

Resultater offentliggjort i 2012

Peer reviewed publikationer:

Brøndum R F, Ma P, Lund M S, Su G. Short communication: Genotype imputation within and across Nordic cattle breeds. J. Dairy Sci. 95:6795–6800.

Brøndum R F, Su G, Lund M S, Bowman P J, Goddard M E, Hayes B J. Genome position specific priors for genomic prediction. BMC Genomics 2012, 13:543 doi:10.1186/1471-2164-13-543.

Buch, Line Hjortø; Kargo, Morten ; Berg, Peer; Lassen, Jan; Sørensen, Anders Christian. The value of cows in reference populations for genomic selection of new functional traits. Animal, Vol. 6, Nr. 06, 06.2012, s. 880-886.

Buch, Line Hjortø; Sørensen, Morten Kargo; Berg, Peer; Pedersen, Louise Dybdahl; Sørensen, Anders Christian. Genomic selection strategies in breeding programs: Strong positive interaction between application of genotypic information and intensive use of young bulls on genetic gain. Journal of Animal Breeding and Genetics, Vol. 129, Nr. 2, 04.2012, s. 138-151.

Edriss V., Guldbrandtsen B., Lund M. S., Su G., 2012. Effect of marker-data editing on the accuracy of genomic prediction. J. Animal Breeding and Genetics, doi:10.1111/j.1439-0388.2012.01015.x.

Gao H., Christensen O. F., Madsen P., Nielsen U. S., Zhang Y., Lund M. S., Su G., 2012. Comparison on genomic predictions using a GBLUP model and two single-step blending methods in the Nordic Holstein population. Gen Sel Evol, 44:8 doi:10.1186/1297-9686-44-8.

Henryon, Mark; Berg, Peer; Sørensen, Anders Christian; Ostensen, Tage; Nielsen, Bjarne. Most of the benefits from genomic selection can be realised by genotyping a proportion of selection candidates. Journal of Animal Science, 2012.

Höglund, Johanna Karolina; Guldbrandtsen, Bernt; Lund, Mogens Sandø; Sahana, Goutam 2012. Analyses of genome-wide association follow-up study for calving traits in dairy cattle. BMC Genetics 13(71):1-9.

Jensen J., Su G., Madsen. P., 2012. Partitioning additive genetic variance into genomic and remaining polygenic components for complex traits in Dairy Cattle. BMC Genetics 13:44 doi:10.1186/1471-2156-13-44.

Koivula M., Strandén I., Su G., Mäntysaari E. A., 2012. Different methods to calculate genomic predictions- Comparisons of BLUP at the single nucleotide polymorphism level (SNP-BLUP), BLUP at the individual level (G-BLUP), and the one-step approach (H-BLUP). J. Dairy Sci. 95:4065-73.

Pedersen, Louise Dybdahl; Kargo, Morten ; Berg, Peer; Voergaard, Jacob; Buch, Line Hjortø; Sørensen, Anders Christian. Genomic selection strategies in dairy cattle breeding programmes: Sexed semen cannot replace multiple ovulation and embryo transfer as superior reproductive technology. Journal of Animal Breeding and Genetics, Vol. 129, Nr. 2, 04.2012, s. 152-163.

Sahana G; Lund MS, Guldbrandtsen B, Thomsen B, Bendixen, C, Panitz FB. 2012. Genetic markers for mastitis resistance. Danish Patent Application No. PA 2012 70337.

Su G, Brøndum R. F., Ma P., Guldbrandtsen B, Aamand G. P., Lund M. S., 2012. Comparison of genomic predictions using medium-density (~54,000) and high-density (~777,000) single nucleotide polymorphism marker panels in Nordic Holstein and Red Dairy Cattle populations. J. Dairy Sci. 95 :4657–4665.

Su G., Madsen P., Nielsen U. S., Mäntysaari E. A, Aamand G.P., Christensen O. F., Lund M. S., 2012. Genomic prediction for the Nordic Red Cattle using one-step blending and selection index blending. *Journal of Dairy Science*, 95:909–917.

Thomasen J. R., Guldbrandtsen B., Su G., Brøndum R. F., Lund M. L., 2012. Reliabilities of genomic estimated breeding values in Danish Jersey. *Animal*, 6:789-796.

Internationale konferencebidrag:

Bouquet, Alban; Pedersen, Louise Dybdahl; Henryon, Mark; Sørensen, Anders Christian; Juga, Jarmo. Comparing Predictions of Response to Genomic Selection using Selection Index Theory and Genotype Simulations. I: *Book of Abstracts, ICQG2012*. Edinburgh, 2012. s. 137-137.

