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1 **Dissection of genomic correlation matrices of US Holsteins using multivariate factor analysis**

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13

14 **Summary**

15 The aim of this study was to compare correlation matrices between direct genomic predictions for
16 31 traits at the genomic and chromosomal levels in US Holstein bulls. Multivariate factor analysis
17 carried out at the genome level identified seven factors associated with conformation, longevity,
18 yield, feet and legs, fat and protein content traits. Some differences were found at the chromosome
19 level; variations in covariance structure on BTA 6, 14, 18 and 20 were interpreted as evidence of
20 segregating QTL for different groups of traits. For example, milk yield and composition tended to
21 join in a single factor on BTA 14, which is known to harbor the *DGATI* locus that affects these
22 traits. Another example was on BTA 18, where a factor strongly correlated with sire calving ease
23 and conformation traits was identified. It is known that in US Holstein there is a segregating QTL
24 on BTA18 influencing these traits. Moreover, a possible candidate gene for daughter pregnancy rate
25 was suggested for BTA28. The methodology proposed in this study could be used to identify
26 individual chromosomes which have covariance structures that differ from the overall (whole
27 genome) covariance structure. Such differences can be difficult to detect when a large number of
28 traits are evaluated, and covariances may be affected by QTL that do not have large allele
29 substitution effects.

30

31 **Introduction**

32 High-throughput marker platforms are the fundamental tools of the genomic (r)evolution
33 that has caused major changes in dairy cattle breeding over the last five years. Cattle are currently
34 genotyped in many countries using SNP chips with different densities (VanRaden et al., 2011).
35 Marker data are used both for predicting the genetic merit of individuals and for performing
36 genome-wide association studies aimed at identifying genomic regions that control the expression
37 of traits of economic importance.

38 Different methods are used to predict genomic estimated breeding values (GEBV), which
39 include direct genomic values (DGV) that are calculated as the sum of genotype*SNP effects on the
40 trait across the whole animal genome, as well as information from conventional genetic evaluation.
41 Direct chromosomal values (DCV) can be computed by summing the genotype*SNP marker effects
42 separately by each chromosome, and the sum of the DCV is the DGV. The DCV may be useful for
43 developing mating plans (Cole and Null, 2013). However, they also can be used to compute
44 genomic correlation matrices for individual chromosomes (G_CHR) as well as the whole genome
45 (G_GEN). The G_GEN matrix summarizes relationships among traits averaged across the whole
46 genome, while G_CHR depicts the relationships at a local level.

47 Genetic relationships between traits are the result of the pleiotropic effects of segregating
48 alleles (Mezey and Houle, 2003). Structural differences between G_GEN and G_CHR or between
49 different G_CHR may therefore indicate differences in the genetic mechanisms controlling groups
50 of traits due, for example, to segregating QTLs. For example, Cole et al. (2009) reported differences
51 in the correlations between sire calving ease and conformation traits when comparing G_GEN to
52 G_CHR for BTA 18 in US Holsteins. This result confirmed the detection of a segregating QTL in
53 US Holsteins on BTA18 affecting reproductive and type traits, reported also by other authors
54 (Qanbari et al., 2011).

55 A key issue when comparing two correlation matrices is the choice of a suitable
56 methodology for performing the analysis. A matrix has several structural elements that cannot be
57 summarized into a single metric. Moreover, genetic correlation matrices are often singular, with
58 rank equal to the number of genetically independent traits (Hine and Blows, 2006). Several
59 approaches to compare G matrices have been proposed, even though none of them seems to be
60 widely accepted (Steppan et al., 2002). One of the most popular is the Common Principal
61 Component (CPC) method (Flury, 1984). It relies on the assumption that, if two matrices are
62 similar, they share one or more eigenvectors, and similarity is measured as the number of principal

63 components two matrices have in common. The CPC method relies on Principal Component
64 Analysis, which is a technique mainly used to explain the variance of a system. However, when
65 comparing matrices to find differences in the genetic control of groups of traits the covariances
66 between variables are of greatest interest.

67 Multivariate Factor Analysis (MFA) is a statistical technique particularly suitable for investigating
68 the correlation structure of complex systems. It has been suggested as a tool for making biologically
69 relevant comparisons among matrices (Houle et al., 2002). The basic theoretical assumption of
70 MFA is that the (co)variance of a multivariate system can be partitioned into two portions
71 (Morrison, 1976): the first is shared by all variables and it is called communality, and the second is
72 peculiar of each variable and is named uniqueness. As a consequence of (co)variance modelling,
73 each of the n original variables can be represented as a linear combination of p common factors that
74 generates the common covariance between variables plus a residual specific variable (Morrison,
75 1976).

76 In the case of genomic matrices, MFA can be carried out separately on G_GEN and
77 G_CHR. Differing (co)variance structures can be interpreted as differing genetic relationships
78 between traits at the whole-genome and chromosomal levels. Such an analysis may represent a first
79 step in the identification of differences in genetic architecture among groups of traits. In this work,
80 multivariate factor analysis is used to dissect the structure of different genomic correlation matrices
81 in US Holsteins.

82

83 **Materials and methods**

84 Direct genomic and chromosomal values for 31 production, functional, and conformation
85 traits were calculated for 182,233 Holstein bulls and cows using the SNP effects estimated in May
86 2012 by the US genomic evaluation system as described in Wiggans et al. (2011). Direct genomic
87 values for each chromosome were obtained by summing the effects for only the SNP markers on

88 that chromosome, and all SNP effects were summed to obtain an animal's overall DGV. The traits
89 included in the analysis are listed in Table 1 together with the corresponding means and standard
90 deviations of the DGVs.

91 The G_GEN and G_CHR matrices were then calculated using the DGV for the 31 traits. The
92 suitability of genomic correlation matrices to factor analysis was evaluated by using the Kaiser
93 measure of sampling adequacy (MSA). This index compares Pearson and partial correlations. An
94 empirical threshold of 0.8 is considered as the optimum value in order to consider a dataset suitable
95 for factor analysis (Cerny and Kaiser, 1973).

