1 **TITLE**

2 **Functional longevity in five rabbit lines founded on different**

3 **criteria: Comparison at foundation and at fixed times after selection**

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28   **Running Head (Short title):** COMPARING FIVE RABBIT LINES IN TERMS OF

29   LONGEVITY.

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ABSTRACT

The objective of the present study was to compare five Spanish rabbit lines in terms of functional longevity. Four of them are maternal lines (A, V, H and LP) founded on different criteria and being selected for litter size at weaning. The fifth line is the paternal line R, founded and selected for post-weaning daily gain from 28 to 63d. The last generations of selection considered in the present study were 44th, 39th, 10th, 8th and 32th generations for lines A, V, H, LP and R, respectively. Cox proportional hazard models under a Bayesian approach were used to perform two comparisons between the lines. The first comparison was done at the origin of the lines, involving the complete data set (from March 1980 to March 2013; records of 15670 does), and the complete pedigree (19405 animals), so the effect of selection was considered. The second comparison was done at two fixed times through the selection processes when all lines shared the same environmental and management conditions (from March 1997 to September 1998 and from March 2011 to September 2012). For the second comparison the same model as the first comparison was used, but excluding the additive effects from the model of analysis, and involving only the data corresponding to each period, so the differences between the lines were not dependent on the additive values of the animals. At their foundation, lines V, H and LP showed a substantial superiority over line A. The line R also had higher risk of death or culling with relevant differences when compared to V, H and LP lines. The line LP had the longest productive life compared to the other lines; this may be a consequence of its foundation process. The maximum relative risks were observed between the lines LP and R (0.239). This means that at foundation it was 0.239 times more likely for a LP doe to be culled/died than for a R female. The interactions between year-seasons and the lines were important and affected the differences

57   between the lines at their origin. During the two periods of the comparison at fixed

58   time, lines A and R showed low longevity compared to the other lines. However, as

59   the selection process evolves, the differences between these two lines and the other

60   lines were reduced, which demonstrate the importance of natural selection in these

61   lines. The predicted differences between the four maternal lines match well the

62   phenotypic differences computed at the fixed times of comparison, indicating that the

63   genetic model is suitable to describe the longevity records in these populations,

64   although, this was not the case for the paternal line R. It could be concluded that the

65   average longevity of a population greatly depends on the criteria followed for the

66   foundation of this population. Along the generations of selection for litter size, the

67   differences of longevity between lines tend to decrease, due to the action of the

68   natural selection in the lines of lower longevity.

69   **KEYWORDS:** line foundation, selection, functional longevity, maternal lines, survival

70   analysis, rabbits.

INTRODUCTION

The success of any selection experiment could be limited by the criteria and procedure used to recruit animals in the base generation, i.e. foundation, this holds for any specie and trait, and it is particularly relevant in rabbit lines. One way to quantify the consequences of considering different foundation criteria is to compare, for the desired traits, performances of lines sharing the same environmental and management conditions at different moments of the selection processes, for example at their origin and after some generations of selection.

Longevity is a functional trait directly related to farm profitability; thus, selective breeding to increase the length of productive life could help to reduce costs attributed to replacements. With the aim of creating a maternal line outstanding for its longevity, Sanchez et al. (2008) recruited, from commercial farms, females showing and extraordinary length of productive live (over 25 parturitions) but keeping a prolificacy performance above the mean prolificacy of the Spanish rabbit commercial population. This selection procedure was chosen so because traditional breeding methods, based on limited selection pressure within a close populations, were not expected to be success since the time required to obtain relevant information for accurately ranking the animals within each generation would be rather long (Larzul et al., 2014). The aim of this study was to compare the functional longevity of the aforementioned line, with others raised in the same selection farm. Some of these lines are being selected for litter size at weaning and other is selected for post-weaning daily gain. As the comparisons between the functional longevity of the lines are done at their foundation and also at fixed time periods of the selection process of the lines it is possible to assess how the initial genetic differences evolve as consequence of the different selection procedures implemented for each line.

MATERIALS AND METHODS

Ethical statement

Animal manipulations and the experimental procedures were approved by the Ethical Committee of the Polytechnic University of Valencia, according to Council Directives 98/58/EC (European Economic Community, 1998).

