1 **INTERPRETIVE SUMMARY**

2 **Genetic correlations between claw health and feet and leg conformation in Norwegian Red**

3 **cows.** *By Ødegård et al., page 000.* Genetic correlations between claw disorders recorded at

4 claw trimming, and feet and leg conformation traits scored on 1st lactation cows, were

5 estimated. Three claw disorders and five feet and leg conformation traits were analyzed. All

6 genetic correlations were low or moderate, except between corkscrew claw and hoof quality

7 (which are supposed to measure the same trait). These results indicate that selecting for feet and

8 leg conformation is not an efficient approach to genetically improve claw health in Norwegian

9 Red.

10 **Genetic correlations between claw health and feet and leg conformation in Norwegian Red**

11 **cows**

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36 **ABSTRACT**

37 The aim of this study was to estimate genetic correlations between claw disorders and feet and

38 leg conformation traits in Norwegian Red cows. A total of 188,928 cows with claw health status

39 recorded at claw trimming from 2004 to September 2013 and 210,789 1st lactation cows with

40 feet and leg conformation scores from 2001 to September 2013 were included in the analyses.

41 Traits describing claw health were corkscrew claw, infectious claw disorders (dermatitis, heel

42 horn erosion and interdigital phlegmon) and laminitis related claw disorders (sole ulcer, white

43 line disorder and hemorrhage of sole and white line). The feet and leg conformation traits were

44 rear leg rear view (new and old definition), rear leg side view, foot angle and hoof quality. Feet

45 and leg conformation traits were scored linearly from 1 to 9 with optimum scores depending on

46 the trait. Claw disorders were defined as binary (0/1) traits for each lactation. Threshold sire

47 models were used to model claw disorders, whereas the feet and leg conformation traits were

48 described by linear sire models. Three multivariate analyses were performed; each including

49 the 5 feet and leg conformation traits and 1 of the 3 claw disorders at a time. Posterior means

50 of heritability of liability of claw disorders ranged from 0.10 to 0.20 and heritabilities of feet

51 and leg conformation traits ranged from 0.04 to 0.11. Posterior standard deviation of heritability

52 was ≤0.01 for all traits. Genetic correlations between claw disorders and feet and leg

53 conformation traits were all low or moderate, except between corkscrew claw and hoof quality

54 (-0.86), which are supposed to measure the same trait. The genetic correlations between rear

55 leg rear view (new) and infectious claw disorders (-0.20) and laminitis related claw disorders

56 (0.26), respectively, and between hoof quality and laminitis related claw disorders (-0.33) were

57 moderate. Eight of the 15 genetic correlations between claw disorders and feet and leg

58 conformation traits had 0 included in the 95% highest posterior density interval. These results

59 imply that selection for feet and leg conformation is not an efficient approach to genetically

60 improve claw health in Norwegian Red.

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62 **Key words:** claw disorder, feet and leg conformation, genetic correlation, dairy cow

63

64   **INTRODUCTION**

65 More free-stalls (Simensen et al., 2010) and focus on claw health has raised the interest to breed

66 for better claw health in Norwegian Red. Claw health status at claw trimming has since 2004

67 been reported to the Norwegian Dairy Herd Recording System, and Ødegård et al. (2013)

68 showed that these data are suitable for genetic evaluation of Norwegian Red. The current feet

69 and leg index included in the total merit index (**TMI**) for Norwegian Red contains 3 feet and

70 leg conformation traits: rear leg rear view (**RLRV**), foot angle (**FA**) and hoof quality (**HQ**),

71 with weights 35%, 25% and 40%, respectively. The feet and leg index receives a relative weight

72 of 6% in the TMI (Geno, 2013). All conformation traits are scored on 1st lactation cows by

73 breeding advisors.

74

75 The number of claw health records from claw trimming has gradually increased over time, but

76 the data is still limited (Ødegård et al., 2013). In 2012, about 60,000 Norwegian Red cows had

77 at least 1 claw health record and about 30% of Norwegian dairy herds reported claw health.