96 Multivariate factor analysis was then carried out on both G_GEN and the different G_CHR,
97 separately for each correlation matrix using the maximum likelihood method implemented in the
98 FACTOR procedure of SAS version 9.2 (2008). Factors were rotated using a VARIMAX
99 procedure, and the number of extracted variables was assessed by considering their eigenvalue
100 (only factors with eigenvalue >1 were retained). The interpretation of the extracted factors was
101 assessed by examining the factor loadings, i.e. correlations between factors and original variables
102 (in this case, the 31 considered traits). A minimum threshold of 0.60 was assumed for a loading to
103 be considered "large". A statistical test was performed to test the salience of each loading, i.e. if it
104 was significantly greater than 0.60.

105 Comparisons were carried out on the basis of the following outputs of MFA: i) factor
106 pattern, i.e., the correlations between extracted common factors and the 31 considered traits; ii) the
107 variance explained by each extracted factor; and iii) communalities, i.e., the amount of variance of
108 each trait which is explained by the common factors. A popular method for comparing observed (y)
109 and model-predicted (x) values is by the linear regression of y on x. The slope is interpreted as an
110 indicator of bias (it should not be different from 1 if the two variables are equal) and the intercept is
111 related to systematic error (it should not be different from 0). In this analysis, variables considered
112 in the regression were communalities of each original variable. Values referred to the G:GEN were

113 considered as y whereas corresponding values derived from the different G_CHR were considered
114 as x, respectively.

115 **Results**

116 Statistics of factors extracted from G_GEN (Table S1) and G_CHROM matrices are
117 reported in Table 2. The Kaiser measure of sampling adequacy for G_GEN (0.80) indicates that the
118 partial correlations among the variables are small compared to Pearson correlations, and that the
119 common factor model is appropriate to these data (Cerny and Kaiser, 1973; Morrison, 1976). The
120 seven extracted factors were able to explain a large part (about 0.70) of the variance.

121 Factors extracted from the G_GEN showed a quite readable structure (Table 3), with traits
122 loading onto factors that appear to be functionally related. Each factor had a few large correlations
123 (i.e., significantly larger than 0.60, with $P \leq 0.01$) with considered traits, and several rather small
124 loadings. The same conclusions may be drawn if the table is observed across columns: each trait
125 had a large correlation with just one factor, and small correlations with the other factors. An
126 exception was represented by fat yield, that showed correlations > 0.60 with both factors 3 and 6.
127 The first factor (Table 3), explaining about 26% of the total variance of the system, was mainly
128 correlated with conformation traits (body size and shape, and udder conformation). The second
129 factor explained about half of the variance explained by the first, and could be considered as an
130 indicator of longevity, being related to survival traits, SCS, and daughter pregnancy rate. The third
131 factor was related to yield traits, whereas the fourth showed larger correlation with specific traits of
132 feet and legs. The fifth factor could be interpreted as an indicator of body shape. The final two
133 factors were related to milk composition traits: the sixth is a fat indicator (both for yield and
134 composition), and the seventh is related to protein content. Such a structure reflects quite reasonably
135 the pattern of genetic relationships that exist among the individual traits.

136 Of the 31 traits considered, some showed no relationship with the latent factors (Table 3).
137 One group was represented by traits related to calving ease and stillbirth, both for sires and

138 daughters. Others were morphology measurements of teat, rump and legs. Actually, the salience
139 was related to the communality of variables (Table 4), i.e., the amount of variability of each trait
140 that is generated by the common factors. Traits that did not show any relationship with extracted
141 factors were those characterised by the lowest communality (usually lower than 0.30, except for
142 rear leg (side view), which showed loadings closer to the fixed threshold of 0.60).

143 The MFA carried out on single chromosomes showed, as expected, some differences as
144 compared to genome-wide results. The Kaiser measure of sampling adequacy (Table 2) was
145 generally lower than the value obtained for the G_GEN. The largest observed values were for BTAs
146 5,10, and 26. However, the lowest values (0.65) were not too far from the empirical threshold of 0.80.
147 The total amount of variance explained by the different factors was on average 0.69 (± 0.05), with
148 the lowest and highest values for BTA15 and BTA2 respectively. Moreover, differences between
149 G_GEN and G_CHROM were noted in their distribution across factors. For example, Figure 1
150 reports the pattern of variance explained by the different factors extracted both from G_GEN and
151 G_CHROM for BTAs 6,14,18 and 20. A large reduction in explained variance when moving from
152 the first to the subsequent factors was observed for the G_GEN, with the first factor explaining
153 about 2.5 times as much variance as the second factor. While the amount of explained variance
154 decreased with factor number for individual chromosomes, the magnitude was much smaller,
155 especially for BTA 6.

156 The number of extracted factors by chromosome was very close to that of the G_GEN,
157 ranging from 6 to 8. Their general structure was similar to G_GEN, but specific variations in their
158 pattern have been detected. The communalities of the 31 traits calculated for each chromosome also
159 had similar patterns to the genome-wide matrix (the correlation between communalities calculated
160 from the G_GEN. and those averaged by the 29 autosomes was 0.96) (Table 4). However, some
161 traits exhibited large variation of communality among chromosomes. Examples include strength or
162 body weight that ranged from 0.05 (both on BTA1) to 1.00 (on BTA7 and BTA6 respectively). In

163 general, conformation and functional traits were characterised by the largest variation in
164 communality among chromosomes

165 Although analyses were performed along the whole genome, in order to validate the MFA
166 approach a more detailed examination of results was carried out on four chromosomes known to
167 harbour genes affecting milk production and conformation traits (i.e., BTA 6, 14, 18, and 20)
168 (Chamberlain et al., 2012; Cole et al., 2009; Flori et al., 2009; Grisart et al., 2002). Relevant results
169 obtained for other chromosomes are presented in the paper and reported in the supporting
170 information.

