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Oral presentation

Living longer by dieting: analysis of transcriptional response after caloric restriction

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Caloric restriction extends mean and maximum lifespan in a range of eukaryotic species, including yeast, flies and mice, and retards age-associated pathologies such as cancer in mice. However, the molecular mechanisms for this are not well understood. In rodents, it has been suggested that there is little similarity between the transcriptional responses of different tissues to caloric restriction, but this has not been examined simultaneously in the same sample population. We used gene expression arrays to determine the transcriptional profiles of liver, skeletal muscle, hypothalamus and colon in mice subjected to caloric restriction for 48 hours. All of these tissues are known to be affected by caloric restriction and all appear to be important to the metabolic and physiological adaptations that occur in response to caloric restriction. We compared the transcription changes between our tissues in two ways: based on overlap between lists of differentially expressed genes and overlap in functional annotation categories overrepresented in lists of differentially expressed genes (calculated using EASE).