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Neuregulin 1 in neural development, synaptic plasticity and schizophrenia

Lin Mei¹ and Wen-Cheng Xiong¹

¹ Program of Developmental Neurobiology, Institute of Molecular Medicine and Genetics, Department of Neurology, Medical College of Georgia, Augusta, Georgia 30912, USA.

Abstract

Schizophrenia is a highly debilitating mental disorder that affects ~1% of the general population, yet it continues to be poorly understood. Recent studies have identified variations in several genes that are associated with this disorder in diverse populations, including those that encode neuregulin 1 (NRG1) and its receptor ErbB4. The past few years have witnessed exciting progress in our knowledge of NRG1 and ErbB4 functions and the biological basis of the increased risk for schizophrenia that is potentially conferred by polymorphisms in the two genes. An improved understanding of the mechanisms by which altered function of NRG1 and ErbB4 contributes to schizophrenia might eventually lead to the development of more effective therapeutics.

Schizophrenia is a severe and disabling mental disorder that is characterized by chronic positive symptoms (hallucinations, delusions and thought disorders), negative symptoms (social withdrawal, apathy and emotional blunting) and cognitive deficits. Although schizophrenia is a highly prevalent CNS disorder, it continues to be one of the least understood, primarily owing to its lack of pathological hallmarks. Most, if not all, commonly prescribed antipsychotics are anti-dopaminergic, and their use has been based on the ‘classical’ dopamine hypothesis, which posits that it is the hyperactivity of dopaminergic transmission that causes positive symptoms¹. However, current antipsychotics are only modestly effective treatments for the cognitive dysfunction and negative symptoms that are associated with schizophrenia. Moreover, studies on the mechanism of action of antipsychotics have not been particularly informative about the pathogenesis of the disease².

Recent genetic studies have provided insight into the possible aetiological mechanisms of this devastating disorder. Schizophrenia has a significant genetic component, and several genes have been associated with the disorder in diverse populations³. In particular, the identification of polymorphisms in the genes that encode neuregulin 1 (NRG1) and its receptor ErbB4 has provided a useful starting point from which to better dissect the pathogenic mechanisms of schizophrenia. The past few years have witnessed major progress in our understanding of NRG1 function in neurodevelopment, neurotransmission and synaptic plasticity and of the potential pathological basis of the increased risk that is conferred by polymorphisms in *NRG1* and *ERBB4*. In this Review we briefly discuss the basic signalling machinery of NRG1, review recent findings on the roles of NRG1 and ErbB signalling during development and synaptic plasticity, and explore the implications for the pathophysiology of schizophrenia.

NRG1 and ErbB4 signalling

NRG1

NRG1 is a trophic factor that contains an epidermal growth factor (EGF)-like domain that signals by stimulating ErbB receptor tyrosine kinases. It belongs to a family of growth factors that are encoded by four individual genes (*NRG1–4*), of which NRG1 is the best-characterized. Presumably owing to the use of distinct 5' flanking regulatory elements and alternative splicing, *NRG1* generates six types of protein (I–VI) and at least 31 isoforms (based on analysis of human expressed sequence tags^{4, 5, 6, 7, 8}) (Fig. 1a); these isoforms include Neu differentiation factor (NDF), heregulin, glial growth factor (GGF) and acetylcholine-receptor-inducing activity (ARIA)^{9, 10, 11, 12, 13, 14, 15}. Each of the protein types has a distinct amino-terminal region. The EGF-like domain is located in the membrane-proximal region of the extracellular domain that is necessary and sufficient for activation of the ErbB receptor tyrosine kinases. NRG1 isoforms differ in their levels and patterns of expression in various tissues, including in the brain^{7, 16}. Mice that carry mutations that inactivate particular isoforms show distinct changes in neural development^{7, 17, 18}, suggesting that the different NRG1 isoforms have different functions. Interestingly, some NRG1 isoforms are abnormally expressed in patients with schizophrenia.