171 The largest extracted factor in terms of explained variance for BTA 6 (Table 5) is similar to
172 the longevity factor of the G_GEN (Table 3), with the exception of a large loading for daughter
173 stillbirth, and a loading for daughter calving ease that approaches the threshold of significance. A
174 QTL associated with calving difficulty on this chromosome has been reported for Norwegian Red
175 cattle (Olsen et al., 2009), and a genomic region on the same chromosome affecting calving ease in
176 the Piemontese beef breed has been identified (Bongiorni et al., 2012). Some putative candidate
177 genes related to pelvic morphology, including *LAP3* (leucine aminopeptidase) and *LCORL* (ligand
178 dependent nuclear receptor corepressor-like), have been mapped to BTA6 (Flori et al., 2009). Large
179 SNP effects on this chromosome have been detected in the US Holstein for daughter pregnancy
180 rate, heifer conception rate, and somatic cell score (Cole and VanRaden, 2010). Another relevant
181 difference in comparison with the G_GEN could be found on factor 6 (Table 5), which is
182 unfavourably related to milk yield (with a negative sign) and favourably associated with fat and
183 protein percentage. It is widely known that BTA6 harbors several genes involved in milk yield and
184 composition in a group that maps at around 37 Mbp including *FAM13B1*, *SPPI*, and *ABCG2*, and
185 the casein cluster. As was the case with G_GEN, sire calving traits, rump angle, and some teat
186 measures did not load significantly onto any of the extracted factors.

187 As expected, BTA14 exhibited some variation in comparison with G_GEN as far as milk
188 production traits are concerned (Table 6). The second factor was associated with both yield and
189 composition traits, that were associated with different factors (3, 6 and 7) in the genome-wide
190 matrix (Table 3). It is of interest to note that the correlation of fat yield with factor 2 of BTA14 was
191 of a different sign compared to the other yield traits, while it was of the same sign for percentage
192 traits (Table 6). It is known that the *DGATI* gene maps to this chromosome. The pattern of
193 correlation signs for factor 2 was the same reported for the substitution effects of the K232A
194 mutation on these traits (Grisart et al., 2002). It is also of interest to note that protein yield had a
195 correlation slightly lower than the threshold of significance on factor 2, but it showed a large
196 loading on factor 5. Some studies have suggested the existence of a second QTL affecting milk
197 protein yield and percentage located on BTA14 (Cole et al., 2011; Schnabel et al., 2005), and it is
198 known that the effect of *DGATI* on fat and protein is different (Tetens et al., 2012).

199 An additional peculiarity of BTA14 found in the present study was the splitting of the factor
200 associated with conformation traits into two latent variables related to udders and feet and legs (the
201 first) and to the size of the animals (the third), respectively (Table 6). The US Holstein population
202 has large marker effects on this chromosome for strength and udder cleft (Cole and VanRaden,
203 2010). An effect of *DGATI* on rump width and strength has been reported in German Holsteins
204 (Kaupe et al., 2007), a QTL related to rump width has been mapped in the US Holstein population
205 (Schnabel et al., 2005), and a QTL influencing growth traits has been found in Fleckvieh cattle
206 (Pausch et al., 2011).

207 The results from BTA18 showed relevant variation compared to the genome-wide pattern as
208 far as factor 1 is concerned (Table 7). This variable was strongly correlated with sire calving and
209 conformation traits. As mentioned in the introduction, a QTL affecting sire calving ease and
210 stillbirth and conformation traits was reported in the US (Cole et al., 2009) and German (Brand et
211 al., 2010) Holstein populations. The maternally imprinted *PG3* domain, a mutation which has

212 recently been associated with the expression of the *MIMT1* protein, affects abortion and stillbirth in
213 Finnish Ayrshire cattle (Flisikowsky et al., 2010). Cole et al. (2014) also have recently reported an
214 association between calf birth weight and a sialic acid-binding immunoglobulin-type lectin that
215 maps on BTA18. This result further supports the role of this putative QTL in influencing body size
216 and shape.

217 Finally, BTA20 also exhibited some peculiarities in comparison to the G_GEN matrix
218 (Table 8). There was a division of factors related to conformation into one associated with
219 mammary traits (the first) and the second to the animal size (Table 8), which is similar to results
220 observed for BTA14. There was also a factor related to both milk yield and composition (factor 5),
221 and the US population has a strong signal for protein percentage on BTA20 (Cole and VanRaden,
222 2010). A number of SNP associations with milk production traits have also been reported by other
223 groups (Blott et al., 2003; Chamberlain et al., 2012), and BTA20 harbors some interesting candidate
224 genes for milk production traits, such as the growth hormone receptor (*GHR*; Blott et al., 2003) and
225 the prolactin receptor (*PRLR*). Somatic cell score was not included in the factor associated with
226 longevity, and no reports were found in literature about genomic regions that affect SCS located on
227 this chromosome, but Sodeland et al. (2011) did identify a QTL affecting clinical mastitis in
228 Norwegian Red cattle.

229 The comparisons discussed above were based on visual inspection of factor patterns,
230 evaluating the correspondence of loadings statistically larger than 0.6 between the different factors.
231 However, a more empirical approach may be desirable, particularly as the number of traits
232 continues to grow. Table 9 reports results of regression analyses that compare communalities of
233 different traits estimated by analysing either the whole genome or chromosomal matrices,
234 respectively. It can clearly be seen that all comparisons differed significantly from expectations; the
235 intercept was always different from zero, and the slope from one. Regression models were also used
236 to compare communalities of the G_GEN with those obtained from the G_CHROM of BTA3,

237 which exhibited a factorial pattern similar to the genome-wide (data not reported for brevity). In this
238 case, the intercept was not different from zero, or the slope from one. The BTA3 results are
239 important because they confirm that intercepts and slopes are consistent with expectations when the
240 whole-genome and chromosome-specific matrices have similar covariance structures.

