Origin and Loss of Nested LRRTM/α-Catenin Genes during Vertebrate Evolution

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Abstract

Leucine-rich repeat transmembrane neuronal proteins (LRRTMs) form in mammals a family of four postsynaptic adhesion proteins, which have been shown to bind neurexins and heparan sulphate proteoglycan (HSPG) glypican on the presynaptic side. Mutations in the genes encoding LRRTMs and neurexins are implicated in human cognitive disorders such as schizophrenia and autism. Our analysis shows that in most jawed vertebrates, lrrtm1, lrrtm2, and lrrtm3 genes are nested on opposite strands of large conserved intron of α-catenin genes ctnna2, ctnna1, and ctnna3, respectively. No lrrtm genes could be found in tunicates or lancelets, while two lrrtm genes are found in the lamprey genome, one of which is adjacent to a single ctnna homolog. Based on similar highly positive net charge of lamprey LRRTMs and the HSPG-binding LRRTM3 and LRRTM4 proteins, we speculate that the ancestral LRRTM might have bound HSPG before acquiring neurexins as binding partners. Our model suggests that lrtn gene translocated into the large ctnna intron in early vertebrates, and that subsequent duplications resulted in three lrtn/ctnna gene pairs present in most jawed vertebrates. However, we detected three prominent exceptions: (1) the lrrtm3/ctnna3 gene structure is absent in the ray-finned fish genomes, (2) the genomes of clawed frogs contain ctnna1 but lack the corresponding nested (lrrtm2) gene, and (3) contain lrrtm3 gene in the syntenic position but lack the corresponding host (ctnna3) gene. We identified several other protein-coding nested gene structures of which either the host or the nested gene has presumably been lost in the frog or chicken lineages. Interestingly, majority of these nested genes comprise LRR domains.

Introduction

Members of the leucine-rich repeat transmembrane (LRRTM) family of neuronal proteins contain ten N-terminal LRR repeats, a single pass transmembrane domain, and a C-terminal cytoplasmic tail comprising a PDZ domain binding motif [1]. LRRTMs function as postsynaptic adhesion proteins in excitatory synapses [2] by interacting with presynaptic neurexins, similar to the neureligins [3–7]. LRRTM1 gene is associated with schizophrenia and handedness [8]. In rodents, LRRTM1 and LRRTM2 proteins have been shown to interact with neurexins, but there are also indications that all the four LRRTMs can bind to neurexins [3–6]. Recently, heparan sulfate proteoglycan (HSPG) glypican was identified as an alternative receptor for LRRTM4 and possibly for LRRTM3 [9,10].

In human and mouse genomes LRRTM1 is encoded by a single exon, whereas the first four coding nucleotides (ATGG) of other LRRTM genes (Lrtm2, Lrtm3, and Lrtm4) are located in a separate first exon [1]. Three of the four LRRTM genes (Lrtm1 to Lrtm3) are nested in a large conserved intron of α-catenin genes (Ctnna1 to Ctnna3) [1]. Each mammalian Ctnna gene has 17 coding exons (encoding a protein of about 900 amino acids) and hosts one Lrtm nested in the opposite orientation in a large (~50–450 kb in human) intron between coding exons 6 and 7: Lrtm1 is nested in Ctnna2, Lrtm2 in Ctnna1, and Lrtm3 in Ctnna3. Lrtm4 gene is not nested but is located within a few genes away from the Lrtm1/ Ctnna2 gene pair in mammals [1]. Genes encoding for α-catenins exist in all metazoan animals analyzed [11], whereas LRRTM genes have only been found in vertebrate genomes [1].

Nested genes represent a subgroup of overlapping genes [12]: one gene (“nested”) is situated totally inside another gene (“host”). Nearly all protein-coding nested genes are thought to have emerged by insertion of a corresponding DNA sequence into an intron of a pre-existing gene [13]. Most commonly, the internal/nested gene lies inside an intron of the larger host gene in the opposite orientation [12]. Nested genes that have a single coding exon presumably emerged by retrotransposition [13]. A gene may also become nested by fusion of two flanking genes or by acquisition of new exons. Alternatively, nested genes may originate de novo through accumulation of mutations inside a preexisting gene [12]. Once formed, a nested gene structure can be duplicated or lost during evolution. However, no loss of a nested gene structure encoding conserved proteins was reported in vertebrates in a previous study [13].

Here, we have studied the evolution of the LRRTM family. Our analysis suggests that in early vertebrates an ancestral lrtm gene had become incorporated into a pre-existing ctnna intron that was followed by two duplications of the nested lrtm/ctnna structure. We found that the nested lrtm/ctnna gene structure is conserved in jawed vertebrates. However, the clawed frog (Xenopus) genome contains two notable exceptions. First, the genome contains ctnna1/
but lacks the corresponding nested (lrrtm2) gene. Second, the genome contains a clear lrrtm3 ortholog in syntenic position but lacks the corresponding host (ciona2) gene. A database analysis identified several other phylogenetically old nested gene structures comprising LRR-domain encoding genes that have apparently been lost in amphibian or avian lineages.

