

## Session 02.

## Challenges – Improving genomic prediction (1)

Room: Grote Zaal

Chair: Mario Calus, Andres Legarra, Gustavo de los Campos

- 10:00 [Accuracy of prediction for a genomic evaluation in rotational crossbreeding scheme: Montbéliarde x Holstein x Red Danish](#)  
*Croiseau, P.; Saintilan, R.; Baur, A.; Croué, I.; Ducrocq, V.; Thomasen, J.R.; Karaman, E.; Boichard, D.; Leclerc, H.; Cuyabano, B.C.D.*
- 10:02 [Genomic evaluation for two-way crossbred performance in cattle](#)  
*Mei, Q.; Liu, H.; Xiang, T.; Christensen, O.*
- 10:04 [Improving accuracy of genomic prediction in distant populations by collecting sequence data over generations](#)  
*Nawaz, M.Y.; Gondro, C.*
- 10:06 [Comparison of genomic prediction methods for residual feed intake in broilers](#)  
*He, Z.; Li, S.; Li, W.; Ding, J.; Zheng, M.; Li, Q.; Fahey, A.G.; Wen, J.; Liu, R.; Zhao, G.*
- 10:08 [Impact of foreign phenotype data on single-step genomic evaluation of test-day protein yields for German Holsteins](#)  
*Alkhoder, H.; Liu, Z.; Segelke, D.; Reents, R.*
- 10:10 Discussion
- 10:15 [Extend mixed models to multi-layer neural networks for genomic prediction including intermediate omics data](#)  
*Zhao, T.; Zeng, J.; Cheng, H.*
- 10:30 [The holobiont ‘predictome’ of immunocompetence in pigs](#)  
*Calle-García, J.; Ramayo-Caldas, Y.; Zingaretti, L.M.; Quintanilla, R.; Ballester, M.; Pérez-Enciso, M.*
- 10:45 [The long and short of Nanopore genomic prediction: the effect of read length on prediction accuracy](#)  
*Lamb, H.; Nguyen, L.; Randhawa, I.; Hayes, B.; Ross, E.*
- 11:00 [Accuracy of genomic prediction of dry matter intake in Dutch Holsteins using sequence variants from meta-analyses](#)  
*Gredler-Grandl, B.; Raymond, B.; Chitneedi, P.K.; Cai, Z.; Panzanilla-Pech, C.I.V.; Fischer, D.; Bolormaa, S.; Chud, T.S.; Wang, Y.; Li, C.; Villanueva, B.; Fernandez, A.; Kuehn, C.; Lidauer, M.H.; Pryce, J.E.; Plastow, G.; Baes, C.F.; Charfeddine, N.; Veerkamp, R.F.; Bouwman, A.C.*
- 11:15 [Genomic prediction of bull fertility in Italian Brown Swiss cattle](#)  
*Pacheco, H.A.; Battagin, M.; Rossoni, A.; Cecchinato, A.; Peñagaricano, F.*
- 11:30 [On the use of SNPs of large effect to improve prediction accuracy in pigs](#)  
*Lopes, M.S.; Derks, M.F.L.; Van Son, M.; Gjuvstad, A.B.; Sevilano, C.A.; Grindflek, E.; Knol, E.F.*

11:45 [Including environmental variables in genomic models for carcass traits in Hanwoo beef cattle](#)  
*Makanjuola, B.O.; Rovere, G.; Cuyabano, B.C.D.; Lee, S.H.; Gondro, C.*

## Session 08.

## Challenges – Improving genomic prediction (2)

Room: Grote Zaal

Chair: Mario Calus, Andres Legarra, Gustavo de los Campos

13:30 [Considering chromosomal trait correlations improves accuracy of genomic prediction](#)

*Schmidtman, C.; Segelke, D.; Bennewitz, J.; Tetens, J.; Thaller, G.*

13:32 [Effects of truncation and false positives in selection of markers for genomic prediction](#)

*Loh, Z.; Van Der Werf, J.H.J.; Clark, S.*

13:34 [Genomic selection for breeding values under identity disequilibrium](#)

*Cantet, R.J.C.; Angarita-Barajas, B.K.; Forneris, N.S.; Munilla, S.*

13:36 [Effect of informative polymorphism on accuracy of genomic prediction and heritability](#)

*Tahir, M.S.*

13:38 Discussion

13:45 [Long distance associations generate erosion of genomic breeding values of candidates for selection](#)

*Boichard, D.; Fritz, S.; Croiseau, P.; Ducrocq, V.; Cuyabano, B.; Tribout, T.*

14:00 [Definition of reliabilities for models with metafounders](#)

*Bermann, M.; Misztal, I.; Lourenco, D.; Aguilar, I.; Legarra, A.*

14:15 [A new metric to assess reference populations for genomic selection in Australian beef breeds](#)

*Moore, K.L.; Ferdosi, M.H.; Girard, C.G.; Walkom, S.F.; Johnston, D.J.*

14:30 [Decreasing computing cost of categorical data analysis](#)

*Hidalgo, J.; Misztal, I.; Tsuruta, S.; Bermann, M.; Garcia, A.; Retallick, K.; Lourenco, D.*

14:45 [Within and Across breed Single Step genomic prediction for somatic cell count including foreign information](#)

*Mrode, R.; Winters, M.W.; Coffey, M.*

15:00 [Using convolutional neural networks for image-based genomic prediction in mice](#)

*Perez, B.C.; Savchuk, A.; Duenk, P.; Calus, M.P.L.; Bink, M.C.A.M.*

15:15 [Selection for robustness: exploring the value of genomic prediction, reaction norm models and phenotyping strategies](#)

*Ghaderi-Zefreh, M.; Doeschl-Wilson, A.; Riggio, V.; Matika, O.; Pong-Wong, R.*