241 As far as the other chromosomes are concerned, a difference from genome-wide results was
242 detected on factor pattern extracted from G_CHROM of BTA5 (Table S2). The yield factor showed
243 large correlations only for milk and protein while fat yield had a large loading in the same factor as
244 fat percentage. The US Holstein population has large SNP effects on BTA5 for milk, fat, and
245 protein yields and fat percentage (Cole and VanRaden, 2010). QTLs affecting milk fat content
246 located on BTA5 were reported for German (Wang et al., 2012) and Australian (Hayes et al., 2010;
247 Raven et al., 2014) Holsteins. Epidermal Growth Factor Receptor Pathway Substrate 8 (EPS8), a
248 gene involved in the fat metabolism of mammals, has been suggested as a candidate gene for that
249 QTL region..Moreover, a QTL affecting milk, protein and fat yield was reported on BTA5 for the
250 Fleckvieh breed (Awad et al., 2011).

251 On BTA11 (Table S3), protein percentage exhibited large loadings both in factor 4, mainly
252 associated with measures of longevity, and factor 7, with fat content. The US Holstein population
253 has large SNP effects on BTA11 for protein and fat content (Cole and VanRaden, 2010). A QTL
254 affecting milk protein content on BTA11 has been detected in Holstein Friesians by Schopen et al.
255 (2009) in a position close to the Beta-lactoglobulin (BLG) gene .

256 A different behaviour of fat percentage, in comparison with the results obtained for the
257 G_GEN, was observed on BTA27. The fourth factor (Table S4) showed large correlation values
258 with milk and protein yield, and fat content, but not with fat yield. In the G_GEN (Table 3) yield
259 and composition traits were associated to distinct factors. BTA27 has a large signal for fat
260 percentage in the US Holstein (Cole and VanRaden, 2010). Wang et al. (2012) reported a major
261 QTL for fat content on this chromosome. These authors suggested the Glycerol-3-phosphate

262 acyltransferase 4 (GPAT4) as neighbouring gene for this QTL. Raven et al. (2014), in a multibreed
263 study reported a SNP associated with fat content on BTA27, hypothesizing the GINS complex
264 subunit 4 as a candidate gene.

265 Finally on BTA28 (Table S5), daughter pregnancy rate had a large correlation in the same
266 factor of yield traits (Factor 2). The US Holstein population exhibits large SNP effects on BTA28
267 for daughter pregnancy rate and heifer conception rate (Cole and VanRaden, 2010). A SNP
268 significantly associated with calving ease has been detected on BTA28 in Italian Holstens (Minozzi
269 et al., 2013). The Bone Morphogenetic Protein Receptor Type 1A (BMPRA1) and the Growth
270 Differentiation Factor2 (GDF2) genes could be plausible candidates that could underlie the QTL
271 effect (Pennington and Ealy, 2012).

272

273 **Discussion**

274 Large correlation matrices (31 traits) of genomic breeding values were dissected using
275 MFA. This technique was able to analyse their deep structure, extracting factors with biologically
276 interpretable meanings. These new variables can be considered as indicators of aggregate traits as
277 conformation, longevity, feet and legs, yield, body size, milk composition, respectively. Such a
278 feature is of particular interest for matrix comparisons because most proposed methodologies are
279 unable to give biological explanations of results. The basic assumption of the factorial model, i.e.,
280 that the (co)variance of a multivariate system is generated by causes that may affect either one or
281 many variables, seemed to be adequate to fit the structure of the genomic correlation matrices. This
282 model has previously been used to generate covariance matrices that are both simple and
283 biologically reasonable (Houle et al., 2002), and has been used for finding the dimension of
284 variance-covariance matrices (Hine and Blows, 2006).

285 As expected, differences between the genome-wide and the chromosome-wide correlation
286 matrices of direct genomic predictions were detected. Under a geometrical perspective, basic

287 elements of a genetic correlation matrix are i) its orientation, which can be represented by the
288 structure of its eigenvectors; and ii) its length, which is related to the magnitude of its eigenvalues.
289 Multivariate factor analysis was able to describe these two aspects of the matrices examined in the
290 current study. In particular, the orientation was described by the factor pattern, while the length was
291 summarized by the amount of variance explained by each factor. Differences between G_GEN and
292 G_CHROM were found in both aspects, but most interesting were those detected in factor patterns.
293 Biologically, latent factors may be regarded as a sort of mirror of genes or pools of genes that affect
294 sets of traits. The clustering of traits across different latent variables followed a biologically and
295 technically coherent pattern when genome-wide covariances were examined. Differences detected
296 at the chromosome level involved those traits for which chromosomes were known to harbor
297 significant genes as, for example, the behaviour of morphology and calving ease traits for BTA18.
298 Mezey and Houle (2003) pointed out that two genetic correlation matrices are similar when they
299 present the same modular organisation, i.e., when pleiotropic effects of genes are associated with
300 the same set of traits in both matrices. If this concept is reversed, different factor patterns yielded by
301 MFA may indicate variation in modular organisation, i.e., in the genetic architecture of groups of
302 traits, of the compared matrices.

303 Some differences were detected among groups of traits. Milk yield and composition were
304 associated to distinct factors at the genome-wide level, and they tended to join in chromosomes
305 where genes affecting milk yield are located, such as BTA14. On the other hand, many
306 morphological traits clustered in the same latent variables both at genome and chromosome level.
307 They were also frequently associated to the first or second extracted factor, whereas milk traits had
308 relevant loadings on the later factors in terms of explained variance. Such behaviour could be
309 related to the genetic regulation of the two groups of traits: mainly attributable to a relatively small
310 number of genes with a moderate effect for milk composition, or due to a polygenic background for
311 conformation traits, respectively (Hayes et al., 2010).

312 The MFA also provides an estimate of the amount of variance each variable shares with the
313 others. The lowest communalities were obtained for rump angle, calving traits, and some indicators
314 of teat placement, while the highest values were associated with milk production traits. The
315 uniqueness of each variable (that can be calculated as $1 - \text{communality}$) expresses its specific
316 variability, and it seems to be related with the nature of the trait (either measured directly, or
317 evaluated by an expert). However, variation within the same trait has been observed. The largest
318 communalities were usually found for chromosomes where QTL or genes affecting the trait were
319 located, such as sire calving ease and stillbirth for BTA18. Thus, the communality also yields useful
320 information for the detection of chromosomal regions that affect a specific set of traits. Moreover,
321 also the pattern of variation of this parameter across chromosomes (large variability for functional
322 and conformation traits, low for yield traits) could provide additional information about the genetic
323 background of traits.

