

Bácsalmás-Mosztonga, Dunapataj-Szent Tamás domb. The samples contain the remains of 756 individuals (163 males, 54 females, 207 undetermined, 332 subadults). This skeletal material is collected at the Department of Anthropology, University of Szeged.

The specimens have been analysed for the determination of the age at death and sex and scored for the measurements. Concerning the pathological conditions, the macro-morphological examination was completed - in some cases - with radiological analyses. In one case the molecular analysis was carried out to estimate the DNA of *Mycobacterium tuberculosis*. (This investigation was made at the München University - Institute of Pathology.)

The following disorders have been identified: traumatic lesions, specific and non-specific infections, haematological anomalies, joint diseases, bone-tumor and tumor-like anomalies, developmental disorders, and enthesopathies.

It is the most important to highlight the cases of skeletal tuberculosis (one case) and -syphilitic lesions (two cases) (Nyárlőrinc-Hangár utca; Pálfi et al. 1997; Balázs et al. 2005), for these diseases were among the most important selective factors in human populations in antiquity. In the sample Dunapataj-Szent Tamás domb, the frequency of the developmental anomalies is very significant by the reason of endogamy (Balázs and Marcsik 2007b).

In the Nyárlőrinc-Hangár series (11th-17th centuries; V. Székely 1987), there was excavated a partly mummified foetus which was buried in a crock at the edge of this cemetery and dated to 19th century on the basis of a copper coin which was put into the crock (Balázs and Bölkei 2007a).

This presentation is only a preliminary result.

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## Functional characterization of the plant SET protein: from phosphatase inhibition to heat stress tolerance

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Even small environmental changes can induce expression or repression of hundreds of genes in plants, contributing to their endless adaptation to the changing environment. Regulation of such a synchronized genomic event has to employ chromatin remodelling – a process that involves post-translational modifications of histones. One of the putative proteins involved in the regulation of histone modification patterns is SET. SET, belonging to the NAP/SET family of potential histone chaperones, is a multifunctional protein involved in very diverse cellular processes in mammals.

It was previously shown that human SET inhibits protein phosphatase 2A (PP2A) (Li et al. 1996), a major serine/threonine phosphatase both in plants and animals. It was also demonstrated that SET is associated with transcriptionally active loci in response to heat shock in *Drosophila melanogaster*, and these regions encoding heat shock proteins are marked with phosphorylation of histone H3 at serine 10 (Nowak et al. 2003).

Although the members of the NAP/SET family are well characterized proteins in animals (reviewed in Park and Luger 2006), we have little information on the plant NAP1 (nucleosome assembly protein1)-related proteins. The aim of our studies was hence the characterization of the *Arabidopsis* SET protein.

Our results revealed that the recombinant *Arabidopsis thaliana* SET protein exhibited inhibitory effect on the activity of purified preparations of rabbit PP2A and PP1 (protein phosphatase 1) catalytic subunits against a phospho-histone substrate. In addition, purified SET inhibited the dephosphorylation of histone H3 at serine 10 position by immunoprecipitated *Arabidopsis* PP2A and interacted *in vitro* with purified calf histone H3.

Phosphorylation of serine 10 on histone H3 is coupled with two opposite chromatin states: it is associated with mitotic chromosome condensation, while it occurs also during interphase in correlation with transcriptionally active loci (Johansen and Johansen 2006). Since our results suggest that SET may have a role in the maintaining of this kind of histone modification in plants, we propose a role for SET in transcriptional regulation. The verification of the involvement of the *Arabidopsis* SET in gene expression control, however, needs further investigations.

We also demonstrated that the subcellular localization of SET was influenced by a heat stress treatment at 45°C. In response to heat, SET accumulated in the nucleus, while under standard conditions it is located predominantly in the cytosol. Interestingly, other types of stresses including heat stress at lower temperature (37°C), salt stress, heavy metal stress or genotoxic stress did not cause the nuclear accumulation of SET, suggesting a specific role for SET in certain plant stress responses.



Taken together, the *Arabidopsis* SET protein is a potent inhibitor of animal and plant phosphatases and may have a role in heat shock tolerance as indicated by its altered (nuclear) localization in response to a 1h 45°C treatment. Thus, in the light of our results we can presume that the investigation of SET can be of practical importance, since it might have a role in the stress tolerance of plants. This hypothesis is currently investigated in SET-overexpressing transgenic plants.

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## Cross-talk between cannabinoid CB<sub>1</sub> and GABA<sub>B</sub> receptors in rat brain hippocampus

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Cannabinoid CB<sub>1</sub> and the metabotropic GABA<sub>B</sub> receptors have been shown to display similar pharmacological effects and co-localization in certain brain regions. Previous studies have reported a functional link between the two systems. As a first step to investigate the underlying molecular mechanism, here we show cross-inhibition of G-protein signaling between GABA<sub>B</sub> and CB<sub>1</sub> receptors in rat hippocampal membranes. The CB<sub>1</sub> agonists R-Win55,212-2 displayed high potency and efficacy in stimulating Guanosine-5'-O-(3-[<sup>35</sup>S]thio)triphosphate, [<sup>35</sup>S]GTPγS binding. Its effect was completely blocked by the specific CB<sub>1</sub> antagonists AM251 suggesting that the signaling was via CB<sub>1</sub> receptors. The GABA<sub>B</sub> agonist baclofen and SKF97541 also elevated [<sup>35</sup>S]GTPγS binding by about 60%, with potency values in the micromolar range. Phaclofen behaved as a low potency antagonist with an ED<sub>50</sub> ≈ 1 mM. However, phaclofen at low doses (1 and 10 nM) slightly but significantly attenuated maximal stimulation of [<sup>35</sup>S]GTPγS binding by the CB<sub>1</sub> agonist Win55,212-2. The observation that higher concentrations of phaclofen had no such effect rule out the possibility of its direct action on CB<sub>1</sub> receptors. The pharmacologically inactive stereoisomer S-Win55,212-3 had no effect either alone or in combination with phaclofen establishing that the interaction is stereospecific in hippocampus. The specific CB<sub>1</sub> antagonist AM251 at a low dose (1 nM) also inhibited the efficacy of G-protein signaling of the GABA<sub>B</sub> receptor agonist SKF97541. Cross-talk of the two receptor systems was not detected in either spinal cord or cerebral cortex membranes. It is suggested that the interaction might occur via an allosteric interaction between a subset of GABA<sub>B</sub> and CB<sub>1</sub> receptors in rat hippocampal membranes. Supported by NKTH DNT 08/2004 and OTKA TS 049817 research grants.

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## Functional analysis of *Drosophila melanogaster* histone H4 specific acetylase complex and its role in regulating chromatin structure

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Numerous enzymes and protein complexes are known to bring about changes in the state of chromatin by different mechanisms with resultant effects on gene expression. One class of complexes including the yeast SWI/SNF and a number of others from various organisms, alter the DNA packaging in an ATP-dependent manner. Another class of chromatin structure regulating factors acts by covalently modifying histone proteins. The various modifications include phosphorylation, ubiquitination, ADP-ribosylation, methylation, sumoylation and frequently acetylation, catalyzed by histone acetyltransferases (HATs). In many cases HAT enzymes are components of complexes which also contain among others, ADA-type adaptors.

Recently our laboratory, in parallel with several others, has showed that contrary to the single ADA2 adaptor protein present in *Saccharomyces cerevisiae*, different GCN5-containing HAT complexes of *Drosophila melanogaster* cells contain two related ADA2 proteins encoded by genes referred to as *dAda2a* and *dAda2b*. In several other metazoan organisms, including mouse, human and *Arabidopsis*, there