



# Enhancing the amount of free amino acids and protein fractions in cow milk

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## DESCRIPTION

Regularly assessing intricate milk compositional features necessitates a significant investment of resources. Therefore, in dairy cow breeding programmes, a lack of phenotypic data can impede genetic advancement in these qualities. Utilizing Mid-Infrared Spectroscopy (MIS) predictions commonly taken from milk samples, the goal of the current study was to estimate the possibilities for breeding for improved milk protein and Free Amino Acid (FAA) composition. Few breeding programmes for dairy cows take into account the specific milk composition, even though most breeding programmes focus on milk yield and protein and fat concentration at the macro level. However, the quality of a range of dairy products that can be produced is impacted by the specific milk composition. For instance, the amount of protein that is transferred from milk into cheese curd is positively impacted by the Concentration of Casein (CN) in milk.

The main cause of FAA-rich milk's unfavourable cheese-making qualities is protein hydrolysis. Even Nevertheless, the existence of FAA is crucial for specific products, such as newborn formulae, despite the fact that the FAA composition and concentration of the milk from different mammals varies. In actuality, cow milk has less FAA than human milk. Particularly in babies, certain FAA is known to play a significant influence in the development of the immune system. However, even though some of them, like leucine, valine, and glycine, are necessary or conditionally necessary, bovine milk FAA have typically been disregarded up to this point. When nursing is not an option, products containing amino acids and FAA-enriched infant formulae may be beneficial from a nutritional standpoint. Although expensive, amino acid-based supplements offer proteins in non-allergenic forms, making them appropriate for persons who are allergic to bovine milk proteins. Given these factors, it is important to look at the possibility of modifying the FAA profile of

bovine milk by breeding. Individual protein fractions, such as -lactalbumin (-LA) and -casein (-CN), are known to be heritable. Interbreed variations in the concentration of protein fractions and FAA has been recorded. For protein fractions measured by capillary zone electrophoresis, a heritability of 0.25 (-CN) to 0.80 (-LG) was observed. The percentage of overall phenotypic variance attributed to additive genetic variation, according to a similar report, ranged from 0.33 (s1-CN, s-CN, and s-LA) to 0.68 (s-LG). The estimations may change due to variations in the gold standard techniques used to measure milk protein fractions as well as features of the population under study, such as the researched breeds, parities, and lactational stages represented.

It is now widely known that milk Mid-Infrared Spectroscopy (MIS) analysis can accurately predict milk composition and animal health features on a broad scale. Despite this, only a small number of studies have revealed genetic parameters of MIRS-predicted protein fractions, and there are no estimations for FAA. Therefore, the goal of the current study was to estimate the possibility for breeding dairy cows for milk protein fractions and FAA while utilising the usually accessible MIRS forecasts for individual cows. Response to genetic selection depends on the level of genetic variability, the precision of the selection, the strength of the selection, and the generation gap. Therefore, in order to accomplish genetic gain, the trait must show genetic diversity and there must be enough phenotypic or genomic data on the trait to assure high selection precision. All of the milk quality parameters evaluated in the current study clearly exhibit significant genetic variation, despite having low to moderate heritabilities. This implies that selective breeding may be used to change the protein content as well as the FAA composition of cow milk. The lower the number of progeny records needed to achieve good selection accuracy, the higher the heritability. In other words, the smaller the reference group used to produce genetic predictions, the higher the heritability.

Many contemporary national breeding programmes indirectly select for protein concentration by giving milk yield a negative weight while giving protein yield a positive weight. In the current investigation, the genetic variance coefficients for protein content and milk output were 7.45% and 4.84%, respectively. As well as being lower than the coefficient of genetic variation for FAA (14.30%), these results were comparable to or even lower than the coefficient of genetic variation for the gold standard total casein and total whey.

Positive genetic trends for dairy cow milk production are well established, with lactation milk production per cow increasing over the last 40 years. In other words, the smaller the reference group used to produce genetic predictions, the higher the heritability. If MIS prediction equations are used for phenotyping and anytime dairy chain stakeholders decide that particular protein fractions merit inclusion in the breeding objective, traditional and genomic evaluations of detailed protein composition make sense.