# Cell Adhesion, the Backbone of the Synapse: "Vertebrate" and "Invertebrate" Perspectives

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Synapses are asymmetric intercellular junctions that mediate neuronal communication. The number, type, and connectivity patterns of synapses determine the formation, maintenance, and function of neural circuitries. The complexity and specificity of synaptogenesis relies upon modulation of adhesive properties, which regulate contact initiation, synapse formation, maturation, and functional plasticity. Disruption of adhesion may result in structural and functional imbalance that may lead to neurodevelopmental diseases, such as autism, or neurodegeneration, such as Alzheimer's disease. Therefore, understanding the roles of different adhesion protein families in synapse formation is crucial for unraveling the biology of neuronal circuit formation, as well as the pathogenesis of some brain disorders. The present review summarizes some of the knowledge that has been acquired in vertebrate and invertebrate genetic model organisms.

Synapses are asymmetric, intercellular junctions that are the basic structural units of neuronal transmission. The correct development of synaptic specializations and the establishment of appropriate connectivity patterns are crucial for the assembly of functional neuronal circuits. Improper synapse formation and function may cause neurodevelopmental disorders, such as mental retardation (MsR) and autism spectrum disorders (ASD) (McAllister 2007; Sudhof 2008), and likely play a role in neurodegenerative disorders, such as Alzheimer's disease (AD) (Haass and Selkoe 2007). At chemical synapses (reviewed in Sudhof 2004; Zhai and Bellen 2004; Waites et al. 2005; McAllister 2007; Jin and Garner 2008), the presynaptic compartment contains synaptic vesicles (SV), organized in functionally distinct subcellular pools. A subset of SVs docks to the presynaptic membrane around protein-dense release sites, named active zones (AZ). Upon the arrival of an action potential at the terminal, the docked and "primed" SVs fuse with the plasma membrane and release neurotransmitter molecules into the synaptic cleft. Depending on the type of synapse (i.e., excitatory vs. inhibitory synapses), neurotransmitters ultimately

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Figure 1. (A-C) Different stages of synapse formation. (A) Target selection, (B) Synapse assembly, (C) Synapse maturation and stabilization. (D-F) The role of cell adhesion molecules in synapse formation is exemplified by the paradigm of N-cadherin and catenins in regulation of the morphology and strength of dendritic spine heads. (D) At an early stage the dendritic spines are elongated from motile structures "seeking" their synaptic partners. (E) The contacts between the presynaptic and postsynaptic compartments are stabilized by recruitment of additional cell adhesion molecules. Adhesional interactions activate downstream pathways that remodel the cytoskeleton and organize pre- and postsynaptic apparatuses. (F) Cell adhesion complexes, stabilized by increased synaptic activity, promote the expansion of the dendritic spine head and the maturation/ stabilization of the synapse. Retraction and expansion is dependent on synaptic plasticity.

activate an appropriate set of postsynaptic receptors that are accurately apposed to the AZ.

Synapse formation occurs in several steps (Fig. 1) (reviewed in Eaton and Davis 2003; Goda and Davis 2003; Waites et al. 2005; Garner et al. 2006; Gerrow and El-Husseini 2006; McAllister 2007). Spatiotemporal signals guide axons through heterogeneous cellular environments to contact appropriate postsynaptic targets. At their destination, axonal growth cones initiate synaptogenesis through adhesive interactions with target cells. In the mammalian central nervous system (CNS), immature postsynaptic dendritic spines initially protrude as thin, actin-rich filopodia on the surface of dendrites. Similarly, at the Drosophila neuromuscular junction (NMJ), myopodia develop from the muscles (Ritzenthaler et al. 2000). The stabilization of intercellular contacts

and their elaboration into mature, functional synapses involves cytoskeletal arrangements and recruitment of pre- and postsynaptic components to contact sites in spines and boutons. Conversely, retraction of contacts results in synaptic elimination. Both stabilization and retraction sculpt a functional neuronal circuitry.

In addition to the plastic nature of synapse formation, the vast heterogeneity of synapses (in terms of target selection, morphology, and type of neurotransmitter released) greatly enhances the complexity of synaptogenesis (reviewed in Craig and Boudin 2001; Craig et al. 2006; Gerrow and El-Husseini 2006). The complexity and specificity of synaptogenesis relies upon the modulation of adhesion between the pre- and postsynaptic components (reviewed in Craig et al. 2006; Gerrow and El-Husseini 2006; Piechotta et al. 2006; Dalva et al. 2007; Shapiro et al. 2007; Yamada and Nelson 2007; Gottmann 2008). Cell adhesive interactions enable cell–cell recognition via extracellular domains and also mediate intracellular signaling cascades that affect synapse morphology and organize scaffolding complexes. Thus, cell adhesion molecules (CAMs) coordinate multiple synaptogenic steps.

However, in vitro and in vivo studies of vertebrate CAMs are often at odds with each other. Indeed, there are no examples of mutants for synaptic CAMs that exhibit prominent defects in synapse formation. This apparent "resilience" of synapses is probably caused by functional redundancy or compensatory effects among different CAMs (Piechotta et al. 2006). Hence, studies using simpler organisms less riddled by redundancy, such as *Caenorhabditis elegans* and *Drosophila*, have aided in our understanding of the role that these molecules play in organizing synapses.

In this survey, we discuss the roles of the best characterized CAM families of proteins involved in synaptogenesis. Our focus is to highlight the complex principles that govern the molecular basis of synapse formation and function from a comparative perspective. We will present results from cell culture studies as well as in vivo analyses in vertebrate systems and refer to invertebrate studies, mainly performed in Drosophila and C. elegans, when they have provided important insights into the role of particular CAM protein families. However, we do not discuss secreted factors, for which we refer the reader to numerous excellent reviews (as for example Washbourne et al. 2004; Salinas 2005; Piechotta et al. 2006; Shapiro et al. 2006; Dalva 2007; Yamada and Nelson 2007; Biederer and Stagi 2008; Salinas and Zou 2008).

# THE NEUROLIGINS-NEUREXINS: SUFFICIENCY VERSUS NECESSITY

The Neuroligin (Nlg)–Neurexin (Nrx) proteins play a major role in synapse formation and function (reviewed in Dean and Dresbach 2006; Dalva et al. 2007; Sudhof 2008). Neuroligins are type I membrane proteins consisting of an extracellular, catalytically inactive acetylcholinesterase domain that mediates binding to the following: neurexins, an O-glycosylation motif, a transmembrane (TM) domain, a cytoplasmic PDZ (post synaptic density protein [PSD95]), Drosophila disc large tumor suppressor (Dlg), and a zonula occludens-1 protein (zo-1) domain (Fig. 2) (Craig and Kang 2007; Sudhof 2008). There are four neuroligin genes in vertebrates, but alternative splicing increases the complexity of this protein family (Ichtchenko et al. 1996; Bolliger et al. 2001). Neuroligins, which are enriched postsynaptically, interact with presynaptic neurexins (Song et al. 1999). Three neurexin genes have been reported in mammals (Nrx 1-3), each with dual promoters that enable expression of two distinct protein isoforms, a long  $\alpha$ - and a short  $\beta$ -isoform. The latter short isoforms bind to neuroligins (Tabuchi and Sudhof 2002; Sudhof 2008), neurexins contain adhesive, extracellular laminin, nectin, sexhormone binding globulin (LNS) domains prone to extensive alternative splicing (Fig. 2) (Rudenko et al. 1999, 2001). Though found presynaptically at both excitatory and inhibitory synapses (Ushkaryov et al. 1992; Ullrich et al. 1995; Dean et al. 2003; Graf et al. 2004), neurexins have also been reported to be present on postsynaptic cells (Kattenstroth et al. 2004; Taniguchi et al. 2007).

