

Effects of Maternal Protein Malnutrition and Intrauterine Growth Restriction on Redox State of the Central Nervous System in Offspring Rats

Mehmet Tatlı,¹ Aşlan Guzel,¹ Goksel Kizil,² Vatan Kavak,³ Murat Yavuz,² and Murat Kizil²; ¹Department of Neurosurgery, Faculty of Medicine, University of Dicle, 21280 Diyarbakir, Turkey, ²Department of Chemistry, Faculty of Science, University of Dicle, 21280 Diyarbakir, Turkey, ³Department of Anatomy, Faculty of Medicine, University of Dicle, 21280 Diyarbakir, Turkey (kavakv@dicle.edu.tr)

Nutrition plays a crucial role in the maturation and functional development of the central nervous system (CNS). Both maternal protein malnutrition and intrauterine growth restriction (IUGR) have deleterious effects on brain development, but a comparison of these effects has not been previously reported. The objective of this study was to investigate the effects of these factors on redox status of CNS including spinal cord in offspring rats. We evaluated various parameters of oxidative status, indexes of damage to lipid, and protein damage in addition to antioxidant enzyme activities of superoxide dismutase and catalase in different regions of CNS from rats subjected to pre-postnatal protein malnutrition (middle 12%, low protein 4%) and IUGR. Results were analyzed by one-way ANOVA followed by Tukey's post hoc test. Both, protein malnutrition and IUGR altered various parameters of oxidative status. There was an increase in levels of thiobarbituric acid-reactive substances, the index of lipid peroxidation, in the cerebellum, cerebral cortex and spinal cord ($P < 0.001$) from protein-malnourished rats. Furthermore, IUGR increased lipid peroxidation level in the blood samples ($P < 0.04$) and protein oxidative damage in the cerebellum, and cerebral cortex ($P < 0.005$). The highest decreased in catalase activity was in the cerebellum ($P < 0.001$). In addition, a significant decrease in antioxidant enzyme activities ($P < 0.005$) was observed in the cerebral cortex from protein-malnourished rats. The present data indicated that both protein malnutrition, in different protein contents, and IUGR increased oxidative damage to lipids and proteins from CNS areas.

Taking It to the Edge: Field Studies vs. Museum Studies of Dental Microwear

Mark F. Teaford; *Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, 1830 E. Monument St., Baltimore, MD 21205, USA (mteaford@jhmi.edu)*

Dental microwear analysis takes us into interpretations of how teeth are actually used, rather than focusing solely on what they are capable of doing. As a result, these analyses often raise more questions than they answer, as we begin to grapple with the true complexity and diversity of diet, especially in animals, like primates, with varied diets. Field studies would seem to be the ultimate source of information on diet and dental microwear. Yet such studies are difficult and relatively rare. Meanwhile, analyses of museum material, while more feasible, are often harder to interpret, due to a lack of feeding data on the specimens in question. Still, researchers are pushing analyses to their limits. Recent work with living primates in the wild has begun to sort through the relative effects of exogenous grit and abrasive foods on dental microwear patterns. This raises the hope of gaining new insights into the diet and ecology of prehistoric creatures. Meanwhile, analyses of museum material are using larger and larger sample sizes to begin to document the range of dental microwear exhibited by species found in multiple habitats. This will, at the very least, begin to bracket the extremes of what one might find in fossil assemblages, ultimately leading to insights into intraspecific differences in diet and ecology. By pushing dental microwear analyses to finer levels of resolution, researchers are promoting the development of even better methods of data collection, which, in turn, will make even better interpretations possible.

