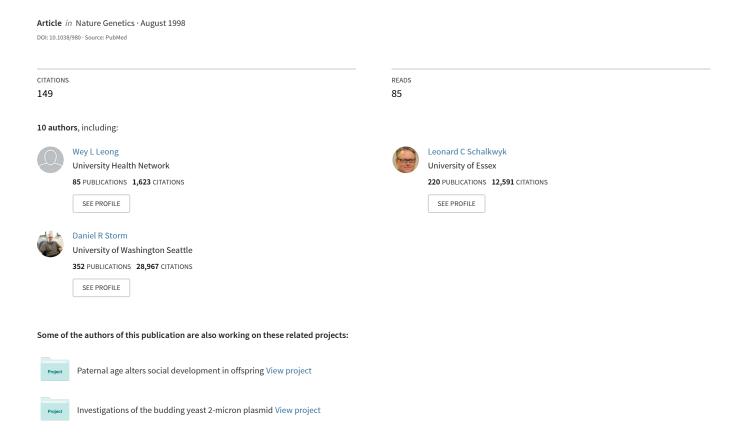
## Loss of adenylyl cyclase I activity disrupts patterning of mouse somatosensory cortex



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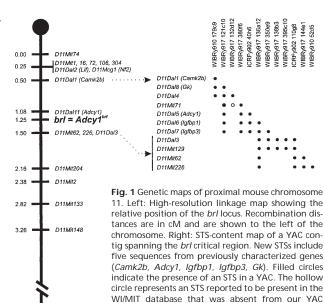
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The somatosensory (SI) cortex of mice displays a patterned, nonuniform distribution of neurons in layer IV called the 'barrelfield' (ref. 1). Thalamocortical afferents (TCAs) that terminate in layer IV are segregated such that each barrel, a readily visible cylindrical array of neurons surrounding a cell-sparse center, represents a distinct receptive field. TCA arbors are confined to the barrel hollow and synapse on barrel-wall neurons whose dendrites are oriented toward the center of the barrel2. Mice homozygous for the barrelless (brl) mutation, which occurred spontaneously in ICR stock at Université de Lausanne (Switzerland), fail to develop this patterned distribution of neurons, but still display normal topological organization of the SI cortex3. Despite the absence of barrels and the overlapping zones of TCA arborization, the size of individual whisker representations, as judged by 2-deoxyglucose uptake, is similar to that of wild-type mice. We identified adenylyl cyclase type I (Adcy1) as the gene disrupted in brl mutant mice by fine mapping of proximal chromosome 11, enzyme assay, mutation analysis and examination of mice homozygous for a targeted disruption of Adcy1. These results provide the first evidence for involvement of cAMP signalling pathways in pattern formation of the brain.

We constructed a high-resolution genetic map of the region around the *brl* locus on proximal chromosome 11 (ref. 3) using intercross and backcross offspring (Fig. 1). Candidate genes Ca<sup>2+</sup>/calmodulin protein kinase type II (*Camk2b*) and leukaemia inhibitory factor (*Lif*), from the region of conserved synteny with human chromosome 22 (ref. 4), were excluded on the basis of sequence analysis and map position. To identify other candidates, we made a sequence tagged site (STS)-content map of a yeast artificial chromosome (YAC) contig spanning the *brl* critical region (Fig. 1). Four genes (*Adcy1*, *Gk*, *Igfbp1*, and *Igfbp3*) from the region of conserved synteny with human chromosome 7 (refs 4,5) were placed on this physical map.

The physical map identified Adcy1 as a candidate gene for brl. Adcy1 (EC 4.6.1.1) is a membrane-bound enzyme that catalyzes the formation of cAMP, an important second messenger. Adcy1 is neurospecific and is expressed in areas of the brain that are associated with neuroplasticity, such as the hippocampus and cerebral cortex<sup>6</sup>. Adcy1 activity is directly stimulated by  $Ca^{2+}$  and calmodulin  $in\ vivo$  with half-maximal stimulation at 150 nM free  $Ca^{2+}$  (refs 7,8). Although it is not stimulated by activation of  $G_s$ -coupled receptors alone  $in\ vivo$ , it is stimulated by receptor activation when paired with  $Ca^{2+}$  (ref. 9).