Neuroligins induce presynaptic differentiation of contacting neurites when expressed in heterologous nonneuronal cells (Scheiffele et al. 2000) and regulate synapse number and spine density in cell culture (Chih et al. 2005). In addition, recruitment of PSD-95 to the Neuroligin PDZ domain clusters NMDA receptors and other postsynaptic proteins (Fig. 2) (Chih et al. 2004). Neurexin overexpression in heterophilic cells induces postsynaptic differentiation of contacting neurites in vitro (Graf et al. 2004; Nam and Chen 2005; Chih et al. 2006). Neurexin signaling induces presynaptic specialization and is linked with the synaptic release machinery, voltage gated calcium channel (VGCC) clustering, and actin cytoskeletal changes (Hata et al. 1996; Butz et al. 1998; Biederer and Sudhof 2000; Atasoy et al. 2007).



Figure 2. Diagram of Nrx – Nlg, LRR, and Ig mediated adhesion at excitatory synapses. Neurexins participate in the organization of presynaptic apparatuses and are linked to the synaptic vesicle cycle through interaction with CASK/Mint/Veli. Neuroligins interact with the postsynaptic PDZ scaffolding molecule PSD-95, which organizes the postsynaptic receptors (mainly NMDAR). Neurexins and neuroligins also participate at inhibitory synapses. Therefore, they are important for the balance of excitatory and inhibitory neurotransmission. Postsynaptic NGL2 binds to presynaptic GPI anchored Netrin G. NGL2 binds to the postsynaptic PDZ scaffolding molecule PSD95 and recruits NMDAR, but not AMPAR, in coculture experiments. SALM family members regulate the differentiation of neurites, organize postsynaptic sites by interacting with PSD-95, and recruit mainly NMDAR, and to a lesser extend AMPAR, in coculture experiments. Although no effects of SALMs on presynaptic organization are known, SALMs form distinct homophilic and heterophilic interactions suggesting adhesive roles on both sides of synapses. Ig molecules participate in both the structural and the functional organization of the synapse. SynCAM forms preferentially heterophilic interactions and induces synapse formation in coculture experiments. Presynaptically, it participates in the functional organization of the terminal through the interaction with CASK/Mint/Veli complexes. Postsynaptically, it interacts with the scaffolding molecule PSD-95. NCAM and L1-CAM form homophilic complexes and regulate cytoskeleton dynamics pre- and postsynaptically through interactions with spectrin and ankyrin.

In summary, the neurexin-neuroligin interactions are sufficient in cell culture assays to induce synapse formation, suggesting that they play a critical role in synapse formation.

The synaptogenic activities of Nlg and Nrx depend on their physical interaction (Scheiffele et al. 2000). These heterophilic associations regulate both excitatory and inhibitory synaptogenesis. Their ability to define different synapse types likely involves cell-type specific localization, as well as particular neuroligin– neurexin combinations (Boucard et al. 2005; Chih et al. 2006). For example, Nlg-1 and -4 exclusively localize to excitatory synapses, whereas Nlg-2 is found only at inhibitory synapses, suggesting distinct roles at these terminals (Graf et al. 2004; Song et al. 1999; Varoqueaux et al. 2004). Nlg-3 can be found at both types of synapses (Budreck and Scheiffele 2007). Interestingly, an insert in splice site B of Nlg-1 disrupts binding to Nrx-1 $\beta$  and favors its localization to excitatory synapses. On the other end, Nlg-1 isoforms without the insert in splice site B bind to both  $\alpha$ - and  $\beta$ -neurexins (Boucard et al. 2005; Chih et al. 2006). Hence, subtype and splice code variants of neurexin and neuroligin may dictate their binding specificity and roles in functional differentiation during synapse formation (Dalva et al. 2007).

The aforementioned data indicate that the Nrx-Nlg axis is sufficient to induce synapse formation in cell culture. However, in vivo studies paint a different picture. Removal of Nlg 1–3 or  $\alpha$ -Nrx in mice does not support a singular inductive role for these proteins (Missler et al. 2003; Varoqueaux et al. 2006). Nlg triple knockout mice die soon after birth from respiratory failure, likely because of a subtle synaptic imbalance of excitatory and inhibitory synapses in the brainstem, although synapse numbers in most areas of the brain, including respiratory centers, are intact (Varoqueaux et al. 2006). Similarly, α-Nrx triple knockout mice exhibit neonatal lethality and reduced synaptic transmission at both excitatory and inhibitory synapses (Missler et al. 2003), though synapse number and morphology are also unaffected (Dudanova et al. 2007). Electrophysiological studies, however, indicate a requirement for a presynaptic function of the neurexins and a role in regulating the activity of synaptic Ca<sup>2+</sup> channels (Missler 2003). Hence, the in vivo analysis indicates that the Nrx-Nlg proteins are sufficient in vitro but not necessary in vivo for synapse formation. Redundancy with other CAM proteins may underlie the apparent discrepancy between in vitro and in vivo studies. Alternatively, the Nrx-Nlg may be required in synapse stabilization at a later stage.

Drosophila contains a single neurexin (*dnrx*) and a single neuroligin gene homologous to the vertebrate counterparts (Tabuchi and Sudhof 2002; Li et al. 2007; Zeng et al. 2007). A neurexin IV has been reported in *Drosophila*, but this protein is clearly less homologous to Nrx I and was later shown to be more similar to the vertebrate Caspr protein (Bhat et al. 2001). Both NrxIV and Caspr were shown to play a role in septate junction formation and axon insulation in flies and mice (Baumgartner et al. 1996; Bhat et al. 2001). dNrx ( $\alpha$ -neurexin) is expressed in neurons and localizes to active zones at the NMJ (Li et al. 2007). dnrx1 controls synapse growth, differentiation, and function, in agreement with a synaptogenic role for neurexin proteins. Overexpression of *dnrx* leads to synaptic overgrowth. Conversely, loss of *dnrx* leads to a reduction of the number of synaptic boutons at the NMJ and misalignment of the pre- and postsynaptic compartments. The SV protein synaptotagmin and the AZ protein Bruchpilot are mislocalized in *dnrx* mutant axons, indicating a role in the recruitment, localization, or transport of key synaptic components (Li et al. 2007). Future studies in Drosophila should shed a better insight into how the neuroliginneurexin system regulates synapse development. An important step will be to determine whether the Drosophila Nlg gene, which reportedly exhibits the same spatiotemporal pattern of expression as dNrx, also affects synapse growth and function (Li et al. 2007).

In summary, neurexins and neuroligins are not absolutely required to form synapses, but they clearly play a role in the formation of the ultrastructural morphological features of synapses in flies and affect synapse function in vertebrates in vivo. These observations also emphasize the importance of carrying out in vivo experiments as they reveal a higher order of complexity than the in vitro cell culture data.

### LEUCINE RICH REPEAT (LRR) PROTEINS

The leucine rich repeat (LRR) motifs are 20–29 amino acid (aa)-long protein interaction sequences, present in extracellular domains of a wide range of transmembrane as well as cytosolic proteins. Many LRR proteins regulate neurite outgrowth and migration (reviewed in Ko and Kim 2007), but two specific members of this family have been implicated in synaptogenesis: the netrin-G ligand (NGL) and the synaptic-like adhesion molecule (SALM) (Fig. 2).