Animals and Management

Data used in the present study were collected from five Spanish lines of rabbits, four of them are maternal (A, V, H, LP) and the fifth is a paternal line (R). These lines are reared at a selection nucleus located in the farm of the Institute for Animal Science and Technology, Universitat Politècnica de València. The records were collected along the generations of selection of these lines from March 1980 to March 2013.

The process of foundation of line A began in 1976 sampling New Zealand White (NZW) rabbits, reared by farmers near Valencia (Spain). After three generations without selection, the line is being selected since 1980 by a family index based on litter size at weaning (Estany et al., 1989). Line V was founded in 1980 as a synthetic line, mating crossbred animals that were progeny of four specialized maternal lines, after three generations without selection, the line is being selected (Estany et al., 1989) to increase litter size at weaning since 1982. Line H was founded applying hyperprolific selection and embryo cryopreservation techniques (García-Ximénez et al., 1996; Cifre et al., 1998). Hyperprolific does were assembled from a large commercial population, spread over different Spanish farms. This line was kept since its foundation in 1996 at the nucleus of selection until May, 2004 (10th generation of selection). Line LP was founded selecting females from commercial farms that

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121 showed extremely long productive lives and prolificacy near or above the average of

122 the Spanish commercial rabbit population (Sánchez et al., 2008). This line is being

123 selected since 2003 to increase litter size at weaning. In V, H and LP, animals are

124 evaluated for litter size using a repeatability animal model. Line R comes from the

125 fusion of two paternal lines, one founded in 1976 with California rabbits reared by

126 Valencian farmers and the other founded in 1981 with rabbits belonging to

127 specialised paternal lines (Estany et al., 1992). The method of selection has always

128 been individual selection on post-weaning daily gain.

129 The farm where the rabbits are housed has isolated roofs and the ventilation is

130 controlled depending on the indoor temperature. The cages for does (90 cm long, 50

131 cm wide and 40 cm high) and progeny (80 cm long, 50 cm wide and 30 cm high) are

132 standard flat deck. Management of animals in the different lines is the same, using

133 natural mating; bucks and does began reproduction from 17 to 18 weeks of age. On

134 the day 12 post-mating each does are tested for pregnancy by abdominal palpation,

135 and non-pregnant does are mated back. Does are mated 11 days after kindling,

136 usually one female is always mated to the same buck; litters are examined each

137 morning during the suckling period to remove dead kits. Kits are reared by their own

138 dams, and weaned at 28 days post kindling. Then animals are individually identified

139 by a number tattooed on the left ear and transferred to the fattening cages (8-9

140 rabbits per cage) until marketing at 63 days. Both breeding animals and progeny are

141 fed *ad libitum* on pelleted commercial rations. The animals were kept under

142 controlled 16-h light: 8-h dark photoperiods.

143 Mating males and females in the maternal lines always belong to the same

144 generation, i.e. non-overlapping generations mating. In these maternal lines does for

145 the next generations are selected from 25 – 30 % of the best evaluated matings, with

146 a limit of 4 does per mating. Each sire contributes a son to the next generation, and

147 is selected from the best mating of the sire.

148 Management of animals in line R is somewhat different compared to other lines,

149 where in the last generations the does were artificially inseminated and the

150 candidates for selection were genetically evaluated exclusively based on their

151 phenotypic values, i.e. individual selection. Similarly to the maternal lines, in the R

152 line each sire contributes a son to the next generation and does are selected at a

153 rate of around 20%, referred to the average growth of the previous four weeks.

154 Mating was conducted in non-overlapping generations until the 25th generation. The

155 generation interval is about 6 months and the estimated response to selection was

156 about 0.5 g/day per generation (Estany el al. 1992). In maternal lines the generation

157 interval is about 9 months and the response to selection ranged from 0.076 (Tudela

158 et al., 2003) to 0.085 (García and Baselga, 2002) kit weaned per parturition by

159 generation.

160 For a suitable genetic evaluation of animals in the nucleus, some common culling

161 criteria in commercial farms are not considered; i.e. does with low levels of

162 production or no strong reproductive delay are not culled.