Although invertebrates, such as fruit fly and nematode have a neurexin (nrxn) gene ortholog [14,15], the evolution of the alternatively spliced nrxn AS4 exon, which encodes a loop sequence required for LRRTM binding in mammals [3–6], has not been investigated. Therefore, we also studied whether the alternative splicing of nrxn AS4 exon would have co-evolved with the appearance of lrrtm. We show that the AS4 exon emerged de novo in chordates, and that the mechanism of its alternative splicing may have evolved in the early vertebrates. Based on analysis of net charge of the extracellular LRR domains, we speculate that the first LRRTMs may have bound HPSGs before acquiring neurexins as binding partners.

Materials and Methods

Identification of Sequences

We searched the Ensembl genome database (release 72, Jun 2013) for the genomic location and structure of the annotated LRRTM and α-catenin gene homologs (by searching for their names/gene symbols) from the following species: human, chicken (Gallus gallus), Western (tropical) clawed frog (Xenopus tropicalis), coelacanth (Latimeria chalumnae), zebrafish (Danio rerio), and sea lamprey (Petromyzon marinus). Lrrtm orthologs were also retrieved from other ray-finned fish genomes (Gasterosteus aculeatus, Orzyas latipes, Takifugu rubripes, and Tetradon nigroviridis). In addition, we searched the tunicates (Ciona intestinalis and Ciona savignyi), amphioxus (Branchiostoma floridae), genome.jgi-psf.org/Brafl1), elephant shark (Callorhinichus miliaris, esharkgenome.imcb.a-star.edu.sg), spotted gar (Lepisosteus oculatus, pre.ensembl.org/Lepisosteus_oculatus), and the African clawed frog (Xenopus laevis, xenopus lah.nig.ac.jp/assembly v7.1) genomes. We also searched the transcriptionalomes of clawed frogs (X. laevis and X. tropicalis, www.xenbase.org) and salamander (axolotl, Ambystoma mexicanum, www.ambystoma.org, assembly v4.0) for lrrtm and ctnna homologs. If some LRRTM or α-catenin homologs seemed to be missing or incompletely annotated, we searched the corresponding genomes by using TBLASTN (blast.ncbi.nlm.nih.gov/) using the corresponding mouse and chicken protein sequences as a query and verified the hits by reciprocal BLAST searches (using default parameters). The N-terminal part of some LRRTM transcripts was curated manually to conform to the splice site consensus sequences. Identified shark and coelacanth CTNNA fragments were aligned and assembled manually. Isoelectric point (pI) values were calculated using Geneious 6.1.7 [Biomatters Ltd] for the extracellular LRR-domains of LRRTMs (excluding the signal sequence and hinge domain). These pI values and accession numbers for the identified LRRTM and sequence and hinge domain). These pI values and accession numbers for the identified LRRTM and CTNNA amino acid sequences were analyzed using the Genomicus database (v73 www.genomicus.biologie.ens.fr).

Alignment and Phylogenetic Analysis

The predicted LRRTM and CTNNA amino acid sequences were aligned using MAFFT v.7 [http://mafft.cbrc.jp/alignment/software/] [17] with default parameters. For LRRTM3 and LRRTM4 orthologs that have alternative C-terminal splice forms, only the shorter isoform (ending to -ECEV) was used. The alignment was edited using Geneious in order to remove positions (amino acid residues) of the LRRTM signal sequence and the extracellular juxtamembrane domain where more than half of the sequences had gaps. The LRRTM alignment is shown in Fig. S1. Phylogenetic trees were inferred using PhyML3.0 under the following model parameters (LG substitution model, empirical equilibrium frequencies, four gamma-distributed substitution rate categories and five random starting trees) with confidence estimates derived from 1000 bootstrap replicates [18]. Trees were rearranged with Geneious and visualized using the MEGA5 software [19].

Analysis of Selected Nested Gene Structures in Vertebrates

We also searched the Ensembl database for vertebrate orthologs for a subset of previously identified human different strand nested gene pairs [12]. We included for the search only those different strand nested gene pairs that were reported to be shared between human and mouse [12], and in which a protein-coding nested gene is flanked by protein-coding exons of the host gene. This selection resulted in 91 protein-coding different strand nested gene pairs for our analysis (Table S3). If annotated orthologs for the nested gene pair were identified (by searching for their names/gene symbols) in coelacanth or zebrafish (or in both), as well as in chicken and clawed frog (X. tropicalis) genomes, the nested structure was designated as conserved. If the nested gene structure was present in coelacanth or zebrafish but either the host or the nested gene, or both, were not annotated in either chicken or clawed frog genomes, the nested gene structure was designated as potentially lost (not conserved). The absence of these nested gene structures in chicken or in X. tropicalis genomes was verified by BLAST searches and by synteny analysis of adjacent genes.

