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Challenges related to introducing genomic selection in sport horse breeding

EAAP 2015



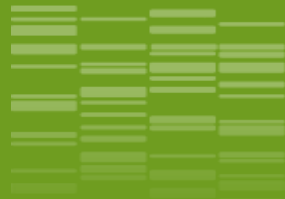
« That is the question... »

- ❖ Genomic selection had radically changed the breeding structure in dairy cattle



- ❖ Why not in sport horses ?





_01

Positive facts

..about horse genomic

Positive facts about horse genomic

❖ Commercial High Density Beadchip available

- Genome Sequence 2007, Equ Cab2.0 2009
- First SNP chip Illumina 54k, 74k (-> publications from 2010)
- High density Affymetrix 670 k (2015)



Genome Sequence, Comparative Analysis, and Population Genetics of the Domestic Horse

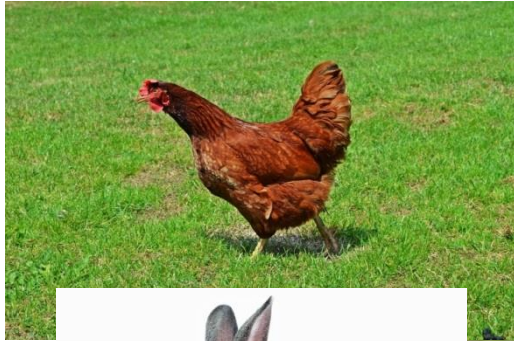
C. M. Wade, *et al.*

Science **326**, 865 (2009);

