

and Sanger sequencing in a larger population of the same three breeds and other 10 breeds. The results revealed that the Reggiana and the Italian Holstein breeds were almost completely fixed for alleles that were almost absent in Modenese breed. Variability in the *ASIP* gene in this breed might be involved in determining its white coat colour. These results provide some first evidence on the elusive role of the *ASIP* gene in affecting coat colour also in cattle, similarly to what already reported in sheep and goat, where variants in this gene are associated with white coat colours.

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#### P291

# Giant Grey rabbit breed: a preliminary study on reproductive traits

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Population size reduction and genetic erosion are aspects of concern in rabbit heritage breed conservation. An objective analysis of reproductive parameters of heritage breeds could provide effective tools for the definition of population management strategy. In addition, the inclusion of reproductive efficiency in selection plans could be very helpful in targeting conservation parameters on productive data. The aim of this study was to investigate reproductive traits in the Giant Grey rabbit (GGR) breed. Nineteen litters from three different rabbitries have been analyzed: origin of the breeders (BRO; 3 levels: 0 = homebred buck and doe, 1 =external buck or doe, 2 = external buck and doe), gestation length (GSL; dd), litter size (LIS; N; born alive), percentage of weaned kits (PWK; %; number of weaned kits/number of born alive kits), percentage of show prospect kits (PSK; %; number of selected kits for conformation show/number of weaned kits) were included in the dataset. Descriptive statistics, correlation (Pearson's) and ANOVA analyses were carried out using SPSS® (vers. 28) software. The GLM model included GSL, LIS, PWK and PSK as dependent variables and BRO as a source of variation. Post hoc Bonferroni test was used to investigate significant differences  $(p \le 0.05)$  between means. The major part (57.9%) of the litter was produced by mating a homebred with an external breeder. Variable mean values ( $\pm$  std. dev.) are GSL (dd)  $32.23 \pm 0.832$ , LIS (N)  $6.26 \pm 2.05$ , PWK (%)  $88.31 \pm 13.29$ , PSK (%)  $83.00 \pm 25.22$ . BRO showed significant effects on PSK and kits out of external parent recorded higher values. Pearson's correlation analysis

confirmed the most favourable choice of kits out of both external breeders for conformation competitions. Furthermore, a significant positive correlation between GSL and LIS was found. In conclusion, reproductive traits have been described in the Giant Grey rabbit breed for the first time and further monitoring may play a pivotal role for the implementation of conservation program and the improvement of production.

#### P309

### Different exposure to heat waves in Italian small ruminant populations

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Last decades have seen a dramatic increase in the number and frequency of heatwaves (HWs), and according to climatic projections, the situation is going to worsen. HWs have a severely detrimental impact on livestock leading to reduced performance, impaired feed intake and immunity, pest outbreaks, and increased mortality. For this reason, we aimed to assess the HW exposure of Italian small ruminant populations.

Geographic data about 2022 goat and 4475 sheep farms, related to 47 and 66 breeds, were provided by the Italian Sheep and Goat Breeders Association (Asso.Na.Pa.). The hourly Temperature Humidity Index (THI) from 1950 to 2022 was calculated using ERA5-land. A HW was defined as a period of at least 3 days, between May and September, with a maximum daily THI exceeding the 99th percentile of the reference period (1950–1979). For each year, the number of HW days (nDays) and the average THI measured during the HWs were calculated. HW parameters were associated with all the farms using ArcGis Pro and then fitted in a model including year, breed, and their interaction as fixed factors.

The locations of the enrolled farms saw a significant increase in nDays (from  $0.9 \pm 2.0$  in 1950s to  $5.4 \pm 5.7$  after 2010) and THI (from  $69.8 \pm 5.3$  to  $71.8 \pm 5.5$ ), especially in Friuli-Venezia Giulia and Liguria regions, respectively. In particular, the mean increase was of 0.08 and 0.07 nDays and 0.02 and 0.01 THI points per year in goat and sheep farms, respectively. All farms showed a notable rise in nDays, with Lariana goat and Istriana-Carsolina sheep farms exhibiting the greatest average value and increase (+0.10/ year and +0.12/year). No significant difference was observed among goat breeds in terms of yearly THI increase, though Grigia dei Monti Picentini farms had the highest mean value. Conversely, the year x sheep breed interaction was significant, with Noticiana





farms having the highest average THI and Garessina farms the greatest increase (+0.04/year).

Many of the breeds exposed to increasing HW are small and reared in localized areas, and thus even more sensitive to changes in their environment. Knowledge of the climatic risks for local livestock populations is useful to identify both breeds to be carefully monitored or showing a good response to HW (e.g. long-selected in regions subjected to HW): indeed, studying them might allow to understand the mechanism underlying their adaptation and thus the most efficient measures to mitigate the negative effects of climate change.

### P340

### The Apennine Rock partridge (Alectoris graeca graeca) a taxon to conserve. But what genes and how to keep them ex situ?

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The Rock partridge (RP, *Alectoris graeca*) is a wild Galliform endemic to Europe. The species is of conservation concern (SPEC 1) and reported in the Annex 1 of 2009/147/EC Directive. Conservation efforts are needed, and appropriate *ex situ* farming protocols should be established. Such types of protocols should include: (i) a preliminary genetic characterization to select native genes, (ii) a breeding technique avoiding morphological and behavioural limits. At these scopes, samples of faeces and feathers from 69 wild specimens of Apennine RP (*A. g. graeca*) were collected. The DNA extraction and PCR amplifications were performed following validated protocols focusing on the D-loop control region. The samples matched to four haplotypes registered in GenBank (H3, H8, H24 and H10), and mutations in the interval between 431 and 896 bp of our improved sequences allowed for the identification of 7 longer haplotypes.

Aiming to assess the effect of the intensive rearing on some morpho-functional traits, live weight, tarsus length and depth, tarsus and head width, head, wing, and beak length, were recorded fortnightly from 14 days after hatching (DAH) up to 98 DAH on offspring reared with intensive (G1, 16 chicks) and wildlike (G2, 14 chicks) approaches. Since morphological changes normally occur in multigenerational captive birds, first generation chicks of a wild breeding pair showing H10 haplotype were involved. This was a forced choice given the unavailability of other wild birds.

Comparisons between groups, at different stage of growth, were performed by an unbalanced full factorial ANOVA and significant differences were declared for  $p \le 0.01$ .

The G1 birds were constantly heavier than G2 ones, although the statistical significance was achieved only at 14 DAH ( $55.66 \pm 6.65 \text{ mm}$  vs.  $49.16 \pm 4.25 \text{ mm}$ ). The first signal of captive morphological changes has been recorded at 84 DAH, when G1 birds showed shorter heads ( $35.43 \pm 1.24 \text{ mm}$ ) and thinner tarsi ( $4.45 \pm 0.31 \text{ mm}$ ) than G2 birds ( $36.84 \pm 1.34$  and  $4.73 \pm 0.29$  respectively), as a possible result of limited physical and cognitive exercise in an artificial environment. Our results provide a list of Apennine RP haplotypes and suggest implementing semi-natural breeding protocols to avoid the occurrence of captive morphological changes and the unintended selection of this characters. Further studies should be focused on other mitochondrial lineages and on how the breeding system affect behavioural attitudes of Apennine RP.

#### P449

## SCALA-MEDI: investigation of genetic and epigenetic adaptation mechanisms in North African livestock

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