78 Daughters groups for claw health at 1st official proof of the sires are small compared to other

79 health traits in the Norwegian Red breeding scheme, where at least 140 daughters are required.

80 In 2012, 123 sires got their first official breeding values. These sires had on average 39

81 daughters with claw health records at the time of their 1st official proof. To utilize the new claw

82 health information from claw trimming, claw disorders will be included in the feet and leg

83 index. Information from genetically correlated traits could be used to increase reliability of

84 breeding values for claw disorders.

85

86   Several authors have estimated genetic correlations between claw disorders and feet and leg

87   conformation traits (e.g. Uggla et al., 2008; Häggman and Juga, 2013; van der Linde et al.,

88   2010) and the results vary between breeds and populations. Uggla et al. (2008) estimated low

89   to moderate genetic correlations in Swedish Red, ranging from -0.31 (hock quality and heel

90   horn erosion) to 0.17 (rear leg side view and heel horn erosion); whereas van der Waaij et al.

91   (2005) estimated higher genetic correlations ranging from -0.35 (rear leg rear view and

92   interdigital hyperplasia) to 0.64 (foot angle and white line disorder) in Dutch dairy cattle. In

93   Finnish Ayrshire cows the genetic correlations between overall claw disorder and feet and leg

94   conformation traits ranged from -0.40 (bone structure) to 0.42 (rear leg side view) (Häggman

95   et al., 2013), whereas Finnish Holstein cows had genetic correlations ranging from -0.51 (foot

96   angle and sole ulcer) to 0.45 (foot angle and heel horn erosion) (Häggman and Juga, 2013).

97   With such large range estimates of genetic correlations in other breeds and populations it is of

98   interest to study these associations in Norwegian Red. The aim of this study was to estimate

99   genetic correlations between claw disorders and feet and leg conformation traits in Norwegian

100 Red.

101

102   **MATERIALS AND METHODS**

103 *Claw health*

104 Claw health status, recorded at claw trimming, from 2004 to September 2013 was used in the

105 analyses. Nine different claw disorders were recorded as healthy or diseased: corkscrew claw

106 (**CSC**), dermatitis, heel horn erosion, interdigital phlegmon, sole ulcer, white line disorder,

107 hemorrhage of sole and white line, lameness and acute trauma. All trimmed cows were

108 recorded, including healthy cows. A cow could have more than one claw disorder recorded at

109 the same day. Also the identification of claw trimmer and date of claw trimming were recorded

110 at each claw trimming. The recording is voluntary and therefore not reported by all herds.

111   Approximately 30% of the cows in a herd had claw health recorded and about 18% of the cows

112   had more than 1 claw health record during a lactation (Ødegård et al., 2013). More details of

113   claw health data in Norway can be found in Ødegård et al. (2013).

114

115   Based on results from Ødegård et al. (2013) 1 single claw disorder (CSC) and 2 groups of claw

116   disorders (infectious (**INF**) and laminitis related (**LAM**) claw disorders) were included in the

117   analyses (Table 1). The group INF included: dermatitis, heel horn erosion and interdigital

118   phlegmon; and LAM included: sole ulcer, white line disorder and hemorrhage of sole and white

119   line. Claw health data was edited as described in Ødegård et al. (2013); only cows and lactations

120   with claw health records, daughters of Norwegian Red AI sires, and herds recording more than

121   10% or at least 10 cows with normal claws were included. In addition, age at calving should be

122   between 16 and 48 months for 1st lactation, 26 and 61 months for 2nd lactation, 36 and 74 months

123   for 3rd lactation, and 45 and 87 months for 4th lactation. After editing the total number of claw

124   health records was 285,581 from 188,928 cows in 6,891 herds; and 2,101 sires had daughters

125   with claw health data in the final data set. A cow was defined as either healthy (0) or diseased

126   (1) for each of the 3 traits CSC, INF and LAM in each lactation where at least 1 claw trimming

127   record was present. If a cow had more than 1 case of a claw disorder during a lactation, only

128   the 1st observation was included in the analyses. Few cows had claw health records for more

129   than 1 lactation, and therefore a possible permanent environment effect was ignored in the

130   analyses. The mean frequency of CSC, INF and LAM was 0.11, 0.06 and 0.07, respectively

131   (Table 1).