DOI: 10.1126/science.1178158

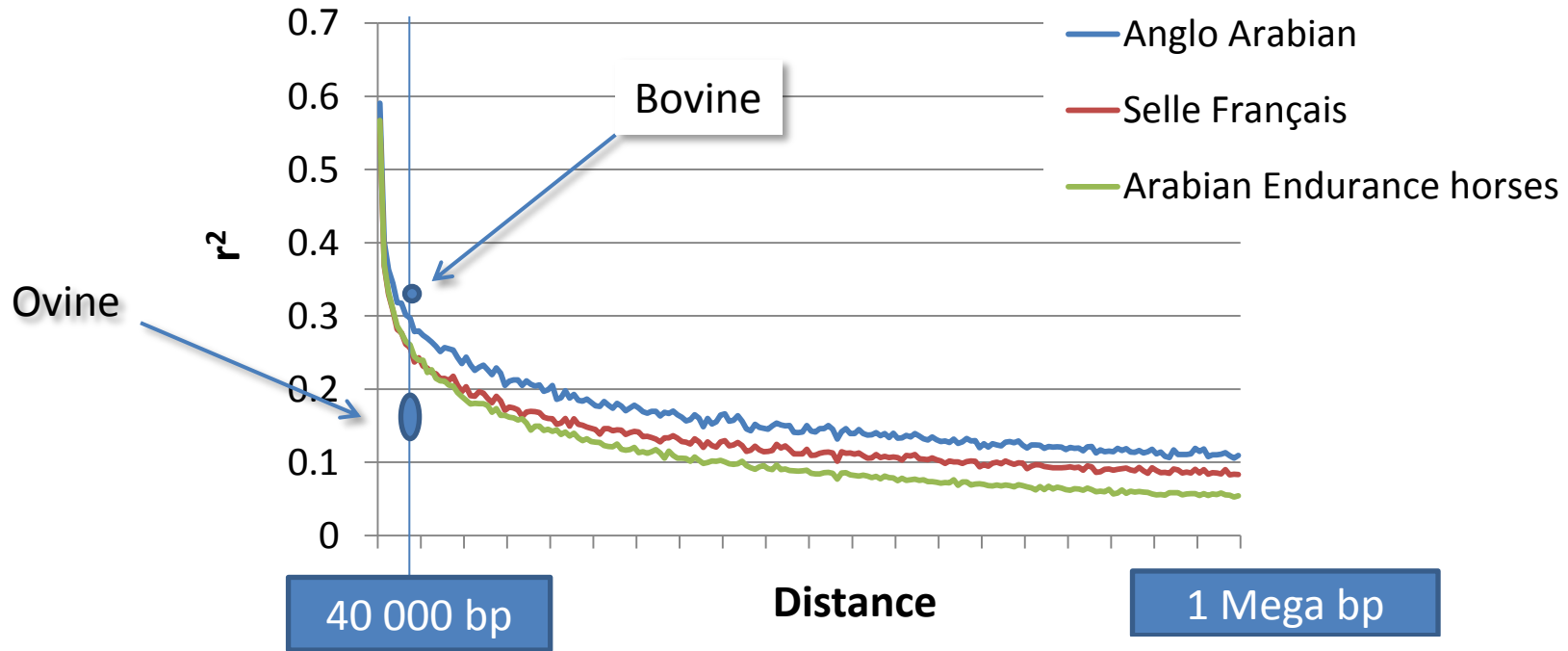
Positive facts about horse genomic

- ❖ Low cost compared to the price of the animal



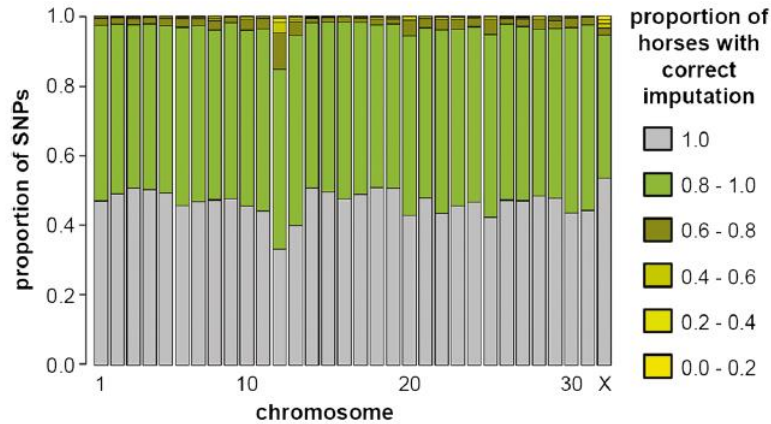
Positive facts about horse genomic

- ❖ Good linkage disequilibrium at small distance between SNPs



Positive facts about horse genomic

❖ Positive feelings about imputation



Practical applications possible at a lower cost

Frischknecht et al. *Genetics Selection Evolution* 2014, **46**:63
<http://www.gsejournal.org/content/46/1/63>

GSE Genetics Selection Evolution

RESEARCH

Open Access

Imputation of sequence level genotypes in the Franches-Montagnes horse breed

Mirjam Frischknecht^{1,2,3,4}, Markus Neuditschko^{1,3}, Vidhya Jagannathan^{2,3}, Cord Drögemüller^{2,3}, Jens Tetens⁵, Georg Thaller⁵, Tosso Leeb^{2,3,1} and Stefan Rieder^{1,3,1}

Corbin et al. *Genetics Selection Evolution* 2014, **46**:9
<http://www.gsejournal.org/content/46/1/9>

GSE Genetics Selection Evolution

RESEARCH

Open Access

The utility of low-density genotyping for imputation in the Thoroughbred horse

Laura J Corbin¹, Andreas Kranis², Sarah C Blott³, June E Swinburne³, Mark Vaudin³, Stephen C Bishop¹ and John A Woolliams^{1*}

Positive facts about horse genomic

❖ Place in breeding plans : optimistic prospects



Proceedings, 10th World Congress of Genetics Applied to Livestock Production

Towards Genomic Selection in Danish Warmblood Horses: Expected Impacts and Selective Genotyping Strategy

Thomas Mark¹, Lina Jönsson^{1,2}, Maiken Holm³ & Karina Christiansen²

¹University of Copenhagen, ²The Danish Warmblood Horse Breeding Society, ³The Knowledge Centre for Agriculture,



Integration of genomic information into sport horse breeding programs for optimization of accuracy of selection

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Positive facts about horse genomic

❖ Place in breeding plans

- Not in the same situation than dairy cattle. In dairy cattle breeding plans, the **accuracy was high** due to progeny test with a **selection intensity moderate** and **long generation interval**. Genomic selection decreased (slightly) the accuracy but also decreased generation interval and increased selection intensity (larger base)
- In sport horse optimized plans (assuming that breeding evaluation are used at each stage of selection which already could be the case, even if not in practice always the case), the selection is mostly based on own performances with **moderate accuracy** but **high selection intensity**. The **long generation interval** is not due to progeny test but to biology of the species (age at first performance) and to the long use of stallions



Available online at www.sciencedirect.com

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Livestock Science 118 (2008) 99–112

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Optimization of breeding schemes for sport horses

