above, progeny testing in dairy cattle implies a high generation interval which can potentially be drastically reduced by GS, even maintaining the accuracy of selection. Conversely, pig breeding schemes have relatively low generation intervals and the genetic gain of GS is mainly improved by increasing the accuracy of selection. Hence, GS is especially interesting for traits where the accuracy of selection is low, such as low heritability traits and traits that can only be recorded directly in one sex (*e.g.* litter size) or in slaughter animals (*e.g.* meat quality traits). Nevertheless, it is important to note that traits with low

heritability will need a larger number of genotypes and phenotypes than high heritability traits in order to obtain an acceptable accuracy (Calus and Veerkamp, 2007). Moreover, GS accuracy also depends on other factors such as the effective population size, the size of the genome, the density of the markers, and the genetic architecture of the trait. In a theoretical study, Goddard (2009) found that the sample size required to obtain an accuracy of 0.88 when a trait is controlled by many polymorphisms with a very small effect (a nearly infinitesimal model) is 10 times larger than when the trait is controlled by 100 quantitative trait loci (QTL) with moderate effects. Consequently, the success of GS is not straightforward for all situations and before it can be applied a thorough study of the selection trait and the population is required.

On the other hand, it is evident that GS offers great opportunities for selection in pigs. In a study of the GS of litter size in pigs, Forni *et al*. (2010) revealed 68% increase in accuracy of the breeding values of the training population over traditional selection (BLUP); Cleveland *et al*. (2010), using training populations of individuals with high accuracy of estimated breeding values (EBVs) in place of female reproduction phenotypes (total born and stillborn), obtained accuracies (0.83-0.63) similar to those reported for a range of traits in dairy cattle when similar-sized training populations (~3,000) were used; and Simianer (2009) showed the potential of applying GS for litter size in a two-breed scheme. This author reported that the genetic progress per year could be increased by 37% compared to the conventional scenario, and that the return on investment is an increase of €6.63 per euro invested in genotyping. Nevertheless, in spite of these results, the profitability of GS is not evident. Recently, simulated results showed a large decrease in accuracy after the second-third generation of GS (Toro and Varona, 2010; Ibáñez-Escriche and Blasco, 2011). Furthermore, these outcomes are in agreement with the results obtained for female reproduction traits in pigs (Cleveland *et al*., 2010). These authors found an important loss of accuracy when the training and validation data sets were separated by age (based on birth year). This seems to indicate that GS will require a constant re-evaluation of the associations between SNPs and, consequently, re-phenotyping and re-genotyping. This fact would increase the economic costs of GS, and it could limit its application in breeding schemes, such as in swine, where the generation interval is short and the value of the selection candidate is relatively low. As a conse-

quence, new genotyping strategies have been proposed to avoid these problems, such as combining the high-density genotyping of individuals selected for breeding with the low-density genotyping of selection candidates, or the use of low-density genotypes and imputing the missing genotypes using the genotype information from relatives.

One of the most important features of GS is that it opens up windows to new selection scheme designs and it evaluates novel phenotypes. In pig production, crossbreeding is widely used in order to take advantage of heterosis and breed complementarity. Genomic selection could use crossbred pigs as a training population in order to select purebreds (Ibáñez-Escriche *et al*., 2009), and it might allow a more effective selection for performance in the field (Kinghorn *et al*., 2010). Additionally, GS models can easily accommodate non-additive effects, which are valuable in crossbreeding performance, particularly in low heritability traits such as litter size. The estimation of dominant effects could allow mating for complementarities, therefore increasing the heterosis. Moreover, this strategy could also be applied to breeding for important traits at the field level which cannot be evaluated in nucleus herds, such as survival or diseases that are commonplace in the field but eliminated by bio-security in nucleus herds. However, this selection scheme has some weak points that have to be taken into account. The recording system in the populations must be well designed and implemented, otherwise the reliability of the field records would be low. Furthermore, there is a generation lag between crossbreeding and selection candidates that is difficult to reduce. Both factors, the reliability of field records and the generation lag, would directly hamper GS accuracy.