The NGL family is composed of three type I transmembrane members, NGL 1–3. The NGL proteins contain nine LRR extracellular

interaction domains, immunoglobulin (Ig) domains, a TM domain, and a PDZ motif, which interacts with PSD-95 (Fig. 2) (reviewed in Ko and Kim 2007). Extracellularly, the NGLs associate with netrin-G1 or netrin-G2, a family of netrin-like cell adhesion molecules, with a great number of spatiotemporally regulated splice variants, mainly expressed in the brain. NGL1 interacts with netrin-G1 (and possibly with other receptors as well) to regulate the growth of thalamocortical axons (Lin et al. 2003).

Interestingly, the NGL/netrin-G system shares key functional features with the Nlg-Nrx axis. Overexpression of NGL in nonneuronal cells in vitro induces the differentiation of presynapses in contacting axons of cocultured neurons, although overexpression of netrin-G does not have the reciprocal capacity of inducing postsynaptic differentiation, as observed for Nrx (Kim et al. 2006). The possibility that netrin-G might not be the only ligand for NGLs may account for the unidirectional synaptogenic activity. For example, NGL3 does not interact with any of the netrin-G ligands (Kim et al. 2006). Furthermore, putative isoform specific interactions increase both the complexity and redundancy of adhesion. A role in synapse formation is further supported by the elevated expression levels of NGL in the brain postnatally and the ability of NGL-2 to induce clustering of NMDA receptors at excitatory synapses (Fig. 2) (Kim et al. 2006).

Interestingly, in *C. elegans*, a molecule distantly related to netrin-G, called netrin (a ligand for netrin receptors), is secreted by glial cells and plays a dual role in a pair of specific interneurons (Colon-Ramos et al. 2007). In this experimental system, netrin guides the axon of the postsynaptic neuron to the glial site of secretion, but unexpectedly, also orchestrates the differentiation of presynaptic boutons.

The SALM family of adhesion molecules contains five members in vertebrates. SALMs contain six LRR domains, an Ig domain, and a fibronectin III domain, followed by a transmembrane region and carboxy-terminal PDZ binding motif that interacts with PSD-95 (Fig. 2) (Ko et al. 2006; Ko and Kim 2007). The SALMs are mainly expressed in the brain. SALM-1 overexpression promotes excitatory synapse maturation and NMDA receptor clustering (Wang et al. 2006). SALM-2 regulates the number of excitatory synapses in cocultured neurons and associates with AMPA receptors more than with NMDA receptors (Ko et al. 2006; Wang et al. 2006). SALMs form distinct homo- and heterophilic interactions, suggesting adhesive roles pre- and postsynaptically (Seabold et al. 2008). However, the ligands and the nature of the molecular interactions of different SALMS need to be further elucidated.

Interestingly, in *Drosophila*, an overexpression genetic screen was recently conducted to identify novel cell membrane and secreted molecules with a role in target selection by the motor neuron axons (Kurusu et al. 2008). Out of 55 genes that were found to affect muscle targeting of motor axons and/or NMJ arborization patterns, 16 belong to the LRR family, including the *tartan* and *capricious* genes. *Capricious* is involved in target selectivity of both motor neuron and photoreceptor axons (Shishido et al. 1998; Shinza-Kameda et al. 2006). Tartan and Capricious cooperate in axonal pathfinding and have interchangeable extracellular domains (Kurusu et al. 2008).

In summary, LRR proteins play an important role in various aspects of neuronal development. However, additional studies are necessary to identify their mode of action in synaptogenesis.

# CONTROL OF SYNAPTOGENESIS BY MEMBERS OF THE IG SUPERFAMILY

The Ig superfamily is the largest, most diverse, and most ancient superfamily represented in the genomes of both vertebrate and invertebrate organisms (Vogel et al. 2003). Members of the Ig protein family are single-pass type I transmembrane proteins that contain variable numbers of globular, extracellular, cysteine looped, Ig or Ig-like domains that mediate homophilic or heterophilic interactions. They are typically followed by fibronectin III type repeats (Fig. 2) (reviewed in Walsh and Doherty 1997; Piechotta et al. 2006).

# The Synaptic Cell Adhesion Molecule (SynCAM)

The family of synaptic cell adhesion molecules (SynCAM) proteins, SynCAM1–4 (Biederer 2006), are expressed in the nervous system, where they constitute a *trans*-synaptic adhesion system (Fig. 2). SynCAMs can undergo further alternative splicing and are often post-translationally modified through glycosylation (Fogel et al. 2007), thus increasing their complexity. The differential expression pattern and the heterophilic pattern of interactions among SynCAMs establish an adhesion code for neuronal circuitry formation (Biederer and Stagi 2008; Thomas et al. 2008).

SynCAM1 (also named nectin-like 2) localizes to both sides of the synaptic cleft. SynCAM1 can trigger the differentiation of functional presynaptic specializations in the axons of cocultured neurons (Fig. 2), similarly to Nlg (Biederer et al. 2002), although the induced synapses may be functionally distinct (Sara et al. 2005). Upon coexpression of SynCAM with glutamate receptors in HEK cells, glutamate-receptor-mediated currents can be detected (Biederer et al. 2002). The synaptogenic effect of SynCAM might be mediated through interaction of intracellular motifs (common among all members of SynCAM) with FERM (fourpoint-one, ezrin, radixin, and moesin) domains of cytoskeletal adaptors and PDZ domains of synaptic scaffolding proteins, such as CASK and syntenin (Fig. 2) (Biederer and Stagi 2008).

Despite the potent synaptogenic activity of SynCAM1 in vitro, SynCAM 1 knockout mutant mice are viable and fertile and synaptogenesis is not altered, possibly because of functional redundancy with other SynCAM proteins or compensation by other adhesion signaling complexes (Fujita et al. 2006; van der Weyden et al. 2006). Hence, redundancy is a recurrent theme to explain the lack of expected phenotypes when these proteins with potent in vitro functions are removed in vivo.

# Neural Cell Adhesion Molecule (NCAM)

Neural cell adhesion molecule (NCAM) was one of the first membrane proteins implicated in cell adhesion between neurons. Three isoforms are produced from a single gene, one of which is glycosyl-phospahtidyl-inositol (GPI) linked to the membrane, whereas the other two are transmembrane molecules. NCAM regulates synapse formation, maturation, and function through homo- and heterophilic interactions (Fig. 2).

In vertebrates, NCAM localizes to developing synapses (Uryu et al. 1999) and its expression is activity-dependent (Schuster et al. 1998). Excitatory synapse density is reduced in NCAM-deficient cells when cocultured with wild-type neurons (Dityatev et al. 2000). Interestingly, synaptogenesis in this context depends on postsynaptic NCAM, its modification with polysialic acid (PSA) and activation of NMDA and fibroblast growth factor (FGF) receptors (Dityatev et al. 2004). However, synapse numbers from cultures of NCAM-deficient neurons alone are not different from wild-type cultures. Furthermore, mice lacking all three isoforms of NCAM are viable and fertile, although synaptic plasticity is impaired (Cremer et al. 1994; Muller et al. 1996; Cremer et al. 2000; Eckhardt et al. 2000; Bukalo et al. 2004). Synaptic transmission and vesicle dynamics at NCAM-deficient neuromuscular junctions are also altered (Polo-Parada et al. 2001). Hence, NCAM is essential for synapse function, but not synapse formation, possibly because of redundancy or compensation by other adhesion molecules. Alternatively, NCAM might only play a role in synaptic plasticity.