Evolution of neurexin AS4 Exon and Alternative Splicing

To study when the nrxn AS4 exon emerged during evolution, we searched selected invertebrate and vertebrate genomes with BLASTP using a 160 amino acid residue fragment of mouse neurexin-1 protein (ENSMMUSP00000125407, Refseq NP_064648.3) that is encoded by the AS4 and flanking exons (see Fig. S6). To estimate the relative percentage of nrxn transcripts in which the AS4 exon is skipped or retained in selected species (that contain the AS4 exon), we searched the NCBI expressed sequence tag database (dbEST) with TBLASTN with default parameters (BLOSUM62 matrix) using the above 160 amino acid fragment of mouse neurexin-1 as a query (Fig. S6). Hits that were considered relevant for the analysis were at least 50 amino acid long, aligned at least partially with the AS4 exon of the query, and had over 30% sequence identity (Table S6). This ruled out short fragments and distant (non-neurexin) sequences. The location of AU-rich sequence motifs in the introns flanking the nrxn AS4 exon (within 200 bp upstream and 200 bp downstream of the exon) was analyzed by text search.

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Genomic PCR with Degenerate Primers

We purified *X. tropicalis* (obtained from the European Xenopus Resource Centre, www.port.ac.uk/research/exrc/) and chicken genomic DNA using the Wizard SV Genomic DNA Purification System (Promega, Madison, WI). Degenerate *ctnna* primers were designed to conform to three conditions. (1) The primers efficiently amplify a corresponding genomic fragment of *ctnna* from other vertebrate species. (2) The primers also amplify a corresponding genomic fragment of *ctnna1* and/or *ctnna2* from *X. tropicalis*, as well as from other vertebrate genomes, although with a lower efficiency compared to the corresponding fragment of *ctnna3*. This would serve as an internal positive control for the quality of genomic DNA, and for the PCR amplification process itself. (3) The PCR product is at least 100 bp and the primer pairs belong to a single (conserved) *ctnna* exonic region.

iCODEHOP (Consensus-DEgenerate Hybrid Oligonucleotide Primers) software [20] was used to design degenerate PCR primers from protein multiple alignments. One pair of degenerate primers that conformed to all the conditions was identified inside the last (and the longest) coding exon of the *ctnna* gene: (a3-F) 5’-GGC TGC CAA RAA YYT NAT GAA YGC-3’ and (a3-R) 5’-GGC TTC TTC TTC GGN GCC TTC GTC AT-3’. Both primers recognize *ctnna3* sequences, which are highly conserved in different vertebrates (Fig. S3). Moreover, the primers amplify the corresponding genomic fragments of *ctnna1* and *ctnna2* from *X. tropicalis* genomic DNA (Fig. S4). The predicted size of the PCR products obtained with these primers for all known *ctnna* genes is 144 bp. Both primers have degeneracy (number of different nucleotide sequences in the primer pool) of 64.

We used a two-step PCR protocol and a PCR machine with a gradient temperature block option. Annealing temperature was kept 45°C for all samples for the first 5 cycles and then was increased up to 54–65°C for 8 different samples (gradient block) for the last 35 cycles. The PCR reactions were run on a 2% agarose gel and an expected product about 150 bp was observed in the reactions with annealing temperatures during the second step kept from 54.1°C up to 56.3°C. These PCR products were extracted from gel, pooled, and sequenced using the a3-F and a3-R primers.

Results

Phylogenetic Analysis of LRRTM and γ-catenin Genes in Vertebrates

The LRRTM family is thought to be vertebrate-specific since clear LRRTM gene homologs were originally identified in several mammalian and teleost fish genomes but not in the fruit fly or nematode genomes [1]. To study the evolution of the LRRTM family in vertebrates, we collected all annotated *lrrtm* and *ctnna* genes, and noted their corresponding genomic structures and locations, from representative model organisms (human, chicken, African clawed frog, coelacanth, zebrafish, and sea lamprey), for which whole genome sequences are available (Fig. 1). Partial *lrrtm* and *ctnna* sequences were also obtained from the elephant shark [21] and spotted gar draft genomes (Tables S1 and S2). No *lrrtm* homologs could be found from the sea squirts (*Branckaustoma floridana*) genomes. The best hits from these species correspond to Slt-like and other LRR-domain containing proteins as confirmed by reciprocal BLAST search (Table S4).