Most NRG1 isoforms are synthesized as membrane-anchored precursors, called pro-NRG1s, with the EGF domain positioned outside of the cell (Fig. 1b). Pro-NRG1s undergo proteolytic cleavage at the juxtamembrane region that lies on the carboxy-terminal side of the EGF-like domain. This leads to the release of diffusible, mature NRG1, except in the case of Type III NRG1. The cleavage is catalysed by three type I transmembrane proteases: tumour necrosis factor- α converting enzyme (TACE, also known as ADAM17)^{19, 20}, β -site of amyloid precursor protein cleaving enzyme (BACE, also known as memapsin 2)^{21, 22} and meltrin beta (also known as ADAM19)²³. Some NRG1 isoforms are synthesized without a transmembrane domain and are thus directly released into the extracellular space⁵. The expression and processing of pro-NRG1 are tightly regulated both temporally and spatially, as well as by neuronal activity^{24, 25, 26, 27}.

ErbB receptor tyrosine kinases

NRG1 acts by stimulating a family of single-transmembrane receptor tyrosine kinases called ErbB proteins²⁸. ErbB proteins have homology with the EGF receptor (EGFR, also known as ErbB1) (Fig. 2). ErbB4 is the only autonomous NRG1-specific ErbB that can both interact with the ligand and become activated by it as a tyrosine kinase. ErbB2, by contrast, functions as a co-receptor by forming heterodimers with other, ligand-bound ErbBs²⁹. ErbB3 can bind to NRG1, but its homodimers are catalytically inactive, indicating that its kinase function is impaired³⁰. EGFR does not bind to NRG1, but it can form heterodimers with ErbB4 (see below). Among the ErbB proteins, ErbB4 is the best-characterized for its function in the CNS. There is no evidence that *ERBB2* and *ERBB3* are susceptibility genes for schizophrenia and, unlike *ErbB4*-mutant mice, mice that carried mutations in *ErbB2* and *ErbB3* did not produce behaviours that were characteristic of schizophrenia³¹. Thus, we review NRG1 signalling and function with a focus on ErbB4.

Canonical forward signalling

In canonical forward signalling, NRG1-induced ErbB dimerization activates the ErbB kinase domain, resulting in auto- and trans-phosphorylation of the intracellular domains. This process seems to require ErbB endocytosis^{32, 33, 34}. The phosphorylated tyrosine residues serve as docking sites for phosphopeptide-binding adaptor proteins or enzymes (Fig. 2). The Raf–MEK–ERK and PI3K–Akt–S6K pathways are frequently activated by the NRG1-induced stimulation of ErbB receptor homo- or heterodimers (Fig. 2). Other downstream kinases

include c-Abl, JNK, CDK5, Fyn and Pyk2 (Refs 35,^{36,37,38}). Similar to *NRG1* transcripts, *ERBB4* transcripts can be alternatively spliced to generate four ErbB4 isoforms that trigger distinct signalling cascades (Fig. 3). Ultimately, NRG1 activates specific transcriptional and translational programmes and thus has various long-term effects.

NRG1 signalling is mediated by heterodimers of ErbB2–ErbB3, ErbB2–ErbB4 and ErbB3–ErbB4 and by the homodimer ErbB4–ErbB4 (Fig. 2). ErbB4 can also form a heterodimer with EGFR. NRG1 stimulation can thus mediate signalling pathways that are typically associated with the EGFR, including the activation of Src family kinases, PLC γ , JNK and Abl³⁷. However, the functional significance of ErbB4–EGFR heterodimers in the CNS remains unclear.

Non-canonical forward signalling

In non-canonical forward signalling, the juxtamembrane-a (JMa) isoform of ErbB4 (Fig. 3) is first cleaved by TACE to release a soluble extracellular peptide that contains the NRG1 binding site (ecto-ErbB4) (Fig. 4). The remaining membrane-anchored 80 kDa fragment (that is, ErbB4-CTF) is further cleaved in its transmembrane domain by presenilin-dependent γ -secretase to release the ErbB4 intracellular domain (ErbB4-ICD)^{39, 40}, which has been shown to translocate to the nucleus and to regulate transcription⁴¹ (Fig. 4). Interestingly, ErbB4 isoforms exhibit distinct tissue-specific and brain-region-specific patterns of expression. Moreover, there is a reduction of JMa ErbB4 in neuronal precursor cells at late stages of embryonic development, providing a potential mechanism for late-onset astrogenesis^{41, 42}.

