FRAP values of twelve hybrids resulting from the cross 'Bergeron' ×'Baneasa 4/11' varied between the values determined for the parents ('Bergeron': 3.57 mmolAA/L and 'Baneasa 4/11': 1.12 mmol AA/L). Three hybrids showed FRAP values very similar to that of the 'Baneasa 4/11', while two others almost reached the level measured in 'Bergeron'.

The closest correlation occurred between the FRAP and DPPH-radical scavenging capacity. Close correlations were also obtained between FRAP, TPC, DPPH and vitamin C content data. Colour values did not show significant correlations with any of the measured parameters of water-soluble antioxidants, since colour values were correlated exclusively with the lipid-soluble carotenoids.

Our results indicate that several valuable genotypes can be selected from a progeny obtained from crosses where at least one of the parents is characterized by enhanced fruit antioxidant properties.

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Regulation of metal responsive transcription factor MTF-1 expression in common carp

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Metal responsive control of gene expression allows organisms to adjust the concentration of essential metal ions such as Zn^{2+} and Cu^{2+}, within an acceptable range and cope with detoxification of heavy metals (Cd^{2+}, Pb^{2+} and As^{3+}) with no biological function. Metallothioneins (MTs) are widely inducible at transcriptional level by a variety of metals and other stress conditions such as accumulation of reactive oxygen species, hormones and cytokines. Transactivation of metallothionein genes involves the Metal-responsive Transcription Factor (MTF-1) a metal responsive element (MRE) binding, zinc sensitive protein.

In this study we present the first evidence for an *mtf-1* splicing variant (*mtf-1.1a*), originated from the brain of unstressed common carp. We have follow the level of *mtf-1.1a* mRNA in the liver, kidney, heart, muscle and brain of unstressed animals and the effect of heavy metal loading (Cd and As) on the alternative splicing of *mtf-1.1* transcript. For the detection and semiquantitative determination, an *mtf-1.1*-specific primer pair was designed. This primer pair has the potential to amplify a segment from both *mtf-1.1* and *mtf-1.1a* in the same PCR reaction, with a well-distinguishable size difference.

The splice variant of *mtf-1.1* mRNA codes for a truncated MTF-1.1 protein. The lack of a 103 nucleotides internally in the *mtf-1.1a* transcript, between positions 1047-1149, results in a frame shift causing an early termination of translation. The putative MTF-1.1a protein consists of the first 349 amino acids of MTF-1.1 followed by an additional 64 amino acids, which don't resemble at all to the corresponding region of MTF-1.1. The 349 amino acid covers the six Zn-finger DNA binding domains, the nuclear localization (NLS) and the nuclear exporting (NES) signals and the first 12 amino acid of the acidic region. Under unstressed conditions *mtf-1.1a* was detected in all tissues examined, but the liver, with the highest level in the brain. Arsenic alters the level of both *mtf-1.1* and *mtf-1.1a* transcripts in an isoform- and tissue-specific manner. Cadmium had no measurable effect on the alternative splicing of *mtf-1.1* in the liver, while the amount of both *mtf-1.1* transcripts gradually decreased in the brain.

The above observations suggest a tissue- and stressor-specific function of the predicted MTF-1.1a protein. In addition, we have already identified another MTF-1-coding gene, *mtf-1.2*, exclusively expressed in the brain of unstressed animals. The possible presence of 3 MTF-1 protein variants in the brain suggests a crucial role of the MTF-1s in this organ. MTF-1.1a might function as a negative regulator of MRE-controlled expressions. However, it is also possible that the introduction of a new C-terminal domain might result in a new level of regulation by recruiting new proteins to MTF-1.1-controlled promoters.