163

164 **Data and Statistical Models**

165 The analysed trait was the length of the productive life (LPL), this trait was measured

166 as the difference in days between the date of the first positive palpation test and the

167 date of death or culling for involuntary causes (Sánchez et al., 2008). Once again,

168 does were never culled based on production results, therefore, LPL reflected a direct

169 measurement of functional longevity. Date and reason for culling or death are

170 systematically recorded, as well as all the information regarding mating and

171   parturition dates, pregnancy status after the abdominal palpation and prolificacy.

172   Does removed to free space for females of the next generation or eliminated

173   because of accidents or other technical reasons not related to health status were

174   treated as censored (Piles et al., 2006b). Thus, the record of each animal included

175   the called censoring code, representing (0 = censored; 1 = uncensored) and all the

176   information regarding physiological status of the female during its entire life

177   (reproductive and lactation status), as well as all the prolificacy records and the line

178   to which the animal belonged. Functional longevity was analysed using Cox models.

179   A Weibull model was discarded because of its misfit due to the high proportion of

180   does dying in the first parturition (Sánchez et al., 2004; Piles et al., 2006b). The

181   pedigree file involved 19,405 animals, and the number of does with records was

182   15,670, out the total number of females with records 5,775 had censored data (Table

183   1), most of these does were removed before the end of their productive life because

184   of space limitations in the nucleus and the followed breeding program. In order to

185   accomplish the comparison of the LPL between the lines this data set was used

186   either completely, for the comparison at the foundation; or different subsets were

187   extracted, for the comparisons at given periods of the selection process. The number

188   of does for the comparisons at foundation and at fixed times are shown in Table 1.

189   In a first analysis, the complete data set from the foundation of each line until March

190   2013 was considered, including the full pedigree. In this analysis a complete genetic

191   model (CM) was used fitting the systematic effects of line-year-season combination

192   (LYS), positive palpation order (OPP), and number born alive at each kindling (NBA)

193   as time-dependent factors; in addition to the additive genetic value of the animal as a

194   random effect. In detail, the CM model was:

195    $$h_i\left(t|\mathbf{x}'_i(t)\right) = h_0\,(t)\exp\{\mathbf{x}'_i(t)_{\mathbf{LYS}}\boldsymbol{\beta}_{\mathbf{LYS}} + \mathbf{x}'_i(t)_{\mathbf{OPP}}\boldsymbol{\beta}_{\mathbf{OPP}} + \mathbf{x}'_i(t)_{\mathbf{NBA}}\boldsymbol{\beta}_{\mathbf{NBA}} + \mathbf{z}'_i\mathbf{u}\}$$

196 where $h_i\left(t|\mathbf{x}'_i(t)\right)$ is the hazard of animal i at time t, for time-dependent factors,

197 affected by covariates indicated by $\mathbf{x}'_i(t) = \{\mathbf{x}'_i(t)_{\mathbf{LYS}},$

198 $\mathbf{x}'_i(t)_{\mathbf{OPP}}, \mathbf{x}'_i(t)_{\mathbf{NBA}}, \mathbf{z}'_i\}$; $h_0\ (t)$ is the baseline hazard function at time t, approximated

199 by a step-wise function given by $h_0(t) = h_{0m}$ for $t \in [\tau_{m-1}, \tau_m]$; $m = 1, \dots, M +$

200 1, where $\tau_1, \dots, \tau_M$ are the M different ordered survival times, $\tau_0 < \tau_1 < \cdots < \tau_M <$

201 τ_{M+1}; $\tau_0 = 0$ and $\tau_{M+1} = \infty$. $\boldsymbol{\beta}_{\mathbf{LYS}}$, is the vector of regression coefficients for the line-

202 year-season (LYS) combinations with 212 levels, where the year-season was defined

203 by 6 months' time intervals. The number of levels were 63, 63, 17, 20 and 49 for the

204 subsets of A, V, H, LP and R lines, respectively. $\boldsymbol{\beta}_{\mathbf{OPP}}$, is the vector including the

205 effect of the three levels of the positive palpation order (OPP) (1, 2 and 3 or more

206 positive palpation orders), the changes of level in this factor occurred after every

207 pregnancy test. $\boldsymbol{\beta}_{\mathbf{NBA}}$, is the vector including the effects of 5 classes of number born

