

firmes these data. *APOB* and *LHCGR*, which map in human to the distal part of HSA2p [7], in pig map to distal SSC 3q24-qter and 3q22-q23 [8] respectively. *IL1A* and *IL1B*, which map in human to the proximal long arm in 2q12-q21 [7], map to proximal SSC 3q11-q14 [8]. *LCT* maps in human to 2q21 [7] but is found in pig on SSC 15 [9], as is the case for other loci from distal HSA2q. These localizations provide evidence that in pig the human Chr 2 is conserved in two segments which are identical to chimp Chr PTR 12 and PTR 13. During evolution to human, these two ancestral chromosome arms are fused and form HSA 2 [10].

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References

1. Zehetner, G., Lehrach, H. (1994). *Nature* 367, 489–491.
2. Leeb, T., Rettenberger, G., Hameister, H., Brem, G., Brenig, B. (1995). *Mamm. Genome* 6, 37–41.
3. Malcolm, S., Barton, P., Murphy, C., Ferguson-Smith, M.A., Bentley, D.L., Rabbits, T.H. (1982). *Proc. Natl. Acad. Sci. USA* 79, 4957–4961.
4. Swan, D., D'Eustachio, P., Leinwand, J., Seidman, J., Keithley, D., Ruddle, F.H. (1979). *Proc. Natl. Acad. Sci. USA* 76, 2735–2739.
5. Rettenberger, G., Bruch, J., Fries, R., Archibald, L., Hameister, H. (1995). Assignment of 19 porcine type 1 loci by somatic cell hybrid analysis detects new regions of conserved synteny between human and pig. Submitted.
6. Rettenberger, G., Klett, C., Zechner, U., Kunz, J., Vogel, W., Hameister, H. (1995). *Genomics* 26, 372–378.
7. Human Gene Mapping 11 (1991). *Cytogenet. Cell Genet.* 58, 1–2200.
8. Yerle M., Lahbib-Mansais, Y., Mellink, C., Goureau, A., Pinton, P., Echard, G., Gellin, J., Zijlstra, C., De Haan, N., Bosma, A., Chowdhary B., Gu, F., Gustavsson, I., Thomsen, P., Christensen, K., Rettenberger, G., Hameister, H., Schmitz, A., Chaput, B., Frelat, G. (1995). *Mamm. Genome* 6, 176–186.
9. Thomsen, P.D., Johansson, M., Troelsen, J.T., Andersson, L. (1995). The lactase-phlorizin hydrolase (*LCT*) gene maps to pig chromosome 15q13, in press.
10. Yunis, J.J., Prakash, O. (1982). *Science* 215, 1525–1530.

Assignment of the choline acetyltransferase gene to porcine Chromosome 14q25-27 by fluorescence in situ hybridization

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Species: Pig (*Sus scrofa domestica*)

Locus name: Choline acetyltransferase

Locus symbol: *ChAT*

Map position: 14q25-27 (Fig. 1)

Method of mapping: Fluorescence in situ hybridization (FISH)

Molecular reagents: A cosmid clone containing a 35-kb insert of porcine genomic DNA, including at least a part of *ChAT* gene, was used as a probe for FISH.

Previously identified homologs: *ChAT* gene was assigned to human Chromosome (Chr) 10q11-q22.2 by in situ hybridization [1,2].

Discussion: *ChAT* catalyzes the biosynthesis of the neurotransmitter acetylcholine in the central and peripheral nervous system

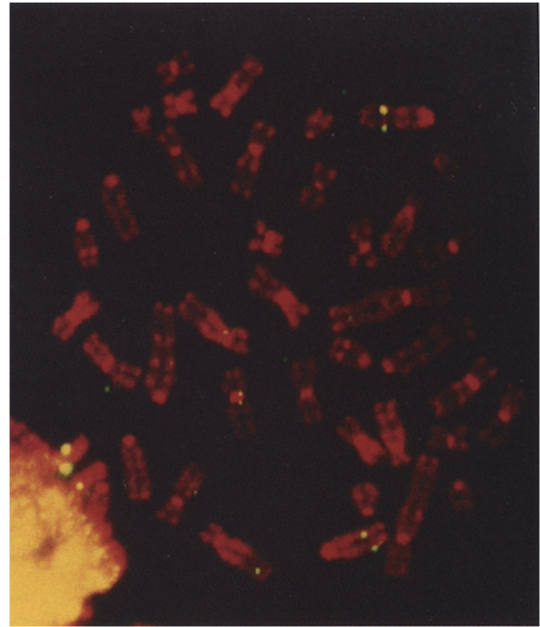


Fig. 1. Assignment of the porcine choline acetyltransferase gene to Chr 14q25-27 by fluorescence in situ hybridization. A representative chromosome-spread displaying fluorescence signals; hybridization sites are indicated by arrows.

[3]. Here, we report mapping of the gene encoding *ChAT* to porcine Chr 14. Several other genes, which have been assigned to the same chromosome, include ubiquitin C (*UBC*; 14q12-15) [4], D-amino acid oxylase (*DAO*; 14q21-23) [5], cardiac ryanodine receptor (*RYR2*; 14q22-23) [6], 5S rRNA (14q23) [7], and urokinase (*PLAU*; 14q24-26) [5]. All of the corresponding genes, including *ChAT*, in humans have already been assigned: *UBC* and *DAO* are mapped to Chr 12, *RYR2* and 5S rRNA to Chr 1, and *ChAT* and *PLAU* to Chr 10 [8]. This means that the porcine Chr 14 contains at least three different conserved regions: the upper part of the porcine Chr 14 is homologous to human Chr 12, the middle part to Chr 1, and the lower part to Chr 10. This will provide useful information for considering a chromosomal rearrangement during the evolutionary process of the porcine genome.

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References

1. Strauss, W.L., Kemper, R.R., Jayakar, P., Kong, C.F., Hersh, L.B., Hilt D.C., Rabin, M. (1991). *Genomics* 9, 396–398.
2. Viegas-Pequignot, E., Berrard, S., Brice, A., Apiou, F., Mallet, J. (1991). *Genomics* 9, 210–212.
3. Berrard, S., Brice, A., Lottspeich, F., Braun, A., Barde, Y-A., Mallet, J. (1987). *Proc. Natl. Acad. Sci. USA* 84, 9280–9284.
4. Rettenberger, G., Fries, R., Engel, W., Scheit, K.H., Dolf, G., Hameister, H. (1994). *Genomics* 21, 558–566.
5. Mellink, C.H., Lahbib-Mansais, Y., Yerle, M., Gellin, J. (1993). *Cytogenet. Cell Genet.* 64, 256–260.
6. Leeb, T., Rettenberger, G., Hameister, H., Brem, G., Brenig, B. (1995). *Mamm. Genome* 6, 37–41.
7. Lomholt, B., Christensen, K., Hallenberg, C., Frederiksen, S. (1995). *Mamm. Genome* 6, 439–441.
8. McKusick, V.A. (1994). *Mendelian Inheritance in Man*, 11th ed. (Baltimore, Md.: The Johns Hopkins University Press).