

CattleQTLdb analysis to increase understanding of the functions of milk proteins genes

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Brazil has one of the largest commercial cattle herds in the world and is the fourth largest milk producer worldwide, yielding approximately 35 billion kg of milk per year. Brazilian herds consist of taurine breeds (*Bos taurus*), indicine breeds (*Bos indicus*) and their crossbreeds. However, the genetic basis underlying the milk features and/or differences above these breeds is only partially known. In a previous study, we identified 64 SNVs and 6 INDELs in genes which codify milk proteins from Guzerá and Gir Genome, such as α S1-casein (*CSN1S1*), α S2-casein (*CSN1S2*), β -casein (*CSN2*), κ -casein (*CSN3*), α -lactalbumin (*LALBA*), β -lactoglobulin (*LGB*) and lactotransferrin (*LTF*). However, despite we study that identified variations in these genes, it is still necessary to have a better understanding of the function of these genes in the yield of milk proteins and if these genes have function in other relevant characteristics economically also, for example analysis in QTLs. In this context, the objective of the present study was to verify *in silico*, if these genes co-locate with QTLs of economic importance deposited in Cattle QTLdb. We search for QTLs associated for *CSN1S1*, *CSN1S2*, *CSN2*, *CSN3*, *LALBA*, *LGB* and *LTF* genes in Cattle QTLdb. We select all QTLs associated with these genes found and analyzed what characteristics are related with gene. QTLs regions (60) were identified co-locating as the seven genes referred above. We found one (1.7%) in *LALBA* gene; two (3.3%) in *CSN1S2* gene; thirteen (21.7%) in *LTF* gene; fifteen (25%) in *CSN3* gene; nine (15%) in *CSN1S1* gene; and twenty (33.3%) in *CSN2* gene. In *LGB* gene, no QTLs were identified. *LTF* and *LALBA* genes co-locate with QTLs for calving interval and clinical mastitis, and fertilization rate, respectively, in addition to milk protein yield. *CSN2* and *CSN3* genes co-located with QTLs for milk alpha-lactalbumin and beta-lactoglobulin content. QTLs analysis is an important tool for understanding of the function and characteristics related with genes. These results suggest the existence of regulatory mechanisms regulating in trans the milk protein content.

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