324 Finally, the proposed approach allows for a preliminary scan across the whole genome to
325 identify regions of potential interest associated with genetic control of a group of traits by using
326 only the information that are currently produced by genomic selection programs. An example is
327 represented by results for pregnancy rate on BTA28. Although it is quite easy to perform, being
328 based upon routine calculations that are normally implemented in most commercial and free
329 statistical software packages, MFA also is able to flag groups of traits that are characterised by
330 different genetic architectures, such as milk yield, composition, or conformation traits (Hayes et al.,
331 2010). In the present paper the method was tested on chromosomes known to harbour some
332 important candidate genes in order to check its reliability. It could be further tested on less-
333 investigated chromosomes within the same population, applied to new phenotypes, or used to
334 compare the same chromosome in different breeds.

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341

342

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455 Table 1. Means and standard deviations (SD) of direct genomic values (DGV) for the 31
 456 production, fitness, and conformation traits used to construct chromosomal and genomic correlation
 457 matrices.

Trait	Mean	SD
Milk yield (kg)	222	302
Fat yield (kg)	11.9	11.7
Protein yield (kg)	8.6	8.6
Fat percentage (%)	0.03	0.09
Protein percentage (%)	0.02	0.04
Productive life (d)	1.93	2.22
Net merit (\$)	295	224
Somatic cell score	2.87	0.16
Daughter pregnancy rate (%)	-0.07	1.19
Sire calving ease (%)	7.6	1.4
Daughter calving ease (%)	7.3	1.4
Sire stillbirth (%)	7.8	0.78
Daughter stillbirth (%)	7.3	1.3
Final score	1.38	1.07
Stature	1.13	1.21
Strength	0.60	0.93
Dairy form	0.99	1.15
Foot angle	1.12	1.07
Rear legs (side view)	-0.10	0.91
Body depth	0.71	0.99
Rump angle	0.19	0.96
Rump width	0.79	1.01
Fore udder attach	1.41	1.25
Rear udder height	1.70	1.36
Udder depth	1.04	1.14
Udder cleft	0.97	1.10
Front teat placement	0.70	0.99
Teat length	0.02	0.96
Rear legs (rear view)	1.08	1.04
Feet and legs	1.25	1.03
Rear teat placement	0.69	1.06

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464 Table 2. Statistics of factor extraction

	Factors (n.)	Variance explained	Kaiser MSA
Genome	7	0.69	0.80
BTA1	8	0.69	0.67
BTA2	7	0.60	0.68
BTA3	8	0.67	0.66
BTA4	7	0.66	0.67
BTA5	7	0.80	0.77
BTA6	7	0.69	0.72
BTA7	7	0.67	0.72
BTA8	8	0.72	0.70
BTA9	7	0.68	0.68
BTA10	8	0.73	0.76
BTA11	7	0.69	0.73
BTA12	7	0.61	0.68
BTA13	8	0.68	0.67
BTA14	6	0.67	0.74
BTA15	7	0.58	0.66
BTA16	7	0.68	0.68
BTA17	7	0.65	0.65
BTA18	7	0.76	0.75
BTA19	7	0.70	0.73
BTA20	8	0.69	0.72
BTA21	7	0.63	0.66
BTA22	7	0.67	0.72
BTA23	8	0.69	0.71
BTA24	8	0.71	0.68
BTA25	8	0.77	0.72
BTA26	7	0.77	0.76
BTA27	7	0.62	0.65
BTA28	7	0.68	0.74
BTA29	8	0.71	0.70

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468 Table 3. Factor pattern of the correlation matrix between direct genomic values for 31 production,
 469 conformation and functional traits.

Trait	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7
Milk	0.29	0.14	0.89	0.02	0.03	-0.17	-0.28
Fat	0.30	0.20	0.66	0.06	0.04	0.65	0.03
Protein	0.31	0.23	0.90	0.05	0.03	-0.03	0.20
Fat percentage	0.04	0.07	-0.20	0.04	0.01	0.92	0.33
Protein percentage	0.01	0.14	-0.09	0.05	-0.01	0.29	0.94
Net merit	0.36	0.75	0.47	0.13	-0.04	0.24	0.07
Productive life	0.22	0.92	0.10	0.09	-0.10	0.04	-0.02
Somatic cell score	-0.16	-0.64	0.11	-0.09	-0.07	-0.11	0.04
Daughter pregnancy rate	-0.22	0.71	-0.30	0.03	0.00	-0.09	0.10
Sire calving ease	0.13	-0.42	-0.16	0.01	0.19	-0.01	-0.05
Daughter calving ease	-0.26	-0.48	-0.17	-0.08	0.03	-0.02	0.00
Sire stillbirth	0.13	-0.33	-0.05	0.00	0.09	0.02	-0.04
Daughter stillbirth	-0.15	-0.40	-0.13	-0.07	-0.01	0.00	0.01
Final score	0.93	0.09	0.12	0.23	0.24	0.07	0.01
Stature	0.72	-0.17	0.09	0.22	0.46	0.02	0.04
Strength	0.41	-0.12	0.08	0.26	0.86	0.04	0.05
Dairy form	0.75	-0.29	0.34	0.04	0.00	0.10	-0.06
Foot angle	0.52	0.08	0.05	0.69	0.27	0.04	0.06
Rear legs (side view)	0.24	-0.14	0.06	-0.58	-0.13	0.02	0.01
Body depth	0.58	-0.28	0.14	0.20	0.67	0.08	0.01
Rump angle	-0.06	0.02	0.11	-0.02	0.08	-0.02	-0.06
Rump width	0.65	-0.14	0.11	0.11	0.50	0.04	0.04
Fore udder attachment	0.85	0.27	-0.06	0.11	0.17	0.06	-0.01
Rear udder height	0.88	0.11	0.15	0.16	0.08	0.06	-0.02
Udder depth	0.73	0.34	-0.21	0.08	0.09	0.00	0.03
Udder cleft	0.81	0.02	0.09	0.06	0.06	0.01	0.00
Front teat placement	0.63	0.16	0.14	-0.03	0.04	0.03	0.02
Teat length	0.00	-0.24	-0.03	0.10	0.24	-0.04	-0.06
Rear legs (rear view)	0.53	0.10	0.07	0.76	0.11	0.06	0.04
Feet and legs	0.65	0.13	0.07	0.73	0.05	0.07	0.05
Rear teat placement	0.62	0.01	0.14	-0.04	0.00	0.01	0.01
Variance explained (%)	0.26	0.12	0.09	0.07	0.06	0.05	0.04