132

133   ***Feet and leg conformation***

134   Feet and leg conformation scores from 1987 to 2013 were available, but only data from 2001

135   to September 2013 were used in the analyses, due to changes of the scoring system in 2001.

136   Breeding advisors score feet and leg conformation together with other conformation traits on

137   1st lactation cows. Four feet and leg conformation traits are recorded: RLRV, rear leg side view

138   (**RLSV**), FA and HQ (Table 1). The definition of RLRV changed in 2010 and was therefore

139   treated as 2 correlated traits: new (**RLRV_N**) and old (**RLRV_O**). Hoof quality from

140   conformation scoring and CSC from claw trimming measures the same trait, but are recorded

141   differently (Table 1). Hoof quality is scored when the cow is standing, whereas CSC is

142   measured when the cow is fixed and the sole is inspected. The feet and leg conformation traits

143   are scored on a scale from 1 to 9, with optimum value depending on the trait (Table 1). Data

144   editing for feet and leg conformation traits was performed as in routine genetic evaluation

145   (Interbull, 2011): only daughters of Norwegian Red AI sires with age at first calving between

146   18 and 33 months, and time for conformation scoring within defined intervals (months after

147   calving) were included. The final dataset had feet and leg conformation scores for 210,789 1st

148   lactation cows in 13,659 herds and by 1,655 sires. The number of records for all trait

149   combinations of claw health and feet and leg conformation are presented in Table 2.

150

151   The total number of sires with daughter information on claw health, feet and leg conformation,

152   or both was 2,145. Of these sires, 1,611 had daughter information on both trait groups. The

153   pedigree of sires with daughters was traced back as far as possible and the final pedigree file

154   contained 18,895 animals.

155

156   ***Statistical model***

157   A Bayesian approach using Gibbs sampling was applied. The 3 claw disorders: CSC, INF and

158   LAM were defined as binary traits and analyzed with threshold models, whereas the 5 feet and

159   leg conformation traits: RLRV_N, RLRV_O, RLSV, FA and HQ were assumed to be normally

160   distributed and analyzed with linear models.

161

162   The threshold sire model used for claw disorders was as described in Ødegård et al. (2013):

163    $$\boldsymbol{\lambda} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z_h}\mathbf{h} + \mathbf{Z_s}\mathbf{s} + \mathbf{e},$$

164   where $\boldsymbol{\lambda}$ is a vector of unobserved liabilities of the trait; $\boldsymbol{\beta}$ is a vector of systematic effects,

165   including lactation number, calving year and month, time for claw trimming (months after

166   calving), and claw trimmer; $\mathbf{h}$ is a vector of herd effects with 6891 levels; $\mathbf{s}$ is a vector of sire

167   effects; and $\mathbf{e}$ is a vector of residuals. $\mathbf{X}$, $\mathbf{Z_h}$ and $\mathbf{Z_s}$ are the corresponding incidence matrices.

168   Lactation number had 4 levels where the 4th class included lactation 4 to 13; calving year and

169   month had 114 levels; time for claw trimming (months after calving) had 12 levels; and claw

170   trimmer were divided into 4 groups: certified claw trimmers, other claw trimmers, farmers, and

171   others (e.g. veterinarian).

