



Evidence for the coevolution of axon guidance molecule Netrin and its receptor Frazzled



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ABSTRACT

Coevolution of a ligand and its receptor is critical for maintaining their function in different species, but how ligand and its receptor coevolve is poorly understood. The axon guidance molecule Netrin and its receptor Frazzled (Fra) are useful to study the mechanisms of ligand–receptor coevolution. Here, we have applied codon substitution models to identify positive selection of the *netrin* and *fra* genes. The sites under positive selection in *netrin* and *fra* were detected in same lineage, such as nematode, dipteran, hymenopteran, hemichordate, and teleost. Several amino acid residues that are under positive selection were identified in the interaction domains. Here we provide evidence that positive selection is essential for the coevolution of Netrin and Fra during central nervous system evolution.

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1. Introduction

The coevolutionary mechanism underlying the conserved interaction between paired-interaction proteins is essential for understanding the evolutionary process of protein interaction networks. Several examples of molecular coevolution of ligands and their receptors have been identified by testing their correlated changes using phylogenetic and interaction methods (de Juan et al., 2013; Pazos and Valencia, 2008; Reitzel and Tarrant, 2010). However, the evolutionary role of interaction domains in paired protein coevolution is largely unknown. As the interaction domains of receptors and their ligands play key functional roles, the correlated changes of amino acid sites in the interaction domains might be critical to their coevolution. The axon guidance molecule Netrin and its receptor Frazzled (Fra) are good models for investigating the role of interaction domains in ligand–receptor coevolution. Netrin and Fra bind to each other and direct the proper wiring of the central nervous system (CNS) (Cebria and Newmark, 2005; Kolodziej et al., 1996). To achieve this interaction, the VI and V domains of Netrin-1 bind to the FN4 and FN5 domains of Deleted in Colorectal Carcinoma (DCC), an ortholog of Fra in vertebrates (Geisbrecht et al., 2003; Kruger et al., 2004). The interaction between Netrin and Fra appears

to have been conserved during the evolutionary process from planarians to humans (Cebria and Newmark, 2005; Chan et al., 1996; Kolodziej et al., 1996; Lai Wing Sun et al., 2011; Rajasekharan and Kennedy, 2009). However, the evolutionary mechanism underlying the conserved interaction between Netrin and Fra remains unclear.

2. Materials and methods

2.1. Sequence collection and alignment

123 *netrin* homologous sequences from 58 species and 82 *fra* homologous sequences from 57 species were identified by BLAST searches against National Center for Biotechnology Information (NCBI) (<http://www.ncbi.nlm.nih.gov>) and Ensembl Genome Browser (<http://asia.ensembl.org/index.html>). Accession numbers were compiled in Tables S1 and S2. Sequence alignments (Files S1–S7) were performed using MUSCLE in MEGA 5 with default parameters (Edgar, 2004; Tamura et al., 2011).

2.2. Phylogenetic tree constructions

The neighbor-joining (NJ) trees (Saitou and Nei, 1987) for Netrin and Fra were constructed by MEGA 5 (Tamura et al., 2011). Bootstrap analysis with 1000 replicates was used to assess the support for tree nodes (Felsenstein, 1985).

2.3. Positive selection tests

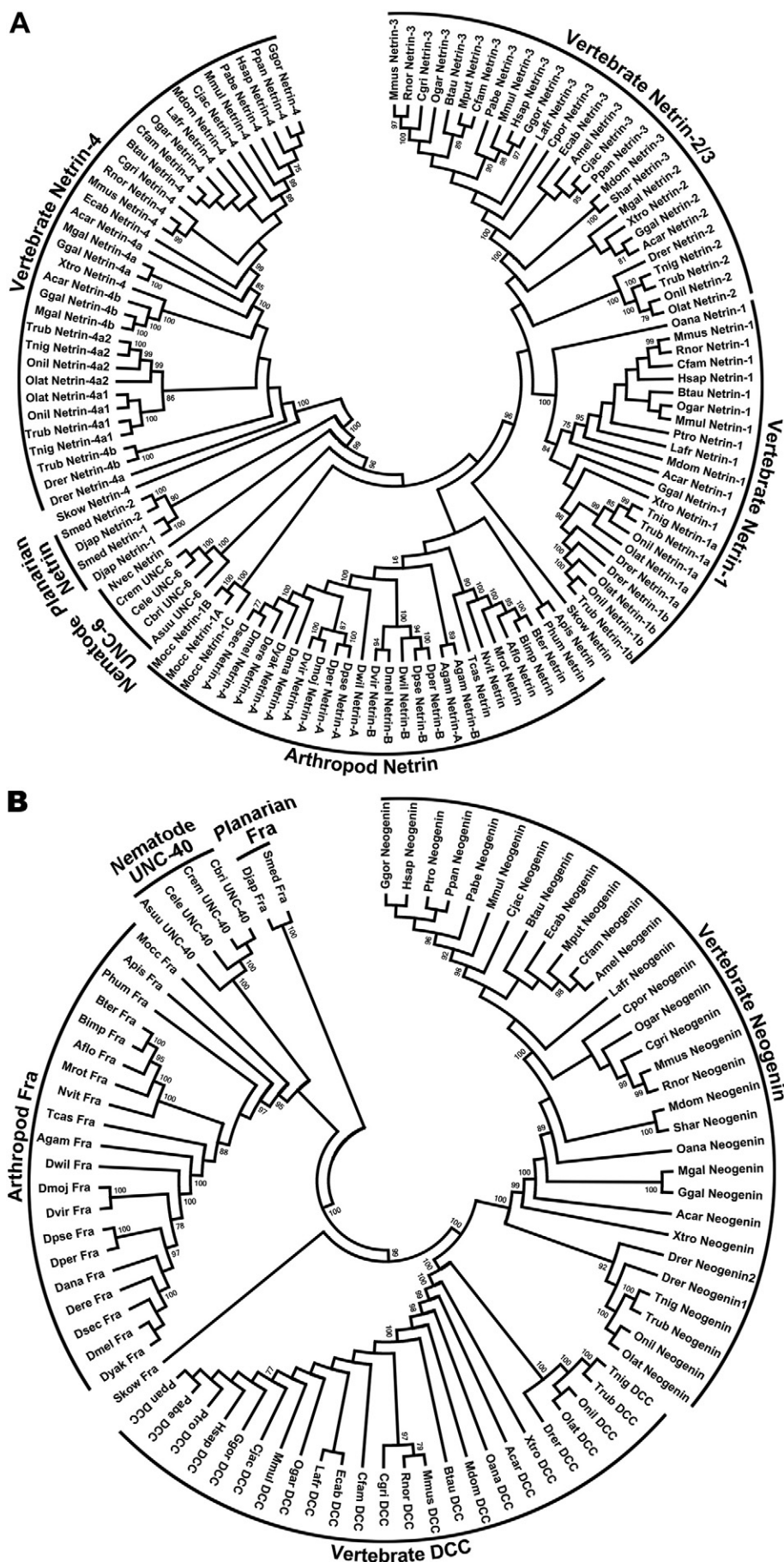
Selective pressure was measured by the ratio of nonsynonymous to synonymous nucleotide substitutions rates ($\omega = dN / dS$). This ratio

Abbreviations: Fra, Frazzled; CNS, central nervous system; DCC, deleted in colorectal carcinoma; NCBI, National Center for Biotechnology Information; NJ, neighbor-joining; LRT, likelihood ratio test; FN, fibronectin; Ig, immunoglobulin.

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