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**Genetic variation in milking efficiency: a novel trait for milkability in automatic milking systems**

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Genetic parameters for milking efficiency, milk flow rate, yield, cell count and milking frequency were estimated for cows intensively recorded in a research station. Milking efficiency was calculated at every milking as kg ECM produced per minute a cow occupy the automatic milking station. The study utilised data from Holstein, Red Dane and Jersey cows (n=556) in first parity over a 7 year period. Milk records were filtered to avoid data from disturbed milkings, (i.e. incomplete milkings, and milking following other incomplete milking). After filtering 280,510 undisturbed records remained of which 146,133 also had composition data. The lactation trajectory was divided into 10 segments of 30 days to allow for co-variance components to change during lactation. Covariance components were estimated for genetic, permanent environmental and residual effects using AI-REML and used to calculate heritability and genetic correlations. Heritability of milking efficiency ranged from 0.34 to 0.50 during lactation. Milking efficiency was positively correlated to higher yield per day but either weakly or negatively correlated to flow rate and somatic cell count indicating that higher efficiency could be obtained without concurrent increase in somatic cell count. This study has introduced a new functional trait that could replace flow rate and milkability in describing the efficiency of cows in utilising the milking station.

**WebLOAD: a web frontend to create a consistent dataset from multiple text files in animal breeding**

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Parameter estimates, genetic analyses and genomic selection – all these methods require consistent data and logically correct pedigrees. If datasets from various sources (farms, teststations or breed societies) are merged, different keys or codes for the same indication or different identifications (IDs) for the same animal are very problematic. Purchases and sales of animals resulting in two IDs for the same animal aggregate the problem. Therefore, to obtain one consistent datapool its initial contributing files need to get harmonized. WebLOAD implements this in a generic manner. WebLOAD is a web frontend for the parameterization of the LOAD software providing a set of rules and filters to clean up heterogeneous data from different sources. This includes the proper treatment of multiple animal ID systems as well as harmonization of codes. The pedigree is checked for consistency and loops. Additionally, alleles of offspring are checked against their parents for consistency. Apart from the data checking there are various possibilities to recode keys or animal IDs or to mark them as invalid. After completion of the analysis the results can be exported to text files or as a normalized database. Being a web application problem definition and configuration is done via a browser otherwise an editor. The WebLOAD is written in Perl with LOAD using the logic of the APIIS-framework. WebLOAD is freely released under the GPL license. The project is supported by funds of the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support programme.