NRG1–ErbB4 interactions also mediate both short- and long-range attraction for tangentially migrating interneurons: ErbB4 is expressed in a subpopulation of interneurons that migrate tangentially towards the cortex through a permissive corridor that expresses Type III NRG1 (Refs 58,⁵⁹). Furthermore, the migration of interneurons from the medial ganglionic eminence towards the developing cortex might be mediated by a diffusible source of immunoglobulin (Ig)-domain-containing Type I or Type II NRG1. Loss of ErbB4 perturbs interneuron migration, leading to an altered number of GABAergic interneurons in the postnatal cortex⁵⁹ (Fig. 5b).

In the adult rodent brain, interneurons in the olfactory bulb are replaced by neural progenitor cells that migrate into the bulb from the subventricular zone through the rostral migratory stream⁶⁰. This process is in part regulated by ErbB4 that is expressed in neuroblasts in the subventricular zone and in the rostral migratory stream, as *ErbB4*-deficient mice exhibit altered neuroblast chain organization and migration as well as deficits in the placement and differentiation of olfactory bulb interneurons⁶¹.

Axon guidance

Recombinant NRG1 stimulates neurite outgrowth in multiple populations of primary neurons, including hippocampal neurons⁶², retinal neurons⁶³, cerebellar granule cells⁶⁴ and thalamic neurons⁶⁵. In addition, NRG–ErbB-signalling-induced neurite outgrowth has been observed in neural cell lines^{66, 67, 68}. Owing to the embryonic lethality of deleting the *Nrg1* gene, the exact function of NRG1 in axon guidance is unclear^{18, 51, 52}.

A recent study provided evidence that the thalamocortical axon (TCA) projection is regulated by NRG1 and ErbB4 (Ref. 65) (Fig. 5b). TCAs convey sensory and motor inputs to the cerebral cortex. They originate in the dorsal thalamus, run rostrally towards the telencephalon, make a sharp turn in a dorsal direction to enter the mantle region of the medial ganglionic eminence, and then advance through the striatum to finally reach the developing cortex⁶⁹. TCA development depends on the migration of a population of lateral-ganglionic-eminence-derived

interneurons towards the diencephalon, where the neurons form a permissive corridor for later-arriving TCAs. GABAergic neurons (or corridor cells) between the medial ganglionic eminence and the globus pallidus express cysteine-rich-domain-containing NRG1 (CRD-NRG1), which is thought to serve as a permissive cue that activates ErbB4 in TCAs, allowing growth into the developing telencephalon. In addition, diffusible Ig-NRG1 in the ventral and lateral pallidum serves as a long-range attractant that facilitates TCA projection through the dorsal striatum and into the cortex⁶⁵. These observations demonstrate that the two isoforms of NRG1 cooperate in the guidance of TCAs.

Glial cell development, axon myelination and axon ensheathment

In the nervous system, specialized glial cells (Schwann cells in the PNS and oligodendrocytes in the CNS) extend plasma-membrane processes that wrap axons with a multilamellar membranous myelin sheath. Myelination increases the conduction velocity of action potentials and is a tightly controlled developmental process. Type III NRG1 has emerged as a key axon-derived regulator at virtually every stage of Schwann cell development^{70, 71, 72, 73, 74} (Fig. 5c).

NRG1 induces the commitment of neural crest cells to the gliogenic fate^{75, 76} and promotes their proliferation^{15, 51, 57, 77, 78, 79} and migration along axons^{51, 80}. It also promotes Schwann cell proliferation and differentiation^{79, 81, 82}. Disrupting NRG1 signalling by ablating all NRG1 isoforms, the Type III isoform or one of its receptors (ErbB2 and ErbB3) leads to an almost complete loss of Schwann cells and the sensory and motor neurons that they support^{49, 52, 71, 83, 84, 85}. Recent studies have suggested that the level of Type III NRG1 in the axon is a key instructive signal for myelination⁷². Small axons (usually ones that are less than 1 micrometre in diameter) contain insufficient amounts of NRG1 to induce Schwann cell myelination and, consequently, they become ensheathed but remain unmyelinated, whereas myelinated axons are usually large and express higher levels of NRG1 (Refs 73, 74) (Fig. 5c). Whether NRG1 signalling affects internode length or axonal calibre awaits further investigation. In one study, NRG1 signalling was implicated in the elaboration of myelin thickness and internodal length, as well as in determining the axonal calibre of myelinating Schwann cells⁸⁶. However, heterozygous *Nrg1*^{+/-} mice did not display an abnormal axonal size distribution, although they did have significant hypomyelination⁷³. Conversely, for non-myelinating Schwann cells NRG1 serves as a pro-survival signal but inhibits proliferation⁸⁷.