208 alive in each kindling (NBA); the first level corresponded to does that had 0 NBA, the

209 second level to parturitions with 1 to 4 born alive, the third to parturitions with 5 to 8

210 born alive, and so on until the fifth level which corresponded to parturition with at

211 least 13 born alive. The changes of levels in this time-dependent factor occurred at

212 parturition. Finally, u_i is the additive genetic effect of the animal i, this factor was

213 assumed to follow *a priori* a multivariate normal distribution with mean 0 and

214 (co)variance **G**. In order to account for the genetic heterogeneity between the five **G**

215 was defined as a block-diagonal matrix formed by elements $\mathbf{A}_i \sigma^2_{a,i}$, where $\mathbf{A}_i$ is the

216 numerator relationship matrix of the line i, and $\sigma^2_{a,i}$ is the additive genetic variance for

217 that particular line. The additive genetic variances ($\sigma^2_{a,i}$) were assumed to be known

218 and equal to 0.17, 0.05, 0.29, 0.29 and 0.07 for A, V, H, LP and R lines, respectively

219 (EL Nagar et al., 2020). The prior distributions for the remaining model parameters

220 were defined in the same way as in Sánchez *et al.* (2006). Baseline hazard step-wise

221   function elements h_{0m} for $m = 1, \dots, M + 1$ were assumed to be independent and

222   identically distributed (i.i.d.) : $p(h_{0m}) \sim \frac{1}{h_{0m}}$, where $0 < h_{0m} < \infty$. This is a long-

223   uniform prior which supposes an uniform distribution for the logarithm of h_{0m}. The

224   elements of all $\boldsymbol{\beta}$ were assumed to be i.i.d. following a uniform distribution.

225   In the analysis of the complete data set using CM additive genetic effects account for

226   the genetic responses in the different lines. Thus, the contrast of the differences

227   between each pair of lines based on the year-season levels shared by both lines

228   reflect the difference between the lines at their foundation, reflecting genetic

229   differences between the lines when the respective populations were created. The

230   periods in which each pair of lines were sharing the same environmental and

231   management conditions were from March 1983 to September 2003 and from March

232   2006 to March 2013 for lines A and V; from March 1997 to September 1998 for lines

233   A and H; from March 2006 to March 2013 for lines A and LP; from March 1990 to

234   March 2013 for lines A and R; from March 1997 to September 1998 for lines V and

235   H; from September 2004 to March 2013 for lines V and LP; from March 1990 to

236   September 2003 and from March 2006 to March 2013 for lines V and R; from March

237   1997 to September 1998 for lines H and R; and from March 2006 to September 2013

238   for lines LP and R. The lines H and LP only shared one year-season, for this reason

239   the contrast between them was not estimated.

240   It is possible to compute actual differences between lines at different periods of time

241   shared by some of them, without relying on the genetic model and by only using the

242   records from those given periods. For the computation of this actual differences

243   between the lines the model should be the same as that previously described but

244   removing the additive genetic effect, we name this as incomplete model (IM). In this

245   case the line effects refer to the real genetic merit of the lines at the time of

246   comparison as a consequence of selection and genetic drift, but not being dependent

247   on the genetic model. The difference between two lines at a defined period was

248   computed as the difference between the averages of the within line year-season

249   effects for that period. The periods chosen for comparison were arbitrarily defined by

250   the last three year-seasons shared by at least four of the lines under the same

251   management conditions. These periods were from March 1997 to September 1998

252   for comparisons between the lines A, V, H and R, and from March 2011 to

253   September 2012 for comparisons between the lines A, V, LP and R. It is also

254   possible to predict the actual differences between the lines (those calculated with the

255   IM) at the defined periods using the results of the analysis with the CM model and the

256   complete data set. The difference between two lines in the abovementioned arbitrary

257   periods can be predicted adding to the contrast between the within line average of

258   the solutions of the year-season effects to the differences between the additive

259   values of the animals of each line performing in those particular year-season levels.

260   The estimated differences between lines for the previously indicated arbitrary

261   periods, calculated with IM model, can be compared with the predicted differences

262   obtained using CM model and the whole data set. This comparison could be seem as

263   a way to check the adequacy of the CM model to explain the complete longevity data

264   set.