Poultry

The sequence genome was first available for poultry in 2004. Since then, the development of SNP panels for poultry has been fast. Three SNP panels of sizes 6, 12 and 42 K have come out in the last five years. In contrast to pigs, some studies of the whole genome evaluation have been published by Long *et al*. (2007) who identified sets of SNPs across the genome as classifiers for mortality, and by González-Recio *et al*. (2008, 2009), who showed a high predictive ability for the conversion rate and mortality in poultry by using non-parametric approaches. Nonetheless, the industry is still very conservative when it comes to implemen-

tation in the field, although an international GS experiment exists for GS implementation in layers (Avendaño *et al*., 2010). The main objective of this GS breeding program is the selection of commercially important traits that can only be directly recorded for one sex (egg production, egg weight, egg shell, etc.).The first results of this breeding program using genomic information revealed a substantial increase in the genetic response per year and a decrease in the inbreeding rate per year compared to the traditional program. These outcomes clearly showed the potential application of GS over traditional selection in these particular traits. The implementation of genomic information in these poultry breeding programs seems to be clear. However, the practical benefits (cost effectiveness) of GS in commercial poultry breeding have not yet been verified.

Poultry and pigs have comparable breeding schemes and comparable traits where GS is promising for genetic improvement. Therefore, the approaches mentioned for pigs could be generalized for the poultry breeding context. Both species also have common challenges for GS implementation, such as the genotyping cost, that might be overcome by redesigning the breeding programs.

Rabbits

The rabbit breeding schemes are similar to those described previously in monogastric animals. Hence, similar advantages are expected with GS implementation. However, there are three main factors that currently limit GS applications: 1) the SNP chip is still not available although the rabbit genome is being sequenced, 2) rabbits have a shorter generation interval and 3) the smaller economic value of a parental rabbit compare to a parental pig. In addition, rabbit production is restricted to certain countries and its economic importance is smaller than the poultry or pig industries. As a consequence, is difficult to justify the economic cost of GS in this particular case. Nonetheless, further research should reduce the genotyping costs for traits of special interest, such as diseases.

Fish

In the last few years aquaculture has become an important production system. However, selection programs are only available for a few species (*e.g.* salmonids, shrimp and tilapia). Most of the aquaculture species use mass selection (for growth) and the breeding programs with higher levels of technology are family-based, using information on siblings of the candidates. This sibling test scheme is used for traits that cannot be directly measured in the selection candidates (*e.g.* disease resistance, slaughter quality traits or maturation), in which only 50% of the genetic variation is exploited. As with other species, GS could be relevant for these particular traits. Moreover, GS might be able to deal with two important challenges in the fish industry: the lack of pedigree recording and the large increase in inbreeding with traditional selection.

In contrast to other species, no dense marker maps and few high-throughput genotyping platforms are currently available for fish. Therefore, actual applications of GS in fish remain unknown and only a few studies based on computer simulations have been performed (Nielsen *et al*., 2009; Sonesson and Meuwissen, 2009; Villanueva *et al*., 2010). All of these studies indicated that aquaculture breeding companies can increase the accuracy of selection when using GS, both in continuous and dichotomous traits. Particularly, Sonesson and Meuwissen (2009) found that GS increased the genetic gain when the re-estimation of marker effects was performed every generation or every second generation, and that inbreeding was reduced by 81% compared to classical selection. These results would make GS a promising tool in breeding schemes for fish because inbreeding is a central problem in the aquaculture industry. Estimates of inbreeding depression in fish clearly showed that the consanguinity negatively affected progeny viability, fertility and growth (Gjerde *et al*., 1983; Su *et al*., 1996). As mentioned before, the GS strategy still involves a high economic cost, which can be partly recovered by genetic gain and the reduction of sibling testing compared to classical selection. However, further research to determine the optimal number of fish to genotype is needed.

Apart from increasing the genetic gain, GS can offer additional advantages over traditional methods in aquaculture. For instance, Ødegård *et al*. (2009a,b) showed the success of GS for the introgression of desirable genes in a population, such as resistance to specific diseases. They found that backcrossing schemes using GS are a fast way of producing a more resistant line that is still commercially competitive. This application could also be generalized to other species and, as the authors pointed out, it could be utilized for the introgression of genetic material from commercial strains into locally adapted populations.

Table 1. Main challenges of genomic selection application

Species	Field implementation status	Main problems	Main advantages and challenges
Dairy cattle	Already implemented	— Industry is reluctant to changes in the breeding management decisions — Accuracies of > 90% are still priority for most farmers — Large relative weight of semen companies in the breeding decisions	— Large generation intervals — Good data recording systems — High economic value of individuals — Well organized populations
Beef cattle	Preliminary	— Small populations — Cross breeding — Lack of well established breeding goals in local populations — Not well established data recording schemes — Limited use of artificial insemination	— Large generation intervals — High economic value of individuals
Sheep &goats	Preliminary	— DNA chips development — Small economic value of individuals	— Paternity and maternity tests
Pigs	Preliminary	— Genotyping cost — Lack of data recording at the farm level	— Increase accuracy in traits that are difficult to measure — Implementations in cross-breeding — Good control of animals in the nucleus — Breeding decisions from in-farms and slaughter house information
Rabbits	Unknown	— DNA chips development — Small economic value of individuals	— Increase accuracy difficult traits
Fish	Unknown	— DNA chips development — Small economic value of individuals	— Reduction of inbreeding — Avoid sib testing

Main advantages and limitations for GS implementation in each species is summarized in Table 1.