The role of NRG1 in myelination in the CNS has not been well-characterized. NRG1 is thought to serve as an axon-derived signal for oligodendrocyte development (Fig. 5d). *In vitro* studies showed that NRG1 promotes oligodendrocyte proliferation and survival^{88, 89, 90, 91}. NRG1 is expressed in the subventricular zone of the rat brain at the critical time for oligodendrocyte differentiation, and it enhances the development of oligodendrocytes from bipotential (O2A) glial progenitor cells⁹¹. Neural tube explants prepared from *Nrg1*-knockout mice failed to produce oligodendrocytes *in vitro*; this effect could be rescued by exogenous NRG1 (Ref. 92). Moreover, disruption of NRG1 signalling suppressed oligodendrocyte differentiation from progenitor cells⁹³. Furthermore, mice that expressed DN-ErbB4 showed reduced myelin thickness and a slower conduction velocity in their CNS axons compared with wild-type mice⁹⁴. However, the reduction in ErbB signalling did not alter the number of myelinated and unmyelinated axons in the optic nerve and the corpus callosum, suggesting that NRG1 is required for the terminal differentiation of oligodendrocytes. This notion is supported by studies of *ErbB2*-null mice in which oligodendrocyte development is halted at the pre-oligodendroblast stage⁹⁵. Although ErbB3 is expressed in oligodendrocytes, it is dispensable for their development⁹⁶, presumably because of expression of autonomous ErbB4.

Synapse formation

NRG1 signalling also has a role in synapse formation. Indeed, ARIA (an Ig-domain-containing NRG1) was identified and purified on the basis of its ability to stimulate the synthesis of the acetylcholine receptor (AChR)^{11, 12}. Furthermore, inhibition of ErbB kinase activity or of its downstream kinases ERK, JNK and CDK5 attenuates NRG1-induced expression of AChR in muscle cells^{35, 36, 97, 98, 99, 100}. *Nrg1* heterozygous-mutant mice exhibited a decreased postsynaptic AChR density and a reduced reliability of neuromuscular transmission¹⁰¹. However, conditional-mutant mice lacking both ErbB2 and ErbB4 in their skeletal muscle form neuromuscular junctions that are structurally and functionally normal in many respects¹⁰². These data indicate that the NRG1–ErbB signalling pathway in muscle might be dispensable for postsynaptic development. Alternatively, NRG1 might signal to muscle cells indirectly through Schwann cells to regulate the formation of neuromuscular junctions^{51, 85, 103, 104} (Fig. 5e). In addition, Type I and Type II but not Type III NRG1s are required for proprioceptive-afferent-evoked induction of muscle spindle differentiation¹⁰⁵.

In the CNS, Type III NRG1 influences the expression level of neuronal AChRs, whereas Type I and Type II isoforms alter the expression of GABA_A receptors^{64, 106, 107, 108}. Alterations in the levels and profiles of various glutamate receptors (NMDA (*N*-methyl-D-aspartate) and AMPA (α -amino-3-hydroxy-5-methyl-4-isoxazole propionic acid) receptors) have been associated with signalling stimulated by Type I, Type II and Type III isoforms^{38, 109}. *Nrg1*^{+/-} mice show a decrease in the number of functional NMDA receptors in their forebrain¹¹⁰. Therefore, there might be differential regulation of glutamate receptors depending on the isoforms that are expressed.

Recently, postsynaptic ErbB4 signalling has been shown to control the activity-dependent maturation of excitatory synapses¹¹¹: synaptic activity triggers NRG1–ErbB4 signalling, which recruits or stabilizes ErbB4 at the synapse in a PSD95-dependent manner and stabilizes synaptic AMPA receptors. Interruption of NRG1–ErbB4 signalling causes the destabilization of synaptic AMPA receptors and spine structure, leading to the impairment of plasticity and, eventually, to the loss of spines and NMDA receptors.