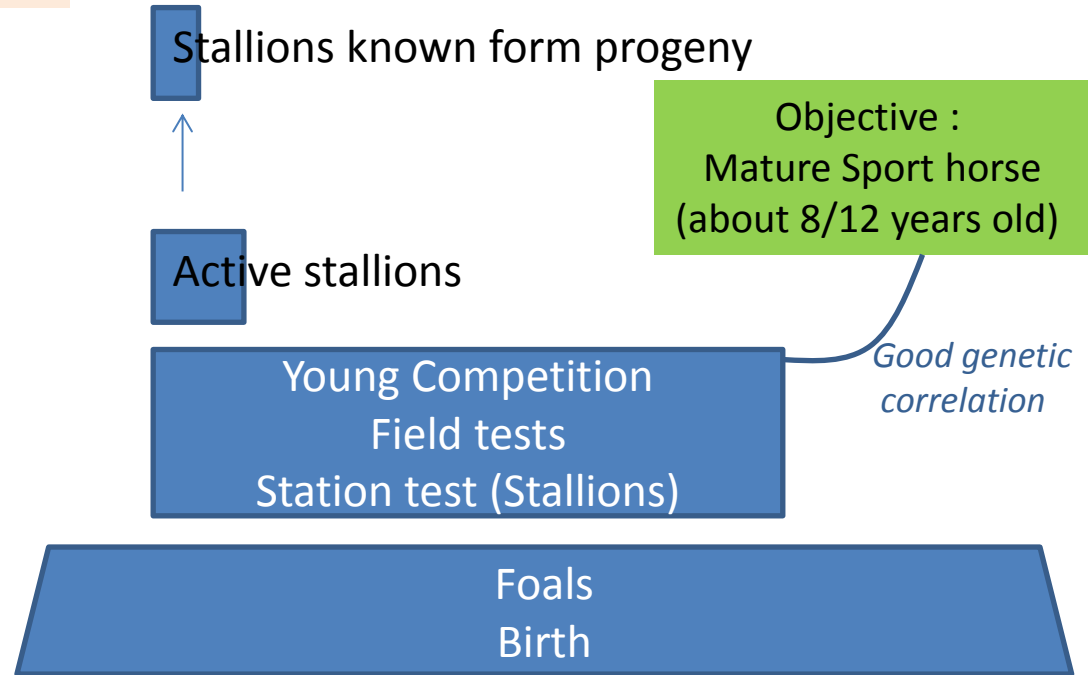
C. Dubois, E. Manfredi, A. Ricard*

Station d'Amélioration Génétique des Animaux, Institut national de la recherche agronomique, 31326 Castanet-Tolosan, France

Received 6 July 2007; received in revised form 9 January 2008; accepted 9 January 2008

Positive facts about horse genomic

Accuracy	Selection rate	Age
0.84-0.77	35%-20%	12 years
0.47- 0.59	2%-4%	3-5 years



Positive facts about horse genomic

Accuracy	Selection rate	Age
0.84-0.77	35%-20%	12 years

0.47- 0.59 2%-4% 3-5 years

Stallions known form progeny

Active stallions

Objective :
Mature Sport horse
(about 8/12 years old)

Young Competition
Field tests
Station test (Stallions)