470 * Values in bold are significantly higher than 0.60 ($P \leq 0.01$)

471 Table 4. Communalities of genomic predictions at genome-wide level and statistics of
472 communalities by chromosome.

<u>NAME</u>	Whole genome	Average	S.D.	Maximum	Minimum
Milk	1.00	1.00	0.00	1.00	0.99
Fat	1.00	1.00	0.01	1.00	0.97
Protein	1.00	1.00	0.00	1.00	0.99
Fat percentage	1.00	1.00	0.01	1.00	0.98
Protein percentage	1.00	0.99	0.01	1.00	0.97
Nett merit	0.99	0.96	0.05	1.00	0.79
Productive life	0.92	0.83	0.13	0.98	0.49
Somatic cell score	0.47	0.50	0.14	0.75	0.21
Daughter pregnancy rate	0.67	0.56	0.13	0.82	0.28
Sire calving ease	0.26	0.25	0.14	0.72	0.08
Daughter calving ease	0.33	0.27	0.10	0.53	0.04
Sire stillbirth	0.14	0.24	0.13	0.65	0.07
Daughter stillbirth	0.21	0.28	0.10	0.46	0.08
Final score	1.00	0.93	0.08	1.00	0.58
Stature	0.81	0.67	0.16	0.86	0.09
Strength	1.00	0.81	0.22	1.00	0.05
Dairy form	0.78	0.66	0.19	0.99	0.33
Foot angle	0.83	0.75	0.12	0.92	0.37
Rear legs (side view)	0.43	0.46	0.14	0.71	0.08
Body depth	0.93	0.83	0.21	1.00	0.05
Rump angle	0.03	0.19	0.08	0.37	0.02
Rump width	0.71	0.57	0.16	0.80	0.08
Fore udder attachment	0.84	0.83	0.14	1.00	0.31
Rear udder height	0.85	0.67	0.11	0.81	0.27
Udder depth	0.71	0.73	0.13	0.91	0.37
Udder cleft	0.67	0.66	0.15	0.93	0.30
Front teat placement	0.45	0.60	0.21	1.00	0.28
Teat length	0.13	0.27	0.14	0.56	0.07
Rear legs (rear view)	0.90	0.83	0.12	0.95	0.44
Feet and legs	1.00	0.93	0.13	1.00	0.48
Rear teat placement	0.41	0.64	0.27	0.99	0.19

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475 Table 5. Factor pattern of the correlation matrix between direct chromosomal values for 31
 476 production, conformation and functional traits for BTA6.

Trait	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7
Milk	-0.11	0.06	0.02	0.64	-0.01	-0.72	0.19
Fat	-0.04	0.14	0.03	0.59	-0.09	-0.01	0.79
Protein	0.08	0.07	0.09	0.99	-0.05	0.01	0.06
Fat percentage	0.08	0.05	0.00	-0.21	-0.08	0.86	0.45
Protein percentage	0.19	-0.02	0.04	0.14	-0.04	0.95	-0.17
Net merit	0.88	0.07	0.28	0.21	0.09	0.15	0.25
Productive life	0.90	0.02	0.16	-0.26	0.13	0.16	-0.02
Somatic cell score	-0.75	-0.22	-0.19	0.28	-0.01	-0.15	-0.01
Daughter pregnancy rate	0.70	-0.09	-0.09	-0.39	0.06	0.22	-0.15
Sire calving ease	-0.29	0.36	0.19	-0.09	0.08	0.11	0.06
Daughter calving ease	-0.57	0.09	-0.09	-0.06	0.02	0.02	0.02
Sire stillbirth	-0.28	0.28	0.16	0.07	0.07	0.08	0.05
Daughter stillbirth	-0.65	-0.01	0.13	-0.05	0.03	0.01	0.00
Final score	0.13	0.53	0.68	0.20	0.34	0.02	0.13
Stature	0.14	0.72	0.30	0.14	0.30	0.02	0.01
Strength	0.00	0.85	0.09	-0.09	0.31	-0.03	0.01
Dairy form	-0.34	0.20	0.13	0.64	-0.11	-0.12	0.08
Foot angle	0.17	0.40	0.43	-0.07	0.67	0.07	-0.04
Rear legs (side view)	0.09	-0.13	0.17	0.21	-0.65	0.08	0.02
Body depth	-0.19	0.93	0.08	0.23	0.17	-0.07	0.03
Rump angle	0.01	-0.01	-0.39	0.05	0.08	0.02	-0.06
Rump width	0.10	0.68	0.30	0.17	0.19	-0.04	0.02
Fore udder attachment	0.34	0.15	0.86	-0.04	0.13	0.09	0.06
Rear udder height	-0.07	0.21	0.51	0.22	0.25	-0.12	0.23
Udder depth	0.54	0.07	0.67	-0.26	0.12	0.20	0.00
Udder cleft	0.14	0.37	0.60	-0.01	0.15	0.00	-0.01
Front teat placement	0.00	0.14	0.51	0.22	0.05	0.02	-0.09
Teat length	-0.27	0.21	-0.14	-0.13	0.12	0.00	-0.02
Rear legs (rear view)	-0.03	0.37	0.18	0.02	0.86	-0.05	0.00
Feet and legs	0.09	0.35	0.31	0.06	0.85	0.02	-0.04
Rear teat placement	-0.13	0.06	0.44	0.19	0.08	0.00	-0.20
Variance explained (%)	0.14	0.13	0.12	0.10	0.09	0.08	0.04

477 * Values in bold are significantly higher than 0.60 ($P \leq 0.01$)

478 Table 6. Factor pattern of the correlation matrix between direct chromosomal values for 31
 479 production, conformation and functional traits for BTA14.

