



In this study, a dataset of 200,000 test day records from 23,000 cows in the period 2008–2019, treating each parity as a separated and correlated trait, has been used. Results showed a moderately negative genetic correlation (-0.29) between intercept and slope, ranging from a minimum of -0.69 (parity 3 for Fat corrected milk) to a maximum of 0.13 (for cheese yield at $24\,\mathrm{h}$), indicating that production is antagonistic to heat tolerance. For protein and fat yield, the genetic correlation was lower in parity 2 respect to parity 1 and 3, probably due to a different production level of the cows. Interestingly, the permanent environment correlation was higher for parity 3 (mean 0.03) and lower for parity 1 (-0.24) indicating that herd condition is critical in younger animals.

P009

Effect of lactic acid bacteria addition or protozoa modulation on the in vitro rumen aflatoxin B1 decontamination

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The ingested Aflatoxin B1 (AFB1) by lactating animals is partially excreted in the milk and this is a serious problem of food safety due to high toxicity and carcinogenic effect. The rumen fermentation partially detoxifies AFB1 and there is a practical interest in the adoption of dietary strategies in dairy cows breeding to further increasing this rumen capacity. This study evaluates the effects of (i) the addition of pure lactic acid bacteria (LAB) inoculants and (ii) the protozoa modulation on fermentative profile and AFB1 recovery. Two in vitro experiments used the same in vitro fermentation apparatus (eight 500 mL bottles immersed in a water bath at 39 °C for 24 h, filled with filtered rumen fluid and buffer (ratio 1:2)) and the same feed substrate (3300 mg of corn silage containing 20 µg AFB1/kg). At the end of the incubation period, the fermentation fluid was collected and sampled for protozoa, volatile fatty acid, and ammonia. The remaining fluid was centrifuged (4600g for 20') and the AFB1 content of supernatant and pellet were analyzed by an HPLC technique.

In Exp 1, three pure bacteria strains ($L.\ plantarum$, $L.\ rhamnosus$ and $L.\ mucosae$) were selected and added, autoclaved (121 °C × 15') or not, in a concentration of 1x10⁸ CFU/mL. After 24 h of incubation, the concentration of AFB1 was evaluated. The levels of AFB1 did not differ between the control and the treated samples, both in pure and autoclaved LAB. The addition of $L.\ plantarum$ only increased the proportion of propionate in fermentation fluid (15.5 vs. 14.5–14.8%, p < .05). Presumably, the rumen

environment and the interaction with other microorganisms may affect the AFB1 binding capacity of LAB tested.

In Exp 2 the protozoa population was changed by the addition of *Stevia rebaudiana* Bertoni extract (S) or Camphor oil (CO) at a dose of 1.5% of incubated DM. The protozoa count in fermenters added with S were lower than those added with CO (213 vs. $293*10^3$ Cell/mL, p < .01), while the AFB1 residue after 24 h fermentation was higher for S than CO (56.0 vs. 42.9 ng, p < .05) then the reduction of total protozoa generates higher AFB1 levels. This phenomenon could be explained by an interaction between protozoa and other rumen microorganisms.

P010

Application of a genomic tool for heifers selection in Italian Holstein cattle

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Recently, genetic improvement of animal health is attracting more attention from both animal sciences and farming. The introduction of genomic methods and tools contributed to enhancing insights into the genetic control of diseases, thus improving animal welfare and resilience. Aim of this study was to evaluate disease-related genomic indexes in animals reared in farms that can be considered virtuous as for the farming practices in comparison with less virtuous farms. A total of 10 farms were selected based on the average Somatic Cell Count (SCC), to obtain a 1:1 ratio between virtuous (V) and less-virtuous (LV) farms. Mean SCC ($\times 1000$) of the two groups ($\pm SD$) was 165.2 ± 365.4 and 289.8 ± 532.1 (V and LV, respectively). A t-test was performed to evaluate the difference between SCC means (t = 4.5574, df =1039.4, p-value <0.001). From the selected farms, 117 heifers were randomly sampled and genotyped using the Zoetis Clarifide chip (61 in V and 56 in LV farms, respectively). Genomic indexes were calculated on the abovementioned animals. The means of the Somatic Cell Score (SCS, calculated as log2(SCC/100,000) + 3) index in the two groups were 2.92 ± 0.14 and 2.97 ± 0.14 (V and LV, respectively). Low values for this index indicate a more favorable SCC. Although not statistically significant (t-test: t = -1.8946, df = 114.6, p-value = 0.06), a trend could be identified. Supporting this trend, 56.5% of the animals with an SCS index lower than the sample average (i.e. lower SCC) were reared in V farms, while 64.5% of the animals with an SCS index higher than the sample average were reared in LV farms. Out of the 5 V farms, 4 had at least one animal in the top ten ranked by SCS index. In particular,