*Good genetic
correlation*

Foals
Birth

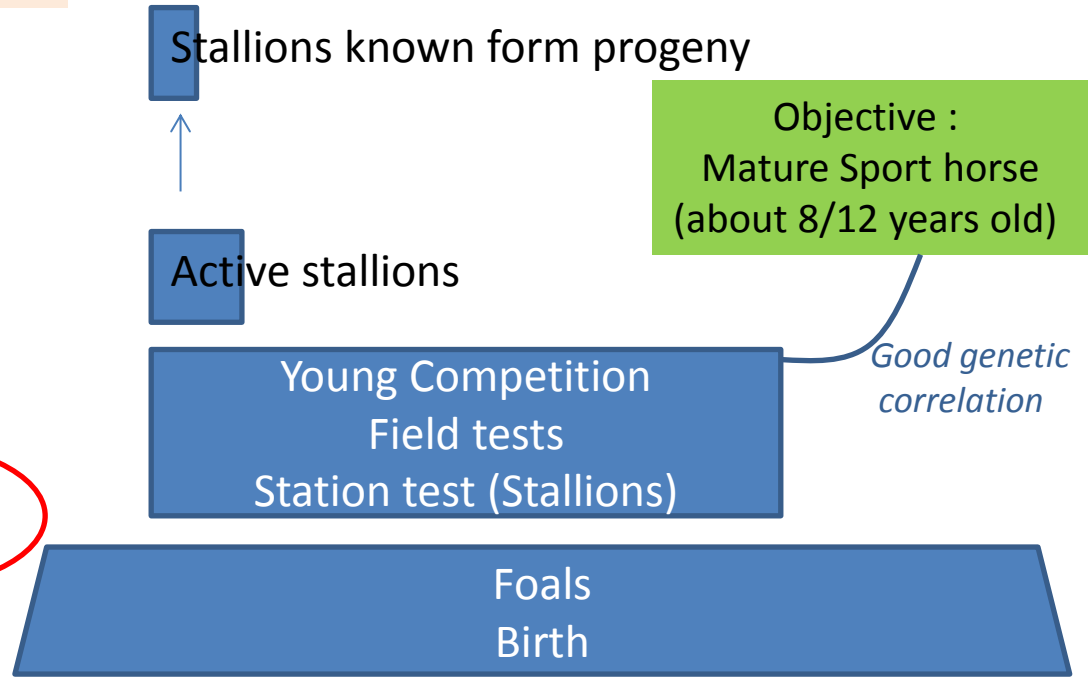
Positive facts about horse genomic

Accuracy	Selection rate	Age
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0.84-0.77	35%-20%	12 years
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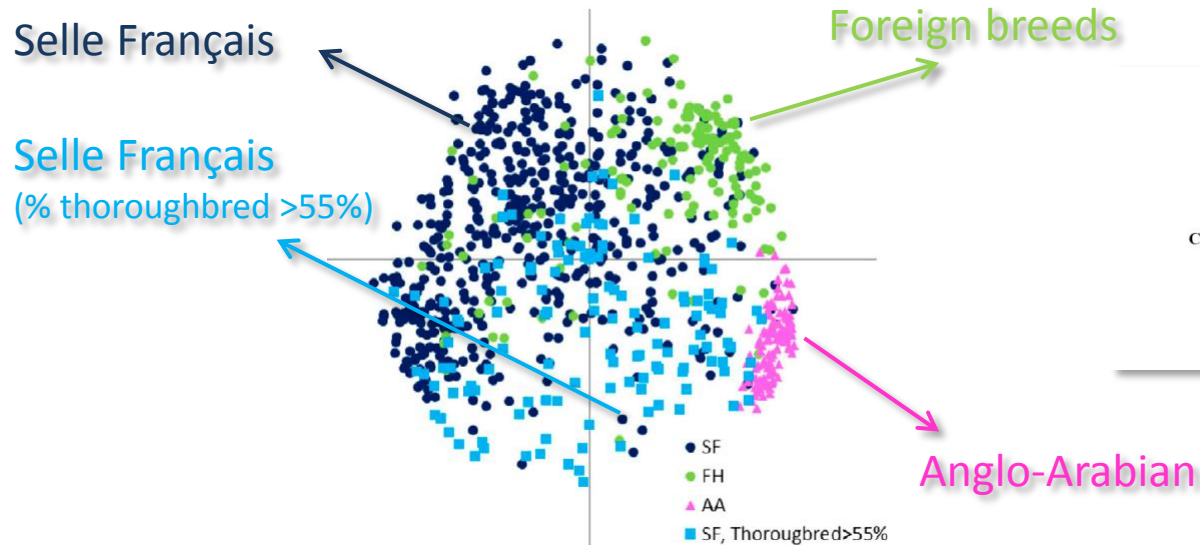
0.47- 0.59	2%-4%	3-5 years
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1-2 years



Positive facts about horse genomic

- ❖ To build international reference population we will need to use multiple European sport breeds which possibly is known to decrease accuracy of genomic evaluation but...