The Auditory Region in the Cainotheriidae: New Information from CT-scans

Jessica M. Theodor; *Department of Biological Sciences, University of Calgary, 2500 University Dr. NW, Calgary AB, T2N 1N4, Canada (jtheodor@ucalgary.ca)*

The Cainotheriidae are well known from numerous specimens and their cranial anatomy is well documented from complete, partial and disarticulated cranial material. However, high resolution CT scans can provide additional data to resolve problems in the interpretation of the auditory region. Hürzeler's 1936 (Abh. Schweiz. Paläont. Gesellschaft)

description of the auditory region in *Cainotherium* is highly detailed. He depicts a large flange of the periotic overlapping the margin of the basioccipital, and reconstructed the petrobasilar canal as running in a sulcus along the medial part of this flange. Norris (1999, J. Vert. Paleol.) could not find any such sulcus on the specimens he was able to examine, and suggested that the specimen figured may have been broken, because the figure showed a discontinuity in the periotic. A MicroCT scan of YPM 25037 shows the morphology is more complex. Anteriorly, the periotic has a small projection over the basioccipital. In this region, the periotic bears a shallow sulcus with a slight ridge along the lateral margin, and no medial flange or ridge. The lateral ridge becomes more pronounced posteriorly, and the medial edge of the periotic becomes depressed, forming a deep sulcus in the periotic and restricting the contact between the basicoccipital and the periotic to the ventral portion. The periotic does not completely roof over the petrobasilar canal at any point. Thus, the basioccipital encloses the petrobasilar canal only on the medial side, unlike the condition seen in camelids, *Bunomeryx*, and *Merycoidodon*.

The Virtual Pig Head: Digital Imaging in Cephalic Anatomy

Justin Tickhill,¹ and Lawrence M. Witmer²; ¹Department of Biological Sciences and ²Department of Biomedical Sciences, Ohio University Athens, OH 45701, USA (jt188600@ohio.edu)

Domestic pigs are commonly used as biomedical animal models for several human disease states such as in temporomandibular joint (TMJ) disorders and mastoid air cell infections. However, unlikely the highly successful Visible Human project and similar imaging projects for laboratory rodents and other model animals, no digital representations of pig anatomy exist to aid biomedical researchers. To address this problem, the Virtual Pig Project uses digital datasets derived from computed tomography (CT scanning) to construct virtual models for research and education. Multiple specimens of domestic pig were CT scanned at O'Blens Memorial Hospital, Athens, OH. Moreover, an explant of the TMJ region of an adult pig was subjected to microCT scanning to probe its fine-scale bony and soft-tissue architecture. All data were imported into powerful 3D visualization software (Amira), and anatomical structures such as bones, muscles, brain, air sinuses, and blood vessels were digitally extracted and visualized, rendering a virtual anatomical atlas of the head. The utilization of these data in visual comparisons to CT imagery of key human systems highlights interspecies similarities and differences. The Virtual Pig Head has already provided a series of often dramatic 3D visualizations, including virtual dissection and vascular traces, ultimately to be delivered through an interactive website. These virtual data provide an important new resource for researchers in the biomedical field and beyond.

Exploring the Molecular Basis of Digit Identity

C. Tickle, L.A. McDonald and M.E. Fisher; *Division of Cell and Developmental Biology, College of Life Sciences, MSI/WTB Building, University of Dundee, Dow Street, Dundee DD1 5EH, UK (c.a.tickle@dundee.ac.uk)*

We are taking two approaches to uncovering genes involved in digit identity. In one approach we are pursuing the idea that the molecular code that specifies the identity of digits in the chick wing may parallel the molecular code that specifies the identity of veins in the fly wing. We have constructed, in the chick wing bud, 3D maps of expression of vertebrate homologs of genes encoding transcription factors involved in fly venation and traced the fate of cells that express different combinations of transcription factors. We are also carrying out functional analysis in developing chick wings to test whether these genes might contribute to digit identity. In a second approach, we are using microarrays to identify genes expressed in primordia of different digits in the chick wing. This analysis has uncovered a number of genes whose expression is restricted to a particular digit primordium. These not only represent candidates for genes involved in generating digit anatomy but may also provide tools for recognising specific digits.

The Expanded Femur of Tardigrada and Its Morphofunctional Implications

Giuseppe Tito,¹ Gerardo De Iuliis²; ¹Dipartimento di Scienze della Terra, Università di Firenze, Firenze, Italy (g.tito@geo.unifi.it), ²George Brown College and University of Toronto, ON, Canada (gerry.deiuliis@utoronto.ca)