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Didier Boichard, Vincent Ducrocq, Pascal Croiseau, Sebastien S. Fritz

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How is genomics changing cattle breeding?

Thursday, July 21, 2016: 2:45 PM

Grand Ballroom J (Salt Palace Convention Center)

Didier Boichard , GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France
Vincent Ducrocq , GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France
Pascal Croiseau , GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France
Sebastien Fritz , GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France

Abstract Text: Genomic selection offers considerable flexibility to increase genetic trends in dairy cattle breeding, through a decrease in generation interval, an increase in selection intensity, and an increase in reliability for females and for low heritability traits. It is also an opportunity for more sustainable breeding, in terms of breeding goal and genetic variability. With a shorter generation interval, there is a big risk of increasing inbreeding if semen dissemination policy of elite bulls is not changed. However, using a large number of young bulls both as service bulls and bull sires is a simple solution for both maximizing genetic trend while reducing inbreeding trend. Female genotyping is a key challenge for within herd selection and, simultaneously, for replacing current reference populations based upon progeny tested bulls, assembling new ones in breeds of more limited size, and for selection of newly recorded traits. At a reasonable price and coupled with use of sexed semen, female genotyping is profitable for the farmers and is becoming a routine practice in an increasing number of herds. New applications are generated such as renovated mating plans, efficient management of genetic defects, prediction of cows' future career and optimization of culling policy. With more diverse bulls on the market and with female genotyping, genomic selection also opens new avenues for more customized breeding across herds or production systems. A big challenge is to reduce the dependency of genomic predictions on relationship between candidates and the reference population. A strong effort is presently dedicated to integrating genome sequence information into predictions, in order to improve their accuracy and persistency. To increase the accuracy, within and especially across breeds, causal variants or very close proxies should be identified and included in the predictions, while discarding or limiting the weight of many other variants generating noise. In the longer term, further customization of selection will be possible by accounting for GxE interactions. Important developments are also necessary to decrease loss of favorable alleles through genetic drift.

Keywords: dairy cattle; genomic selection

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Meeting Information

When:

July 19 - 23, 2016

Where:

Salt Lake City, UT

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