1   **Networks of inbreeding coefficients in a selected population of rabbits**

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3   **Running title:** Inbreeding networks in rabbits

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14

15   **Summary**

16

17   The correlation between pedigree and genomic-based inbreeding coefficients is usually

18   discussed in the literature. However, some of these correlations could be spurious.

19   Using partial correlations and information theory, it is possible to distinguish a

20   significant association between two variables which is independent from associations

21   with a third variable. The objective of this study is to implement partial correlations and

22   information theory to assess the relationship between different inbreeding coefficients

23   using a selected population of rabbits. Data from pedigree and genomic information

24   from a 200K SNP chip were available. After applying filtering criteria, the data set

25   comprised 437 animals genotyped for 114,604 autosomal SNP. Fifteen pedigree- and

26   genome-based inbreeding coefficients were estimated and used to build a network.

27   Recent inbreeding coefficient based on runs of homozygosity had 9 edges linking it

28   with different inbreeding coefficients. Partial correlations and information theory

29   approach allowed to infer meaningful associations between inbreeding coefficients, and

30   highlighted the importance of the recent inbreeding based on runs of homozygosity, but

31   a good proxy of it could be those pedigree-based definitions reflecting recent

32   inbreeding.

33

34   **Keywords:** inbreeding, information theory, partial correlation, rabbit

35

Introduction

The coefficient of inbreeding is defined as the probability that two alleles at a given locus are identical by descent (IBD), and occurs when related individuals are mated (Malécot, 1948). One of the most important consequences of the rise of inbreeding is the reduction in the mean of a trait with economic interest (Falconer & Mackay, 1996). Therefore, obtaining accurate estimates of inbreeding is important for the management of animal populations under selection.

Traditionally, inbreeding coefficients have been estimated in animal populations from pedigree records. With pedigree data, it is also possible to distinguish recent from ancient inbreeding by using deterministic or stochastic methods. However, genomic inbreeding coefficients can be obtained nowadays since the cost of genotyping is no longer a limiting factor. Single nucleotide polymorphisms (SNP) are the most commonly used genomic markers due to their automated and accurate genotyping, and refined pedigree-free inbreeding coefficients based on them have been proposed (McQuillan et al., 2008). Genomic inbreeding coefficients account for Mendelian sampling variance (Hill & Weir, 2011) and do not depend on quality and completeness of the pedigree. Therefore, they are expected to be more accurate than pedigree-based coefficients. Among the former, those obtained from the proportion of the genome covered by homozygous regions called runs of homozygosity (ROH) allow to distinguish recent from ancient inbreeding (Pryce, Haile-Mariam, Goddard, & Hayes, 2014).

60   Correlations between genome- and pedigree-based inbreeding coefficients are usually

61   provided in the literature (e.g. Silió et al., 2013; Pryce et al., 2014; Rodríguez-Ramilo,

62   Elsen, & Legarra, 2019). However, when two inbreeding coefficients (*A* and *B*) evolve

63   similarly along generations it is expected a strong relationship between them.

64   Accordingly, the change of inbreeding coefficient *A* is linked to the change of

65   inbreeding coefficient *B*, and vice versa. However, occasionally the association could be

66   coincidental or caused by a third inbreeding coefficient *C* that affects the first two

67   inbreeding coefficients. In other words, given three inbreeding coefficients (*A*, *B* and *C*),

68   if there is a strong correlation between *AC* and *BC*, the correlation *AB* is likely to be

69   also strong. However, the correlation *AB* could be non-meaningful or dependents on the

70   correlations *AC* and *BC*. This is called a spurious correlation. The occurrence of this

71   kind of correlations can increase with the augmentation of the definition of different

72   inbreeding coefficients. This highlights the importance of assessing spurious

73   correlations.

74

75   In order to identify significant associations between two variables that are independent

76   from a third one, Reverter and Chan (2008) suggested an approach that uses first-order

77   partial correlation coefficients combined with information theory (PCIT) methodology.

78   The objective of this study was to detect significant associations between different

79   inbreeding coefficients in a selected population of rabbits using a PCIT algorithm.

80

81   **Material and Methods**

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83   *Ethical statement*

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85   The current study was carried out under a Project License from the IRTA Scientific

86   Ethic Committee. Animal manipulations were performed according to the Spanish

87   Policy for Animal Protection, which meets the European Union Normative.

88

89   *Data*

90

91   Animals in the study are a sample of the Caldes line, which belongs to IRTA. This line

92   was founded in 1983 by crossing animals from five New Zealand White lines and a

93   California $\times$ New Zealand synthetic line. It has been selected for litter weight and

94   individual growth rate until 1992, for growth rate until 2011. From 2011 to 2016 no

95   selection was performed on these animals (see Piles et al., 2017 for more details).

96   Management of rabbits was performed avoiding matings between animals with common

97   grandparents. The line is currently in its 60th generation. The average number of animals

98   per generation was 2,928 with a minimum of 1,351 and a maximum of 5,016

99   individuals. The average number of does per generation was 179 ranging from 117 to

100   364 dams. The average number of sires per generation was 60, ranging from 37 to 97

101   sires. The mean generation interval was 292 d and the 0.05 and 0.95 quartiles of the

102   absolute value of the age difference of dam and sire was 1 to 310 days, respectively.

103   The pedigree file comprised 173,485 animals, with 1,799 sires and 8,082 dams from

104   generation 1 to generation 60. The pedigree was complete and only individuals from the

105   base generation had unknown parents.