JOURNAL OF ANIMAL SCIENCE

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Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses
A. Ricard, S. Danvy and A. Legarra

J ANIM SCI 2013, 91:1076-1085.
doi: 10.2527/jas.2012-5256 originally published online December 10, 2012

Positive facts about horse genomic

❖ Selection of new/difficult traits



ELSEVIER

Livestock Production Science 88 (2004) 77–84

LIVESTOCK
PRODUCTION
SCIENCE

www.elsevier.com/locate/livprodsci

An overview of breeding objectives for warmblood sport horses

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^b*Irish Horse Board, Maynooth Business Campus, Maynooth Co. Kildare, Ireland*


^c*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Box 7023, S-750 07 Uppsala, Sweden*

Received 30 January 2003; received in revised form 7 October 2003; accepted 10 October 2003

- Health
- Behavior
- Fertility

Positive facts about horse genomic

❖ Selection of new/difficult traits



vit IT-Solutions for Animal Production
S46 (abstract no. 18963)
65th EAAP Annual Meeting, 25-29 August 2014, Copenhagen / Denmark
Systematization of recording and use of equine health data and its potential for horse breeding
K.F. Stock^{1*}, S. Sarnowski¹, E. Kalm², R. Reents¹
¹ Vereinigte Informationssysteme
² Institute for Animal Breeding
Email: friederike.katharina.stoc

Preventive Veterinary Medicine 109 (2013) 92–105

Contents lists available at SciVerse ScienceDirect

Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed



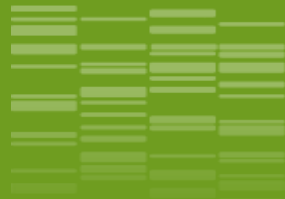
Monitoring of equine health in Denmark: The importance, purpose, research areas and content of a future database

Wendy Hartig^{a,*}, Hans Houe^a, Pia Haubro Andersen^b

^a University of Copenhagen, Faculty of Health and Medical Sciences, Large Animal Sciences, Groennegårdsvej 8, 1870 Frederiksberg C, Denmark
^b Swedish University of Agricultural Sciences, Faculty of Veterinary Medicine and Animal Science, Box 7054, 75007 Uppsala, Sweden

- Health
- Behavior
- Fertility

Genomic selection is well known to help selection for these traits because measurement on a smaller reference population can be used for the whole population.



_02

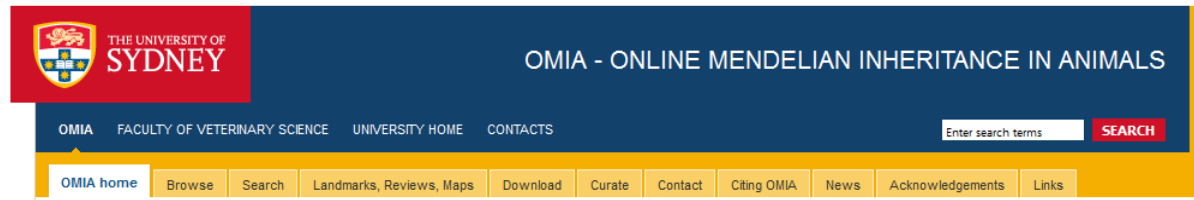
Challenges

..about horse genomic

Technical Challenges about horse genomic

❖ Lower entries in the Online Mendelian Inheritance in Animals (OMIA) database

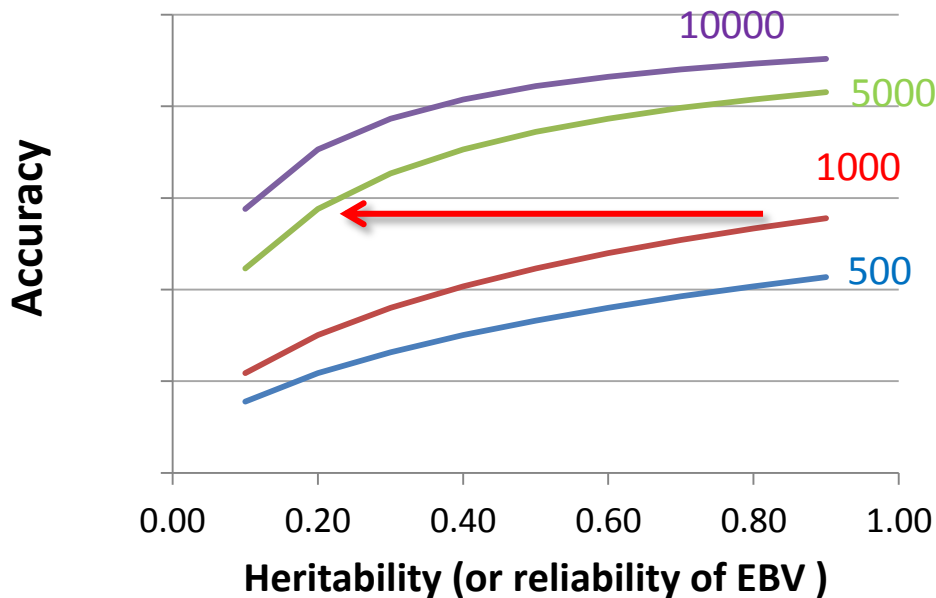
- Horse genome is not as well annotated than others



➤ Which may cause problems to exploit GWAS

Technical Challenges about horse genomic

- ❖ The size of potential reference population is small because thousands of stallions do not exist as thousands of bulls...



