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Assignment* of the 5-hydroxytryptamine (serotonin) receptor 5A gene (HTR5A) to human chromosome band 7q36.1

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Rationale and significance

Serotonin (5-hydroxytryptamine) plays a role in the regulation of diverse processes including sleep, appetite, aggression, and anxiety. It acts through a variety of distinct receptor subtypes which are differentially expressed in both the central and peripheral nervous systems (Peroutka, 1988). A novel receptor subtype, HTR5A, was recently identified that appears to be expressed uniquely in the central nervous system (Rees et al., 1994). We used PCR analysis of somatic cell hybrid panels and a collection of chromosome 7-specific yeast artificial chromosome (YAC) clones to map the HTR5A gene to chromosome 7, sub-band q36.1.

Materials and methods

The primary chromosome assignment to 7q was done using a panel of 19 human × Chinese hamster hybrid cell lines derived from several fusion experiments (Francke et al., 1986). Further sublocalization to 7q32→qter was achieved using a regional mapping panel (Tsui et al., 1995). PCR screening of YACs from the region assigned HTR5A to a YAC contig.

Primer names	Primer sequences: (from GenBank X81412)
5HTR5A-F	5' CCTGTCAGTGTCCAGGCTCA 3' (nt 6–25)
5HTR5A-R	5' GCGGACCGTGAACACCAT 3' (nt 125–108)

Amplicon: 120 bp
PCR Conditions: 1 mM $MgCl_2$
Cycle: Denaturation at 95 °C for 5 min, followed by 28 cycles at 95 °C for 30 s, 62 °C for 30 s, and 72 °C for 30 s with a final extension at 72 °C for 10 min. Under these conditions, no amplification was obtained from rodent parental DNA.

Results

Table 1. Segregation of HTR5A with human chromosomes in somatic cell hybrids

Gene/ chromosome	Chromosome number																						
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Y
+/+	0	0	1	1	0	1	3	1	2	1	1	1	1	1	3	0	0	2	1	2	1	2	2	0
+/–	3	3	2	1	2	2	0	2	1	2	2	2	1	1	0	3	3	1	2	1	2	0	0	2
–/+	6	4	9	6	5	10	0	9	2	2	7	7	10	12	6	9	2	7	10	7	10	10	2	3
–/–	9	11	5	8	11	5	14	6	12	14	7	9	5	3	10	5	14	9	5	9	5	6	4	13
% discordant	50	39	65	44	39	67	0	61	18	21	53	47	65	76	32	71	26	42	67	42	67	56	20	28

Data for chromosomes with rearrangements or present at very low copy (<0.1) were excluded. The % discordance is calculated as the sum of the discordant hybrids over the total number of informative hybrids for each chromosome.

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* To our knowledge this is the first time this gene has been mapped

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Regional mapping results

Hybrid designation	Chromosome region present	HTR5A present (+) or absent (–)
XXI-23A-2c	7p	–
Ru-Rag6-19	7q	+
2068Rag22-2	7q22–qter	+
GM1059-Rag5	7pter–q22::q32–qter	+

Three YAC clones were identified that contained the gene, HSC7E769, CEPH clone 744a8, and CEPH clone 868g12. These clones are part of a YAC contig anchored by the Généthon microsatellite marker D7S637 (unpublished data) which is localized to 7q36.1 (Thacker et al., 1995). In addition, YAC clone HSC7E769 was previously mapped to 7q36 by FISH (Kunz et al., 1993).

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