106

107   DNA was extracted from blood samples from $N = 437$ rabbits born in 2013, 2014 and

108   2016 (corresponding to generations 49, 50, 51 and 54). Genotyping was performed

109   using the Axiom rabbit array of 200,000 SNP (Affymetrix). No pruning of SNP for

110   linkage disequilibrium was performed, and after the exclusion of SNP with a minor

111   allele frequency (MAF) < 0.05, 114,604 autosomal SNP were available.

112

113   *Inbreeding computation from pedigree*

114

115   Following Ragab, Sánchez, and Baselga (2015), we defined F_u^t as the inbreeding of an

116   animal from generation u considering generation t as the base generation, being $t < u$.

117   For $t = 0$, F_u^0 represents the inbreeding accumulated since the foundation of the line,

118   which is divided into several components that account for the inbreeding accumulated

119   during different periods of time. Thus, for two given generations t_1 and t_2, being $0 <$

120    $t_1 < t_2 < u$, we defined the inbreeding accumulated until generation t_1 as $F_{0,t1}^0$, the

121   inbreeding accumulated from generation t_1 to generation t_2 as $F_{t1,t2}^0$ and the inbreeding

122   accumulated from generation t_2 to generation u as $F_{t2,u}^0$. These components are

123   computed from the following formulas derived from the equation for inbreeding in

124   hierarchically structured populations (Wright, 1922):

125

$$1 - F_u^0 = \left(1 - F_{0,ti}^0\right)\left(1 - F_u^{ti}\right) \text{ for } i = 1,2$$

126   Thus,

$$1 - F_u^0 = 1 - F_u^{ti} - F_{0,ti}^0 + F_{0,ti}^0 F_u^{ti}$$

$$F_u^0 = F_u^{ti} - F_{0,ti}^0 \left(1 - F_u^{ti}\right)$$

$$F_{0,ti}^0 = \frac{\left(F_u^0 - F_u^{ti}\right)}{\left(1 - F_u^{ti}\right)} \qquad \{\text{Formula 1}\}$$

127   and

$$1 - F_u^0 = 1 - F_{0,ti}^0 - F_{ti,u}^0 = \left(1 - F_{0,ti}^0\right)\left(1 - F_u^{ti}\right)$$

$$F_{ti,u}^0 = \left(1 - F_{0,ti}^0\right) - \left(1 - F_{0,ti}^0\right)\left(1 - F_u^{ti}\right)$$

$$\qquad\qquad\qquad\qquad\qquad\qquad\qquad \{\text{Formula 2}\}$$

$$F_{ti,u}^0 = \left(1 - F_{0,ti}^0\right)\left[1 - \left(1 - F_u^{ti}\right)\right] = \left(1 - F_{0,ti}^0\right)F_u^{ti}$$

128   The part of F_u^0 accumulated between generations t_1 and t_2 corresponds to:

$$F_{t1,t2}^0 = F_{t1,u}^0 - F_{t2,u}^0 = F_{0,t2}^0 - F_{0,t1}^0$$

129

130   F_u^0, F_u^{t1} and F_u^{t2} were computed using the program inbupgf90 that implements the

131   algorithm developed by Aguilar and Misztal (2008). $F_{0,t1}^0$, $F_{0,t2}^0$, $F_{t1,t2}^0$ were computed

132   from the Formulas 1 and 2. Finally, $F_{t1,u}^0 = F_u^0 - F_{0,t1}^0$ and $F_{t2,u}^0 = F_u^0 - F_{0,t2}^0$.

133

134   Three periods of 20 generations were considered, and $t_1 = 20$ and $t_2 = 40$. The recent

135   pedigree-based inbreeding coefficient (*FpedR*) is the inbreeding accumulated in the

136   period immediately preceding individual birth, the intermediate pedigree-based

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137   inbreeding coefficient (*FpedI*) is the inbreeding accumulated during the 20 generations

138   period before this, and the ancient pedigree-based inbreeding coefficient (*FpedA*) is the

139   inbreeding accumulated during the first 20 generations period of time. An animal born

140   before generation 20 has only accumulated *FpedR*, calculated as F_u^0, whereas *FpedI* and

141   *FpedA* are set to 0. An animal born between generations 20 and 40 has accumulated

142   *FpedR*, calculated as $F_{20,u}^0 = F_u^0 - F_{0,20}^0$, and *FpedI*, calculated as $F_{0,20}^0$, whereas *FpedA*

143   is set to 0. An individual born after generation 40 has accumulated *FpedR* calculated as

144     $F_{40,u}^0 = F_u^0 - F_{0,40}^0$, *FpedI* calculated as $F_{20,40}^0 = F_{0,40}^0 - F_{0,20}^0$, and *FpedA* calculated as

145     $F_{0,20}^0$. Inbreeding coefficients with all pedigree information were also calculated

146   (*FpedAll*).

147

148   The software "Grain" (Baumung et al., 2015) version 2.2 (Doekes et al., 2020) was used

149   to calculate the ancestral inbreeding coefficients and the ancestral history coefficient

150   (see below their definitions). The correlation between the inbreeding coefficients

151   calculated using the deterministic recursive algorithm proposed by Aguilar and Misztal

152   (2008) with all the genealogy (*FpedAll*) and the ones obtained with the stochastic gene

153   dropping process (Baumung et al., 2015) (*FpedAllDrop*) was high (0.9) with 800,000

154   replications (gene drops). Consequently, only results from *FpedAll* will be shown. The

155   ancestral inbreeding coefficient defined by Ballou (1997) was also calculated (*Fbal*).