In *Drosophila*, fasciclin II (Fas II) is the only ortholog of vertebrate NCAM (reviewed in Packard et al. 2003; Kristiansen and Hortsch 2008). Similar to NCAM, there are three major protein isoforms of Fas II, two of which are transmembrane proteins and one that is GPI-anchored to the cell membrane. However, unlike the vertebrate homologs, none of the Fas II protein isoforms is modified by PSA. Fas II is expressed in numerous tissues, including the developing nervous system. Notably, the GPI-anchored isoform is expressed in nonneuronal cell types, especially glial cells where it provides an adhesive signal for guiding extending axons. The role of Fas II has been studied in the context of axonal pathfinding, synapse growth, and function at the NMJ and in the CNS.

Fas II is expressed in motor neuron axons and is especially enriched in their growth cones (Schuster et al. 1996a,b). Upon contact of the motor axon with the target muscle at the NMJ and initiation of synapse formation, Fas II becomes enriched pre- and postsynaptically. Overexpression of Fas II in the muscle affects target-selection and changes neuronal connectivity (Davis et al. 1997). However, in the absence of Fas II, synapses still form but eventually retract, suggesting that Fas II is not required for synapse induction, but rather stabilizes the nascent synapse (Schuster et al. 1996a,b). Lack of stability allows or induces dynamic structural changes during synapse growth. Indeed, reduced levels of Fas II allow synapse growth and sprouting in mutant flies (Schuster et al. 1996a,b). Interestingly, mutations that presynaptically increase synaptic activity by affecting cyclic AMP (cAMP) degradation result in reduction of FasII and expansion of the NMJ arborization pattern (Budnik et al. 1990; Zhong et al. 1992). Postsynaptically, Fas II localization at the NMJ is regulated through interaction with Dlg (the fly homolog of PSD-95) (Thomas et al. 1997). Ca<sup>2+</sup>-calmodulin protein kinase II (CaMKII) phosphorylates Dlg in an activity-dependent manner, causing the dissociation of Dlg from the postsynaptic density, reducing the binding of Dlg with FasII. This results in declustering and removal of Fas II from the synapse, thereby allowing an expansion of the synapse (Koh et al. 1999).

In the CNS, Fas II is not required for initial synapse formation, similarly to the principles of NMJ development, but a lack of balance between the pre- and postsynaptic levels of Fas II causes a decrease in synaptic input to the motor neurons and a reduction of the number of synapses (Baines et al. 2002). Fas II regulates synaptic function, and this has been documented in learning and memory related studies. Fas II is expressed in the axons of the mushroom bodies, the learning centers of the fly brain, where it is involved in memory storage, and maintenance and retrieval of memory (Cheng et al. 2001).

# L1-CAM

In vertebrates, L1-CAM, neurofascin, Nr-CAM, and CHL1 comprise the L1-type CAM protein group. L1-CAM interacts both homophilicaly and heterophilicaly. L1 is present in the CNS at the onset of differentiation. The highly conserved intracellular domains of most L1-type proteins contain ankyrin and FERM binding motifs linking it to spectrin and the actin cytoskeleton (Fig. 2) (Davis and Bennett 1994; Dickson et al. 2002; Cheng et al. 2005). However, L1 can also interact with microtubule stabilizing proteins such as doublecortin (Kizhatil et al. 2002).

L1-type proteins play a role in cell migration, neurite extension, axon pathfinding, myelination, fasciculation, synapse targeting, and long term potentiation (LTP) (Crossin and Krushel 2000; Gerrow and El-Husseini 2006; Piechotta et al. 2006; Maness and Schachner 2007). The L1-CAM gene is causally related to a variety of neurological disorders that are associated with mental retardation, hydrocephalus, and spasticity of the lower limbs (CRASH syndrome) (Fransen et al. 1995, 1997; Bateman et al. 1996; Fransen et al. 1997; Kenwrick and Doherty 1998; Kenwrick et al. 2000; De Angelis et al. 2002). Two L1-CAM knockout mice strains were independently generated (Dahme et al. 1997; Cohen et al. 1998). Dahme et al. (1997) reported that deletion of L1-CAM causes a high rate of embryonic lethality and compromises the postnatal survival of knockout mice, which also display a deficiency of peripheral sensory and motor innervation, a reduction of the corticospinal tract, an enlargement of the cerebral ventricles, and an impaired axon-Schwann cell association (Dahme et al. 1997). In other studies, the L1 knockout mice were viable but exhibited an axon guidance defect in the corticospinal tract, disturbed axonal targeting, altered dendritic morphology and orientation, and abnormalities of spatial learning and exploratory behavior (Cohen et al. 1998; Fransen et al. 1998; Demyanenko et al. 1999, 2001). An electrophysiological study of L1 mice has revealed a reduction of y-aminobutyric acid (GABA)-ergic transmission in the CA1 region of the hippocampus. Morphologically, a corresponding decrease in the density of perisomatic symmetrical synapses has been observed and synaptic vesicles show a more diffuse distribution (Saghatelyan et al. 2004). In a hippocampus-specific conditional L1-CAM knockout mouse model, basal excitatory transmission is enhanced in the mutant neurons and behavioral deficits are only partly similar to those observed in constitutive  $L1^{-/-}$  mice (Law et al. 2003). The above findings suggest an involvement of L1 in the formation and/or maintenance of inhibitory synapses and imply that L1 might be functioning along with other cell adhesion systems.

The only homolog of L1-CAM in the fly is neuroglian (Nrg) (Bieber et al. 1989; Walsh and Doherty 1997; Kristiansen and Hortsch 2008). Two transcripts are generated encoding a short and a long isoform (Hortsch et al. 1990; Hall and Bieber 1997). The two isoforms differ in their cytoplasmic domains and the short isoform is expressed in epidermis, muscle, trachea, and glia, whereas the long isoform is restricted to the nervous system (Hortsch et al. 1990). Nrg plays a role in axon growth in the peripheral nervous system during embryonic and postembryonic development. Null nrg mutations are lethal, and motor axons are stalled in embryos (Bieber et al. 1989; Hall and Bieber 1997; Martin et al. 2008). Neuronal expression of Nrg rescues the mutant phenotype suggesting that Nrg mediates heterophilic adhesion of the advancing axons with their substrate (Martin et al. 2008). In the adult ocellar sensory system, Nrg establishes two distinct axonal pathways, one originating from the bristle mechanoreceptors and the other originating from the ocellar pioneer neurons (Garcia-Alonso et al. 2000; Kristiansen et al. 2005). Especially in the ocellar pioneer neurons, Nrg functions redundantly with Fas II. Interestingly, it has been proposed that Nrg mediated activation of epidermal growth factor (EGF) and FGF receptors is needed for the pathfinding process (Garcia-Alonso et al. 2000).

It has been suggested that ankyrin-binding to L1-type CAMs provides a "master switch," so that L1-type adhesive proteins can function in different contexts: in an ankyrin-independent manner during neurite outgrowth and axonal pathfinding, or in ankyrin-dependent manner during synaptogenesis (Hortsch et al. 2009). Indeed, Nrg also functions along with the intracellular adaptor ankyrin to suppress axonal sprouting and dendritic branching in a subset of multidendritic neurons (Yamamoto et al. 2006) and control proper synapse formation and function in the giant fiber synapse by organizing the microtubules in the presynaptic terminals (Godenschwege et al. 2006). The significance of ankyrin in organizing the stability of presynaptic cytoskeleton is further supported by experiments at the fly NMJ, which show that in the absence of the neuronally expressed ankyrin 2, synapses retract, leaving behind "footprints" of postsynaptic specializations (Koch et al. 2008; Pielage et al. 2008). In addition, postsynaptic spectrin is necessary for the development and organization of both the presynaptic active zone and the opposing postsynaptic density (Pielage et al. 2006). It would be interesting to assess whether Nrg participates in these processes as well.