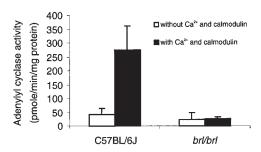
Basal adenylyl cyclase activity in brain membrane preparations from brl/brl mice was one-half that of wild-type mice, but this difference was not statistically significant (Fig. 2). There was a significant difference in enzyme activity in the presence of  $Ca^{2+}$  and calmodulin (t=5.7, df=3.0, P=0.01); adenylyl cyclase activity



D11Mit78

increased sixfold in wild-type mice, whereas no increase in enzyme activity was observed in mutants. Comparable results were reported in *Adcy1* knockout mice<sup>10</sup>. Sequencing of *Adcy1* cDNA from B6 and *br1* mutant mice revealed two differences: a polymorphism in the 5´ end of the coding region (*D11Dal11*) found in other ICR-derived lines that mapped proximal to *br1*, and an early retrotransposon (ETn) insertion that co-segregated with the *br1* phenotype (Fig. 3). Insertion of an ETn has been associated with loss-of-function mutations in other genes due to alter-

clone, suggesting a deletion.



**Fig. 2** Adenylyl cyclase activity in two-week wild-type and *brl* mutant mice. Enzyme activity in brain membrane protein fractions was measured in the absence (white bars) or presence (black bars) of free Ca<sup>2+</sup> (estimated to be 300–500 nM) and calmodulin.

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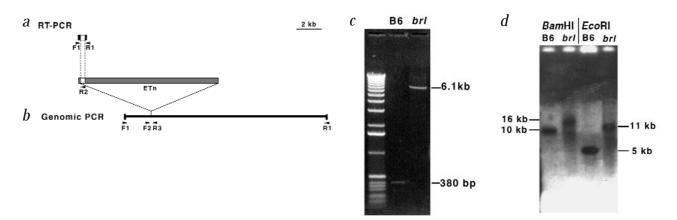


Fig. 3 Mutational analysis of *Adcy1* in *brI* mutant mice. *a*, RT-PCR of *brI* brain RNA using primers F1 and R1 yielded an aberrant amplicon with a 183-bp insert (white box) after nucleotide 2158 of our partial cDNA sequence. The sequence of the 183-bp insert was identical to part of the long terminal repeat (LTR) of ETn. *b*, Extended genomic PCR and DNA sequencing with primers F1 and R2 of *brI* genomic DNA was used to amplify the 5' end of the intron and to develop primer F2, which was used with primer R1 to amplify the 3' end of the intron from B6 mice. *c*, Primers F2 and R3 were used to amplify the inserted sequence in *brI* mice. The amplicon from *brI* genomic DNA is approximately 5.7 kb larger than the amplicon from B6, consistent with the presence of a complete ETn. *d*, Southern-blot analysis of genomic DNA confirmed the presence of a 5.7-kb insert in *brI* mutant mice. The probe was generated from PCR of B6 genomic DNA with primers F2 and R3 (see Methods). There were no *Bam*HI or *Eco*RI restriction sites in ETn.

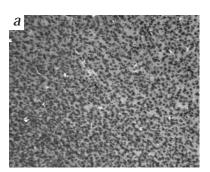
native splicing and premature termination of transcripts  $^{11,12}$ . The causal relationship between Adcy1 and the brl phenotype was confirmed by the absence of barrels in mice homozygous for a targeted disruption of Adcy1 (Fig. 4). In contrast, mice homozygous for a targeted disruption of Adcy8, another neurospecific  $Ca^{2+}/$  calmodulin-responsive adenylyl cyclase gene, have barrels indistinguishable from wild-type mice (Fig. 4).

The cAMP signaling system plays an important role in neuroplasticity in both invertebrates and vertebrates. In *Drosophila melanogaster*, disruption of genes involved in cAMP pathways, including adenylyl cyclase type I (rutabaga), impairs learning and memory<sup>13</sup>. In *Aplysia*, calmodulin-sensitive adenylyl cyclase may play a role in the association of conditioned and unconditioned stimuli in short-term and long-term sensitization, perhaps through synergistic activation by serotonin and  $Ca^{2+}$  (refs 14,15). Similarly, disruption of Adcy1 in mice alters performance in the Morris water task and depresses long-term potentiation<sup>8</sup>.