BTA14	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
Milk	0.02	-0.90	0.01	0.10	0.34	0.27
Fat	0.24	0.94	0.09	0.03	0.03	0.20
Protein	-0.06	-0.58	0.02	0.12	0.80	0.04
Fat percentage	0.13	0.98	0.05	-0.03	-0.15	-0.01
Protein percentage	-0.07	0.92	0.01	-0.07	0.06	-0.38
Net merit	0.50	0.71	-0.10	-0.39	0.20	0.20
Productive life	0.50	0.19	-0.36	-0.73	0.06	0.07
Somatic cell score	-0.40	-0.30	-0.06	0.56	0.31	-0.14
Daughter pregnancy rate	-0.16	-0.01	-0.25	-0.62	-0.03	-0.15
Sire calving ease	-0.14	-0.13	0.19	0.53	-0.17	-0.07
Daughter calving ease	-0.35	-0.02	-0.01	0.35	-0.24	0.00
Sire stillbirth	-0.03	-0.12	0.03	0.43	0.03	0.12
Daughter stillbirth	-0.22	-0.18	0.28	0.36	-0.26	0.27
Final score	0.89	0.10	0.42	0.10	0.05	-0.03
Stature	0.28	-0.01	0.73	0.18	0.03	0.05
Strength	0.13	0.01	0.99	-0.01	0.01	0.03
Dairy form	0.42	0.04	0.29	0.63	0.22	0.14
Foot angle	0.53	-0.03	0.45	-0.22	-0.02	0.07
Rear legs (side view)	-0.10	0.23	-0.09	0.49	0.10	-0.09
Body depth	0.21	0.12	0.89	0.24	0.05	0.11
Rump angle	-0.39	-0.06	0.03	-0.01	-0.05	-0.01
Rump width	0.27	0.03	0.81	0.24	-0.12	0.04
Fore udder attachment	0.82	0.19	0.15	-0.15	-0.15	-0.14
Rear udder height	0.85	-0.10	0.03	0.01	0.06	-0.05
Udder depth	0.65	0.21	-0.07	-0.33	-0.25	-0.16
Udder cleft	0.71	-0.02	0.28	0.06	-0.12	0.16
Front teat placement	0.67	0.12	0.18	-0.05	0.03	-0.18
Teat length	-0.09	-0.18	0.26	0.10	0.04	0.38
Rear legs (rear view)	0.54	0.09	0.25	-0.29	0.14	0.07
Feet and legs	0.69	0.15	0.14	-0.27	0.13	0.13
Rear teat placement	0.69	0.00	0.13	0.04	-0.07	0.02
Variance explained (%)	0.21	0.15	0.13	0.11	0.04	0.02

481 Table 7. Factor pattern of the correlation matrix between direct chromosomal values for 31
 482 production, conformation and functional traits for BTA18.

BTA18	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7
Milk	-0.08	0.04	0.05	0.01	0.95	-0.20	-0.20
Fat	0.18	-0.09	-0.01	-0.07	0.80	0.55	0.01
Protein	-0.16	0.05	0.13	-0.04	0.94	-0.09	0.26
Fat percentage	0.31	-0.15	-0.07	-0.10	-0.10	0.89	0.23
Protein percentage	-0.17	0.01	0.18	-0.11	0.05	0.20	0.94
Net merit	-0.31	0.13	0.78	0.22	0.46	0.09	0.11
Productive life	-0.41	0.13	0.83	0.26	0.15	-0.03	0.09
Somatic cell score	0.00	-0.12	-0.71	-0.10	0.01	0.00	0.00
Daughter pregnancy rate	-0.22	-0.08	0.82	0.25	-0.13	0.00	0.06
Sire calving ease	0.72	0.01	-0.41	0.12	-0.04	0.12	-0.01
Daughter calving ease	0.46	-0.09	-0.50	0.09	-0.17	0.08	-0.12
Sire stillbirth	0.69	0.11	-0.31	0.19	-0.01	0.17	-0.02
Daughter stillbirth	0.38	0.08	-0.44	-0.07	-0.26	0.08	-0.10
Final score	0.47	0.69	0.22	0.46	0.02	0.00	-0.08
Stature	0.83	0.21	-0.03	0.19	-0.06	-0.05	-0.11
Strength	0.96	0.01	-0.08	0.09	-0.03	0.09	0.02
Dairy form	0.34	0.37	-0.36	0.11	0.28	-0.06	-0.22
Foot angle	0.52	0.32	0.10	0.67	-0.10	-0.03	0.00
Rear legs (side view)	-0.03	-0.04	-0.10	-0.46	-0.03	0.08	0.07
Body depth	0.93	0.05	-0.23	0.09	-0.01	0.10	-0.06
Rump angle	-0.37	0.05	-0.14	-0.24	0.11	-0.23	-0.05
Rump width	0.84	0.21	-0.07	0.17	-0.05	0.05	-0.06
Fore udder attachment	0.30	0.67	0.44	0.33	-0.10	0.01	-0.01
Rear udder height	0.04	0.71	0.22	0.36	0.07	-0.12	-0.08
Udder depth	0.17	0.51	0.51	0.27	-0.25	-0.08	-0.11
Udder cleft	0.04	0.85	0.14	0.18	0.03	-0.09	0.06
Front teat placement	0.01	0.81	-0.06	0.04	-0.02	0.00	0.00
Teat length	0.44	-0.27	-0.13	-0.17	0.17	-0.05	-0.10
Rear legs (rear view)	0.29	0.26	0.16	0.84	-0.01	0.11	-0.03
Feet and legs	0.13	0.33	0.16	0.91	-0.04	0.00	0.01
Rear teat placement	-0.03	0.84	-0.17	0.00	0.07	0.00	0.04
Variance explained (%)	0.20	0.14	0.13	0.10	0.10	0.04	0.04

484 Table 8. Factor pattern of the correlation matrix between direct chromosomal values for 31
 485 production, conformation and functional traits for BTA20.