### Synaptogenesis Abnormal (SYG) -1 and -2

In the *C. elegans* egg-laying circuitry, two transmembrane proteins, SYG-1 and SYG-2, control target recognition and synapse formation of the hermaphrodite specific motor neuron HSNL. SYG-2 is present on vulval epithelial cells and interacts with SYG-1, which is expressed on HSNL neuron (Shen and Bargmann 2003; Shen et al. 2004). Upon interaction with SYG-2, SYG-1 initiates the hierarchical assembly of presynaptic specializations in HSNL (Patel et al. 2006) by recruiting SYD-1 (a rhoGTPase activating protein factor) and SYD-2 (liprin- $\alpha$ ). Furthermore, the interaction of SYG-1 and SYG-2 enables SYG-1 to bind to SKR-1, an E3 ubiquitin ligase, and inhibit its activity, protecting the nascent synapses from proteasome mediated, aberrant elimination (Ding et al. 2007). *syg-2* mutants lack synapses at the normal location and instead exhibit ectopic synapses and a reduced number of active zones (Shen et al. 2004). In *syg-1* mutants, vesicles fail to accumulate at normal synaptic locations and form ectopic clusters instead (Shen and Bargmann 2003).

There are two SYG-1 homologs in Drosophila, irregular chiasm C-roughest (IrreC-Rst) and kin of IrreC also named dumbfounded (Kirre or Duf), and two SYG-2 homologs, sticks and stones (Sns) and Hibris (Chao and Shen 2008). SYG-1/IrreC/Kirre are homologous to Neph receptor and SYG-2/ Hibris/Sns are homologues of nephrin ligands (Chao and Shen 2008). IrreC-Rst, Kirre, and Hibris are involved in patterning of the Drosophila eye and in synaptic wiring of the visual system (Ramos et al. 1993; Bao and Cagan 2005; Carthew 2005, 2007; Bazigou et al. 2007). Heterophilic interactions between IrreC-Rst and Kirre, which are expressed in muscle founder cells with Hibris and Sns, respectively (which are expressed on fusion competent myoblasts), are important for Drosophila myoblast fusion (Bour et al. 2000; Ruiz-Gomez et al. 2000; Artero et al. 2001; Dworak et al. 2001; Strunkelnberg et al. 2001; Dworak and Sink 2002). Neph/nephrin are instrumental in kidney function (Patrakka and Tryggvason 2007). However, their expression pattern in the nervous system and their ability to interact with CASK implies that the vertebrate homologs may be involved in synapse formation as well (Gerke et al. 2006).

# THE INSTRUMENTAL ROLE OF LIPRIN-α AND LEUCOCYTE-COMMON ANTIGEN RELATED (LAR) PROTEINS IN SYNAPSE FORMATION AND ACTIVE ZONE MORPHOGENESIS

Liprin- $\alpha$  family proteins contain an aminoterminal coiled coil domain and a carboxyterminal liprin homology domain, comprised of three sterile  $\alpha$  motifs (SAMs) (reviewed in Stryker and Johnson 2007). Through these motifs, liprin- $\alpha$  proteins interact with leucocyte-common antigen related (LAR) proteins. In vertebrates, there are four liprin- $\alpha$ (liprin  $\alpha$  1–4) and three LAR (LAR, PTP- $\sigma$ , and PTP- $\delta$ ) paralogues. Members of the LAR family are transmembrane tyrosine phosphatases with highly conserved extracellular and cytoplasmic domains. Their extracellular region is structurally similar to cell adhesion molecules of the Ig family. Intracellularly, the phosphatase domain proximal to the membrane possesses the majority of the catalytic activity, whereas the distal one seems to interact with numerous downstream effectors, including  $\beta$ -catenin and members of the liprin- $\alpha$  protein family (reviewed in Stryker and Johnson 2007) (Fig. 3).

LAR and liprin- $\alpha$  regulate synapse formation and function (reviewed in Spangler and Hoogenraad 2007; Stryker and Johnson 2007). Presynaptically, mammalian liprin- $\alpha$ associates with two major synaptic complexes. One of the complexes is formed by liprin- $\alpha$ interacting through the coiled coil regions with the cytomatrix at the active zoneassociated structural protein (CAST) and Rab3-interacting molecule (RIM) (Fig. 3) (Ohtsuka et al. 2002; Schoch et al. 2002; Ko et al. 2003). The other complex liprin- $\alpha$  associates with is the mammalian-LIN-seven protein (MALS)-CASK-Mint complex (Olsen et al. 2005). Postsynaptically, liprin- $\alpha$  interacts with glutamate receptor interacting protein 1 (GRIP1), an AMPA receptor binding protein (Wyszynski et al. 2002)(Fig. 3). The interaction of LAR and liprin- $\alpha$  regulates AMPA receptor clustering and dendritic spine morphology. Intriguingly, the phosphatase activity of LAR and its interactions with liprin- $\alpha$  and GRIP1 regulate the delivery of cadherin/β-catenin complexes during the development and maintenance of excitatory synapses (Dunah et al. 2005). Liprin- $\alpha$  is regulated by CAMKII. Overexpression of nondegradable mutant forms of liprin or dominant negative forms of LAR that cannot bind to liprin impair signaling



Figure 3. Diagram of LAR-liprin- $\alpha$  signaling and cadherin-nectin mediated adhesion at excitatory synapses. Liprin- $\alpha$  is the mediator of LAR signaling in both pre- and postsynaptic compartments. Thus, LAR/liprin- $\alpha$  complexes control neurotransmitter release and active zone formation through interactions with CAS/Mint/ Veli, RIM, and ERC. LAR/liprin- $\alpha$  complexes regulate the postsynaptic organization of neurotransmitter receptors through interaction with GRIP, an AMPAR interacting protein. Cadherins are localized at *puncta adherentia*, the region flanking the active zone, along with nectins. Cadherins form homophilic complexes. The intracellular domain of cadherins interacts with catenins that ultimately link cadherins to the cytoskeleton. Cadherins are the physical link between synaptic activity and dendritic spine morphology (see text and Fig. 1C–F). Cadherins also control the organization of postsynaptic receptors. Nectins form heterophilic complexes and are able to recruit cadherins, but they can also interact with other adhesions systems, such as ephrins. Nectins are indirectly linked to the cytoskeleton through Afadin.

and lead to a reduction of dendritic branching and spine density (Hoogenraad et al. 2007).

LAR-liprin- $\alpha$  signaling has been studied in *C. elegans* and *Drosophila* (reviewed in Stryker and Johnson 2007). In *C. elegans*, SYD-2 (liprin- $\alpha$ ) is required presynaptically for the formation of active zones and synaptic function (Zhen and Jin 1999). In addition, the localization of PTP-3A, one of the protein isoforms of LAR, is disrupted in *syd-2* mutants. Mutants lacking PTP-3A phenocopy *syd-2* mutants in terms of active zone organization (Zhen and Jin 1999). The precise localization at the synapse of PTP-3A also depends on interactions of the extracellular Ig domains with

nidogen, a sulfated glycoprotein, and animals lacking nidogen phenocopy *ptp-3a* and *syd-2* mutants (Ackley et al. 2005).