To correctly identify the subtypes of the new LRRTM protein sequences in the novel species and to provide a relative time point for the divergence of the different subtypes within each family, we aligned the predicted LRRTM sequences (Fig. S1) and generated phylogenetic trees using PhyML (Fig. 2A) and MrBayes (Fig. S2). Orthologs of each LRRTM family member (*LRRTM1* to *LRRTM4*) from different jawed vertebrate species group together forming a clade. Individual family members in the tree are located in general as expected from the known vertebrate phylogeny. Among the four LRRTMs, the highest amino acid sequence identity is seen between LRRTM3 and LRRTM4 proteins in all the analyzed jawed vertebrate species (with average pairwise sequence identities of ~60%, Table S5). Consistent with this, the LRRTM3 and LRRTM4 clades cluster together in the phylogenetic trees. LRRTM2 proteins show higher (47–49%) pairwise sequence identity to LRRTM1 than to LRRTM3 or LRRTM4 proteins (~40%) in all the analyzed species (Table S5). Consistent with this, the LRRTM1 and LRRTM2 clades branch together (Fig. 2A).

In a similar way, we aligned CTNNA proteins and inferred phylogenetic trees (Fig. 2B and Fig. S2). The resulting tree topology has high bootstrap support and, in agreement with a previous study [11], shows that orthologs of CTNNA1 and CTNNA2 from different jawed vertebrates form separate clades that apparently originated by duplication from a common ancestor. The CTNNA3 orthologs from different jawed vertebrates also form a distinct clade that originated before the split of the CTNNA1 and CTNNA2 proteins. However, the CTNNA3 clade has diverged clearly more from the common ancestor than CTNNA1 and CTNNA2 clades.

Structure of lrrtm/ctnna Genes in Jawed Vertebrates

In all analyzed jawed vertebrate genomes (except the amphibians, see below), *lrrtm1* and *lrrtm2* are nested in a large intron between conserved coding exons 6 and 7 of *α*-catenin genes *ctnna2* and *ctnna1*, respectively. Similarly, *lrrtm3* gene resides in a homologous position (inside the large intron between coding exons 6 and 7) of the *ctnna3* gene in all annotated genomes of amniotes (mammals, reptiles, and birds), as well as in the lobe-finned fish coelacanth (*Latimeria chalumnae*) and the ray-finned fish spotted gar (*Lepisosteus osseulus*) genomes (Figs. 1 and 3, and Tables S1 and S2). Clear orthologs of all four *lrrtm* and three *ctnna* genes have also been found in the elephant shark genome. Nested gene structures of *lrrtm2/ctnna1* and *lrrtm3/ctnna2* are annotated, while the expected *lrrtm1/ctnna2* gene structure could not be verified because of the short size of the scaffold_422 which contains *lrrtm1* (esharkgenome.imcb.a-star.edu.sg). In contrast, the genomes of ray-finned fishes (other than the spotted gar, which diverged before the teleost fish-specific whole genome duplication [22]) lack both *lrrtm3* and *ctnna3*. Clear *lrrtm4* orthologs were found in all jawed vertebrate species analyzed. In mammals, *lrrtm4* is located near the nested *lrrtm1/ctnna2* gene structure, whereas in other vertebrates, *lrrtm4* is located in a different chromosome than the *lrrtm1/ctnna2*. In contrast to other jawed vertebrates (shark, coelacanth, and tetrapods), which have a single *lrrtm4* ortholog, the analyzed genomes of ray-finned fishes (other than the spotted gar) contain four *lrrtm4* orthologs located as two closely situated genes in two chromosomes, each pair on a single chromosome being phylogenetically closer to each other (Figs. 1 and 2A, and data not shown).

Analysis of paralogous clusters of genes using the Synteny Database (syntendb.oregon.edu/synteny_db/) found suggestive evidence of conserved synteny between human *CTNNA1*, *CTNNA2*, and *CTNNA3* gene regions: a few genes (including *EGR1-4* and *REEP1-4*) that are located near the *CTNNA1* genes have four paralogs in the human genome (Fig. S5). This is consistent with the idea that the three nested *lrrtm/ctnna* gene structures may have originated from two rounds of whole-genome

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duplications in the early vertebrate lineage [23–25]. However, tracing back to these events is difficult. The conserved paralogous genes in human genome (EGRI-1 and REEP1-A) are not immediately adjacent to the CTNXA genes and similar regions of conserved synteny (paralogous pairwise clusters) containing lrrtm/ cttna were not found in other vertebrate (e.g. chicken or clawed frog) genomes. Lrrt4 neighboring genes are not even syntenic between chicken and clawed frog and the lrrtm4 locus is not assembled in coelacanth genome to allow analysis of synteny.