NRG1 in synaptic plasticity and neuronal survival

NRG1 and ErbB4 are expressed in multiple regions in the adult brain^{58, 112, 113}. Notably, the expression of NRG1 isoforms seems to be lamina-specific and largely non-overlapping in the cortex: Type I and Type II isoforms are expressed in layers 2, 3 and 6b; Type III isoforms are expressed in layer 5. Type I, Type II and Type III isoforms are also all expressed in the reticular nucleus of the thalamus, in the piriform cortex and throughout the hippocampus. By contrast, ErbB4 transcripts are detectable in cortical layers 2–6b and are present at high levels in regions where interneurons are enriched, including the medial habenula, the reticular nucleus of the thalamus and in the intercalated masses of the amygdala^{58, 112, 113}. These findings suggest additional functions of NRG1–ErbB4 signalling in the mature nervous system. Indeed, NRG1 regulates both excitatory and inhibitory synaptic transmission in the adult brain. These observations are exciting because abnormal neurotransmission and/or synaptic plasticity have been observed in both glutamatergic and GABAergic pathways in the schizophrenic brain^{114, 115, 116, 117}.

Short-term plasticity: glutamatergic transmission

ErbB4 interacts and co-localizes with PSD95, a postsynaptic scaffold protein that is essential for the assembly and function of glutamatergic synapses^{118, 119}. This interaction enhances NRG-dependent intracellular signalling¹¹⁸. Further studies have indicated that ErbB4 is localized in anatomically defined PSDs in the brain¹²⁰ (Fig. 6a). The targeting of ErbB4 to

the PSD suggested that NRG1 might have a role in synaptic transmission or plasticity at excitatory synapses. Indeed, in collaboration with Salter and colleagues, we showed that bath application of NRG1 blocked tetanus-induced long-term potentiation (LTP) at Schaffer collateral/CA1 synapses in hippocampal slices within 20 minutes¹¹⁸, suggesting that protein synthesis might not be involved. The effect of NRG1 on LTP requires ErbB4, as both pharmacological inhibition and genetic ablation of ErbB4 prevented it¹²¹. When NRG1 was applied soon after LTP induction by theta-burst stimulation, it had a depotentiating effect in the hippocampus¹²². However, this effect was lost if NRG1 was added 50 min after induction¹²². These observations are in good agreement with the notion that NRG1–ErbB4 signalling suppresses both the induction and the expression of LTP.

Studies of *Nrg1*(ΔEGF)^{+/-} mice, which have a heterozygous deletion of the NRG1 EGF domain, suggest that the effect of NRG1 on LTP depends on the level of endogenous NRG1 (Ref. 38). Theta-burst-induced but not tetanus-induced LTP was deficient in hippocampal slices of adult mutant mice, suggesting that developmental disruption of NRG1 signalling impairs neurotransmission in adult animals. Intriguingly, at low doses NRG1 increased both tetanus- and theta-burst-induced LTP in hippocampal slices from adult *Nrg1*(ΔEGF)^{+/-} mice, but higher doses of NRG1 suppressed LTP³⁸. These observations suggest that the regulation of synaptic plasticity by NRG1 might depend on an initial NRG1 activity that is controlled by local concentrations of NRG1 isoforms, levels of ErbB kinases and neuronal activity that regulates NRG1 expression. An ‘inverted-U model’ has been proposed that might explain why both low and high levels of NRG1–ErbB activity could impair synaptic function¹²³.

The mechanism by which NRG1 regulates LTP remains unclear. Basal synaptic transmission at the Schaffer collateral/CA1 synapses in hippocampal slices from adult mice was not affected by bath application of NRG1 (Refs 38, 118, 122, 124), by acute inhibition of ErbB4 (Ref. 121) or by *ErbB4*^{-/-} and *Nrg1*^{+/-} mutation^{38, 121}. NRG1 does not alter paired-pulse facilitation ratios^{118, 121, 122, 124}, suggesting that NRG1 has no effect on short-term plasticity and acts through a postsynaptic mechanism. Moreover, the effect of NRG1 on LTP is observed in the presence of the GABA_A-receptor blockers bicuculine and picrotoxin^{38, 121, 122} and thus cannot be explained by changes in GABA transmission (see below). A recent study reported that NRG1 depression of LTP at CA1 synapses is independent of GABAergic inhibition¹²⁴. The activity of NMDA receptors is subject to modulation by tyrosine phosphorylation^{125, 126, 127}, but the NRG1-induced suppression of LTP could not be attributed to an effect on basal NMDA currents because NRG1 did not alter basal NMDA-receptor-mediated synaptic responses in hippocampal slices^{118, 122, 124}. These results might suggest that NRG1–ErbB4 signalling acts at a point downstream of NMDA receptor stimulation. Intriguingly, NRG1 has been shown to downregulate AMPA receptor currents and reduce surface glutamate-receptor-1-containing AMPA receptors in dissociated hippocampal neurons¹²².

