

be compatible in scale, it is rarely true in dairy-cattle data because the pedigree is long but partially missing and the genotypes are mainly available for the last few generations. Unknown parent-groups (UPG) and metafounders (MF) can be used to fill the missing relationships in the relationship matrices and to make them compatible in scale. The objectives of this study were to show a reasonable relationship matrix with UPG or MF in ssGBLUP, to implement this matrix in genetic prediction software, and to apply this technique to production traits in US Holstein. We have derived \mathbf{H}^{-1} in which UPG are considered only for pedigree relationships. We also derived an alternative \mathbf{H}^{-1} from a joint density function. This alternative form is equivalent to one derived from the MF theory. Although UPG and MF are equivalent under some assumptions, MF seems to be more flexible to keep the compatibility among the relationship matrices. The alternative \mathbf{H}^{-1} showed that the computation of \mathbf{A}_{22}^{-1} with MF is greatly simplified with sparse matrix techniques. The newly-derived \mathbf{H}^{-1} was implemented in the BLUPF90 programs. The genotypes, pedigrees, and phenotypes of 305-d milk, fat, and protein yield were provided by the Council of Dairy Cattle Breeding (CDCB). The data included more than 72 million phenotypes for each trait, 80 million pedigree animals, and 2.3 million genotyped animals. The validation predictability and inflation of genomic predictions with UPG or MF will be presented.

Key Words: genomic prediction, metafounder, unknown-parent group

468 Alternative input parameters for Wood's curve within best prediction used by USDA-AGIL for genetic evaluation of production traits in the United States. E. S. Houdek*¹, B. J. Heins¹, A. R. Hazel¹, L. B. Hansen¹, and J. B. Cole², ¹University of Minnesota, St. Paul, MN, ²Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD.

Best Prediction (BP) was developed by USDA-AGIL to predict 305-d lactational production for genetic evaluation in the US. Mean and SD of test days for all production traits are used by BP to predict either primiparous or multiparous 305-d production based on a Wood's lactation curve. Fixed Holstein (HO) breed parameters for Wood's curve (a, b, c, and SD of a, b, c) currently used by BP since 2009 were compared with alternative parameters that were newly estimated. The new parameters were implemented to determine if increased production of cows and reduced use of rBST over the past decade has impacted the effectiveness of BP to predict 305-d production of milk, fat, and protein. Test-day observations of HO cows from 7 high-production dairies in Minnesota that have participated in research with the University of Minnesota were

used to estimate the alternative BP parameters. The primiparous cows calved from 2011 to 2016, and the multiparous cows calved from 2012 to 2016. All lactations of cows were required to have at least 250 d in milk and were also required to have at least 6 test days by 265 d in milk. Shapes of Wood's lactation curves for these 3 production traits from BP were noticeably different for the currently used versus alternative fixed breed parameters. However, when the 305-d production records of cows were deviated within months of calving according to procedures used for genetic evaluation in the US, the differences between the 2 alternative predictions of 305-d production were of no practical consequence.

Key Words: best prediction, lactation curve

469 A genome-wide analysis using runs of homozygosity in Italian Holstein cattle. A. Cesarani¹, G. Gaspa², C. Dimauro¹, M. Usala¹, F. Correddu¹, and N. Macciotta*¹, ¹Università di Sassari, Dipartimento di Agraria, Sassari, Italy, ²Università di Torino, Dipartimento di Scienze Agrarie Alimentari e Forestali, Grugliasco, Italy.

Current dairy cattle populations are the result of years of selection that lead to high production levels, but also to a reduction of the within breed genetic diversity. This genomic similarity can be investigated using runs of homozygosity (ROH). Apart from being indicators of inbreeding, ROH are also useful for detecting selection sweeps. In the present study, ROHs were used for GWAS study in dairy cattle production traits. A total of 2,818 Italian Holstein bulls were genotyped with the Illumina HD bead chip. After edits, 609,074 SNPs were retained. Minimum number of SNP and length for a ROH were fixed at 50 and 1Mb, respectively. To account for genotyping/imputation errors one heterozygote was allowed into a ROH. Phenotypes were EBVs for milk yield, fat yield and percentage, protein yield and somatic cell score. A linear model was used to test the effects of ROH presence/absence and year of birth (5 levels according to 7-years interval from 1979 to 2014: 1 = 1979–1986; ... 5 = 2007–2014). In the model, only ROHs shared by at least 20 animals were considered. Year of birth affected almost all investigated traits (at least $P < 0.00001$). The significance threshold was fixed as the negative logarithm of the ratio between 0.05 and the number of ROH tested, which was 1,083. Several genes found to be associated with dairy traits in previous studies have been found in the present work. Examples are the *ARHGAP39*, *CYHRI*, *CPSF1*, *DGATI* and *GRINA* loci. Results of the present study confirms the usefulness of ROH as indicators of selection sweeps.

Key Words: runs of homozygosity, milk production trait, cattle

Table 1 (Abstr. 468). Mean currently used and alternative Holstein parameters

	Currently used parameters			Alternative parameters			
	a	b	c	n	a	b	c
Primiparous				1922			
Milk	13.010	0.267	0.00262		13.376	0.300	0.00238
Fat	0.784	0.120	0.00130		0.762	0.172	0.00125
Protein	0.463	0.203	0.00161		0.462	0.247	0.00158
Multiparous				1730			
Milk	22.009	0.216	0.00357		21.391	0.278	0.00370
Fat	1.287	0.073	0.00213		1.173	0.139	0.00228
Protein	0.854	0.132	0.00232		0.801	0.197	0.00257