172

173   The linear sire model for feet and leg conformation traits included the same effects as the linear

174   animal model used in routine genetic evaluation for Norwegian Red (Interbull, 2011):

175    $$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z_{hy}}\mathbf{hy} + \mathbf{Z_s}\mathbf{s} + \mathbf{e},$$

176   where $\mathbf{y}$ is a vector of observations of the trait; $\boldsymbol{\beta}$ is a vector of systematic effects including year

177   and month of calving, time from calving (months) and time from milking (hours) to scoring,

178   and age at scoring (in months); $\mathbf{hy}$ is a vector of herd-year effects; $\mathbf{s}$ is a vector of sire effects;

179    $\mathbf{e}$ is a vector of residuals; and $\mathbf{X}$, $\mathbf{Z_{hy}}$ and $\mathbf{Z_s}$ are the corresponding incidence matrices. Year and

180   month of calving had 46 levels for RLRV_N, 116 for RLRV_O and 151 levels for RLSV, FA

181   and HQ; time from calving (months) and time from milking (hours) to scoring had 96 levels for

182   all traits; age (in months) at scoring had 7 levels for all traits; and number of herd-year classes

183   were 10,395 for RLVR_N, 50,199 for RVLR_O and 60,594 for RLSV, FA and HQ. Classifier

184   (breeding advisor) was not included in the model because this effect is confounded with the

185   herd-year effect.

186

187   Because of computational time the 5 feet and leg conformation traits were analyzed together

188   with 1 of the 3 claw disorders at a time. It was assumed that $var(\mathbf{h}) \sim N(0, \sigma_h^2)$,

189    $var(\mathbf{hy}) = \mathbf{HY} \otimes \mathbf{I}$, $var(\mathbf{s}) = \mathbf{G} \otimes \mathbf{A}$, and $var(\mathbf{e}) = \mathbf{R} \otimes \mathbf{I}$; where σ_h^2 is the herd variance for claw

190   disorders, $\mathbf{HY}$ is the 5×5 matrix containing herd-year variances among the 5 feet and leg

191   conformation traits, herd-year covariances were assumed to be 0 among these traits (same as in

192   the routine evaluation), $\mathbf{I}$ is the identity matrix, $\mathbf{A}$ is the additive genetic relationship matrix,

193   and $\mathbf{G}$ and $\mathbf{R}$ are the 6×6 genetic and residual (co)variance matrices for the 5 feet and leg

194   conformation traits and 1 of the 3 claw disorders. For the binary claw disorders the residual

195   variance was assumed to be 1. Residual covariance was assumed to be 0 between RLRV_N and

196   RLRV_O, because no cows had observation for both new and old RLRV, and between claw

197   disorders and the 5 feet and leg conformation traits. These assumptions reduced computational

198   time without affecting the results.

199

200   To analyze the data the RJMC procedure in DMU (Madsen and Jensen, 2010) was used. The

201   Raftery and Lewis method in BOA (Smith, 2005) was used for convergence diagnostics. The

202   length of burn in was set to 10,000 iterations for all 3 models. The total number of iterations,

203   after burn in, was 200,000 for the models including CSC and INF and 350,000 for the model

204   including LAM.

205

206   Heritability (h^2) was calculated using

207    $$h^2 = \frac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_e^2}$$

208   where σ_s^2 is the sire variance and σ_e^2 is the residual variance.

209

210   **RESULTS AND DISCUSSION**

211   **Heritabilities**

212   Posterior mean of heritability of liability of CSC, INF and LAM was 0.20, 0.12 and 0.10,

213   respectively (Table 3), which corresponds well with Ødegård et al. (2013). Estimated

214   heritabilities were also in accordance with other studies (e.g. van der Waaij et al., 2005; Swalve

215   et al., 2008; Buch et al., 2011). Van der Spek et al. (2013) found that the underlying heritability

216   of some claw disorders changed when including herds where at least 70% of the cows were

217   trimmed compared to herds were less than 35% of the cows where trimmed. At present our

218   editing criteria were less strict due to limited data. The heritability estimates may therefore be

219   affected, and higher heritabilities may be obtained with more complete data in the future. The

220   heritabilities for the 5 feet and leg conformation traits ranged from 0.04 (HQ) to 0.11 (RLSV),

221   with small standard deviations (**SD**) ($\leq$0.01, Table 3), and were in accordance with heritabilities

222   used in routine genetic evaluations for these traits in Norwegian Red (Geno, 2013).