156   This coefficient can be defined as the probability that any allele in an individual has

157   been IBD in previous generations at least once. Alternatively, the ancestral inbreeding

158   coefficient according to Kalinowski, Hedrick, and Miller (2000) (*Fkal*) represents the

159   probability that any allele in an individual is currently IBD and has been IBD in

160   previous generations at least once. It is also possible to calculate the recent inbreeding

161   (*FpedRDrop*) as the part of the classical inbreeding coefficient whereby alleles are IBD

162   for the first time, and it has been calculated as $FpedRDrop = FpedAllDrop - Fkal$

163   (Doekes et al., 2019). Finally, we computed the ancestral history coefficient (Ahc)

164   defined as the number of times that a random allele in an individual has been IBD in the

165   individual's pedigree. Alleles which have experienced inbreeding more often in the past

166   are less likely to be deleterious than alleles which have undergone IBD less often

167   because those alleles have survived to purging and therefore, it is probably that they

168   have a neutral or even positive effect on the selected traits. Thus, high values of $Fbal$,

169    $Fkal$ or Ahc are expected to have a positive effect on the phenotype.

170

171   *Inbreeding computation from genomic data*

172

173   Genomic inbreeding coefficients based on runs of homozygosity ($Froh$) were obtained

174   using PLINK v1.90 software (Chang et al., 2015). The criteria used for defining a ROH

175   were: (i) the minimum number of SNP was 100; (ii) the minimum density was 1 SNP

176   per 50 kb; (iii) the maximum distance allowed between two consecutive homozygous

177   SNP in a run was 1 Mb; (iv) a maximum of 5 missing genotypes, and (v) one

178   heterozygous genotype within a particular ROH was permitted. The minimum length

179   that constituted a ROH was set to > 1.25 and < 2.5, > 2.5 and <10, and > 10 Mb to

180   reflect ancient ($FrohA$), intermediate ($FrohI$) and recent ($FrohR$) ROH-based inbreeding

181   coefficients, respectively. These are the ROH minimum sizes that match to 40, 20 and 5

182   generations from the common ancestor (Curik, Ferenčaković, & Sölkner, 2014),

183   respectively. Recent inbreeding seems to generate long ROH while shorter ROH mainly

184   proceed from IBD segments shared by old ancestors, which were fragmented by

9

185   recombination along generations (Kirin et al., 2010). Genomic inbreeding coefficients

186   based on runs of homozygosity (*Froh*) were calculated as

187
$$Froh = \frac{\sum L_{roh}}{L_{genome}}$$

188   where $\sum L_{roh}$ is the sum of the length of all ROH detected in an animal in bp, and

189   L_{genome} is the total length of the genome in bp covered by SNP and where the criteria

190   used for defining a ROH were fulfilled.

191

192   Genomic-based inbreeding coefficients were also calculated as in VanRaden (2008)

193   (*Fvan*). Then, the inbreeding coefficient based on VanRaden (2008) for individual *j* was

194   estimated from the self-coancestry of individual *j* as

195
$$Fvan_j = 2f_{jj} - 1 = 2\left(\frac{1}{L}\sum_l \frac{(g_{jl} - p_l)(g_{jl} - p_l)}{p_l(1 - p_l)}\right) - 1$$

196   where g_{jl} is half of the number of copies of the reference allele *A* in the locus *l* for

197   individual *j*, p_l is the allele frequency, and *L* is the total number of SNP.

198

199   The proportion of homozygous genotypes (*Fsnp*) and the proportion of homozygous

200   SNP for the minor allele (*PHoMA*) were also calculated.

201

202   Expressing the genotype compressed file size relative to its uncompressed form is

203   possible to obtain a measure of compression efficiency (*CE*) as follows:

204
$$CE = \frac{Sb - Sa}{Sb}$$

205   where *Sb* and *Sa* represent the size of the SNP genotype file in bytes before and after

206   compression, respectively. This relates to the order and proportion of homozygote and

207   heterozygote SNP positions (Hudson et al., 2014).

208

209   *Identification of correlations and network reconstitution*

210

211   Pearson's correlation coefficients and first order partial correlation coefficients

212   combined with an approximation of information theory (Reverter & Chan, 2008) were

213   used to identify significant associations between the different inbreeding coefficients.

214   The first order partial correlation coefficients together with a similarity of information

215   theory were calculated with the software PCIT (Watson-Haig, Kadarmideen, &

216   Reverter, 2010). The PCIT algorithm contains two distinct steps as follows:

217

218   1) Partial correlations: For every trio of inbreeding coefficients, *x*, *y* and *z*, the three

219   first-order partial correlation coefficients are computed as

220

221
$$r_{xy,z} = \frac{r_{xy} - r_{xz}r_{yz}}{\sqrt{(1 - r_{xz}^2)(1 - r_{yz}^2)}}$$

222

223   and similarly for $r_{xz,y}$ and $r_{yz,x}$.

