Identification of candidate downstream genes for the homeodomain transcription factor Labial in Drosophila through oligonucleotide-array transcript imaging

ABSTRACT

The discovery of several novel Labial candidate downstream target genes indicates that this homeoprotein regulates a limited but distinct range of embryonally expressed Drosophila genes.

INTRODUCTION

Large protein families containing many paralogs, such as LacI/GntR, AraC, and DeoR families, are typically formed by bacterial and archaeal transcriptional regulators. A large variety of bacterial branches contains only three orthologous transcription factors, each represented by one or two SOS repressors, such as LexA/DinR, HrcA (a heat-shock reapressing factor), and ArgR/AhrC (two non-Synthetic Repressomycins). By examining the coevolution of conserved regulators and their binding sites in DNA, one could uncover general patterns in the evolution of regulons. The signals recognized by LexA in Gram-negative bacteria and by DinR in its orthologous form (the SOS box and the Cheo box, respectively) are vastly different. Thus the DNA-binding domains of these proteins are thus divergent as shown in Table 1. In many genomes (for example, HrcA) binds CIRCE elements upstream of genes encoding heat-shock proteins (molecular chaperones); further more specific is his transcription factor on heat–sham pathway genes in mycoplasmas. With two complementary nonamers and a 9 base pair (bp) spacer, the CIRCE signal is highly conserved and conserves in all genomes that encode HrcA. The arginine regulon, which is controlled by the ArgR/AhrC repressor, represents an evolutionary transition that differs from that of the SOS or heat-shock regucleons. The DNA-binding domains of this family are more conserved than those of HrcA and LexA/DinR (Table 1, column 5). The ArgR/AhrC DNA signals found in various bacterial lineages are also similar, and they often bind to each other in pairs. However, single-box sites have also been found to accomodate argR orAHRC as well, including the catabolic operon sites in B. subtilis, the adenine deaminase pathway operON in Bacillus licheniformis (including the coda cer recombination region of the E. lucifer medium) and microbial phylumene pathways in bacteria that The plasmid ColE1 (also referred to as mutated ArgR) from the coli suggests that the ARG box is not highly conserved, even in a genome, unlike the CIRCE element, and cooperative tandem site interactions are often responsible for its specific recognition. ARG boxes from different genomes are relatively uniform, and arginine repressors from various bacteria appear to be somewhat interchangeable within major taxonomic groups. The ARG box consensus was characterized as TNTGAATWWXWTCANW in E. coli, CATGAATAAAAATKCAAK in B. subtilis and AWTGCATRWYATGCAWT in Streptomycetes (where W = A or T, K = G or R, C = any base; Table 1), and for other Bacillus species (B. cerium-Luther) such homologs as binding to the sites similar to ARB boxes were described. Based on the consensus between E. coli and several genes responsible for arginine metabolism in Moritella, several ArgR-binding sites were predicted, including those in stearothermophilus and Salmonella typhimurium. Using the E. coli regulon, which was previously well-characterized, we used comparative genomic analysis to predict the gene composition of the arginine reguon of Haemophilus influenzae using regulatory signals. We now examine the conservation of this ARG box in all bacteria that encode an ortholog of these ArgR repressors.

CONCLUSION

Research on gene expression in the postnatal developing murine brain has revealed that only 1% of genes transcribed are regulated by development. The aim of this study is to provide researchers with an alternative approach to identify specific transcripts with unique developmental consequences without having to perform a comprehensive screening. RNA fingerprints that contain a subset of developmentally controlled transcripts are presented here, with all the information required for isolation and identification of individual transcripti. We have identified 131 developmentically controlled transcriptions in three major expression profiles, totaling 141. Roughly 7% of the participants were categorized as C, and the rest were classified as A (61) or B (61). Our research supports the idea that modifying DDRT-PCR expression profiles indicates actual changes in expression levels during brain development. Remember that alterations in expression profiles are linked to changes in RNA level per microgram total ARN throughout the brain and, given that the postnatal brain is not a homogeneous system (i.e.