265   Both for CM and IM parameter estimation was performed by a Bayesian approach,

266   based on statistics computed from samples of the marginal posterior distributions

267   obtained using a Gibbs sampling algorithm. The Gibbs sampler algorithm comprised

268   200,000 iterations, discarding the first 20,000 in order to allow for the algorithm to

269   reach convergence to the marginal posterior distributions. Afterwards, one sample in

270   each 20 was saved to avoid high correlations between consecutive samples. The

271 post-Gibbs analysis used to calculate the parameters of interest of the marginal

272 posterior distributions was implemented with the coda package of the R program

273 (Plummer et al., 2006). Convergence of the chains for the parameters and contrasts

274 of interest was assessed using the Z-criterion of Geweke (Geweke, 1992).

275

RESULTS AND DISCUSSION

277 **Comparison between lines at foundation**

278 Monte Carlo standard errors were very small in all cases and they are not showed in

279 the tables. Geweke test did not detect lack of convergence in any case. The

280 comparison among lines at their foundation is shown in Table 2. The contrasts are

281 estimable functions between each pairs of lines through the years-season in which

282 both lines were subjected to the same environmental and management conditions.

283 Using all data and the full pedigree, the additive effects of the animals were

284 considered in the model, the selection response was accounted for by this effect, and

285 consequently, the effects of the lines (included in the line-year-season combination)

286 expressed the values at their foundation. The lines V, H and LP showed a substantial

287 superiority over line A. The line R had higher risk of death or culling with relevant

288 differences when compared to V, H and LP lines. The maximum relative risks were

289 observed between the lines LP and R, and between LP and A. The relative risk

290 describes how much more likely it is that culling or death occurs within one level of a

291 given factor relative to another level of the same factor. For instance, at foundation it

292 was 3.152 times more likely for an A doe to be culled/died than for a LP doe (Table

293 2). Line LP was created from does that had at least 25 parities (Sánchez et al.,

294 2008). The results presented in Table 2 could seem to show inconsistencies, for

295 example, the difference between lines A and V at their foundation was 0.495 and

296 between lines A and LP was 1.148. Their difference, (1.148-0.495) is not exactly

297 0.436, the contrast between lines V and LP. This deviation between the two values is

298 due to the different sets of year-seasons involved in each particular contrast and also

299 to the fact that the model included the interaction line-year-season. The interaction

300 terms involved in the contrasts A-V and A-LP are, obviously, different to that involved

301 in that estimated between V and LP lines, thus the last one cannot be exactly

302 reconstructed from the previous.

303 The longer productive life of LP does could be considered as an indicator of the

304 successful foundation procedure of this line. The line A was created by mating does

305 and bucks of the New Zealand White breed belonged to populations maintaining the

306 standard morphological characteristics of the breed. This line was shown to have a

307 high susceptibility to enterocolitis disease, which was a condition present during

308 some periods shared with the other lines (Ragab and Baselga, 2011). Piles et al.

309 (2006a) also found, in a diallel cross experiment, relevant differences in the genetic

310 effects for functional longevity between maternal rabbit lines A, V and Prat and the

311 crossbred females from them. They stated that a A doe was twice as likely to be

312 replaced than a crossbred Prat × A doe, and in general, the genetic groups with the

313 highest relative risks were those in which the A line participated. All these results,

314 particularly those presented in this study that refer to the situation at the foundation,

315 suggest the hypothesis that founding line A based on morphological aspects of the

316 animals created a genetic load, related with susceptibility to diseases or longevity,

317 that still segregating in the population. We could speculate that if the founder animals

318 would be selected based on any performance criteria, this genetic load would be

319 minimized, since those animals with the putative deleterious alleles would not be

320 selected since their performance phenotypes would be deteriorated.

321 In another study comparing lines LP and V, Sánchez et al. (2008) indicated the

322 superiority of the line LP over the line V with respect to survival ability, especially at

323 later cycles. They attributed this result to the foundation procedure in the LP line

324 which was focused on late life survival. In spite this result is the same as the one we

325 have reported in this study, this comparison between LP and V lines was not a

326 comparison at foundation time, because for V line only the closest relationships sibs

327 were considered in the study. In contrast, in the present study all the available

328 pedigree information was used.

