

in dairy systems. The objective of this study was to estimate heritabilities ( $h^2$ ) and additive genetic correlations ( $rg$ ) of enteric methane emission (EME) traits predicted with milk FTIR-spectra (Direct-IR) and predicted indirectly using fatty acids (Indirect-IR). Data included the detailed milk composition of 42,462 Brown Swiss cows from 669 herds during 8 years. The traits included were daily milk yield (dMY, kg), fat (%), protein (%), the predicted milk fatty acids related to EME (FAs: C4, C16iso, C18:1t10, C18:1t11, C18:1c9, C18:2c9c12), methane yield per unit dry matter intake ( $CH_4$ -DMI, g/kg), daily methane production ( $dCH_4$ , g/d), and methane intensity per kg of corrected milk ( $CH_4$ -CM, g/kg), fresh cheese ( $CH_4$ -FC, g/kg), and cheese solids ( $CH_4$ -CS, g/kg). Univariate models were used to estimate  $h^2$  and bivariate models were used for the estimation of  $rg$  between traits. All models included the effects of parity (1–3), days in milk, and year-season interaction as fixed effects. The herd, additive genetic animal and permanent environmental effects were included as random. The program used for calculations was AIREMLF90. The  $h^2$  for dMY, fat and protein were 0.09, 0.26 and 0.40, respectively (SE <0.008) and for FAs it ranged from 0.03 to 0.13 (SE <0.004). The methane traits had similar  $h^2$  in Direct-IR and Indirect-IR methods, from 0.04 to 0.11 (SE <0.004). The  $rg$  between dMY, fat, protein and FAs ranged from -0.79 (fat – C18:1t11) to 0.55 (fat – protein). The  $rg$  between dMY, fat, protein and Direct-IR EME varied from -0.92 (dMY –  $CH_4$ -CM) to 0.47 (protein –  $CH_4$ -DMI), while the  $rg$  between dMY, fat, protein and Indirect-IR EME ranged from -0.53 (protein –  $CH_4$ -FC) to 0.73 (dMY –  $dCH_4$ ). The  $rg$  between Direct-IR EME and Indirect-IR EME were high (0.89–0.96) except for  $dCH_4$  with 0.30. The  $rg$  between FAs and Direct-IR EME had a wide interval of -0.77 (C18:2c9c12 –  $CH_4$ -DMI) and 0.95 (C18:1t10 –  $CH_4$ -CS). The  $rg$  between FAs and Indirect-IR EME varied from -0.88 (C18:2c9c12 –  $CH_4$ -DMI) to 0.45 (C16iso –  $CH_4$ -DMI). Results show the feasibility of using Direct-IR and indirect-IR EME in animal breeding programs, except for  $dCH_4$  because it is better estimated by multiplying  $dMY \times CH_4$ -CM.

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### Genetic evaluation and variance component estimation in an Italian honey bee population

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In all domestic species, mating control is a key aspect of any breeding program. In *Apis mellifera* the problem is crucial due to the free mating of the virgin queen in its single nuptial flight and to the variable number of haploid drones. Controlled matings via,

for instance, geographic isolation is an effective approach but it is not a common practice yet. In such a situation, pedigree is not complete because drone origin is missing and selection occurs only on the maternal path. Since 2015, 108 colonies from five sites of a honey bee breeding company from Lombardy have been evaluated for honey production (HP), hygienic behaviour (HB) and docility (DOC). A pedigree with information about breeding queens (BQ) and drone producing queens (DPQ) have also been recorded. The objective of this study is to present the results of a genetic evaluation developed using the aforementioned information. The original dataset included 494 records for HP, HB and DOC. A pedigree with 1267 individuals was also available, including information on drone origin. A total of 6 DPQ were used and traced back. Considering that in honey bees the observed performance is due to the contribution of both the worker bees and their queen, a direct and maternal genetic effect model was used to estimate variance components and breeding values. The model included the fixed effect of year of production, the random effect of the interaction of mating site and year of production, and the random genetic effects of the worker and the queen of the colony. The inverse additive relationship matrix was calculated by combining the classical inversion strategy of Henderson with the bee-specific properties of haploid drones. The random interaction of the mating site and year of production was included to mitigate the unbalanced distribution of DPQ across mating sites. The BLUPF90 programs were used to estimate variance components and to compute EBV fitting each trait separately. Heritability of the worker direct genetic effect ranged from 0.20 for DOC to 0.45 for HP. For all traits, the random non-genetic component accounted for more than 40% of the phenotypic variance. Residual variances accounted for about 10%. Heritability of maternal genetic effect ranged from 0.40 for HP to 0.65 for HB. The correlation between direct and maternal genetic effects was negative for all traits.

#### Acknowledgements

This research was funded by the BEENOMIX and BEENOMIX 2.0 projects funded by the Lombardy Region (FEASR programme), PSR 2014–2020 (grant number 2016/00361532-G42F16000540002) and PSR (grant number 201801057971 – G44I19001910002).