

RESEARCH

Open Access

Molecular genetic analysis of a cattle population to reconstitute the extinct *Algarvia* breed

Catarina Ginja¹, Maria CT Penedo¹, Maria F Sobral², José Matos³, Carla Borges³, Dina Neves⁴, Teresa Rangel-Figueiredo⁵ and Alfredo Cravador^{*6}

Abstract

Background: Decisions to initiate conservation programmes need to account for extant variability, diversity loss and cultural and economic aspects. Molecular markers were used to investigate if putative Algarvia animals could be identified for use as progenitors in a breeding programme to recover this nearly extinct breed.

Methods: 46 individuals phenotypically representative of Algarvia cattle were genotyped for 27 microsatellite loci and compared with 11 Portuguese autochthonous and three imported breeds. Genetic distances and factorial correspondence analyses (FCA) were performed to investigate the relationship among Algarvia and related breeds. Assignment tests were done to identify representative individuals of the breed. Y chromosome and mtDNA analyses were used to further characterize Algarvia animals. Gene- and allelic-based conservation analyses were used to determine breed contributions to overall genetic diversity.

Results: Genetic distance and FCA results confirmed the close relationship between Algarvia and southern Portuguese breeds. Assignment tests without breed information classified 17 Algarvia animals in this cluster with a high probability ($q > 0.95$). With breed information, 30 cows and three bulls were identified ($q > 0.95$) that could be used to reconstitute the Algarvia breed. Molecular and morphological results were concordant. These animals showed intermediate levels of genetic diversity ($MNA = 6.0 \pm 1.6$, $R_t = 5.7 \pm 1.4$, $H_o = 0.63 \pm 0.19$ and $H_e = 0.69 \pm 0.10$) relative to other Portuguese breeds. Evidence of inbreeding was also detected ($F_{is} = 0.083$, $P < 0.001$). The four Algarvia bulls had Y-haplotypes H6Y2 and H11Y2, common in Portuguese cattle. The mtDNA composition showed prevalence of T3 matriline and presence of the African-derived T1a haplogroup. This analysis confirmed the genetic proximity of Algarvia and Garvonesa breeds ($F_{st} = 0.028$, $P > 0.05$). Algarvia cattle provide an intermediate contribution ($CB = 6.18$, $CW = -0.06$ and $D1 = 0.50$) to the overall gene diversity of Portuguese cattle. Algarvia and seven other autochthonous breeds made no contribution to the overall allelic diversity.

Conclusions: Molecular analyses complemented previous morphological findings to identify 33 animals that can be considered remnants of the Algarvia breed. Results of genetic diversity and conservation analyses provide objective information to establish a management program to reconstitute the Algarvia breed.

* Correspondence: acravad@ualg.pt

⁶ IBB/CGB - Universidade do Algarve, Campus de Gambelas, 8005-139 FARO Portugal

Full list of author information is available at the end of the article