224

225   The partial correlation coefficient between *x* and *y* given *z* (here denoted by $r_{xy,z}$)

226   indicates the strength of the linear relationship between *x* and *y* that is independent of

227   (uncorrelated with) *z*. Calculating the ordinary (or unconditional or zero-order)

228   correlation coefficient (r_{xy}, r_{xz} and r_{yz}) and comparing it with the partial correlation, it

229   is possible to see whether the association between the two inbreeding coefficients has

230   been sharply reduced after eliminating the effect of the third inbreeding coefficient.

231

232   2) Information theory: For every trio of inbreeding coefficients, and in order to obtain

233   the tolerance level (ε) to be used as the local threshold for capturing significant

234   associations, the mean ratio of partial to direct correlation is calculated as:

235

236
$$\varepsilon = \frac{1}{3}\left(\frac{r_{xy,z}}{r_{xy}} + \frac{r_{xz,y}}{r_{xz}} + \frac{r_{yz,x}}{r_{yz}}\right)$$

237

238   In the context of the network reconstruction, a connection or edge between inbreeding

239   coefficients *x* and *y* is discarded if:

240

241
$$\left|r_{xy}\right| \leq \left|\varepsilon \times r_{xz}\right| \text{ and } \left|r_{xy}\right| \leq \left|\varepsilon \times r_{yz}\right|$$

242

243   Otherwise, the association is defined as significant, and a connection or edge between

244   the pair of inbreeding coefficients is established.

245

246 Once Pearson's correlations and the significant associations were identified, the analysis

247 of inbreeding coefficients networks and its visualization were performed with the

248 software Cytoscape 2.8.3 (Shannon et al., 2003).

249

250 **Results and Discussion**

251

252 The estimates of the different inbreeding coefficients and their associations in a selected

253 rabbit population were compared. Table 1 shows the descriptive statistics for the

254 different inbreeding coefficeints. Average values for pedigree-based inbreeding

255 coefficients (*FpedA*, *FpedI* and *FpedR*) decreased from ancient to recent inbreeding.

256 However, no similar tendency was observed for ROH-based inbreeding coefficients,

257 where the intermediate coefficients (*FrohI*) showed the highest mean value compared

258 with the ancient (*FrohA*) and the recent (*FrohR*). This is probably because the majority

259 of ROH fell into the intermediate category. However, it should be noted that some

260 parameters used for the definition of a ROH and the thresholds imposed during the

261 filtering of the genotypic data can influence the number and length of ROH (Howrigan,

262 Simonson, & Keller, 2011). Accordingly, the number of allowed heterozygous

263 genotypes (Mastrangelo et al., 2016), and the density of the SNP chip and the frequency

264 of SNP genotyping errors (Ferenčaković, Sölkner, & Curik, 2013) can affect *Froh*. In

265 addition, linkage disequilibrium, recombination and mutation rate can influence the

266 frequency, size and location of ROH (Gibson, Newton, & Collins, 2006).

267

268 As expected, the mean *Fkal* was significantly lower than the mean *Fbal*. When

269 comparing recent inbreeding coefficients, the mean *FpedRDrop* was lower than *FpedR*,

270 and this one was lower than *FrohR*.

271

272 The genomic coefficients not related with ROH were very different. The mean values

273 were 0.03, 0.11, 0.63 and 0.85 for *Fvan*, *PHoMA*, *Fsnp* and *CE*, respectively. The

274 average *Fsnp* (0.63) was much higher than the different *Fped* (ranging between 0.01

275 and 0.15) because the latter refers to a base population where no homozygosity exists.

276 Thus, in *Fsnp* alleles that are IBD and identical by state (IBS) can not be distinguished.

277 Several approaches have been proposed to express the proportion of homozygous SNP

278 in the same scale as pedigree-based coefficients (Toro, García-Cortés, & Legarra, 2011)

279 but they (e. g. *Fvan*) require the knowledge of the base population allele frequencies.

280 However, given that these frequencies are usually unknown, usually the allele

281 frequencies of the studied population are used providing, generally, inaccurate

282 inbreeding estimates (Toro et al., 2002). In addition, the different approaches are

283 equivalent to move the base population several generations ago (*Fsnp*), the present

284 (*Fvan*), to the most ancient ancestors known (*Fped*) or to different intermediate points

285 with different ROH lengths (Morales-Gonzalez et al., 2020).

286

287 - Table 1 -

288

289 Emphasis in the partitioning of the inbreeding coefficients based on the distance to a

290 common ancestor has been performed both for pedigree- and genomic-based inbreeding

291 coefficients. This is important because inbreeding arising from a distant common

14

292 ancestor should has less effect on fitness and economically important related-traits

293 compared with inbreeding from a recent common ancestor because natural and artificial

294 selection along time should act to purge deleterious alleles from the population (Holt,

295 Meuwissen, & Vangen, 2005).

296

297 Figure 1 shows that the highest Pearson's correlations between pedigree-based

298 inbreeding coefficients were observed between *FpedR*, *FpedAll*, *Fkal*, *FpedRDrop* and

299 *Ahc*. Within the genome-based inbreeding coefficients, the highest Pearson's

300 correlations were obtained between *FrohR*, *Fsnp*, *PHoMA* and *CE*. Moderate Pearson's

301 correlations (between 0.32 – 0.45) were observed between the pedigree-based

302 inbreeding coefficients *FpedR*, *FpedAll*, *Fkal* and *FpedRDrop*, and the genome-based

303 inbreeding coefficients *FrohR*, *Fsnp* and *PHoMA*.

