

Increasing concentrations of PEG as well as IBA resulted in shortening of primary root (PR), enhancement of lateral root (LR) number and significant increase of NO generation. Time-dependence investigations revealed that in the case of IBA treatments, the LR number increased in parallel with an intensified NO generation, while elongation of PR was not followed by changes in NO levels. Under osmotic stress, the time curve of NO development was distinct compared to that of IBA-treated roots, since significantly, the appearance of lateral initials was preceded by a transient burst of NO. This early phase of NO generation under osmotic stress was clearly distinguishable from that which accompanied LR initiation. It is concluded that osmotic stress and the presence of exogenous auxin resulted in partly similar root architecture but different time courses of NO synthesis. We suppose that the early phase of NO generation may fulfill a role in the osmotic stress-induced signalization process leading to the modification of root morphology (Kolbert et al. 2008a).

As we already know, NO functions in variable physiological and developmental processes in plants (Bartha et al. 2005; Kolbert et al. 2005) however, the source of this signaling molecule in the diverse plant responses is not well understood. Therefore in our further work we provide genetic and pharmacological evidence that the production of NO is associated with the nitrate reductase (NR) enzyme during IBA-induced lateral root development and under osmotic stress conditions (PEG treatments) in *Arabidopsis thaliana* L. NO production was detected in the NR-deficient *nia1*, *nia2* and *Atnoa1* (former *Atnos1*) mutants of *Arabidopsis thaliana*. As inhibitor for nitric oxide synthase (NOS) N^G-monomethyl-L-arginine (L-NMMA) was applied. Our data clearly show that IBA has increased LR frequency in the wild-type plant and the LR initials emitted intensive NO-dependent fluorescence of the triazol product of NO and DAF-2DA. The presence of increased level of NO was restricted only to the LR initials in contrast to PR sections where it remained at the control level. 200 and 400 mOsm PEG treatments also increased NO fluorescence in roots of *Arabidopsis*. The role of NR in IBA or PEG-induced NO formation in the wild type was shown by the zero effects of the NOS inhibitor L-NMMA. In cases of both treatments the NO synthesis could be inhibited by tungstate treatment, which is a specific inhibitor of NR enzyme. The mutants had different NO levels in their control state (*i.e.* without IBA or PEG treatment), as *nia1*, *nia2* showed lower NO fluorescence than *Atnoa1* or the wild type plant. Finally it was clearly demonstrated that IBA as well as PEG induced NO generation in both the wild type and *Atnoa1* plants, but it totally failed in the NR-deficient mutant. It is concluded that the IBA or osmotic stress-induced NO production is nitrate reductase-associated during lateral root development in *Arabidopsis thaliana* (Kolbert et al. 2008b).

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Comparative anthropological analysis of non-Hungarian skeletal populations from the 16-17th centuries

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The period of the 16th to the 17th centuries was the age of the Turkish occupation of Hungary. Therefore many Hungarians from the southern region of the country escaped to the north, which was not invaded. On the basis of the archaeological and historical data, it is known that appreciable mass of southern Slav populations immigrated from the Balkan-peninsula and settled down mainly to this deserted, empty, southern countryside (Wicker 2006).

The subject of this research is the comparative anthropological examination of these non-Hungarian skeletal populations from the 16-17th centuries. The project has two aims: 1) to describe these populations from an anthropological point of view using osteological age and sex determination, metrical analyses and pathological investigations; 2) to find out the relationship among these non-Hungarian groups and the late medieval Hungarian populations, as well as the origin of the immigrated populations.

The material of this survey is the skeletal population of 6 burial sites (ca. 900 skeletons), which the archaeologists suggest belonged to this immigrated community: Győr-Gabonavásártér, Bácsalmás-Óalmás, Madaras-Bajmoki út, Katymár-Téglagyár, Csávoly-Határ út, Zombor-Repülőtér, (Zombor-Bükkszállás).

To determine the sex and age of death we have used common anthropological methods. The Martin and Saller's (1957) method was applied for measuring the skeletons, and the obtained data have been statistically evaluated with cluster analyses (R Development Core Team 2006). Southern Slav and Romanian series were also involved in the comparison. Paleopathological examinations have been carried out using macromorphological methods, though in certain cases radiographic, histological and molecular biological analyses have been applied as well.

After determination of sex and age, we could establish that in each examined populations the sex ratio was 50% : 50% except Győr-Gabonavásártér series, where the male:female ratio is 70% : 30% – this result might be due to the uncompleted excavation. It is also interesting that in the Bácsalmás-Óalmás series the percentage of infants is high compared to other series, which is due to the well-preserved skeletons and the precise excavation methods.

Many of the skeletons showed different forms of paleopathological lesions, the most common disorders being joint diseases and minor developmental anomalies. According to the prevalence of traumas, the analysed populations could be classified into two groups: a quiet agro-pastoralist population and another group with a more violent lifestyle. Infectious bony lesions were also frequent in each series, many of these cases possibly due to TB-infection (Lovász et al. 2007a). In addition, in the Bácsalmás-Óalmás series 6 cases of scurvy (proved by the histological analyses) were found, a disease rarely described in paleopathological literature (Lovász et al. 2007b). The large number of pathological alterations might indicate a poor state of health in each examined populations.

The results of the statistical analyses indicated that the foreign populations of this study were separated from the late medieval Hungarian series in a distinct group. The comparison of the examined series with the Southern Slav and Romanian data showed that only the southern Bosnian Raška Gora series revealed a close relationship with the foreign ethnic groups in Hungary.

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Applications of protein and small molecule microarrays

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While DNA microarrays measure changes at the transcription level, protein microarrays can provide information on the protein expression in a parallel way (Tao et al. 2007). Several disease-specific genes and their protein products are overexpressed reflecting the specific genotype of the disease. The direct inhibition of such proteins and the relevant signaling pathways could provide novel opportunities for targeted therapy. Small molecule microarrays (small molecule library printed with high density on a modified glass surface) can be used to screen potential inhibitors of these proteins (Darvas et al. 2004; Walsh et al. 2004).

Protein microarrays manufactured up to date are focused on a specific field (apoptosis, cell cycle, cancer etc.) of the proteome. We tested two different commercially available microarrays for our protein expression studies. We applied the Panorama Ab Microarray Cell Signaling Kit (Sigma-Aldrich) to compare protein extracts from *cerebellum* and *hippocampus* of fat-1 transgenic and wild type (control) mice. The Apoptosis Antibody Microarray (Full Moon BioSystems) was used to investigate the effects of the Ac-177 anticancer compound (from the immunomodulatory drug chemical library of Avidin Ltd.) on apoptosis-related protein expression/phosphorylation.

Small molecule microarrays with 8800 compounds of diverse structures in duplicates were applied for high-throughput screening of protein-ligand interaction studies. A purified serine protease was fluorescently labeled with Cy5 dye and incubated on the microarray. The binding intensity data of each spot representing each compound on the array were determined. To identify its potential inhibitors (molecules which bind to the active site) we incubated the labeled protease with its known substrate on the microarray. Competition for binding between the substrate and the spotted compounds resulted a decreased fluorescence intensity when compared to the substrate-free experiment.

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