329 Line R showed higher risk at foundation compared to the other lines, and the

330 differences between line R and both LP and V lines were relevant. Considering that

331 line R was created by mating animals maintaining the standard morphological

332 characteristics of the Californian breed with animals from another synthetic line

333 created by mating animals from three commercial paternal lines (Estany et al., 1992),

334 the argument considered with regard to A line about the genetic load that was

335 created during the foundation of the line only apply partially. For the case of the R

336 line part of the founders came from populations selected for growth performances.

337 Thus, the lower survival ability of the R line with respect to the other lines could be

338 also linked to a certain genetic antagonism between early growth and length of the

339 reproductive life.

340

341 **Comparison between lines at fixed periods**

342 The estimated differences between the lines A, V, H and R from March 1997 to

343 September 1998 and between the lines A, V, LP and R form March 2011 to

344 September 2012 are presented in Table 3. These contracts reflect differences at the

345 foundation of the lines plus the differences generated as a consequence of the

346   selection process. Lines A and R had a greater risk of death or culling than lines V

347   and H. These overall trends were the same as those observed in the comparison at

348   the foundation time of these lines. The contrasts show the inferiority of the line A for

349   longevity over the other maternal lines during the two periods of comparison. This

350   result is in agreement with those of Ragab et al. (2011) who found that line A was

351   more sensitive to the risk factors compared to V and LP lines. The LP does had a

352   lower risk of death or culling compared to A, V and R lines, this result could be

353   explained, again, as a direct consequence of the foundation process of the LP line.

354   The same result was found by Sánchez et al. (2008) who reported that the LP line

355   had a longer reproductive life than the V line. In general, as the selection process

356   evolves, the differences between the lines were reduced. This may be a

357   consequence of a natural selection process, which is more intense for the lines of

358   lower longevity. For animals with lower longevity, the probability of dying before

359   leaving progeny selected for litter size is higher than for animals having higher

360   longevity. Moreover, the selected progeny of parents with low longevity would have a

361   higher probability of dying before reaching the maturity, thus not leaving offspring for

362   the next generation. This phenomenon can be clearly observed in line A, which had

363   low longevity at its foundation, but it has greatly improved its longevity along many

364   selection generations, thus in the comparisons at fixed times the magnitude of the

365   differences with the other lines are clearly lower than at foundation. Other evidence

366   of these natural selection process in the A line can be seen in the differences

367   between the breeding values of animals of each line involved in the comparison,

368   which seem to favour the line A (Table 4). This progress of the line A is consistent

369   with the genetic trend drawn by its relatively higher additive genetic variance (0.17)

370   (EL Nagar et al., 2020).

371 The case of the R line is different to that of the A line. In the comparisons done
372 between March 1997 and September 1998, a certain improvement with respect to
373 the situation at the foundation was observed, but this improvement was less evident
374 than that for the A line, this is compatible with the low additive variance estimated for
375 this line (0.07) (EL Nagar et al., 2020). In the second period of comparison (March
376 2011 – September 2012) an opposite pattern was observed; for example, with
377 respect to the V line, R line log-hazard was slightly worse than that at foundation, -
378 0.697 and -0.620, respectively. The comparisons involving R line should be
379 considered with caution, since, as it has been previously stated, the reproduction of
380 this line has been organized in a different way to that of the other populations: in the
381 last generations artificial insemination has been used and mating between animals
382 from different generations has been allowed. The change from natural mating to
383 artificial insemination was a management decision adopted to overcome the low
384 fertility observed in the population, this has been a serious handicap to properly
385 generate candidates for the selection. Even after the change to reproduction by
386 artificial insemination these fertility problems remained, probably associated to an
387 excess of body fat in the females. This low fertility issues have had strong
388 consequences in the correct implementation of the selection process for post-
389 weaning growth and they are probably also the reason why in the last generations
390 the LPL of the R line seems to be deteriorated. Nonetheless, the genetic trend seems
391 to be favourable, as reported by EL Nagar et al., (2020) and it is also observed when
392 comparing contrasts between breeding value prediction averages in table 4. Thus,
393 the observed deterioration of the LPL in the R line, during the last generations, must
394 be explained by the involvement of the interaction between lines and year-seasons
395 effects. As it has been stated, for R line, the environmental factors could be said to

