showed that, as the parity order increases, sire effect becomes more relevant while the herd effect decreases in relevance. Sires' and herds' solutions were then converted from the liability to the probability scale (0–1). Considering the whole set of sires and herds, correlations between bulls' EBVs across parities ranged from 0.608 to 0.656, while correlations for herds' solutions ranged between 0.597 and 0.718. Considering sires and herds with at least 50 records, correlations between bulls' EBVs range between 0.756 and 0.798, while herds' solutions range between 0.789 and 0.832. In conclusion, it is shown that on cow's longevity there is a genetic impact of sire and herd.

O36
Genetic aspects of heifer fertility in Italian Holstein population

Valentina Ferrari[a], Giulio Visentin[b], Jan-Thijs Van Kaam[a], Mauro Penasa[c], Maurizio Marusi[a], Raffaella Finocchiaro[a] and Martino Cassandro[a]

[a]ANAFIBJ, Cremona, Italy
[b]Department of Veterinary Medical Sciences, University of Bologna, Bologna, Italy
[c]Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Padova, Italy

Fertility is fundamental to enhance the production efficiency of the dairy herd and thus it is a contributor to annual farm profitability. Cow fertility has been included in Italian Holstein breeding objectives since 2009. Heifer fertility is another key trait that deserves attention as it has direct connection with overall efficiency. In general, the main goal is to improve conception and daughter pregnancy rates, favour shorter calving interval in lactating cows, and reduce failure of conceiving in heifers. The advantages of heifer over cow fertility traits are the early availability in life and, overall, the moderate to strong genetic correlations with fertility of lactating cows. The aims of the present study are to assess genetic parameters of Italian Holstein heifers and develop an aggregate selection index to improve heifer fertility. Data (ANAFIBJ, Cremona, Italy) included information on insemination, calving, and pregnancy diagnosis dates of Italian Holstein heifers. The investigated traits (mean ± standard deviation) were age at first insemination (AFI, mo; 17.25 ± 2.89), nonreturn rate at 56 d from the first insemination (NRR56, binary; 0.78 ± 0.41), conception rate at first insemination (CR, binary; 0.61 ± 0.49), and interval from first to last insemination (IFL, d; 26.09 ± 51.85). Genetic parameters were estimated using a 4-trait animal model that included the fixed effects of herd-year of birth and month of birth for AFI, and herd-year-season of birth and month-year of insemination for IFL, NRR56, and CR. The animal additive genetic effect was included as random term. An aggregate index was developed from the estimated additive genetic (co)variance matrix by considering CR as the breeding goal and AFI, NRR56, and IFL as selection criteria. Heritability ranged from 0.012 (CR) to 0.015 (IFL), except for AFI (0.071). Conception rate at first insemination was strongly correlated with both IFL (-0.730) and NRR56 (0.668), and weakly to AFI (-0.065). The relative emphasis placed on each selection criteria in the aggregate index was 10%, 47%, and 43% for AFI, IFL, and NRR56, respectively. Results of the present study suggest that heifer fertility should be considered as an additional trait in the breeding objectives of Italian Holstein.

O146
Influence of genetic background and the effect of liquid whey supplementation on the faecal microbiota composition in Nero siciliano and commercial crossbreed pigs

Viviana Floridia, Letterio Giuffrè and Enrico D'alessandro

Università degli Studi di Messina, Messina, Italy

The genetic background of the host, together with several other biotic and abiotic factors, including feeding, plays a crucial role in modulating the gut microbiota composition of many animal species. Furthermore, several authors have reported that the microbiota of native pig breeds reflects distinctive traits that commercial crossbreeds have lost. Nero Siciliano pig is an important autochthonous Sicilian pig breed that has a marked lipolytic capacity. The aim of this study is to assess the composition of the faecal microbiota of two different genetic types of pigs reared within a farm where liquid whey was integrated in the feeding as dairy by-product. The faecal bacterial composition has been investigated at three time points, T0, T1 (after 30 days) and T2 (after 60 days), in two pig groups (Control and Treatment). Microbial genomic DNA has been extracted from stool samples collected directly from the rectal ampoule of 20 crossbreed (Large White × Landrace) pigs (10 Control and 10 Treatment) and 10 autochthonous (Nero Siciliano) pigs (5 Control and 5 Treatment). The 16S rDNA gene has been sequenced using an Illumina MiSeq platform and the clean reads (Phred-score ≥20) have been classified at phylum, family, and genus level, with an identity threshold of 75%, 87% and 95%, respectively, by using QIIME2. In both groups and population sets, *Firmicutes* (51%) was the most abundant phylum followed by *Bacteroidetes* (36%) whereas the most abundant genera were *Prevotella, Treponema* and *Lactobacillus*. The two pig genetic types have showed a different attitude towards liquid whey diet. In fact, as shown by beta diversity analysis, measured by Bray-Curtis distances, the microbiota of crossbreed samples has been significantly affected by liquid

Taylor & Francis
Taylor & Francis Group