...So you can also use performers.
But in that case a very larger
population is needed.

Journal of
Animal Breeding and Genetics

J. Anim. Breed. Genet. ISSN 0931-2668

ORIGINAL ARTICLE

Using the genomic relationship matrix to predict the accuracy of genomic selection

M.E. Goddard^{1,2}, B.J. Hayes² & T.H.E. Meuwissen³

- 1 Department of Agriculture and Food Systems, University of Melbourne, Melbourne, Vic., Australia
- 2 Biosciences Research Division, Victorian Department of Primary Industries, Bundoora, Vic., Australia
- 3 Norwegian University of Life Sciences, Ås, Norway

Technical Challenges about horse genomic

❖ Few QTLs regardless bovine breeds

- DMRT3 / MSTN are the success stories for performances but not very useful in sports (for example the frequency of A allele at DMRT3 <1% in SF)



BMC
Genomics



A genome-wide SNP-association study confirms a sequence variant (g.66493737C>T) in the equine myostatin (MSTN) gene as the most powerful predictor of optimum racing distance for Thoroughbred racehorses

Hill et al.

BioMed Central

Hill et al. BMC Genomics 2010, 11:332
<http://www.biomedcentral.com/1471-2164/11/332> (11 October 2010)

Technical Challenges about horse genomic

❖ Few QTLs regardless bovine breeds

- DMRT3 / MSTN are the success stories for performances but not very useful in sports (for example the frequency of A allele at DMRT3 <1% in SF)
- Some Genes for Mendelian diseases and coat colors
- One strong QTL on height (but not always polymorphic in interested populations, $p < 2\%$ in Arabian for example)

OPEN ACCESS Freely available online



A Genome-Wide Association Study Reveals Loci Influencing Height and Other Conformation Traits in Horses

Heidi Signer-Hasler¹, Christine Flury¹, Bianca Haase^{2,3}, Dominik Burger⁴, Henner Simianer⁵, Tosso Leeb², Stefan Rieder^{4*}

¹ School of Agricultural, Forest and Food Sciences, Bern University of Applied Sciences, Zollikofen, Switzerland, ² Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, ³ Faculty of Veterinary Science, University of Sydney, New South Wales, Australia, ⁴ Agroscope Liebefeld-Posieux Research Station Agroscope Liebefeld-Posieux (ALP) Haras, Swiss National Stud Farm (SNSTF), Avenches, Switzerland, ⁵ Department of Animal Sciences, Georg-August-Universität, Göttingen, Germany

Technical Challenges about horse genomic

❖ Few QTLs regardless bovine breeds

ANIMAL GENETICS Immunogenetics, Molecular Genetics
and Functional Genomics

doi:10.1111/j.1365-2052.2011.02265.x

A genome-wide association study for quantitative trait loci of show-jumping in Hanoverian warmblood horses

W. Schröder, A. Klostermann, K. F. Stock and O. Distl

Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Bünteweg 17p, 30559 Hannover, Germany



- ... but there were also GWAS on Jumping (eventing) that did not reveals interesting QTL -> impact on genomic selection ?

ANIMAL GENETICS Immunogenetics, Molecular Genetics
and Functional Genomics

SHORT COMMUNICATION

doi: 10.1111/age.12245

Genome-wide association study for jumping performances in French sport horses

S. Brard^{*†‡} and A. Ricard^{§¶}

^{*}INRA, GenPhySE (Génétique Physiologie et Systèmes d'Élevage), F-31326 Castanet-Tolosan, France. [†]INP, ENSAT, GenPhySE (Génétique Physiologie et Systèmes d'Élevage), Université de Toulouse, F-31326 Castanet-Tolosan, France. [‡]INP, ENVT, GenPhySE (Génétique Physiologie et Systèmes d'Élevage), Université de Toulouse, F-31076 Toulouse, France. [§]INRA, UMR 1313, 78352 Jouy-en-Josas, France. [¶]IFCE, Recherche et Innovation, 61310 Exmes, France.

