Assignment¹ of neuronal pentraxin I (NPTX1) gene to porcine chromosome 12pter by somatic cell and radiation hybrid panel mapping

S. Kierstein^a and B. Brenig^b

^aInternational Livestock Research Institute, Nairobi (Kenya)

^bInstitute of Veterinary Medicine, Georg August University of Göttingen, Göttingen (Germany)

¹ To our knowledge this is the first time this gene has been mapped in swine.

Rationale and significance

The neuronal pentraxin I belongs to a family of functionally diverse proteins sharing some structural features like the formation of pentameric complexes (Goodman et al., 1996). The NPTX1 gene is expressed in neurons and the protein was shown to bind the presynaptic toxin taipoxin. Therefore it is supposed to play a role in mediating synaptic uptake. The mouse and human neuronal pentraxin I genes were assigned to chromosomes 11E and 17q25 respectively. The mapping of the NPTX1 gene to the human chromosome regions for Russell-Silver syndrome and campomelic dysplasia-1 makes it a potential candidate for genetic disorders (Omeis et al., 1996). The gene including the 5'- and 3'-UTR is highly conserved among different species. The mapping of the porcine gene will enable further investigations on its possible role in inherited diseases.

Materials and methods

A porcine genomic PAC library (IVM PAC 714, Al-Bayati et al., 1999) was screened by PCR. PAC DNA was isolated with Qiagen Plasmid purification Kit according to the manufacturer's instructions. Sequencing was car-

ried out on a LI-COR DNA Sequencer Model 4000L (MWG) as described previously (Middendorf et al., 1992). Chromosomal localization of the PAC clone was confirmed by PCR analysis of a porcine × rodent somatic cell hybrid panel (Yerle et al., 1996) as well as a porcine whole genome radiation hybrid panel (Yerle et al., 1998). PCR results were analyzed using the interpreting web pages at INRA (<http://www.toulouse.inra.fr/lgc/pig/pcr/pcr.htm>, and <http://imprh.toulouse.inra.fr/>). The following primers were used for both PCR analysis NPTX4.1 with the sequence 5'-GAGAAAGTGGTTGA-GAGG-3' and NPTX4.2 with the sequence 5'-GTAATCAACGACGG-CAAG-3'. The 415-bp product was amplified in a total volume of 25 µl using 25 ng template DNA under the following conditions 3 min 94 °C, 30 cycles with 45 sec at 94 °C, 45 sec at 52 °C, and 45 sec at 72 °C.

Results

Regional mapping results

Somatic porcine × rodent cell hybrid panel analysis of 27 hybrids resulted in the following vector: 00000 00000 00001 10001 11101 11. Statistical evaluation showed significant correlation between the NPTX1 gene and chromosome 12 with the highest probability and correlation values (82 and 92 % respectively) for the region p15. However, the survey of the whole genome radiation hybrid panel showed the following distribution within the 118 lines: 00000 00101 01000 00000 00000 01011 00001 10000 00000 00001 00001 01011 10100 1010 10100 00010 10010 00000 01011 10010 01100 10000 0000 100, with the most significantly linked marker (LOD score 13.71) Sw2490 (Alexander et al., 1996). Multipoint analysis revealed that the NPTX1 gene appears to be the most distal marker currently mapped on SSC12 as the linkage group is NPTX1–Sw2490.

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Corresponding author: Bertram Brenig, Institute of Veterinary Medicine
University of Göttingen, Gröner Landstrasse 2
37073 Göttingen (Germany); telephone: +49 551 3933 83
fax: +49 551 3933 99; e-mail: bbrenig@gwdg.de

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