**Lrtrm and cttna Genes in Lamprey**

The genome of sea lamprey (*Petromyzon marinus*), a jawless fish, contains two genes encoding for LRRTMs (annotated in Ensemble as LRRTM3 and LRRTM2, but named here as lrrtm4 and lrrtmB, respectively), of which lrrtm4 is situated adjacent to, but is not nested in, the single lamprey cttna homolog (Figs. 1 and 3). Both lrrtm4 and lrrtmB possess two protein-coding exons: the first coding exon provides only the first four nucleotides [ATGG] of the open reading frame. The structures of the predicted lamprey LRRTM (PmLRRTM-A and PmLRRTM-B) proteins with 10 LRRs, a single transmembrane domain, and a short cytoplasmic domain (with a C-terminal PDZ binding motif ECEV) are similar to that of mammalian LRRTMs [1,2]. PmLRRTM-A and PmLRRTM-B show higher amino acid sequence identity to LRRTM3 and LRRTM4 (50–55%), than to LRRTM1 and LRRTM2 (40–45%) of other vertebrates (Table 1). In the phylogenetic trees (Fig. 2A and Fig. 2B) both lamprey LRRTM3 branches basal to the LRRTM3-LRRTM4 divergence. Since the lrrtm4 and lrrtmB reside in short scaffolds and many lamprey sequences have unresolved orthologies (possibly due to lineage-specific sequence modifications [26] and independent genome duplications [27]), it is not possible to assign origins to the two lamprey LRRTM sequences by conserved synteny analyses comparing them to other vertebrate genomes. In other words, it remains unclear whether the two sea lamprey LRRTMs originated by an independent duplication after the divergence of lampreys from the vertebrate lineage.

The lamprey cttna gene has a similar structure as other vertebrate β-catenin genes with 17 coding exons, but is much shorter (about 31 kb, compare e.g. to human CTNNB1 that spans 1.8 Mb). However, the longest intron of lamprey cttna gene (~5.8 kb) is the one between the exons 6 and 7 that hosts lrrtm genes in other vertebrates. In the phylogenetic tree, the lamprey β-catenin (PmCTNNA) is basal to the jawed vertebrate branches (Fig. 2B), suggesting that it represents the common ancestor of the tree jawed vertebrate CTNNA subtypes.

**Lack of Lrtrm2 and cttna3 in Amphibian Genomes**

Although the nested lrrtm/cttna gene structure is conserved in most of the analyzed jawed vertebrate species, the genomes of the clawed frogs *Xenopus tropicalis* and *X. laevis* have two notable exceptions. First, the *X. tropicalis* genome [28] lacks an ortholog of lrrtm2 (Fig. 1). The *X. tropicalis* cttna1, otherwise similar in structure to β-catenin genes of other jawed vertebrates, is very compact (its length is about 16.5 kb). In particular, the intron between exons 6 and 7 of *X. tropicalis* cttna1 (that would be expected to host lrrtm2) is unusually short (434 bp) compared to the corresponding intron of *X. tropicalis* cttna2 (~469 kb) hosting lrrtm1, or to the corresponding intron of other jawed vertebrates. Second, an ortholog for cttna3 is absent in the *X. tropicalis* genome, although an apparent lrrtm3 ortholog is present (Fig. 1). Analysis of synteny confirmed that the clawed frog lrrtm3 is indeed an ortholog of human LRRTM3 (Fig. 3). Similar to *X. tropicalis*, the draft *X. laevis* genome (*xenopus.lab.nig.ac.jp/assembly v7.1 at www.xenbase.org*) lacks orthologs of lrrtm2 and cttna3 but contains orthologs for all the other LRRTMs and β-catenin genes. We also searched for transcripts corresponding to β-catenins in the extensive *X. tropicalis* and *X. laevis* mRNA databases (www.xenbase.org). While multiple hits are present for cttna1 (XB-GENE-PAGE-479598) and cttna2 (XB-GENE-PAGE-595200), no cttna3 mRNAs were found by reciprocal BLAST searches. Similarly, the recently available salamander (*axolotl, Ambystoma mexicanum*) transcriptome ([www. ambystoma.org)] lacks orthologs of both lrrtm2 and cttna3, while clear transcripts of all the other LRRTMs and β-catenin genes are present.

**Experimental Support that the X. tropicalis Genome Lacks cttna3**

The apparent lack of cttna3 in the current amphibian genomes and transcriptomes suggests loss of the cttna3 gene in the amphibian lineage during evolution. To obtain further support for this, we carried out polymerase chain reaction (PCR) with degenerate cttna3 primers (a3-F and a3-R) designed to amplify cttna sequences from various species (Fig. S3). As a positive control for our strategy, we first used these degenerate primers to amplify corresponding cttna fragments from the chicken genome (Fig. 4A). The primers have no mismatches with chicken cttna3, but have one mismatch with a corresponding region of cttna1 and two mismatches with cttna2 (Fig. S3). Thus, the primers are expected to primarily amplify cttna3, but may also amplify cttna1 though with a lower efficiency. Consistent with this, most of the amplified
A product from chicken genomic DNA corresponded to *ctnna3*, but a minor part corresponded to *ctnna1* (Fig. 4A).