BTA20	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7	Factor8
Milk	-0.16	-0.10	-0.27	-0.04	-0.76	0.55	0.12	0.01
Fat	0.13	0.18	-0.22	-0.08	0.31	0.78	0.43	-0.04
Protein	0.00	0.25	-0.08	0.00	0.04	0.95	-0.19	0.01
Fat percentage	0.23	0.23	0.07	-0.03	0.90	0.13	0.23	-0.04
Protein percentage	0.15	0.32	0.23	0.04	0.84	0.17	-0.28	0.00
Net merit	0.39	-0.03	0.56	0.26	0.26	0.59	0.13	-0.02
Productive life	0.39	-0.24	0.80	0.32	0.04	0.14	0.06	-0.01
Somatic cell score	0.18	0.18	-0.47	-0.26	-0.03	0.06	0.12	-0.03
Daughter pregnancy rate	0.15	-0.23	0.63	0.08	0.14	-0.13	-0.03	0.00
Sire calving ease	-0.43	0.25	0.03	-0.03	-0.14	0.19	-0.06	-0.01
Daughter calving ease	-0.07	0.10	0.06	-0.19	-0.43	-0.03	-0.05	0.00
Sire stillbirth	-0.10	0.44	-0.13	0.01	0.07	0.03	-0.05	-0.02
Daughter stillbirth	-0.01	0.17	-0.14	0.06	-0.40	-0.29	-0.04	-0.02
Final score	0.69	0.48	0.24	0.40	0.15	0.14	0.06	-0.04
Stature	0.11	0.82	0.20	-0.03	0.04	0.09	-0.04	-0.07
Strength	0.10	0.51	0.02	0.20	-0.03	-0.01	-0.05	0.35
Dairy form	0.17	0.53	-0.47	0.09	-0.06	0.27	0.11	-0.13
Foot angle	0.23	0.26	0.30	0.66	-0.05	0.12	-0.10	0.01
Rear legs (side view)	0.15	0.38	-0.08	-0.32	0.09	0.14	0.29	-0.07
Body depth	0.14	0.65	-0.26	0.18	-0.08	0.08	0.06	0.11
Rump angle	0.11	0.05	-0.17	-0.33	-0.03	0.12	-0.08	-0.01
Rump width	0.14	0.61	-0.23	0.20	0.11	-0.03	0.09	-0.01
Fore udder attachment	0.76	0.25	0.46	0.19	0.14	0.02	0.06	-0.03
Rear udder height	0.63	0.41	0.30	0.32	0.16	0.16	0.07	-0.03
Udder depth	0.52	0.28	0.66	0.09	0.21	-0.05	0.04	-0.08
Udder cleft	0.76	0.27	0.21	0.21	0.14	-0.03	0.00	-0.02
Front teat placement	0.98	0.00	-0.10	0.08	0.10	0.04	-0.02	0.03
Teat length	-0.67	0.07	-0.10	0.07	0.01	-0.23	-0.10	-0.02
Rear legs (rear view)	0.24	0.14	-0.01	0.88	0.12	0.00	-0.06	0.05
Feet and legs	0.34	0.28	0.13	0.83	0.11	0.07	0.00	-0.02
Rear teat placement	0.89	0.11	-0.05	0.07	0.08	-0.01	-0.10	0.02
Variance explained (%)	0.18	0.12	0.10	0.09	0.09	0.08	0.02	0.01

487 Table 9. Regression analysis of communalities extracted from the genomic correlation matrix on
 488 those extracted from the different chromosome matrices

BTA	Intercept	P^I	Slope	P^2
6	0.32 ± 0.09	0.01	0.66 ± 0.10	0.02
14	0.30 ± 0.10	0.02	0.68 ± 0.12	0.03
18	0.51 ± 0.03	<0.001	0.48 ± 0.03	<0.001
20	0.41 ± 0.01	<0.001	0.58 ± 0.02	<0.001
3	-0.12 ± 0.13	0.390	1.12 ± 0.16	0.453

489 P^I = Statistical significance of the test H0: intercept = 0; Ha: intercept \neq 0.

490 P^I = Statistical significance of the test H0: slope = 1; Ha: slope \neq 1.

491 Test are declared statistically significant if $P < 0.05$

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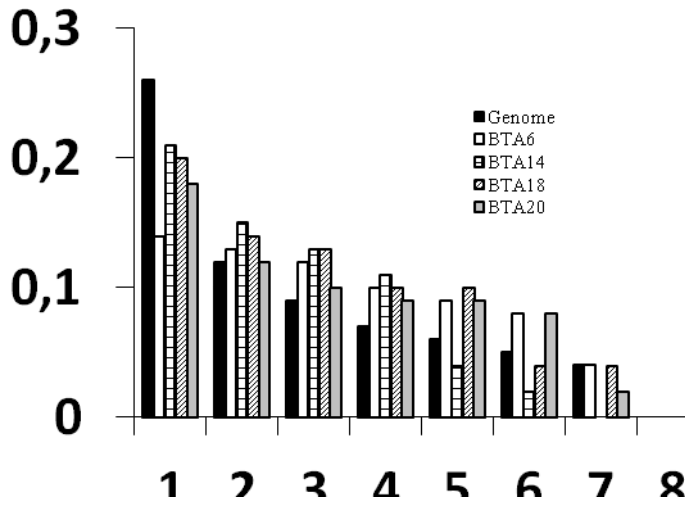
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498 Captions of figures

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500 Figure 1. Pattern of explained variance of factors extracted from the genomic and some
501 chromosomal correlation matrices.

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