Technical Challenges about horse genomic

❖ Low accuracy for the only reference in sport horses

Table 1. Correlation and regression between pseudo-phenotypes for show jumping and genetic evaluation from genealogy (BLUP), or from SNP using genomic BLUP method (GBLUP) or BayesC π method (BayesCPI) in 3 different validation data sets.

Genetic evaluation	Correlation		Regression	
	All breeds	SF + FH ¹	All breeds	SF + FH
Validation set 1 ²				
<i>N</i>	103	84	103	84
BLUP	0.36	0.28	0.99	0.87
GBLUP	0.39	0.30	0.77	0.72
BayesCPI	0.39	0.29	0.74	0.69

JOURNAL OF ANIMAL SCIENCE

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Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses

A. Ricard, S. Danvy and A. Legarra

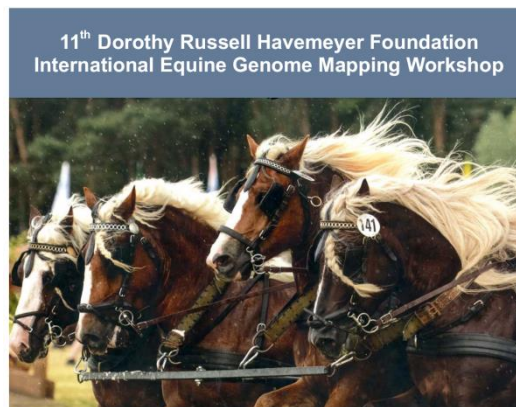
J ANIM SCI 2013, 91:1076-1085.

doi: 10.2527/jas.2012-5256 originally published online December 10, 2012

Technical Challenges about horse genomic

❖ But perhaps just bad luck :

- Hill et al., in thoroughbred
- Brard et al. (see this session also) in trotters



Wednesday, July 22 - Saturday, 25, 2015

Technical Challenges about horse genomic

❖ but we have to be precocious about expected reliability of genomic in species other than dairy cattle where the efficiency is proved.

OPEN ACCESS Freely available online

PLOS one

Accuracy of Predicting the Genetic Risk of Disease Using a Genome-Wide Approach

Hans D. Daetwyler^{1,2*}, Beatriz Villanueva³, John A. Woolliams¹

¹ Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Roslin, Midlothian, United Kingdom, ² Animal

Genetics (2009) 136:245–257
DOI: 10.1007/s10709-008-9308-0

Genomic selection: prediction of accuracy and maximisation of long term response

Mike Goddard

J. Anim. Breed. Genet. ISSN 0931-2668

ORIGINAL ARTICLE

Using the genomic relationship matrix to predict the accuracy of genomic selection

M.E. Goddard^{1,2}, B.J. Hayes² & T.H.E. Meuwissen³

¹ Department of Agriculture and Food Systems, University of Melbourne, Melbourne, Vic., Australia
² Biosciences Research Division, Victorian Department of Primary Industries, Bundoora, Vic., Australia
³ Norwegian University of Life Sciences, Ås, Norway

ANNUAL REVIEWS

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Selection

Theo Meuwissen,¹ Ben Hayes,² and Mike Goddard³

¹Department of Animal and Aquaculture Sciences, Norwegian University of Life Sciences, Ås, Norway 1430; email: theo.meuwissen@umb.no

²Biosciences Research Division, Department of Primary Industries, Bundoora 3083, Australia; email: ben.hayes@dpi.vic.gov.au

³Melbourne School of Land & Environment, University of Melbourne, Victoria 3010, Australia; email: mike.goddard@nrc.vic.gov.au

- All optimistic results about interest of genomic selection in horse breeding plans were obtained using theoretical formulae from publication of Daetwyler, Goddard and Meuwissen
- All these formulae made a lot of assumptions and widely depended on two parameters : the effective number of segments (Me) and the effective size of the population (Ne) , both unknown and hardly variable.

.024

03/09/2015

Technical Challenges about horse genomic

❖ ? Theoretical reliability ?

- ❖ This figure represents the difference between observed accuracy and predicted accuracy in 145 published results in 13 references (mainly dairy cattle) according to the effective number of segments (M_e) calculated using 5 different formulae from the effective size (N_e) and 4 equations proposed by Goddard, Meuwissen and Daetwyler.