The same PCR protocol was then applied to the *X. tropicalis* genomic DNA. Sequencing of the PCR fragment revealed spectra matching only to *X. tropicalis ctnna1* and *ctnna2* (Fig. 4B). Digestion with diagnostic *Hind* III and *Stu* I restriction enzymes confirmed that no other PCR products except for the frog *ctnna1* and *ctnna2* were amplified (Fig. 4C, D).

Evolution of Neurexin Alternative Splice Segment

The alternatively spliced segment (AS4) of neurexin protein comprises a loop structure in the binding domain, and deletion of this loop structure (by exon skipping) is required for LRRTM binding in mammals [3–6]. We used BLASTP search to investigate whether an exon homologous to the AS4 exon was present in *nrxn* genes of other species than the jawed vertebrates.

Amino acid alignment shows that the fruit fly and sea urchin neurexin proteins lack exactly the region that is homologous to the AS4 amino acid sequence of vertebrate neurexins (Fig. S6). Moreover, in fruit fly and sea urchin *nrxn* genes, the intron between the exons that are homologous to vertebrate AS4-flanking exons is very short. In contrast, an exon homologous to the AS4-exon of mouse *Nrxn1* gene is present in the sea squirt and lamprey *nrxn* genes (Fig. S6). This suggests that the *nrxn* AS4 exon sequence appeared early in chordate evolution.

To further analyze the expression of *nrxn* isoforms lacking AS4 during evolution, we searched the available vertebrate EST databases for *nrxn* transcripts with deletion of the AS4 sequence (Table S6). As in mammals, zebrafish *nrxn* pre-mRNAs are known to undergo alternative splicing, including exon AS4 skipping [13]. We found 9 out of 23 (39%) *nrxn* ESTs that lack AS4 in human, 5 out of 27 (19%) in mouse, 1 out of 9 (11%) in clawed frog, and 1 out of 6 (17%) hits in zebrafish, confirming that this splice variant is expressed throughout the jawed vertebrate class. However, no
nrxn EST transcripts (with or without the AS4 sequence) were found in lamprey, and therefore it remains unclear whether the alternative splicing of nrxn was present in jawless vertebrates. In the sea squirt (C. intestinalis), none of the few nrxn ESTs revealed the AS4 exon deletion according to our selection criteria (Table S6). Recently it has been reported that alternative splicing of nrxn AS4 exon is regulated by RNA binding proteins of KHDBRS family (T-STAR and SAM68) [29,30], which are known to recognize specific tandem repeats of UAAA/UUAA sequences in the introns adjacent to the AS4 exon [29,31]. We therefore analyzed intronic sequences surrounding the nrxn AS4 exon in sea squirt (C. intestinalis) and sea lamprey for the presence of these repeats. In sea squirt nrxn, the introns surrounding the AS4-like exon are short (441 and 430 bp compared to 13620 and 1598 bp in lamprey) and contain only one UWAA (W = U/A) repeat in the upstream and three of them in downstream introns. In contrast, markedly more of the UWAA repeats can be found in both upstream and downstream proximal regions of the large introns surrounding the “AS4-exon” in two out of three lamprey nrxn genes (Fig. S7).

Discussion

We show here that the nested lrrtm/ctnna gene structure was established in early jawed vertebrates and that a conserved structure of three nested lrrtm/ctnna pairs is present in lobe-finned fish (and presumably also in cartilaginous fish) as in amniotes (Fig. 5A). Based on the available data, we propose a hypothetical sequence of events to explain the evolution of the nested lrrtm/ctnna genes (Fig. 5B).

The available genomes of invertebrates (including uro- and cephalochordates) lack clear homologs of lrrtm, whereas the jawless vertebrate lamprey has two copies of lrrtm. Thus, the first lrrtm presumably emerged (by exon shuffling of pre-existing genes containing extracellular LRR, transmembrane, and intracellular domains) in the early vertebrate ancestor. The α-catenin (ctnna) gene emerged early in metazoan evolution, presumably from a vinculin-like gene [11]. The first nested lrrtm/ctnna gene structure arose presumably by retrotransposition of lrrtm into the large intron of the nearby ctnna gene. Since the nested lrrtm1/ctnna2, lrrtm2/ctnna1, and lrrtm3/ctnna3 gene structures are similar in all jawed vertebrates (except for amphibians), they share a single ancestral nested lrrtm/ctnna gene structure that was duplicated twice presumably as a part of the two-round whole genome duplications (2R-WGD) at the origin of vertebrates [23–25,27]. The two duplications resulted in four nested lrrtm/ctnna pairs followed by a loss of ctnna around lrrtm4. Presumably, one of the two lrrtm/ctnna-ancestral gene structures that emerged from the first lrrtm/ctnna duplication diverged to become lrrtm1/ctnna2, lrrtm2/ctnna1, and lrrtm3/ctnna3 gene structures. The other nested gene pair diverged to become lrrtm3/ctnna3 and lrrtm4/ctnna4.
Table 1. Nested gene structures lost in clawed frog or chicken genomes.