304

305 - Figure 1 -

306

307 The network between the different evaluated inbreeding coefficients is difficult to

308 interpret from Pearson's correlations even when positive and negative edges are

309 represented separately (Figure 2) because there were 105 different edges linking the

310 different inbreeding coefficients.

311

312 - Figure 2 -

313

15

314   Different studies show the correlation between pedigree- and genomic-based inbreeding

315   coefficients. For example, strong correlations between pedigree and genomic-based

316   inbreeding coefficients have been reported in human populations with complete and

317   reliable pedigree (McQuillan et al., 2008). High correlations were also detected in cattle

318   populations with complete generation equivalent values larger than 5 (Purfield, Berry,

319   McParland, & Bradley, 2012; Doekes et al., 2019).

320

321   The use of partial correlation and information theory on inbreeding coefficients is novel,

322   and the network from PCIT allowed clarifying the relation between the different tested

323   inbreeding coefficients (Figure 3). Thirty-three significant edges were detected in

324   Figure 3.

325

326   - Figure 3 -

327

328   Genomic-based inbreeding coefficients were not correlated with their corresponding

329   pedigree-based inbreeding coefficients, except for the case of recent inbreeding.

330   Significant and positive correlations were detected for *FpedAll*, *FpedRDrop*, and

331   *FpedR*. This cluster also included significant and positive correlations with some

332   genomic-based inbreeding coefficients such as *FrohR*, *Fsnp*, *PHoMA*, *Fvan* and *CE*.

333   *Fvan* is mostly correlated with *PHoMA* suggesting that *Fvan* is giving more importance

334   to minor allele frequencies. In fact, the method 2 from VanRaden (2008) has been

335   implemented to estimate *Fvan*, and it has been suggested that loci with lower MAF get

336   higher weight in method 2 than in VanRaden's method 1 (Toro et al., 2011).

337

Interestingly, *Fkal* was also comprised in this group and non-significant correlations were observed between *Fkal* and *Fbal* or *Ahc*. Parland, Kearney, and Berry (2009) indicated that the correlation between *Fkal* and *Fbal* was weak, ranging from 0.28 to 0.38. Also Schäler et al. (2020) suggested that this correlation was small (0.22), indicating that the two coefficients are measuring different population statistics. The correlation between *Fbal* and *Ahc* was positive and strong, as well as those between both of them and *CE*. *FpedRDrop* coefficient was negatively correlated with *FpedI*.

345

Correlations between inbreeding coefficients vary between studies. Both, population structure and introgression seem important factors affecting this variability found in the literature (e. g. Schäler et al., 2020). It seems that commercial lines present a high and positive correlation for *FpedAll* and *Fkal* (0.90 in the present study), whereas lines with introgression or local lines show a small correlation between *FpedAll* and *Fkal*. In addition, the correlation between *FpedAll* and *Fbal* is higher within local or introgressed lines (Schäler et al., 2020). However, further research on correlations is needed to validate such statements.

354

In addition, the inbreeding coefficient *FrohA* was negatively correlated with *FrohR* and *CE*. *FrohR* was the central coefficient having 9 edges that link it to different inbreeding coefficients and, as expected, it is negatively correlated with *FrohA*. *FpedI* was negatively correlated with *FpedRDrop* and *Fkal*.

359

360 The PCIT approach allows inferring meaningful associations between inbreeding

361 coefficients and emphasizes the importance of *FrohR* from other coefficients. In order

362 to limit the increase in inbreeding in a population under selection or not, it could be

363 recommended to monitor this coefficient, but a good proxy of it could be those

364 pedigree-based definitions reflecting recent inbreeding (*FpedR* and *FpedRDrop*).

365

366 **Acknowledgements**

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374

375 **Conflict of Interest**

376

377 The authors declare no conflict of interest.

378

379 **Data availability statement**

380

381 Data will be available upon reasonable request.

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502

503 **Table 1.** Descriptive statistics for the different inbreeding coefficients. *FpedA*: Ancient

504 pedigree-based inbreeding coefficient; *FpedI*: Intermediate pedigree-based inbreeding

505 coefficient; *FpedR*: Recent pedigree-based inbreeding coefficient; *FpedAll*: Pedigree-

506 based inbreeding coefficient from all the genealogy; *Fbal*: Pedigree-based inbreeding

507 coefficient from Ballou (1997); *Fkal*: Pedigree-based inbreeding coefficient from

508 Kalinowski et al. (2000); *FpedRDrop*: recent pedigre-based inbreeding coefficient

509 calculated from gene drop; *Ahc*: Ancestral history coefficient; *FrohA*: Ancient ROH-

510 based inbreeding coefficient; *FrohI*: Intermediate ROH-based inbreeding coefficient;

511 *FrohR*: Recent ROH-based inbreeding coefficient; *Fvan*: Inbreeding coefficient from

512 VanRaden (2008); *Fsnp*: Proportion of homozygous SNP; *PHoMA*: Proportion of

513 homozygous SNP for the minor allele; *CE*: compression efficiency.