In *Drosophila*, fly LAR and liprin- $\alpha$  homologs are required in the visual system, along with N-cadherin, at an early developmental stage for unbundling the R1–R6 afferent photoreceptor growth cones, so that they can project properly into assembling laminal cartridges (Clandinin et al. 2001; Choe et al. 2006) (also see Fig. 4). Unlike N-cadherin, which is required both pre- and postsynaptically (see the following discussion), liprin- $\alpha$  and LAR are required only in the presynaptic terminals, where they may regulate N-cadherin



Figure 4. Synaptic wiring in the visual system of Drosophila. The compound eye of Drosophila is comprised of 750 ommatidia, each of which has eight photoreceptors, named R1-R8. Light stimulates the photoreceptors at the outer level of the retina, where the cell bodies lie. The signal is transmitted to the postsynaptic partners at the inner neuropils of the lamina and the medulla. R1-R6 photoreceptor axons from each ommatidium stop at the lamina, where they defasciculate and innervate nearby synaptic cartridges according to the principle of neural superposition. R7 and R8 photoreceptor axons continue to the medulla, where they terminate at distinct layers. In loss of function of N-cadherin, R1 and R6 fail to defasciculate, whereas R7 retracts to the wrong R8 specific layer. In loss of function of Flamingo cadherin, R1-R6 defasciculate but innervate abberrantly the synaptic cartridges, whereas the R8 photoreceptor axons terminate in the R7 layer (see text and also Mast et al. 2006; Ting and Lee 2007).

activity to establish a form of functional asymmetry (Clandinin et al. 2001; Choe et al. 2006). LAR and liprin- $\alpha$  are required for proper layer target selection of the R7 photoreceptor axons (Newsome et al. 2000; Maurel-Zaffran et al. 2001; Hofmeyer et al. 2006), where LAR and liprin- $\alpha$  form physical complexes. Although there is evidence of LAR independent liprin-α function in certain contexts (Hofmeyer et al. 2006), at the NMJ they control synapse growth and active zones formation together (Kaufmann et al. 2002). In the absence of LAR or liprin- $\alpha$ , synapses are smaller and less elaborate than in wild-type animals, whereas presynaptic overexpression of LAR is adequate to increase synaptic size in a liprin- $\alpha$  dependent manner. Interestingly, liprin- $\alpha$  is normally down-regulated by the ubiquitinating activity of anaphase promoting complex (APC), which, when absent, results in stabilization of liprin- $\alpha$  and overgrown synapses (van Roessel et al. 2004). The interaction between liprin- $\alpha$  and APC is conserved in vertebrates (Hoogenraad et al. 2007).

Another parallel among Drosophila and C. elegans is the interaction with glycoproteins. Two heparin sulfate proteoglycans, syndecan (sdc) and *dallylike* (dlp) regulate in opposite ways LAR activity. Sdc promotes LAR activity and synapse growth presynaptically, whereas Dlp inhibits it (Johnson et al. 2006). In the absence of sdc, synapse growth is impaired, similar to LAR and liprin-a mutants (Johnson et al. 2006). However, overexpression of Dlp postsynaptically inhibits LAR and results in decreased synaptic growth, whereas in parallel it increases the area of the active zones (Johnson et al. 2006), phenocopying in this manner LAR and liprin- $\alpha$  mutations (Kaufmann et al. 2002). Interestingly, in both mammalian cells and Drosophila, liprin-α interacts with KIF1A, a neuron specific motor transport protein, capable of interacting with synaptic proteins (Shin et al. 2003; Miller et al. 2005), indicating that LAR-liprin interactions regulate the recruitment of molecular complexes that mediate active zone and synapse formation.

# CADHERIN SUPERFAMILY

Cadherins are involved in cell adhesion in numerous cell types in invertebrate and vertebrate organisms (reviewed in Shapiro et al. 2007; Takeichi 2007; Tai et al. 2008). Structurally, cadherins are single pass transmembrane molecules whose ectodomain contains a variable number of calcium binding cadherin repeats (Fig. 3). On the basis of their protein sequence, the domain structure, and the genomic organization, cadherins belong to two major branches, the cadherins and the cadherin related proteins, further subdivided into a total of six subfamilies (Nollet et al. 2000; Hulpiau and van Roy 2009). We mainly refer to the classical cadherins and protocadherins with respect to their role in the nervous system.

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# Nonclassical Cadherins: Protocadherins and Flamingo (Fmi)

Protocadherins (Pcdh) are considered the primordial type of classical cadherins (reviewed in Frank and Kemler 2002). Protocadherins bear a variable number of cadherin repeats (Fig. 3). Based on their genomic organization and protein sequence, protocadherins are divided into the clustered and the nonclustered protocadherins (Redies et al. 2005; Morishita and Yagi 2007). All protocadherins undergo alternative splicing, and some members of the protocadherin family have region-specific expression patterns in the developing brain (Kohmura et al. 1998; Carroll et al. 2001; Hirano et al. 2002; Wang et al. 2002b; Phillips et al. 2003), providing an adhesive code for the establishment of specific brain structures (Serafini 1999; Shapiro and Colman 1999; Redies 2000; Shapiro et al. 2007). Moreover, protocadherins are localized to synaptic junctions and may modulate synaptic structure and transmission properties (Fig. 3) (Phillips et al. 2003).

The role of protocadherins in synapse formation and maturation has been documented genetically in null mutants for the Pcdh- $\gamma$ gene cluster. In *Pcdh*- $\gamma^{-/-}$  animals, there is an apoptotic degeneration of spinal interneurons, which leads to neonatal death (Wang et al. 2002a). Although prevention of cell death in mutants by removal of the proapoptotic Bax protein rescues the survival of the neurons, the density of synaptic puncta and of currents recorded from in vitro cultured neurons are still reduced, indicating a role of Pcdh- $\gamma$  in synaptogenesis (Weiner et al. 2005). The lack of general effects of Pcdh- $\gamma$  on the nervous system could be caused by compensation by Pcdh- $\alpha$  and Pcdh- $\beta$ . Further genetic analysis of Pcdh-a and Pcdh-B mutants is needed.

CELSR1-3 belong to the Flamingo/CELSR group of cadherins and are characterized by seven transmembrane domains (Takeichi 2007). CELSR2 and 3 have been implicated in nervous system development. Knockdown of CELSR2 results in retraction of dendrites, suggesting that the CELSR2 mediated homophilic interactions are important for maintenance of dendritic branching (Shima et al. 2004). Ablation of CELSR3 results in axonal tract defects (Tissir et al. 2005). The fly protein Flamingo (Fmi) is a unique nonclassical cadherin with seven transmembrane domains, that regulates planar cell polarity in epithelial cells (Lu et al. 1999), dendritic tiling of peripheral neurons (Gao et al. 1999, 2000; Grueber 2002), and axon target selection in the visual system of Drosophila (Lee et al. 2003; Senti et al. 2003; Chen and Clandinin 2008). In the visual system, Fmi plays a role in both the lamina and the medulla neuropils (Fig. 4). In the medulla, Fmi is expressed in the afferent R7 and R8 photoreceptor axons, as well as in their target neurons. Fmi controls the layer target selection of R8 photoreceptor axons, which in the absence of Fmi retract to superficial layers (Lee et al. 2003; Senti et al. 2003). In addition, Fmi controls the tiling pattern of R8 axons, because mutations in Fmi cause a significant degree of overlap among the growth cones, as if the repulsion is impaired (Lee et al. 2003; Senti et al. 2003). In the lamina, Fmi functions strictly nonautonomously as a short-range, homophilic adhesive signal between specific R1-R6 photoreceptor cell growth cones, ensuring that the proper trajectory toward the assembling cartridges is followed (Chen and Clandinin 2008).

# **Classical Cadherins**

Multiple classic cadherins exhibit distinct spatiotemporal patterns of expression (Suzuki et al. 1997; Inoue et al. 1998; Bekirov et al. 2002), suggesting that homophilic interactions among the extracellular cadherin repeats of different types of cadherins play a role in target recognition and synapse formation (Inoue et al. 1998; Miskevich et al. 1998; Wohrn et al. 1998; Ranscht 2000).