A barrelless phenotype similar to that observed in  $Adcy1^{brl}$  mutants has also been found in mice homozygous for a targeted disruption of monoamine oxidase A (Maoa; refs 16,17). In these knockout mice, a ninefold increase in serotonin (5-HT) concentrations in the brain has been implicated in the pathogenesis of the barrelless phenotype. Early depletion of 5-HT delays the development of barrels, reduces their size and decreases the growth of TCAs (ref. 18). The shared phenotypic features of

*Maoa* and *Adcy1* mutants suggest the involvement of serotonergic and cAMP signaling pathways in the formation of barrels. Thalamic neurons transiently express the serotonin transporter<sup>19</sup> and the  $5\text{-HT}_{1B}$  receptor<sup>20</sup> during the perinatal period, coincident with barrel formation. As the  $5\text{-HT}_{1B}$  receptor decreases adenylyl cyclase activity<sup>21</sup>, both *Maoa* and *Adcy1* loss-of-function mutations should reduce cAMP levels and cAMP-dependent protein kinase (PKA) activity in TCAs. Decreased Adcy1 activity may lead to absence of barrels through reduced glutamate release, as 5-HT<sub>1B</sub> mediates serotonin's presynaptic inhibition of thalamocortical transmission<sup>22</sup> and NMDA receptor antagonists produce a barrelless phenocopy<sup>23</sup>. Alternatively, the barrelless phenotype may result from loss of Adcy1 in cortical neurons; because cAMP directly stimulates neurite outgrowth in vitro<sup>24</sup>, any contribution of cortical neurite outgrowth to barrel formation may be impaired. The cAMP second messenger system may influence barrel formation and other forms of neuroplasticity in SI cortex through phosphorylation of protein targets and/or changes in gene expression.

The demonstration that the barrelless phenotype results from disruption of adenylyl cyclase type I provides the first evidence that cyclic nucleotide signal transduction systems are important for barrel formation. As many mechanisms of cortical pattern formation are not specific to the barrel cortex, cAMP may play a more general role in cortical specification.



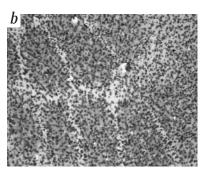


Fig. 4 Digitized images of layer IV of SI cortex from seven-month Adcy1 (a) and Adcy8 (b) knockout mice. Adcy1 knockouts display a barrelless phenotype, whereas Adcy8 knockouts have the normal pattern of barrels separated by cell-sparse septa. Sections (50 μm) were cut parallel to the pial surface overlying SI and stained with cresyl violet (NissI).

## Methods

Linkage map. Independent linkage maps for the intercross (n=469) and backcross (n=607) populations were constructed and combined by calculating the weighted averages. In addition to the marker D11Mcg1 (ref. 25), thirteen of the microsatellites from proximal chromosome 11 in the WI/MIT database (http://www-genome.wi.mit.edu; refs 4,26) were found to be polymorphic between brl/brl and C57BL/6J inbred mice. PCR products were separated in 15% polylacrylamide gels and visualized by a reducing silver stain method. Camk2b was mapped using an amplicon length polymorphism in the 3' untranslated region (D11Dal1), which corresponds to nucleotides 3203–3499 in the cDNA sequence. The C57BL/6J-derived allele was 14 bases longer than the allele in brl mutant mice, which

was identical to the published sequence. Lif was mapped using a restriction fragment length polymorphism (RFLP, D11Dal2); an additional AluI restriction site was found in the second intron of the allele in brl mutant mice. Primers that correspond to bases 2493 and 3723 in the genomic sequence were used to generate amplicons for restriction digestion. After Adcy1 was physically mapped to this genomic region, it was placed on the genetic map using RFLP (*D11Dal11*); a G→T transition at nucleotide 143 in the cDNA sequence of ICR-derived lines, including barrelless, is associated with loss of a BanI restriction site. D11Dal11 primers correspond to nucleotides 99 and 435 in the cDNA sequence.

Physical map. The YAC contig was initiated by screening two YAC libraries, ICRFy902 (ref. 27) and WIBRy910 (ref. 28) with D11Dal1 and D11Mit226, extended by screening these libraries and the WIBRy917 library29 with STSs from YAC end-clones (D11Dal3 and D11Dal4) and completed after the addition of Whitehead Institute contig WC11.0. All YAC clones were obtained from the RZPD, Ressourcenzentrum/Primaerdatenbank des deutschen Humangenomprojektes. PCR products were visualized using 1.5-2.5% agarose gels stained with ethidium bromide.