Metric	Mean	Standard Error	Minimum	Maximum
FpedA	0.0674	0.0000	0.0674	0.0674
FpedI	0.0535	0.0000	0.0519	0.0547
FpedR	0.0250	0.0010	0.0065	0.1615
FpedAll	0.1459	0.0010	0.1272	0.2824
Fbal	0.8546	0.0007	0.8246	0.8819
Fkal	0.1414	0.0009	0.1221	0.2632
FpedRDrop	0.0054	0.0001	0.0029	0.0200
Ahc	2.7155	0.0088	2.3773	3.0936
FrohA	0.0364	0.0003	0.0191	0.0581
FrohI	0.1485	0.0009	0.0727	0.2043
FrohR	0.0749	0.0017	0.0000	0.2347
Fvan	0.0299	0.0033	-0.1414	0.3521
Fsnp	0.6327	0.0009	0.5884	0.7231
PHoMA	0.1063	0.0004	0.0803	0.1446
CE	0.8458	0.0003	0.8145	0.8584

514

515

516   **Figure legends**

517   **Figure 1.** Heat map of Pearson's correlation coefficients among the different inbreeding

518   coefficients. Above the diagonal: blue indicates strong positive correlation, white

519   illustrates no correlation and red denotes strong negative correlation. Below the

520   diagonal: correlation values. *FpedA*: Ancient pedigree-based inbreeding coefficient;

521   *FpedI*: Intermediate pedigree-based inbreeding coefficient; *FpedR*: Recent pedigree-

522   based inbreeding coefficient; *FpedAll*: Pedigree-based inbreeding coefficient from all

523   the genealogy; *Fbal*: Pedigree-based inbreeding coefficient from Ballou (1997); *Fkal*:

524   Pedigree-based inbreeding coefficient from Kalinowski et al. (2000); *FpedRDrop*:

525   recent pedigree-based inbreeding coefficient calculated from gene drop; *Ahc*: Ancestral

526   history coefficient; *FrohA*: Ancient ROH-based inbreeding coefficient; *FrohI*:

527   Intermediate ROH-based inbreeding coefficient; *FrohR*: Recent ROH-based inbreeding

528   coefficient; *Fvan*: Inbreeding coefficient from VanRaden (2008); *Fsnp*: Proportion of

529   homozygous SNP; *PHoMA*: Proportion of homozygous SNP for the minor allele; *CE*:

530   compression efficiency.

531

532   **Figure 2.** Network of Pearson's correlation coefficients for different inbreeding

533   estimates. Blue edges show the positive correlations and red edges the negative ones.

534   *FpedA*: Ancient pedigree-based inbreeding coefficient; *FpedI*: Intermediate pedigree-

535   based inbreeding coefficient; *FpedR*: Recent pedigree-based inbreeding coefficient;

536   *FpedAll*: Pedigree-based inbreeding coefficient from all the genealogy; *Fbal*: Pedigree-

537   based inbreeding coefficient from Ballou (1997); *Fkal*: Pedigree-based inbreeding

538   coefficient from Kalinowski et al. (2000); *FpedRDrop*: recent pedigree-based

539   inbreeding coefficient calculated from gene drop; *Ahc*: Ancestral history coefficient;
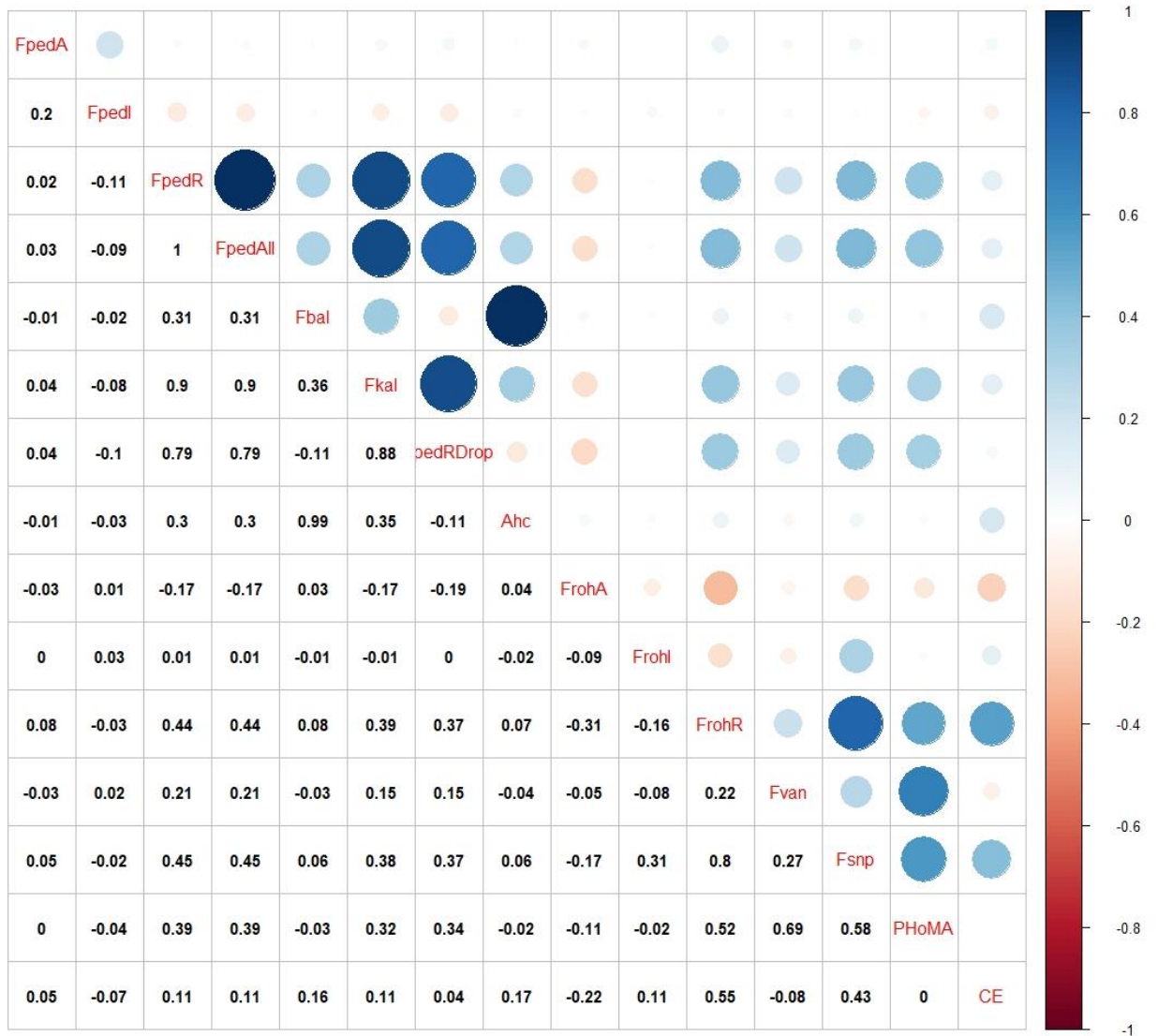
540   *FrohA*: Ancient ROH-based inbreeding coefficient; *FrohI*: Intermediate ROH-based