Classic cadherins and their associated partners, the catenins, localize at synapses preand postsynaptically (Fig. 3) (Yamagata et al. 1995, 2003; Fannon and Colman 1996; Uchida et al. 1996). In the mature synapse, the

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cadherin-catenin complexes are present in puncta adherentia, which are the regions flanking the active zone and are considered sites of mechanical adhesion (Uchida et al. 1996). N-cadherin is cotransported with active zone components to sites of synapse formation (Jontes et al. 2004) and colocalizes with other synaptic markers (Benson and Tanaka 1998). Interestingly, N-cadherin is retained mostly in excitatory and lost from inhibitory synapses (Benson and Tanaka 1998). The proximal region of the cytoplasmic domain of cadherins binds to p120-catenin family members, whereas the distal region binds to  $\beta$ -catenin (Fig. 3). β-catenins contain a PDZ domain that enables interactions with synaptic proteins (Arikkath and Reichardt 2008). The PDZ domain interacts with  $\alpha$ -catenin, which interacts with cytoskeletal actin binding proteins, such as  $\alpha$ -actinin or profilin (Fig. 3) (Pokutta and Weis 2007; Arikkath and Reichardt 2008). Clustering of cadherins may increase the critical concentration of  $\alpha$ -catenin locally, which may favor the formation of stable cell contacts by suppressing the Arp2/3 mediated actin polymerization (Pokutta and Weis 2007). Notably, the extracellular cadherin repeats are also able to bind to calcium  $(Ca^{2+})$ , which rigidifies the molecular structure of cadherins, enhances their dimerization, and stabilizes them by rendering them resistant to proteolytic degradation for extended periods of time (Fig. 1) (Shapiro et al. 2007).  $Ca^{2+}$  also reverses the inhibitory effect of peptides or antibodies directed against the extracellular domain of N-cadherin (Tang et al. 1998). Thus, cadherins become trans-synaptic sensors of synaptic activity and regulators of both presynaptic and postsynaptic components. Indeed, synaptic activity stabilizes dimers of N-cadherin and renders them more resistant to proteolytic degradation (Tanaka et al. 2000). NMDA activation retains N-cadherin at the membrane by inhibiting its endocytosis (Tai et al. 2007). Activation of AMPA receptors on the other hand, leads to lateral expansion of the dendritic spine heads, during which N-cadherin is redistributed to facilitate enhanced adhesion (Fig. 1) (Okamura et al. 2004).

Morphological changes in dendritic spines reflect alterations in synaptic strength (synaptic plasticity). Loss of function of N-cadherin,  $\beta$ -catenin, or  $\alpha$ -catenin results in a less stable spine structure, reduction in the accumulation of pre- and postsynaptic markers, and impaired synaptic function (Elia et al. 2006; Jungling et al. 2006; Tanabe et al. 2006; Togashi et al. 2006; Okuda et al. 2007; Saglietti et al. 2007). N-cadherin also regulates the trafficking of AMPA receptors (Nuriya and Huganir 2006; Saglietti et al. 2007) and postsynaptic loss of N-cadherin causes defects in neurotransmitter exocytosis by presynaptic wild-type neurons (Jungling et al. 2006), suggesting a role in retrograde signaling. Loss of function of p120 (pre or post) catenin leads to decreased spine density, fewer mature spines, and mislocalization of pre- and postsynaptic components (Elia et al. 2006). Conversely, overexpression of  $\alpha$ -catenin increases dendritic spine density and stability (Abe et al. 2004).

Genetic analysis in Drosophila has greatly contributed to determining the function of N-cadherins in vivo. Loss of N-cadherin in Drosophila embryos causes the trajectories of longitudinal CNS axons and the guidance of growth cones to be affected (Iwai et al. 1997). The role of N-cadherins in synaptic "wiring" was more clearly shown by elegant studies in the visual (Fig. 4) and olfactory systems in Drosophila. N-cadherin is instrumental in the assembly of the visual neuronal circuitry, where it functions in the afferent axons of the R1-R6 photoreceptor sensory neurons as well as their target neurons in the lamina neuropil of the fly visual system (Prakash et al. 2005). Similarly, N-cadherin is crucial for the coordinated targeting of multiple neuronal types, such as R7 photoreceptor axons and L1-L5 lamina neurons, to the correct target layer in the medulla neuropil of the visual system (Lee et al. 2001; Nern et al. 2005, 2008; Ting et al. 2005). There are 12 isoforms of N-cadherin in the fly visual system, but the expression of a single isoform is able to rescue null mutations, suggesting functional redundancy (Ting et al. 2005). In the olfactory system, loss of N-cadherin does not affect the pathfinding of olfactory receptor neuronal axons, but it influences their ability to converge onto a single glomerulus and form synapses (Hummel and Zipursky 2004). Similarly, the dendritic projections of the N-cadherin mutant second-order neurons, which also innervate the olfactory lobes, expand on nonappropriate glomeruli (Zhu and Luo 2004). In both systems, N-cadherin probably provides the adhesive force that mediates and stabilizes the attraction between neurites. The functions of N-cadherins appear to be evolutionarily maintained. For example, misrouting of axon fibers has also been observed in the developing optic tract of N-cadherin mutated zebrafish (Masai et al. 2003). Neurite nonextension/retraction has also been observed in cadherin blocked horizontal cell dendrites in the chicken retina (Tanabe et al. 2006).

### **NECTINS-AFADIN**

Nectins (nectins 1-4) (reviewed in Takai et al. 2008a,b) are Ig-like transmembrane molecules with a pleiotropic role in cell-cell adhesion, cell movement, proliferation, survival, differentiation, polarization, and the entry of viruses (Fig. 3). All nectin genes have two or three splicing variants and are ubiquitously expressed (Takai et al. 2008a,b). Nectins interact in trans, in a Ca<sup>2+</sup>-independent manner through their extracellular regions with each other or with other Ig-like molecules (Takai et al. 2008a,b). They are anchored to the actin cytoskeleton, through the interaction of the carboxy-terminal of nectins with the PDZ domain of the actinbinding protein afadin, which, like nectins, are expressed ubiquitously (Takai et al. 2008a,b).

The nectin-afadin system resembles the cadherin-catenin system. Both systems colocalize at *puncta adherentia* junctions (Fig. 3) (Fannon and Colman 1996). Nectins recruit cadherins through the interaction with afadin,  $\alpha$ -catenin, and their binding proteins (Fig. 3) (Tachibana et al. 2000; Pokutta et al. 2002; Asada et al. 2003; Honda et al. 2003, 2006; Ooshio et al. 2004), with which they cooperate in vitro to regulate neurite overextension (Togashi et al. 2006). Afadin also binds to other cell adhesion systems, such as Eph receptors (Hock et al. 1998; Buchert et al. 1999), indicating how multiple cell adhesion complexes may operate cooperatively in the formation of junctional complexes (Fig. 3).

At synapses between mossy fiber terminals and the dendrites of CA3 pyramidal cells in the hippocampus of the adult brain, nectin-1 and -3 localize at presynaptic and postsynaptic sides, respectively, whereas afadin is symmetrically present at both sides (Fig. 3) (Mizoguchi et al. 2002). When presynaptic nectin-1 is blocked and interaction with postsynaptic nectin-3 is lost, the formation of synapses in hippocampal cell culture is impaired (Mizoguchi et al. 2002). However, nectin-1 and nectin-3 mutant mice are viable and fertile (except for male nectin-3 knockout mice). The mutant mice display micropthalmia, impairments of the mossy fiber tract, aberrantly localized afadin and N-cadherin, and reduced number of puncta adherentia junctions at hippocampal synapses (Honda et al. 2006). In spite of these deficits, basic synaptic transmission and LTP at the mossy fiber synapse of nectin-1 knockout mice are identical to wild-type mice (Honda et al. 2006). These results suggest that there might be functional redundancy among different members of the family. However, disruption of the single afadin locus in mice, which consequently disrupts the function of all nectins (but also of other binding proteins) leads to embryonic lethality with pleiotropic defects, suggesting a widespread role of nectin-afadin in cell adhesion, migration, and differentiation (Ikeda et al. 1999).