Generation of knockout mice. Adcy1 knockouts8 used in this study were taken from a congenic inbred strain that was produced by backcrossing to 129/JR2448 inbred mice for 12 generations. Targeted disruption of Adcy8 was achieved using the method described for the Adcv1 knockout<sup>8</sup>. Briefly, an isogenic *Adcy8* clone was isolated from a 129/Sv murine genomic library (Stratagene). A 6.2-kb fragment of Adcy8, which included DNA sequences 4.7-kb upstream and 1.8-kb downstream of the translational start codon, were replaced by a neo<sup>r</sup> cassette. To enrich for homologous recombinants, a herpes simplex viral thymidine kinase (TK) gene was ligated to the 3´ end of the construct. ES cells containing the disrupted Adcy8 gene were injected into blastocysts. Chimeric mice were obtained and bred for germline propagation. Disruption of Adcy8 was confirmed by PCR analysis. Ca<sup>2+</sup>-stimulated adenylyl cyclase activity in the neocortex and hypothalamus were reduced 30% and 100%, respectively.

Adenylyl cyclase assay. Membrane protein fractions were prepared from whole brains of two-week mice as described<sup>30</sup>. Protein concentration was determined using the BCA Protein Assay Reagent (Pierce). The enzyme assay was performed, with and without free Ca<sup>2+</sup> (estimated to be 300-500 nM) and calmodulin (2.4 µM), in a 250 µl volume containing membrane preparation (30 µg), Tris-HCl (20 mM, pH 7.4), ATP (1 mM), MgCl<sub>2</sub> (5 mM), 3-isobutyl-1-methyl-xanthine (1 mM), EDTA (1 mM), BSA (0.1%), creatine phosphate (20 mM), creatine phosphokinase (60 U/ml),

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myokinase (20 U/ml) and adenosine deaminase (8 U/ml). Free Ca<sup>2+</sup> concentration was estimated using the Bound and Determined program. The assay was incubated at 30 °C for 20 min, and the reaction was stopped by the addition of 2% SDS (250 µl) followed by boiling for 2 min. A cAMP enzymeimmunoassay system (Amersham) was used to determine cAMP levels.

RT-PCR. RNA was prepared from brains of six-week-old mice, reverse transcribed into cDNA and PCR amplified by standard techniques. The primers were F1, 5'-GCTATCCTGCTGTTCTCATGC-3' and R1, 5´-GGCAGGAGATTGAAGAGGATC-3´. Cycling parameters were 94 °C (3 min), [94 °C (45 s) -57 °C (45 s), 72 °C (90 s)]×35, 72 °C (5 min), 15 °C. Amplicons were analysed by 1.5% agarose gel electrophoresis and DNA sequencing using a Cyclist Taq DNA sequencing kit (Stratagene).

Extended genomic PCR. GeneAmp XL PCR kit (Perkin-Elmer) was used for extended PCR on genomic DNA templates as detailed by the manufacturer. Cycling parameters were 94 °C (3 min), [94 °C (45 s), 62 °C (45 s), 72 °C (8 min)]×15, [94 °C (45 s), 62 °C (45 s), 72 °C (8min+10s increment/ cycle)]×20, 72 °C (10 min), 15 °C. The following primers (Fig. 3b) were used to generate extended PCR products: F1, R1 (see above); F2, 5'-TCCCAA-CCCAAGTTGCCCAGA-3´; R2, 5´-GCTCCGATAGTCCGATACGA-3´; and R3, 5´-TACAGTGGACGGACAGTCGA-3´. Amplicons were analysed by 0.8% agarose gel electrophoresis and DNA sequencing as above.

Southern-blot analysis. Genomic DNA (10 µg) digested with BamHI and EcoRI was fractionated by electrophoresis in a 0.6% agarose gel and transferred to a charged nylon membrane by Southern blotting. The probe was generated by PCR using primers F2 and R3 on B6 genomic DNA, [32P]labelled by random priming (1.5×10<sup>6</sup> cpm/100 ng) and used in a standard hybridization reaction. The blot was visualized using autoradiography.

GenBank accession numbers. Adcy1 coding sequence (partial) from C57BL/6J inbred mice, AF053980; sequence of 183 bp insert in Adcy1 cDNA from brl mutant mice, AF053979; sequence of an ETn, U06639; mouse Camk2b cDNA, X63615; genomic sequence of mouse Lif, M63419.

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