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the farm with the higher number of animals in the top ten was the first in terms of lower SCC mean. From these preliminary results it is possible to notice that the absence of a rigorous selection on health-related traits almost nullifies the positive effects of good management and animal care. It should be noticed that only heifers were tested. Thus, future farm data will be required to find out if any genetics effect can increase the positive results of the V farms (considering that at least two of these farms are currently under mastitis resistance selection). Breeders should be encouraged to improve their breeding plans to involve health-related traits, to further increase their animals' welfare, and to support the efforts they put into animal management.

PEN28; farrowing rate: 85% PEN3 vs. 75% PEN28) nor on litter size (total born: 13.4 PEN3 vs. 13.3 PEN28; born alive: 12.1 PEN3 vs. 11.8 PEN28, mummified: 0.5 PEN3 vs. 0.5 PEN28) even considering all categories of animal included in study (weaned sows, gilts and repeated breeder sows).

Results of the study suggest that the practice of mixing sows into groups early post-insemination could be done without adversely affecting herd productivity. However, more aspects must be investigated before to reach a definitive conclusion such as the effects of day of mixing also on welfare indicators such as sow behaviour (conflict and aggression), injuries and physiological indicator of stress.

P011

How the stage of gestation for moving at the group housing can affect sow's reproductive performance?

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Confinement in individual stalls of pregnant sows is a controversial welfare issue, as it precludes the freedom of movement, social interaction and expression of other natural behaviours. The legislation on the protection of pigs in the farm environment (2008/120/EC) allows to use the individual gestation stalls for 4 weeks after service, but there is an increasing request by the public opinion to reduce and /or ban their use. However, high levels of aggression are commonly observed in newly formed groups after mixing, pose a concern about the impact of mixing sows in early gestation on their performances. The aim of this study was to determine the impact of mixing sows in group pen on day 3 from insemination (PEN3) instead of 28 (PEN28) evaluating reproductive performance and litter size. At total of 326 sows were used in the study, divided in 234 weaned sows of different parity (from 2 to 11), 60 gilts and 32 sows that had reproductive failure before. The Group pens hosted 20 sows, had a concrete floor and a space allowance of 2.25 m². Data collected allowed to calculate: pregnancy rate (proportion of sows inseminated that results pregnant at 28 d by a real-time ultrasound examination), farrowing rate (proportion of sows inseminated that farrowed) and litter size (total born, born alive, stillborn, mummified piglets).

Data were processed by chi-square test for the analysis of reproductive performance and by Mann-Whitney test for the analysis of litter size. No treatment effects were observed neither on reproductive parameters (pregnancy rate: 85% PEN3 vs. 80%

P012

What consumers perceive from geographical information and welfare of lambs?

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Recently, the geographical origin of food is considered one of the key information which influences the consumers' acceptance. Lamb meat is considered a local and typical food with high quality attributes for the consumers, being characterized by shorter transport and as consequence, a good welfare condition. The aims of the present work were the (i) exploitation of the role of information about geographical origin, transport duration, and welfare condition of lambs for consumers and their actual liking, (ii) and the evaluation of meat quality. Thirty Merinos-derived male lambs were subjected to two different transport distance, fifteen lambs were subjected to a short transport duration (STR), approximately around 1 h, starting from local farm to the slaughterhouse located at Foggia. A second group of lambs was subjected to a long transport (LTR), around 22 h going through 1250 km. At slaughterhouse, welfare issues (percentage of active animals, ambulatory animals, injuries, lameness, dead), were monitored by veterinarian. On longissimus dorsi lumborum (LDL) muscle was assessed the colour, pH, mechanical properties and the chemical composition. A preliminary focus group was carried out to evaluate the interest of consumers regarding the consumption of lamb meat from different geographical origins and with different welfare conditions. Furthermore, a number of 120 consumers were recruited in order to set up the consumer test. Nutritional, textural and quantitative descriptive sensory data were processed