223   Heritabilities of RLRV_N, RLSV and FA were lower (0.09-0.11) in this study than estimates

224   by Laursen et al. (2009), Uggla et al. (2008) and van der Waaij et al. (2005). However,

225   heritabilities of RLRV_N and FA were in accordance with Häggman et al. (2013).

226

227   **Herd variance**

228   The herd variance for CSC, INF and LAM was 0.55, 1.15 and 0.36, respectively (Table 3). For

229   the feet and leg conformation traits the herd-year variance varied between 0.08 (RLRV_O) and

230   0.89 (HQ, Table 3). The models did not include a permanent environment effect for claw

231   disorders, meaning that the herd effect could possibly include a permanent effect of the cow.

232

233   **Genetic correlations**

234   The posterior distributions of the genetic correlations between claw disorders and feet and leg

235   conformation traits were in general symmetric (Figure 1), with SD varying between 0.03 and

236   0.08 (Table 4). Figure 1 show that many of the distributions overlap and have means close to

237   0. The strongest genetic correlation (-0.86) was found between CSC and HQ (Table 4) with the

238   95% highest posterior density interval (**HPD**) ranging from -0.92 to -0.79. The high genetic

239   correlation was expected because CSC and HQ are supposed to measure the same trait. The

240   genetic correlation has a negative sign because of opposite scaling (Table 1) and indicates a

241   favorable genetic correlation. The result shows that CSC can replace HQ in the feet and leg

242   index, which is preferable because CSC is expected to be a more accurate measure of the trait.

243   However, the high genetic correlation indicates that HQ can be used as an indicator trait for

244   CSC. The genetic correlation between RLRV_N and INF (-0.20) and LAM (0.26), respectively,

245   were moderate, and in opposite directions, meaning that bowed-legs are associated with more

246   INF and toes out are associated with more LAM. The genetic correlation of -0.33 between HQ

247   and LAM is favorable in the sense that selection for better HQ will reduce LAM. Between

248   RLRV_O and INF and LAM, respectively, the genetic correlations were not significantly

249   different from 0. Foot angle had genetic correlations that were low but significantly different

250   from 0 to LAM (0.17) and INF (0.16). The genetic correlations between claw disorders and feet

251   and leg conformation traits were in general low, and the 95% HPD included 0 for 8 out of 15

252   correlations (Table 4). Despite relatively few cows with information on both claw health and

253   feet and leg conformation (Table 2) the estimated genetic correlations were relative precise

254   (Table 4 and Figure 1).

255

256   Uggla et al. (2008) showed that dermatitis and heel horn erosion, which are infectious claw

257   disorders, and sole hemorrhage and sole ulcer, which are laminitis related claw disorders, had

258   genetic correlation to RLSV that differed significantly from 0 in Swedish Red. However, they

259   found no significant genetic correlation between the mentioned claw disorders and RLRV. Also

260   van der Linde et al. (2010) found significant genetic correlation between RLSV and SU (0.41)

261   for 1st lactation cows. These results differ from the present study where no significant genetic

262   correlation between RLSV and INF or LAM were found, whereas moderate genetic correlations

263   were found between RLRV_N and both INF and LAM. Häggman and Juga (2013) estimated

264   negative correlation between RLRV and heel horn erosion (-0.29) and a significant positive

265   genetic correlation between FA and heel horn erosion (0.45), whereas most other genetic

266   correlations were not significant different from 0. Van der Waaij et al. (2005) found high genetic

267   correlation between FA and white line disorder (0.64), whereas in the present study FA and

268   LAM (which includes white line disorder) had low genetic correlation (0.17). The different

269   result could be due to a low genetic correlation between FA and the other traits included in

270   LAM. Moderate genetic correlation between RLRV and digital dermatitis (-0.32) and

271   interdigital dermatitis (-0.23) for 1st lactation cows was found by van der Linde et al. (2010),

272   which was in agreement to the genetic correlation found between RLRV_N and INF in this

273   study (-0.20).

