

MiRNA in raw cow milk: any contribution to the nutritional quality?

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BACKGROUND

With its content of miRNAs, cow milk may act as an epigenetic regulator of milk recipients' gene expression. Bovine miRNAs are identical to human analogs and recognize the same target mRNAs. Type and amount of certain miRNAs, as well as bacterial cell count (TBC), somatic cell count (SSC), antioxidant activity, and fatty acid profile, may contribute to modulate the nutritional quality of cow milk and dairy derivatives.

AIM OF THE STUDY

To investigate the nutritional value of raw cow milk, inflammatory miR-148, miR-29 and miR-21, total bacterial cell count (TBC), somatic cell count (SSC), antioxidant activity, and fatty acid profile were assessed.

MATERIALS AND METHODS

After total RNA extraction and retro-transcription, miR-148, miR-29 and miR-21 were quantified by qPCR. Antioxidant activity of raw milk was calculated according to the Oxygen Radical Absorbance Activity (ORAC) test. The lipid profile was evaluated by gas chromatography.

CONCLUSION

The expression levels of inflammatory miRNAs, fatty acids composition and antioxidant properties of cow milk are influenced by its inflammatory profile (expressed in terms of TBC and SSC). This pilot study suggests that inflammation can negatively affect the nutritional value of cow milk.

RESULTS