Journal of
Animal Breeding and Genetics

J. Anim. Breed. Genet. ISSN 0931-2668

ORIGINAL ARTICLE

Is the use of formulae a reliable way to predict the accuracy of genomic selection?

S. Brard^{1,2,3} & A. Ricard^{4,5}

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2 Université de Toulouse, INP, ENSAT, GenPhySE (Génétique, Physiologie et Systèmes d'Élevage), Castanet-Tolosan, France

3 Université de Toulouse, INP, ENVT, GenPhySE (Génétique, Physiologie et Systèmes d'Élevage), Toulouse, France

4 INRA, UMR 1313, Jouy-en-Josas, France

5 IFCE, Recherche et Innovation, Exmes, France

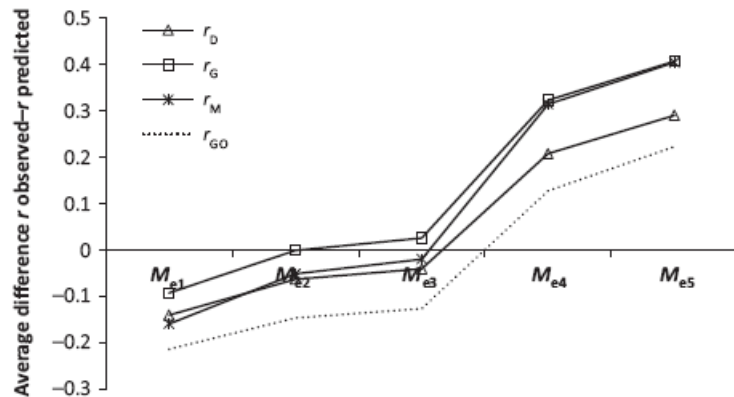


Figure 5 Average differences between the observed and predicted accuracies depending on the formulae for accuracy r and for the number of effective segments M_e .

Political Challenges about horse genomic

- ❖ Building an international reference population
 - The experience of Interstallion (European jumping)

Political Challenges about horse genomic

❖ Building an international reference population

- The experience of Interstallion (European jumping)



Available online at www.sciencedirect.com



Livestock Science 118 (2008) 147–156

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Connectedness among five European sport horse populations

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^b Interbull Centre, Swedish University of Agricultural Science

Received 15 August 2006; received in revised form 5 December



Available online at www.sciencedirect.com



Livestock Science 120 (2009) 75–86

LIVESTOCK
SCIENCE

www.elsevier.com/locate/livsci

Genetic connectedness between seven European countries for performance in jumping competitions of warmblood riding horses

C. Ruhlmann^{a,*}, E. Bruns^b, E. Fraehr^c, J. Philipsson^d, S. Janssens^e, K. Quinn^f,
E. Thorén Hellsten^d, A. Ricard^a

^a Station d'Amélioration Génétique des Animaux (SAGA), Institut National de la Recherche Agronomique (INRA),

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Received in revised form 23 April 2008; accepted 24 April 2008

Livestock Science 122 (2009) 234–240

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci



Genetic correlations between horse show jumping competition traits in five European countries

C. Ruhlmann^a, S. Janssens^b, J. Philipsson^c, E. Thorén-Hellsten^c, H. Crolley^d, K. Quinn^e,
E. Manfredi^a, A. Ricard^{a,*}

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Genetic correlation mostly
 ≥ 0.86

Political Challenges about horse genomic

❖ Building an international reference population

- The experience of Interstallion (European jumping)
- The Nordic project

Journal of
Animal Breeding and Genetics

J. Anim. Breed. Genet. ISSN 0931-2668

ORIGINAL ARTICLE

Genetic conditions of joint Nordic genetic evaluations of lifetime competition performance in warmblood sport horses

Å. Viklund¹, S. Furre², S. Eriksson¹, O. Vangen² & J. Philipsson¹

¹ Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

² Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway

Conclusion

❖ Positive facts

- High linkage disequilibrium at small distance
- Commercial High Density Beadchip available
- Low cost compared to the price of the animal
- Positive feelings about imputation
- Place in breeding plans : optimistic prospects
- Close European breeds
- Selection of new/difficult traits

❖ Challenges

- Lower annotation of the genome
- The size of potential reference population is small
- Few QTLs regardless bovine breeds
- Low accuracy for the only reference in sport horses
- ? Theoretical reliability ?
- Building an international reference population



- ❖ Acceptation by breeders ?
Easier than for traditional genetic ?