274

275   Rear leg side view is not included in the current TMI in Norway, and results from the present

276   study show that claw disorders will not gain additional information from RLSV (Table 4). This

277   was in contrast to a study by Häggman et al. (2013) who estimated moderate genetic correlation

278   between RLSV and overall claw health (0.42) in Finnish Ayrshire and suggested to use it as

279   indicator trait for claw disorders. Gernand et al. (2013) estimated favorable genetic correlation

280   between claw disorder and RLSV and FA. The contradicting results found between different

281   studies could be due to differences in trait definitions and frequency of claw disorders between

282   breeds and populations. Battagin et al. (2012) investigated the genetic correlation of the trait

283   overall feet and leg conformation among different countries and found a correlation of 0.68

284   across countries. Another study by Battagin et al. (2013) estimated changes in genetic

285   correlation of overall feet and leg conformation over time, and concluded that a further

286   harmonization is needed to obtain better genetic correlations across countries. In the Nordic

287   countries, a harmonization of conformation traits and claw disorders will be implemented, and

288   this will provide a better comparison of these traits between the Nordic breeds.

289

290   Although the results indicate that selection for feet and leg conformation traits is not an efficient

291   approach to genetically improve claw health , feet and leg conformation traits may be of value

292   to other health and welfare aspects of the cow.

293

294   Other possible indicator traits for claw health are locomotion and lameness (e.g. Laursen et al.,

295   2009; van der Waaij et al., 2008; Weber et al., 2013). Van der Waaij et al. (2005) concluded

296   that locomotion was useful for predicting claw disorders later in life, but more investigation

297   was needed. Several authors concluded that direct selection against claw disorders is the most

298   efficient way to improve claw health (e.g. Laursen et al., 2009; Häggman et al., 2013; Weber

299   et al., 2013). Gernand et al. (2013) discussed selection strategies for claw health, comparing

300   direct and indirect selection, and concluded that including direct claw health in the ultimate

301   breeding goal was the most promising alternative. In Norwegian Red, locomotion and lameness

302   are not recorded routinely, and direct selection against claw disorders would be the best choice

303   for genetic improvement of claw health.

304

305   **CONCLUSIONS**

306   Genetic correlations between claw disorders and feet and leg conformation traits were in

307   general low, and selection for feet and leg conformation is therefore not an efficient approach

308   for genetic improvement of claw health in Norwegian Red. The exception was HQ which, with

309 a genetic correlation of -0.86 to CSC, is a useful indicator trait that can provide additional

310 information to CSC.

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384 **Table 1.** Definition and optimum value of claw disorders and feet and leg conformation traits[1],

385 frequency of the claw disorders and average scoring of feet and leg conformation traits with

386 standard deviation (SD) in the analyzed data

Trait	Abbreviation	Definition	Scoring	Optimum value	Average score	SD
Corkscrew claw	CSC	Small to large twist in the abaxial wall on the lateral hind claw	0 = healthy 1 = disorder	0	0.11	0.3
Infectious claw disorders	INF	Heel horn erosion, dermatitis and interdigital phlegmon	0 = healthy 1 = disorder	0	0.06	0.2
Laminitis related claw disorders	LAM	Sole ulcer, white line disorder and hemorrhage of sole and white line	0 = healthy 1 = disorder	0	0.07	0.3
Rear leg rear view (new)	RLRV_N	Rear legs should be parallel (from 2010)	1 = toes out 9 = bow-legged	8	6.27	1.5
Rear leg rear view (old)	RLRV_O	Rear legs should be parallel (before 2010)	1 = toes out 9 = bow-legged	5	4.60	0.9
Rear leg side view	RLSV	Optimum angle is 150-155 degrees	1 = straight 9 = sickled	5	4.80	1.1
Foot angle	FA	Optimum angle is 45 degrees	1 = low 9 = steep	5	4.80	1.0
Hoof quality	HQ	Small to large twist in the abaxial wall on the lateral hind claw	1 = severe twisted 9 = no twist	9	8.00	1.7