396 be particular unfavourable, associated with the low fertility of the line in the last year-

397 seasons considered in the comparison. The reported responses for LPL in the

398 studied maternal lines are most likely associated, as previously indicated, to natural

399 selection and not to selection for criteria considered in each line, i.e. correlated

400 response. We proposed this idea because EL Nagar (2015) reported that, in the

401 maternal lines under study, the genetic correlation between longevity and prolificacy

402 traits (the selection criteria) were nearly null. For the case of the R line, the

403 hypothesis of the observed response on LPL to be a correlated response cannot be

404 discarded since for this population the correlation between longevity and post-

405 weaning growth has not been estimated.

406 The differences between lines at fixed times, obtained using the dataset limited to

407 these times with the CM are presented in Table 4. Comparing these differences with

408 those estimated using the IM; we can see that, for the case of the maternal lines (A,

409 V, H and LP) they are fairly relatively similar. This can be interpreted as an evidence

410 about the suitability of the genetic model to describe this longevity data in order to

411 predict the breeding values and to estimate differences between the lines at their

412 origins. Similar conclusions were obtained by Ragab and Baselga (2011) regarding

413 reproductive traits and by Mínguez et al. (2016) in relation to growth traits for the

414 same four lines. For the paternal line R, the differences predicted using CM did not

415 match well those estimated using IM. Thus, according to our previous reasoning for

416 this line it should be concluded that the model is not suitable for fitting the available

417 LPL data. As it has been stated previously, this line presents physiological

418 characteristics very different to that of the other lines considered in this study. These

419 peculiar characteristics get reflected in the statistical model, for example by making

420 the year-season effect to have a completely different meaning than that in the

421 maternal lines, and as these interaction terms are also included in the contrasts we

422 have reported they completely alter the results. In any case the output of our study

423 on this regard is that it seems that for the R line the model for fitting LPL should be

424 reviewed.

425

426 # CONCLUSIONS

427 By studying functional longevity data from five populations raised partially under the

428 same management and environmental conditions we have observed than the

429 differences between the lines at their foundation clearly respond to the selection

430 criteria used for recruiting the animals for the base population. On this regard, two

431 clear extreme examples have been reported: i) LP line, selected for LPL at its

432 foundation, which clearly favoured the trait. ii) A line, selected not attending to any

433 performance criteria, but according to fulfilling the morphological characteristics of a

434 breed, this procedure seems to have created a genetic load in the population that still

435 segregating and penalizes performances and fitness. Along the generations, at least

436 for the maternal lines under study, it seems to exist a natural selection or unintended

437 artificial selection process that have improved the survival ability of the females

438 reducing the differences between lines with regard to their LPL or risk of being culled.

439 The R line, selected for post-weaning growth, show a clearly different pattern

440 probably associated with the unsuitability of the used model to properly fit the

441 peculiar physiological characteristics of this line that alter its management.

442

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451

CONFLICT OF INTERESTS

453 The authors declare that they have no competing interests.

454

DATA AVAILABILITY STATEMENT

456 The datasets used and analysed during the current study are available from the

457 corresponding author on reasonable request.

458

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TABLES

528 **Table 1** Number of rabbit does involved in the study

Line	Foundation[†]	First period[‡]	Second period[§]
A	4986	348	320
V	5275	350	362
H	1156	317	-
LP	1224	-	333
R	3029	243	266
All lines	15670	1258	1281

529 [†]Total number of does. [‡]Number of does at first period comparison. [§]Number of

530 does at second period comparison.