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<th>Host gene</th>
<th>Nested gene</th>
<th>Explanation</th>
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<td>TRIM32</td>
<td>nested absent in frog</td>
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<td>LRTM1</td>
<td>both absent in frog</td>
</tr>
<tr>
<td>CASK</td>
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<tr>
<td>PCD1</td>
<td>AMGO3</td>
<td>nested absent in frog</td>
</tr>
<tr>
<td>SOD1</td>
<td>LRC4</td>
<td>host gene absent in chicken</td>
</tr>
<tr>
<td>SYN1</td>
<td>TIMP1</td>
<td>nested absent in frog</td>
</tr>
<tr>
<td>TB1M</td>
<td>CLDN20</td>
<td>nested absent in frog</td>
</tr>
</tbody>
</table>

The table lists human protein-coding different strand nested gene structures that are also found in coelacanth and/or zebrafish but are absent in clawed frog (X.tropicalis) or chicken genomes. The genes were selected (as described in the Methods and Table S3) from a previously published list of human nested genes [12]. The missing host or nested genes are marked in bold. Nested genes that encode LRR-superfamily proteins are underlined.

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The loss of lrtn3 in the amphibian lineage may have occurred concomitant with (or before) the deletion of most parts of the large ctnna1 intron. Loss of one LRRTM family member is not critical for survival in mice under laboratory conditions [2,10,35,36]. We suggest that LRRTM1, which has an overlapping expression and synaptic function with LRRTM2 [1-6], was likely able to compensate, at least partially, for the lack of LRRTM2 in amphibians.

The precursor of lrtn4, which is not nested in ctnna of any vertebrates, may have been initially nested in a ctnna that became inactive and was lost in the early vertebrates (Fig. 5B). In the teleost fish lineage, a local (probably a head-to-tail tandem) duplication followed presumably by the teleost-specific whole genome duplication [33,34] resulted in four lrtn4 orthologs. As LRRTM3 and LRRTM4 proteins show highest amino acid similarity to each other, the extra copies of lrtn4 gene may have taken over the lack of lrtn3 in teleosts.

No conserved protein-coding nested gene structures were reported in a previous study to have been lost in vertebrates [13]. Therefore, it was rather unexpected that our bioinformatic analysis of 91 protein-coding different strand nested genes conserved between mouse and human [12] (see Table S3) identified 19 protein-coding nested gene structures present also in zebrafish and/or coelacanth but lost in the clawed frog or chicken genomes (Table 1). Interestingly, in 12 out of 19 cases the nested genes encoded LRR superfamily proteins. Therefore, nested LRR superfamily genes may have remained mobile during vertebrate evolution consistent with the idea that many of them have presumably derived via retrotransposons [13].

In mice, LRRTMs have been reported to bind specifically those neurexin isoforms that lack the alternatively spliced segment 4 (AS4) [5,6]. Nrxn gene structure, including the AS4 exon, is conserved in jawed vertebrates, and nrxn1-3 transcripts lacking this segment are expressed in zebrafish [14,15]. Hence, the alternative splicing mechanism to skip nrxn AS4 exon had apparently evolved already prior to the nrxn gene duplications in early vertebrates. The corresponding AS4 exon is also present in the lamprey and sea squirt nrxn gene orthologs. However, nrxn gene orthologs in the fruit fly and nematode, as well as in the urochordate sea urchin, lack the sequence corresponding to the AS4 exon. This indicates that the nrxn AS4 exon emerged de novo in evolution of the chordate lineage. Recently, cerebellin (Clnh) family proteins were identified as novel neurexin ligands that may directly bind the AS4 loop [37,38]. Interestingly, putative cerebellin gene orthologs are annotated in vertebrates, as well as in the sea squirt (C.intestinalis) but not in the fruit fly or nematode genomes (www.ensembl.org/Homo_sapiens/Gene/Compara_Tree?db = core;g = ENSG00000102924). We speculate that the nrxn AS4 exon appeared de novo at the same time as the gene for its new binding partner cerebellin emerged (by duplication of a related C1q/TNF-superfamily gene) in early chordates.

