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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