Advances in the use of low density chips

As stated throughout this work, the cost of genotyping is one of the main limitations of the implementation of GS in most breeding programs. Low density SNP panels (LD-SNP) are an interesting strategy for reducing the genotyping cost of selecting candidates. Habier *et al.* (2009) and Weigel *et al.* (2009; 2010b) confirmed small losses in accuracy on the genomic predictions of selection candidates genotyped by LowD-SNP panels compared to use high density SNP panels (HD-SNP).

Two main approaches have been proposed in order to construct reduced SNP panels: 1) selecting SNPs that show strong associations with phenotype (*e.g.* Weigel *et al.*, 2009), and 2) panels of evenly spaced SNPs (Habier *et al.*, 2009) to exploit co-segregation information within families in order to track SNPs in the high-density SNP panel. Both strategies have shown valuable results. Weigel *et al.* (2009) showed that the evenly spaced LD-SNP strategy led to worse results than using the same amount of SNPs pre-selected by a strong association with the phenotype. This approach is less attractive for multiple traits selection and across populations, as it requires specific SNPs for each trait and population (Cleveland *et al.*, 2010). Moreover, a re-selection of SNPs would be necessary because the allele frequency may vary with selection over generations and thus resulting in a loss of accuracy in GEBV predictions.

The second alternative is to use the information from low-density panels from evenly spaced SNPs to impute dense genotypes on individuals with sparse genotypes

(Goddard and Hayes, 2008). Based on this central idea, Goddard and Hayes (2008) proposed a genotyping strategy where the key ancestors are genotyped with dense panels and the selection candidates are genotyped with standard low-density panels. Then, the chromosome segments in the selection candidates are traced back to the key ancestors and thus their genotypes are inferred at all markers assayed on the key ancestors. Nevertheless, this strategy requires the pedigree and its success depends on two main factors: the effective size of the founder population and the choice of the ancestors (Goddard, 2009). Weigel *et al.* (2010a) demonstrated that missing genotypes can be inferred from genotypes or haplotypes of relatives or from matching allele patterns in the general population, and that this could be useful for combining genotypes of different densities in a reference population. These authors showed that Low-D panels of 2,994 SNPs could be achieved, and that after imputation to 42 K SNPs, an equal predictive accuracy as for the real 42 K panel for milk yield and only a slight reduction by 4% for protein percentage and pregnancy rate were found. This strategy could make GS cost effective in species where it is currently not possible. Furthermore, it could also solve the problem of new generations of high-density SNP panels because only the key ancestors need to be genotyped. In the near future, the density of markers might become obsolete due to full genome sequencing. This information will be integrated to combine full sequences and imputed missing genotypes (*in silico* genome sequence; Daetwyler *et al.*, 2009). Additionally, this technology will allow the accuracy of genomic breeding values to be increased, since further knowledge of causal polymorphisms is expected to appear. Nonetheless, some pre-selection of markers or genome pieces is likely to be performed with current state of the art computations, although it is expected that new software and hardware will be available in the future.

Conclusions

Genomic selection offers new breeding challenges and possibilities in livestock species. We have highlighted the necessity of adapting the breeding program of each species and even each population to GS, because the most efficient way to proceed is usually case and current status dependent. The incorporation of genomic information into the breeding programs must be care-

fully considered. The available information, selection objectives, production circumstances and benefit/cost analysis must be evaluated in order to decide whether or not the population is suitable for GS implementation, and which would be the most convenient way, if any, for its implementation.

The challenges, opportunities and weaknesses that have been raised here are valid under current technologies and circumstances, and it must be pointed out that they may change in the future if new genotype sequencing methodologies come into the picture. In the meantime, breeding programs should take advantage of the state-of-the-art methods and technologies to increase their profitability.

The authors of this article are aware that the state of the art in genomic selection and its application in the breeding programs is evolving fast, and many of the questions, challenges and pitfalls may be solved in the near future without precluding the overview in the general problems and opportunities commented in this article at the present time.

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