Guldbrandtsen, Bernt; Lund, Mogens Sandø; Sahana, Goutam. 2012. Patterns of Genomic Diversity among three Danish Dairy Cattle Breeds. *Book of Abstracts*. Vol. 18, Wageningen Academic Publishers 2012. s. 351.

Kadri, Naveen Kumar; Guldbrandtsen, Bernt; Sørensen, Peter; Sahana, Goutam. 2012. Comparison of Association Mapping Methods in Admixture Population. *Programme & Book of Abstracts of ICQG 2012*. Edinburgh, s. 232-232.

Liu, Huiming; Berg, Peer; Sørensen, Anders Christian; Norberg, Elise. Changes in allele frequency. I: *Book of Abstracts, ICQG2012*. Edinburgh, 2012. s. 158-159.

Sahana, Goutam; Guldbrandtsen, Bernt; Bendixen, Christian; Thomsen, Bo; Lund, Mogens Sandø. 2013. Genome-Wide Association Study with Sequence Variants Identifies Candidate Genes for Mastitis Resistance in Dairy Cattle. Abstract p *International Plant & Animal Genome XXI*, January 12-16, 2013 San Diego, CA, USA.

Sahana, Goutam; Guldbrandtsen, Bernt; Bendixen, Christian; Thomsen, Bo; Lund, Mogens Sandø. 2013. Candidate causative mutations for two mastitis QTL in Holstein dairy cattle' are presented. Poster presented at *International Plant & Animal Genome XXI*, January 12-16, 2013 San Diego, CA, USA.

Sahana, Goutam; Guldbrandtsen, Bernt; Lund, Mogens Sandø. 2012. Genetic Architecture of clinical mastitis traits in dairy cattle. *Programme & Book of Abstracts of ICQG 2012*. Edinburgh, s. 224-224.

Sahana, Goutam; Guldbrandtsen, Bernt; Lund, Mogens Sandø. 2012. Refining QTL with high-density SNP genotyping and whole genome sequence in three cattle breeds. *Book of Abstracts*. Vol. 18, Wageningen Academic Publishers, 2012. s. 354.

Brøndum R. F., Su G., Lund M. S., Bowman P. K., Goddard M. E., Hayes B. J., 2012. BayesRS : Genome Location Specific Priors To Improve Genomic Prediction. I: *Programme & Book of Abstracts, ICQG2012*. Edinburgh, 2012. s. 141-141.

Brøndum R. F., Ma P., Lund M. S., Su G., 2012. A multi breed reference improves genotype imputation accuracy in Nordic Red cattle I: *Book of Abstracts of 63rd Annual Meeting EAAP 2012*, Bratislava, Slovakiet. Vol. 18 2012. The Netherlands : Wageningen Academic Publishers, 2012. s. 356.

Castro Dias Cuyabano B., Su G., Lund M. S., 2012. Haplotype Blocks Built from High Density Marker Map for Genomic Prediction. I: Programme & Book of Abstracts, ICQG2012. Edinburgh, 2012. s. 149-149.

Edriss V., Fernando R. L., Su G., Lund M. S., Guldbrandtsen B., 2012. Genealogy Haplotypes in Genomic Prediction. I: Programme & Book of Abstracts, ICQG2012. Edinburgh, 2012. s. 153-153.

Ma P., Brøndum R. F., Zhang Q., Lund M. S., Su G., 2012. Comparison of methods to impute missing SNP markers in Swedish and Finnish Red Dairy Cattle population. I: Programme & Book of Abstracts. Edinburgh : ICQG, 2012. s. 144-144.

Nielsen U. S., Pösö J., Madsen P., Mäntysaari E. A., Pedersen J., Su G., Aamand G P. 2012. Effect of genomic preselection on the stability of EBV's from traditional BLUP procedure for production traits – a practical illustration. The 2012 Interbull Open Meeting (Cork, Ireland, May 29-30).

Zhou L., Ding X., Zhang Q., Wang Y., Lund M. S., Su G., 2012. Genomic prediction using the combined Chinese and Nordic Holsteins reference population. I: Programme & Book of Abstracts, ICQG2012. Edinburgh, 2012. s. 150-150.

Ph.d.-afhandling:

Zhan, B. Global characterization of genetic variation by using high-throughput technologies. 2012. Ph.d.-afhandling, Århus universitet. ISBN 978-87-91949-90-6.

Nationale/nordiske indlæg for kvægbrugere mv.:

Byskov, K. Test dine hundyr – og får større avlsfremgang. Avlsnyt Juni 2012.

Langdahl, C. Holstein breeding program with focus on genomic selection. Afholdt i Danmark, Finland, England og Polen.

Liu, Huiming; Berg, Peer; Sørensen, Anders Christian. The prediction of allele frequency under selection: A simulation study. MBG Annual PhD-days 2012. Aarhus University, 2012. s. 19-19.