541   inbreeding coefficient; *FrohR*: Recent ROH-based inbreeding coefficient; *Fvan*:

542   Inbreeding coefficient from VanRaden (2008); *Fsnp*: Proportion of homozygous SNP;

543   *PHoMA*: Proportion of homozygous SNP for the minor allele; *CE*: compression

544   efficiency.

545

546   **Figure 3.** Network of significant associations obtained from PCIT for different

547   inbreeding estimates. Blue edges show the positive correlations and red edges the

548   negative ones. *FpedA*: Ancient pedigree-based inbreeding coefficient; *FpedI*:

549   Intermediate pedigree-based inbreeding coefficient; *FpedR*: Recent pedigree-based

550   inbreeding coefficient; *FpedAll*: Pedigree-based inbreeding coefficient from all the

551   genealogy; *Fbal*: Pedigree-based inbreeding coefficient from Ballou (1997); *Fkal*:

552   Pedigree-based inbreeding coefficient from Kalinowski et al. (2000); *FpedRDrop*:

553   recent pedigree-based inbreeding coefficient calculated from gene drop; *Ahc*: Ancestral

554   history coefficient; *FrohA*: Ancient ROH-based inbreeding coefficient; *FrohR*: Recent

555   ROH-based inbreeding coefficient; *Fvan*: Inbreeding coefficient from VanRaden

556   (2008); *Fsnp*: Proportion of homozygous SNP; *PHoMA*: Proportion of homozygous

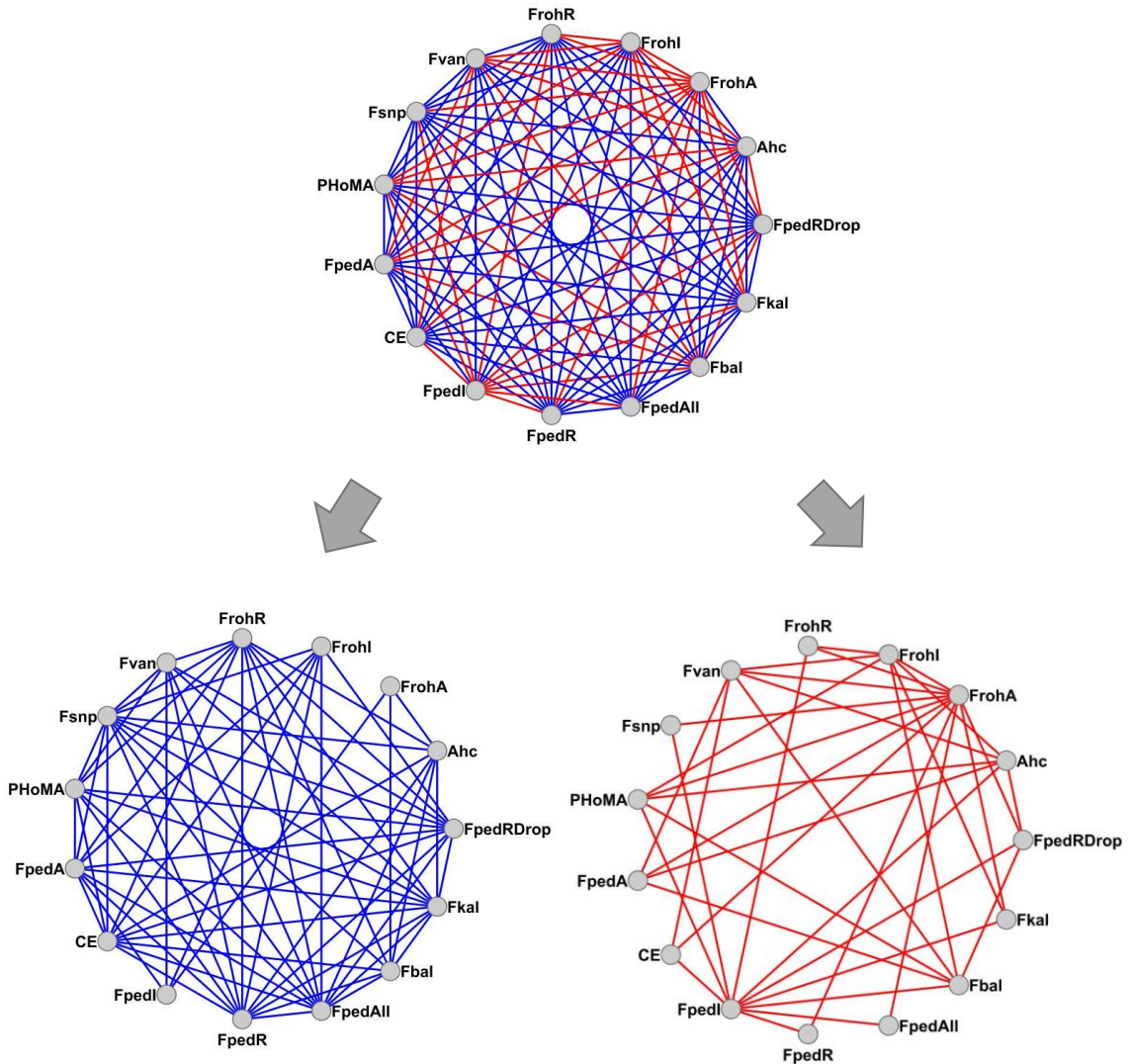557   SNP for the minor allele; *CE*: compression efficiency.