387   [1](Geno, 2011; Refsum, 2012)

388 **Table 2.** Number of records for trait combinations of corkscrew claw (CSC), infectious claw

389 disorders (INF), laminitis related claw disorders (LAM), rear leg rear view new (RLRV_N),

390 rear leg rear view old (RLRV_O), rear leg side view (RLSV) foot angle (FA) and hoof quality

391 (HQ)

	CSC	INF	LAM	RLRV_N	RLRV_O	RLSV	FA	HQ
CSC	285,581							
INF	285,581	285,581						
LAM	285,581	285,581	285,581					
RLRV_N	11,850	11,850	11,850	47,474				
RLRV_O	14,888	14,888	14,888	0	163,315			
RLSV	26,738	26,738	26,738	47,474	163,315	210,789		
FA	26,738	26,738	26,738	47,474	163,315	210,789	210,789	
HQ	26,738	26,738	26,738	47,474	163,315	210,789	210,789	210,789

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395 **Table 3.** Posterior mean and standard deviation (SD) of heritability, sire variance (σ_s^2), herd

396 variance (σ_h^2) of claw disorders and herd-year variance (σ_h^2) of feet and leg conformation

397 traits

Trait	Heritability[1]		σ_s^2		σ_h^2	
	Mean	SD	Mean	SD	Mean	SD
Corkscrew claw	0.20	0.01	0.05	<0.01	0.55	0.02
Infectious claw disorders	0.12	0.01	0.03	<0.01	1.15	0.04
Laminitis related claw disorders	0.10	0.01	0.02	<0.01	0.36	0.01
Rear leg rear view (new)	0.09	0.01	0.03	<0.01	0.54	0.01
Rear leg rear view (old)	0.07	<0.01	0.01	<0.01	0.08	<0.01
Rear leg side view	0.11	0.01	0.03	<0.01	0.13	<0.01
Foot angle	0.10	0.01	0.02	<0.01	0.15	<0.01
Hoof quality	0.04	<0.01	0.02	<0.01	0.89	0.01

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399 [1] Heritability: $h^2 = \dfrac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_e^2}$

