Natural expression of immature Ucn antisense RNA in the rat brain. Evidence favoring bidirectional transcription of the Ucn gene locus

Paola Haeger, Rolando Cuevas, María Inés Forray, Rolando Rojas, Claudia Daza, Juan Rivadeneira, Katia Gysling

Abstract

Recently, it has been shown the endogenous expression of an antisenseurocortin (Ucn) transcript in the rat brain and other tissues. In the present work, by means of two complementary techniques, specific-strand RT-PCRand in situ hybridization, we showed the natural expression of a second novel antisense Ucn RNA of higher size. Specific-strand RT-PCR of total RNA, cloning and sequence analysis together with the different subcellular localization observed for both antisense Ucn RNAs indicated that this novel antisense Ucn transcript corresponded to the immature form of the previously described antisense Ucn RNA. Sequence analysis indicated that this immature antisense Ucn transcript uses non-consensus CT–AC splice sites, exactly complementary to its sense counterpart. The mature antisense Ucn transcript was also amplified after specific-strand RT-PCR of poly(A)-RNA, suggesting that the mature antisense Ucn transcript is polyadenylated. We also proved that the region complementary to the promoter of sense Ucn RNA, including the TATA box, is part of the antisense Ucn RNA. Finally, we showed that the region complementary to the 3′-end of Ucn mRNA behaves as a functional promoter for the transcription of antisense Ucn RNA. Thus, the results indicate that the 3′-ends of both sense and antisense Ucn RNAs are the only non-complementary sequences between them. In conclusion, the present findings suggest that the Ucn gene locus naturally undergoes bidirectional transcription yielding a sense and an antisense RNA expanding the spectrum of antisense RNAs originated from the same genomic loci to antisense transcripts that are spliced using these non-consensus CT–AC splice sites.