Abstract Submitted
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Partitioning of copper isotopes reveals changes in metabolism due to prion protein expression in transgenic mice KERRI MILLER, Dept. of Physics and Astronomy, Univ. Calgary, Canada, CATHERINE M. KEENAN, Hotchkiss Brain Inst, Univ. Calgary, Canada, GARY R. MARTIN, The McCaig Inst. for Bone & Joint Health, Univ. Calgary, Canada, KEITH A. SHARKEY, Hotchkiss Brain Inst., Univ. Calgary, Canada, FRANK R. JIRIK, The McCaig Inst. for Bone & Joint Health, Univ. Calgary, Canada, MICHAEL WIESER, Dept. of Physics and Astronomy, Univ. Calgary, Canada — The partitioning of copper isotopes has provided a wealth of information regarding metal interactions in physical systems. Metabolic activities in animals can partition copper isotopes as the metal is assimilated into the body. Therefore variations in copper isotope abundances in organs and tissues may act as a biomarker for changes in metabolism and may vary in disease. Prion protein is a naturally occurring copper binding protein of importance in neurodegenerative conditions. Mice that lack prion, over express this protein and lack the copper binding motif are available and we used these animals to investigate whether changes in copper isotopic composition were present in the organs and tissues of these mice. The copper isotope amount ratios were measured using an MC-ICP-MS. Changes in the copper isotope amount ratios due to the presence of this protein or its ability to bind copper were observed, most notably in the kidneys and the colon. These results suggest that isotope abundance data may be an innovative tool for identifying alterations in biological homeostasis and may provide novel diagnostic approaches in disease.

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