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Activator region analysis of the murine dopamine receptor regulating factor (DRRF) gene.

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The murine dopamine receptor regulating factor (DRRF) gene is transcribed from a TATA-less promoter that has several putative Sp1 binding sites. The present investigation identifies functional transcription factors that modulate the expression of this gene. In the D_2-expressing NB41A3 cells, Sp1 potently activates transcription from the DRRF promoter in pCAT-DRRF-1153/+17, but DRRF effectively inhibits it. Deletion of the 31 bp fragment between -1153 and -1122 decreased transcription down to about 60%. This fragment contains a functional AP1 binding site. In addition, deletion of the 129 bp region between -901 and -772 further decreased transcription. The latter region has a functional AP2 binding site. Using a DRRF_AP1 (bases -1153 to -1121) probe, a specific retarded band was observed, and the unlabeled AP1 consensus competitor could effectively compete away this retarded band. In addition, using a DRRF_AP2 (bases -873 to -846), a specific retarded band was observed, and the unlabeled AP2 consensus competitor could effectively compete away this retarded band. The present observations suggest that Sp1 and DRRF regulate the DRRF promoter and that both AP1 and AP2 also modulate this gene.

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