

Corrigendum

Corrigendum to “Mammalian mitochondrial nitric oxide synthase: Characterization of a novel candidate” [FEBS Lett. 580 (2006) 455–462][☆]

Tomasz Zemojtel^{a,b,*}, Mateusz Kolanczyk^{b,c}, Nadine Kossler^c, Sigmar Stricker^c, Rudi Lurz^d, Ivan Mikula^e, Marlena Duchniewicz^b, Markus Schuelke^f, Pedram Ghafourifar^g, Pavel Martasek^e, Martin Vingron^a, Stefan Mundlos^c

^a Department of Computational Molecular Biology, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany

^b In silico Miners, Chopina 13/10, 81-782 Sopot, Poland

^c Department of Development and Disease, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany

^d Microscopy Group, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany

^e Department of Pediatrics, Center of Applied Genomics, First School of Medicine, Charles University, 121 09 Prague, Czech Republic

^f Department of Neuropediatrics, Charite, University Medical Center, Berlin, Germany

^g Department of Pharmacology, Joan C. Edwards School of Medicine, Marshall University, Huntington, WV 25704, USA

Available online 17 April 2007

Since the time of our report on the mitochondrial localization of mouse ortholog of AtNOS1, mAtNOS1 [1], the following data has been acquired.

Importantly, both ours and Dr. Durner's labs have failed to detect any NO-synthase activity in purified AtNOS1 protein [2]. Similarly, purified mAtNOS1 and hAtNOS1 did not produce NO in our assays [2]. In response to that, Dr. Crawford reported that his data no longer supports the view that AtNOS1 is an arginine-dependent NOS enzyme and suggested renaming AtNOS1 to AtNOA1 (nitric oxide associated 1) [3]. Following that, we rename mAtNOS1 to mAtNOA1.

Based on information learned from data mining, we have hypothesized an involvement of eukaryotic orthologs of AtNOA1 in mitochondrial ribosome biogenesis and/or processes of translation [2]. mAtNOA1 (and AtNOA1) is an evolutionary conserved protein that contains a circularly permuted GTP-binding domain [4]. Its bacterial ortholog, YqeH protein (CAB14509, *Bacillus subtilis*), was shown to bind GTP and GDP. Deletion of this gene revealed its essentiality for *B. subtilis* viability [5]. YqeH was assigned to a YlqF/YawG protein family (characterized by a circularly permuted GTPase domain) that includes members involved in ribosomal biogenesis and/or the translation process [6]. Recently, work on *YqeH* gene has been reported which suggested YqeH protein to be required for proper 70S ribosome formation and, in particular, 30S subunit assembly/stability in *B. subtilis* [7]. Moreover, the yeast genome contains a homolog of mAtNOA1, YOR205c, that localizes to the mitochondria and co-purifies with mitochondrial ribosomal proteins of the small subunit [8]. *YOR205C*-deficient yeast mutant has a severe defect in phosphorylative oxidation [9]. An inner membrane localization of mAtNOA1 [1] overlaps with that of mitochondrial ribosomes and might imply a function within the mitochondrial translational machinery. In this light, an observed deregulation in levels of reactive oxygen species (ROS) in AtNOA1^{-/-} plant [10] might result from defective translation of the mitochondrial respiratory chain subunits that are encoded by the mitochondrial genome.

Further works undertaken in our laboratories, including a generation of *mAtNOA1* K.O. mouse, are expected to shed some more light on the role of this evolutionary conserved gene.

References

- [1] Zemojtel, T., Kolanczyk, M., Kossler, N., Stricker, S., Lurz, R., Mikula, I., Duchniewicz, M., Schuelke, M., Ghafourifar, P., Martasek, P., Vingron, M. and Mundlos, S. (2006) Mammalian mitochondrial nitric oxide synthase: characterization of a novel candidate. FEBS Lett. 580, 455–462.
- [2] Zemojtel, T., Frohlich, A., Palmieri, M.C., Kolanczyk, M., Mikula, I., Wyrwicz, L.S., Wanker, E.E., Mundlos, S., Vingron, M., Martasek, P. and Durner, J. (2006) Plant nitric oxide synthase: a never-ending story? Trends Plant Sci. 11, 524–525, author reply 526–528.
- [3] Crawford, N.M., Galli, M., Tischner, R., Heimer, Y.M., Okamoto, M. and Mack, A. (2006) Response to Zemojtel et al.: Plant nitric oxide synthase: back to square one. Trends Plant Sci. 11, 526–527.
- [4] Zemojtel, T., Penzkofer, T., Dandekar, T. and Schultz, J. (2004) A novel conserved family of nitric oxide synthase?. Trends Biochem. Sci. 29, 224–226.
- [5] Morimoto, T., Loh, P.C., Hirai, T., Asai, K., Kobayashi, K., Moriya, S. and Ogasawara, N. (2002) Six GTP-binding proteins of the Era/Obg family are essential for cell growth in *Bacillus subtilis*. Microbiology 148, 3539–3552.
- [6] Leippe, D.D., Wolf, Y.I., Koonin, E.V. and Aravind, L. (2002) Classification and evolution of P-loop GTPases and related ATPases. J. Mol. Biol. 317, 41–72.

[☆] DOI of original article: [10.1016/j.febslet.2005.12.038](https://doi.org/10.1016/j.febslet.2005.12.038).

*Corresponding author. Address: Department of Computational Molecular Biology, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany. Fax: +49 30 8413 1152.
E-mail address: zemojtel@molgen.mpg.de (T. Zemojtel).

- [7] Uicker, W.C., Schaefer, L., Koenigsnecht, M. and Britton, R.A. (2007) The essential GTPase YqeH is required for proper ribosome assembly in *Bacillus subtilis*. *J. Bacteriol.* 189, 2926–2929.
- [8] Gavin, A.C., Aloy, P., Grandi, P., Krause, R., Boesche, M., Marzioch, M., Rau, C., Jensen, L.J., Bastuck, S., Dumpelfeld, B., Edelmann, A., Heurtier, M.A., Hoffman, V., Hoefert, C., Klein, K., Hudak, M., Michon, A.M., Schelder, M., Schirle, M., Remor, M., Rudi, T., Hooper, S., Bauer, A., Bouwmeester, T., Casari, G., Drewes, G., Neubauer, G., Rick, J.M., Kuster, B., Bork, P., Russell, R.B. and Superti-Furga, G. (2006) Proteome survey reveals modularity of the yeast cell machinery. *Nature* 440, 631–636.
- [9] Steinmetz, L.M., Scharfe, C., Deutschbauer, A.M., Mokranjac, D., Herman, Z.S., Jones, T., Chu, A.M., Giaever, G., Prokisch, H., Oefner, P.J. and Davis, R.W. (2002) Systematic screen for human disease genes in yeast. *Nat. Genet.* 31, 400–404.
- [10] Guo, F.Q. and Crawford, N.M. (2005) Arabidopsis nitric oxide synthase1 is targeted to mitochondria and protects against oxidative damage and dark-induced senescence. *Plant Cell* 17, 3436–3450.