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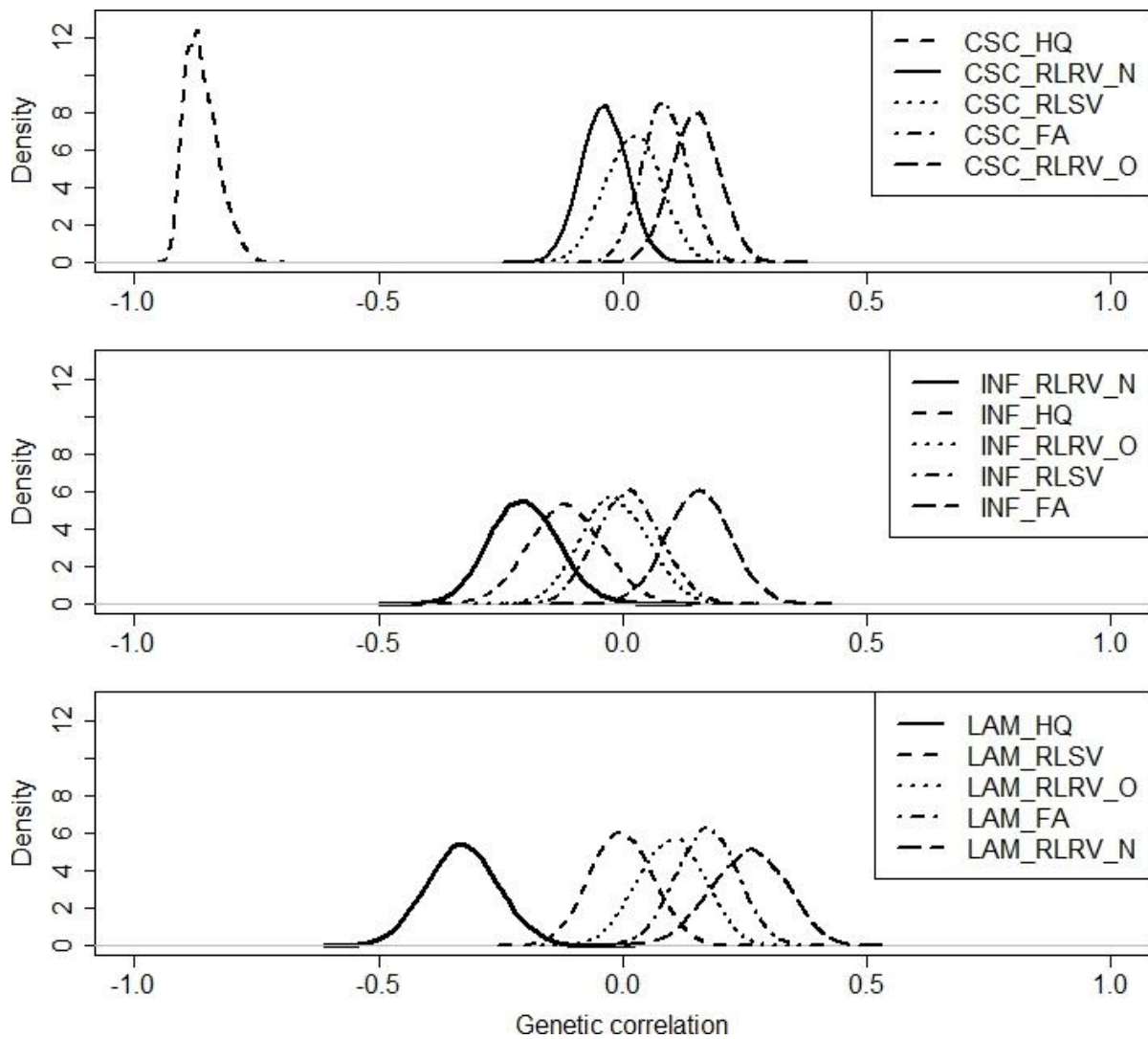402   **Table 4.** Genetic correlation between claw disorders and feet and leg conformation traits.

403   Posterior mean (standard deviation) and [95 % highest posterior density interval]

	Rear leg rear view new	Rear leg rear view old	Rear leg side view	Foot angle	Hoof quality
Corkscrew claw	0.02 (0.06) [-0.09; 0.13]	0.15 (0.05) [0.05; 0.25]	-0.04 (0.05) [-0.13; 0.05]	0.09 (0.05) [-0.01; 0.18]	-0.86 (0.03) [-0.92; -0.79]
Infectious claw disorders	-0.20 (0.07) [-0.33; -0.05]	-0.02 (0.07) [-0.15; 0.12]	0.01 (0.07) [-0.11; 0.14]	0.16 (0.07) [0.03; 0.29]	-0.12 (0.08) [-0.26; 0.04]
Laminitis related claw disorders	0.26 (0.08) [0.11; 0.41]	0.10 (0.07) [-0.03; 0.23]	0.00 (0.07) [-0.13; 0.13]	0.17 (0.06) [0.05; 0.30]	-0.33 (0.07) [-0.47; -0.18]

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Figure 1. Posterior distribution of genetic correlations between claw disorders (corkscrew

claw (CSC), infectious claw disorders (INF), laminitis related claw disorders (LAM)) and feet

and leg conformation traits (rear leg rear view new (RLRV_N), rear leg rear view old

(RLRV_O), rear leg side view (RLSV), foot angle (FA) and hoof quality (HQ)).