Recent studies have identified RNA binding proteins of KHDBRS family as key regulators of neurexin AS4 exon splicing in mice [29,30]. Multiple AU-rich sequence elements in introns preceding and following AS4 exon act as the response elements including UWAA-rich regions closely downstream of AS4 that are conserved in jawed vertebrates [29,30]. Similar UWAA-rich regions are conserved also in lamprey neurexin genes (Fig. S7), and the lamprey genome is known to contain KHDBRS protein orthologs [29]. In contrast, the adjacent short introns in sea squirt neurexin contain few UWAA motifs, and all identified neurexin EST transcripts from sea squirt retain the AS4 exon sequence, suggesting that the AS4 exon is not skipped in this species. Although additional studies are needed to confirm that the neurexin
transcripts lacking AS4 are expressed in lamprey, the present evidence suggests that the LRRTMs and the mechanism of alternative splicing that enabled LRRTM binding to neurexins probably both emerged in early vertebrate evolution, before the divergence of jawed vertebrates.

Several synaptic adhesion molecules, such as neurexins, can be found in less complex metazoan organisms with a simple nervous system. However, the number of genes encoding synaptic adhesion proteins, along with other synaptic components, increased dramatically during the evolution of vertebrates [39]. LRRTMs represent an example of such adhesion proteins that are required to fine tune the formation and maintenance of synapses in the vertebrate brain, while simultaneous diversification of neurexin splice variants contributed towards the same task [7].

Recently it has been found that LRRTM4 and possibly LRRTM5 (but not LRRTM1 or LRRTM2) bind heparan sulphate proteoglycan (HSPG) glypican as a presynaptic ligand [9,10]. We looked at the properties of the vertebrate LRRTM proteins to see if there would be any clues to how the proteins might differ, and when this function might have appeared. We noticed a correlation in total positive charge and the reported HSPG binding function in the LRRTM family: The calculated pI values are higher for the LRR-domains of mouse LRRTM3 and LRRTM4 (pI values of 9.3 and 9.4) than for mouse LRRTM1 and LRRTM2 (pI values of 6.9 and 8.1), resulting in substantial positive charge of LRRTM3 and LRRTM4 that is typical for heparin binding proteins. Similar situation is observed in case of the frog and zebrafish LRRTMs (Table S1). Interestingly, both of
the LRRTMs present in lamprey are highly positively charged (pI values of 9.55 and 9.3). Thus, it seems possible that the HSPG-binding function of LRRTMs might have been present prior to their neurexin binding and then later the HSPG-binding might have been lost in the evolution of LRRTM1 and LRRTM2, which specialized to bind only neurexins. Additional experiments comparing the binding of lamprey LRRTMs to neurexins versus HSPGs are necessary to test this hypothesis.

Conclusions

Our study provides a plausible scenario on how the LRRTMs emerged as new binding partners of neurexins. We show that *lrrtm* became nested in *&-catenin* gene in the early jawed vertebrates followed by gene duplications that resulted in three nested *lrrtm/&-catenin* gene structures in most vertebrates. The clawed frog genome contains a clear *lrrtm3* ortholog but lacks the corresponding host (*&-catenin3*) gene. We identified several other protein-coding nested gene structures that are conserved in jawed vertebrates but either the host or the nested gene is missing in the frog or chicken lineages. Interestingly, majority of these nested genes comprise LRR domains.

Supporting Information

**Figure S1** Alignment of LRRTM family protein sequences from selected vertebrates.

(PDF)
Figure S2 Bayesian phylogenetic trees of LRRTM and α-catenin proteins.

Figure S3 Alignment shows that the degenerate ctnna3 forward (a3-F) and reverse (a3-R) primers have no mismatches with chicken ctnna3 genomic sequence.

Figure S4 Sequence alignment of the predicted 144 bp ctnna1 and ctnna2 PCR fragments.

Figure S5 Paralogous clusters containing α-catenin genes in human genome.

Table S1 Presence of neurexin AS4 exon in selected animal species.

Table S2 Accession numbers for the α-catenin sequences used.

Table S3 Conservation of selected human different strand nested gene structures in vertebrate genomes.

Table S4 BLAST analysis of tunicle and lancelet genomes using lamprey LRRTM sequences as query and reciprocal BLAST analysis against vertebrate genomes.

Table S5 Amino acid sequence identity (%) between vertebrate LRRTMs.

Table S6 Alternative splicing of neurexin AS4 exon in selected species.

Author Contributions

Conceived and designed the experiments: PU TK MSA. Performed the experiments: PU TK MSA. Analyzed the data: PU TK MSA. Contributed reagents/materials/analysis tools: PU TK MSA. Wrote the paper: PU TK MSA.

References