In *Drosophila*, the nectin–afadin system could be paralleled by the echinoid–canoe complexes (Tepass and Harris 2007). Canoe is the fly homolog of afadin, which plays a pleiotropic role in morphogenesis. However, it is unknown if it serves a role in synapse formation and function. There is no clear homolog of nectins in *Drosophila*. The homophilic Ig-type adhesion protein Echinoid binds to canoe, as nectins bind to afadin, but there are many functional differences between echinoid and nectins (Tepass and Harris 2007).

# CONCLUDING REMARKS: GENETICS OF **CELL ADHESION AND NEUROPSYCHIATRIC** DISEASES

Cell adhesion plays an important role in the maintenance and modulation of synaptogenic activity within neuronal circuitries. Synaptogenic cell adhesion molecules have been identified by a wide variety of methods, and their activity has been clearly assessed in in vitro synaptogenesis assays, where the complexity of trans-synaptic signaling is greatly simplified (Biederer and Scheiffele 2007; Sudhof 2008). However, "loss of function" in vivo studies often do not corroborate the in vitro results because of redundancy within a protein family and among different adhesive systems or because of subtle or different function. The intrinsic complexity and redundancy may also account for why so few components have been identified in forward genetic screens in flies and worms. Perhaps the lack of sensitivity of the screening assays in the past will be compensated for by current, more sophisticated tools. For example, screens for neuronal connectivity in the visual system of Drosophila (reviewed in Mast et al. 2006; Ting and Lee 2007) and synaptogenesis in C. elegans (Zhen and Jin 1999; Shen and Bargmann 2003) have illustrated the power of these approaches. Genetic screens can now be carried out in sensitized genetic backgrounds using GFP basedmarkers, such as GRASP (a split GFP method that relies upon reconstitution of GFP along synaptic partners) (Feinberg et al. 2008), and a combination of genetic methodologies and transcriptional profiling or computational methods (Jin and Garner 2008).

Synaptic function and structure may be the converging point of malfunction in neuropsychiatric disorders, such as mental retardation and autism (Geschwind and Levitt 2007; Geschwind 2008; Walsh et al. 2008; Kramer and van Bokhoven 2009). Subtle changes in the connectivity patterns of a subset of synapses or in their basal function (Geschwind and Levitt 2007; Krey and Dolmetsch 2007; Abrahams and Geschwind 2008; Geschwind 2008; Sudhof 2008) and plasticity (Ramocki and Zoghbi 2008) might alter dramatically the output of the neuronal circuitry. Interestingly, mutations in neurexin 1 and neuroligins 3 and 4 are associated with autism spectrum disorders and mental retardation (Sudhof 2008). The scaffolding molecule and interacting protein of neuroligin SHANK3 (ProSAP2) is also associated with autism (Durand et al. 2007). More than 140 different mutations in L1-CAM have been associated with neurological disorders, including mental retardation (Bateman et al. 1996; Kenwrick and Doherty 1998; Kenwrick et al. 2000; De Angelis et al. 2002).

The heritability of psychiatric disorders, such as bipolar disorder, schizophrenia, and autism, has been estimated to be significantly higher than that of cancer (Burmeister et al. 2008). However, the genetics of neuropsychiatric disorders are obscured by incomplete penetrance, variable expressivity, complex interactions among genetic and environmental factors, and imprecisely defined traits (Burmeister et al. 2008). Intriguingly, most of the genes associated with mental retardation are evolutionarily conserved in Drosophila (Inlow and Restifo 2004), which is regarded as a succesful model for human diseases (Bier 2005).

In conclusion, it is important to provide more candidate genes and a better, more detailed understanding of their in vivo role in model organisms in order to further unravel the complexity of synaptogenesis and its role in neuronal development, function, and disease.

### **ABBREVIATIONS**

CASK	Ca <sup>2+</sup> /calmodulin-dependent
	serine protein kinase
aa	amino acid
Alk	Anaplastic lymphoma kinase
AMPA	α-amino-3-hydroxy-5-methyl-4-
	isoxazole propionic acid (AMPA)
AMPAR	AMPA receptors
APC	Anaphase Promoting Complex
ASD	Autism Spectrum Disorders
BDNF	Brain Derived Neurotrophic
	Factor
BMP	Bone Morphogenetic Protein

Cell Adhesion, the Backbone of the Synapse

$Ca^{2+}$	Calcium	Pcdh
CABAR	GABA receptors	PDZ
CAM	Cell Adhesion Molecule	
CAMKII	Ca2+/calmodulin dependent	
	protein kinase II	
CASK	Calcium/calmodulin-dependent	PSA
	serine protein kinase	PSD
CAST	cytomatrix at the active zone-	PTP
	associated structural protein	RIM
CNS	Central Nervous System	SALI
DGC	dystrophin glycoprotein complex	SAM
dNrx	Drosophila Neurexin	S-SC
Eph	Erythropoietin-producing	SV
-	hepatocellular carcinoma	SYD
FAK	focal adhesion kinase	SynC
FERM	Four-point-one, Ezrin, Radixin	TEM
	Moesin	
FGF	fibroblast growth factor	ТМ
Fmi	Flamingo	Veli
GABA	γ-aminobutyric acid	
GAD	glutamate decarboxylase	ACK
GEF	guanine exchange factor	Wea
GPI	glycosyl-phospahtidyl-inositol	Obv
GRB2	growth factor receptor-bound	the
	protein 2	Giag
GRIP	glutamate receptor interacting	Furo
	protein	nost
HEK	Human Embryonic Kindey	Hug
Ig	Immunoglobulin	port
LAR	leucocyte-common antigen	Rese
	related	Insti
LNS	Laminin, Nectin, Sex-hormone	Strol
	binding globulin	Med
LRR	Leucine Rich Repeat	cont
MALS	Mammalian-LIN-seven protein	cont
Mint	Munc-18 interacting protein	RFFF
MR	Mental Retardation	IXEI E
Narp	Neuronal activity-regulated	Abe K
	pentraxin	der N-
NCAM	Neural Cell Adhesion Molecule	Abrah
NGL	Netrin-G Ligand	gen
Nlg	Neuroligin	Reı
NMDA	N-methyl-D-aspartate	Ackley
NMDAR	NMDA receptors	CJ, Ca
NMJ	Neuromuscular Junction	rela
Nrx	Neurexin	ind
N-terminal	aminoterminal	J IN Arikb
PAK	p21-activated kinase	

h	protocadherins
Z	post synaptic density protein
	(PSD95), <i>Drosophila</i> disc large
	tumor suppressor(Dlg), zonula
	occludens-1 protein (zo-1)
L	polysialic acid
)	PSD
)	Protein tyrosine phosphatase
1	Rab3-Interacting Molecule
M	Synaptic Adhesion Like Molecule
Λ	sterile $\alpha$ motifs
CAM	synaptic scaffolding molecule
	Synaptic Vesicles
<b>)</b> -2	synaptogenesis defective
CAM	Synaptic Cell Adhesion Molecule
Л	Transmission Electron
	Microscopy
	Transmembrane
	vertebrate LIN-7

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P21-activated kinase

PAK

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