558

559   **Figure 1**

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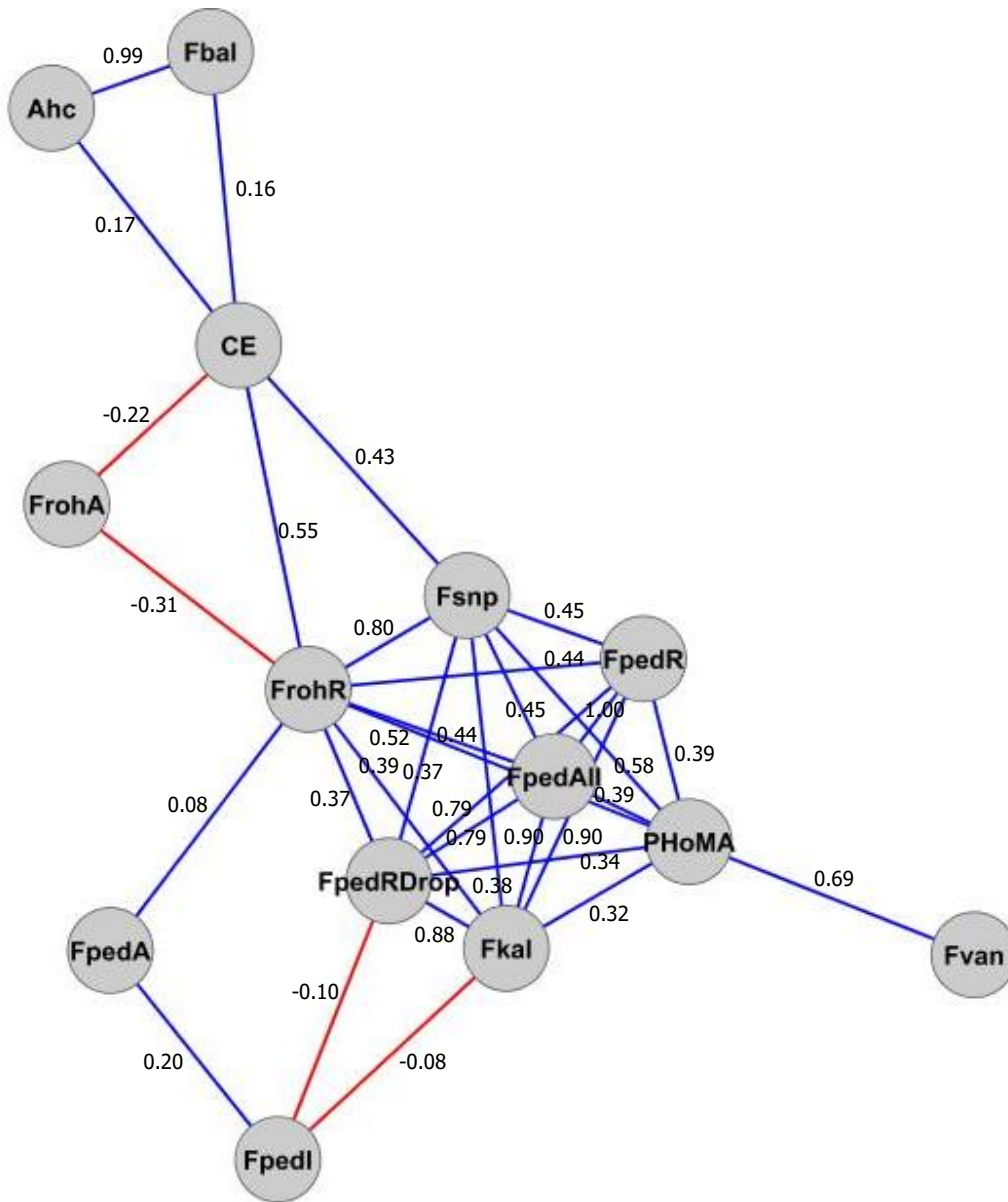**Figure 2**

Figure 3

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572