531 **Table 2** Differences between the lines at foundation for longevity (log-hazard) estimated with the complete genetic model and all

532 data set

Contrast	PM[*]	PSD[**]	RR[***]	HPD95%[†]	P(%)[‡]
A-V	0.495	0.230	1.640	0.029 , 0.936	99
A-H	0.699	0.280	2.012	0.162 , 1.270	99
A-LP	1.148	0.321	3.152	0.510 , 1.753	100
A-R	-0.125	0.240	0.882	-0.611 , 0.345	77
V-H	0.050	0.192	1.051	-0.333 , 0.418	60
V-LP	0.436	0.192	1.547	0.072 , 0.819	99
V-R	-0.620	0.158	0.538	-0.935 , -0.321	100
H-R	-0.344	0.185	0.709	-0.734 , -0.003	97
LP-R	-1.432	0.156	0.239	-1.725 , -1.119	100

533 [*]Marginal posterior mean. [**] Marginal posterior standard deviation. [***]Relative risk = exp(contrast). [†]Marginal posterior highest

534 density region covering 95% of the density.

535 [‡]Probability of the difference being >0 when the contrast >0 and probability of the difference being <0 when the contrast <0.

536

537 **Table 3** Differences between the lines for longevity (log-hazard) at fixed times estimated with the incomplete model and data set of

538 the fixed times

Contrast	PM[*]	PSD[**]	RR[***]	HPD95%[†]	P(%)[‡]
March 1997 - September 1998 (First period)					
A-V	0.395	0.111	1.484	0.177 , 0.611	99
A-H	0.295	0.119	1.343	0.052 , 0.515	99
V-H	-0.099	0.121	0.906	-0.347 , 0.129	79
A-R	0.148	0.115	1.160	-0.078 , 0.374	90
V-R	-0.247	0.121	0.781	-0.488 , -0.012	98
H-R	-0.147	0.128	0.863	-0.400 , 0.102	88
March 2011 - September 2012 (Second period)					
A-V	0.122	0.120	1.130	-0.121 , 0.365	83
A-LP	0.564	0.156	1.758	0.270 , 0.881	99
V-LP	0.442	0.150	1.556	0.145 , 0.735	99
A-R	0.015	0.134	1.015	-0.248 , 0.271	54
V-R	-0.107	0.132	0.899	-0.364 , 0.149	79
LP-R	-0.550	0.163	0.577	-0.852 , -0.227	100

539 [*]Marginal posterior mean. [**] Marginal posterior standard deviation. [***]Relative risk = exp(contrast). [†]Marginal posterior highest

540 density region covering 95% of the density.

541 [‡]Probability of the difference being >0 when the contrast >0 and probability of the difference being <0 when the contrast <0.

542

543

Table 4 Differences between the lines for longevity (log-hazard) at fixed times estimated with the complete genetic model and data
545 set of the fixed times

Contrast	PM[*]	PSD[**]	RR[***]	HPD95%[†]	P(%)[‡]	D1[§]	D2[¶]
March 1997 - September 1998 (First period)							
A-V	0.314	0.113	1.369	0.087 , 0.532	99	0.648	-0.334
A-H	0.251	0.120	1.285	0.008 , 0.479	98	0.699	-0.448
V-H	-0.063	0.125	0.939	-0.302 , 0.181	69	0.050	-0.113
A-R	-0.073	0.111	0.930	-0.285 , 0.143	74	0.355	-0.428
V-R	-0.387	0.114	0.679	-0.622 , -0.179	100	-0.293	-0.094
H-R	-0.324	0.122	0.723	-0.570 , -0.089	100	-0.344	0.020
March 2011 - September 2012 (Second period)							
A-V	0.104	0.127	1.110	-0.152 , 0.345	80	0.655	-0.551
A-LP	0.710	0.157	2.034	0.412 , 1.029	100	1.332	-0.623
V-LP	0.605	0.153	1.831	0.298 , 0.896	100	0.677	-0.072
A-R	-0.592	0.127	0.553	-0.835 , -0.341	100	-0.251	-0.342
V-R	-0.697	0.121	0.498	-0.930 , -0.456	100	-0.906	0.209
LP-R	-1.302	0.154	0.272	-1.614 , -1.010	100	-1.583	0.281

546 [*]Marginal posterior mean. [**]Marginal posterior standard deviation. [***]Relative risk = exp(contrast). [†]Marginal posterior highest
547 density region covering 95% of the density. [‡]Probability of the difference being >0 when the contrast >0 and probability of the
548 difference being <0 when the contrast <0. [§]Part of PM due to differences between lines at foundation. [¶]Part of PM due to
549 differences in the additive genetic values of the animals belonged to each line involved in the comparison.