Valuable insight has been provided by studies that used loss-of-function approaches. In the hippocampus of *Nrg1*(ΔTM)^{+/-} (a heterozygous deletion of the NRG1 transmembrane domain) and *ErbB4*^{-/-} mice, the expression of NMDA receptors is decreased and Tyr 1472 of the NMDA receptor subunit NR2B, a site that is key to NMDA receptors’ channel property, is hypophosphorylated³⁸. Inhibition of NRG1–ErbB4 signalling in hippocampal slices from postnatal mice destabilizes synaptic AMPA receptors and leads to the loss of synaptic NMDA currents and spines¹¹¹. Tyrosine phosphorylation of NR2B was reduced in the hippocampus of *Nrg1*(ΔTM)^{+/-} and *ErbB4*^{-/-} mice³⁸, but tyrosine phosphorylation of the NR1, NR2A and NR2B subunits was not changed in NRG1-treated neurons under conditions in which NMDA currents were inhibited³². Therefore, the question of whether these mechanisms contribute to the rapid NRG1 regulation of synaptic transmission or synaptic plasticity warrants further investigation. The reduction in NMDA receptor levels in the hippocampus of the mutant mice³⁸ is unlikely to occur after brief NRG1 stimulation that suppresses LTP.

It is worth pointing out that the regulation of neurotransmission by NRG1 might vary between brain regions. For example, NRG1 administration decreased NMDA-receptor-mediated excitatory postsynaptic currents in slices of prefrontal cortex (PFC), an area in which altered activity has been implicated in schizophrenia, and reduced whole-cell NMDA receptor currents in acutely isolated PFC pyramidal neurons³² by elevating intracellular Ca^{2+} and stimulating ERK. This resulted in enhanced actin depolymerization and subsequent internalization of NMDA receptors³². Moreover, NRG1 depressed entorhinal CA1 synaptic transmission but increased the dentate field excitatory-postsynaptic-potential response to entorhinal cortical stimulation in anaesthetized rats¹²⁸. These observations indicate that the role of NRG1 in regulating synaptic plasticity might be more complex than was previously thought. More studies are needed to figure out whether the reported differential effects were due to variation in NRG1 (isoforms, timing and local concentration), to the activation of other ErbB kinases, to variation in the age of the animals from which brain slices were cultured and/or to other experimental particulars¹²⁹.

Short-term plasticity: GABAergic transmission

Cognitive processes such as working memory and executive function are mediated by the PFC. The functions of the PFC are executed by pyramidal neurons, and the activity of these neurons is intricately controlled by inhibitory and excitatory synaptic inputs. Abnormal GABAergic and glutamatergic transmission in this area has been implicated in schizophrenia and is thought to contribute to the cognitive deficits that are associated with the disorder¹¹⁵. Despite the fact that ErbB4 is prominently expressed in interneurons^{113, 118}, most studies have focused on its role in pyramidal cells. We showed that there was ErbB4 immunoreactivity at the terminals of GABAergic neurons that seemed to innervate pyramidal neurons in the PFC¹¹² (Fig. 6b). Biochemical and electrophysiological studies have shown that exogenous NRG1 stimulates GABA release in response to depolarization, with no discernible effect on basal release¹¹². This effect of NRG1 was blocked by an ErbB4 inhibitor and did not occur in cortical slices from *ErbB4*-mutant mice. Intriguingly, treatment with ecto-ErbB4 or inhibition of NRG1–ErbB4 signalling attenuated activity-dependent GABA release, indicating that GABA transmission is determined by the level of NRG1–ErbB4 signalling¹¹².

Glutamatergic activity is known to increase GABAergic transmission¹³⁰; it is therefore possible that the NRG1 regulation of evoked GABA release might be mediated by a glutamatergic mechanism. However, the NRG1-mediated enhancement of GABA release was not attenuated by inhibitors of NMDA and AMPA receptors¹¹². Therefore, it is likely that NRG1 regulates GABA release by directly activating ErbB4 receptors on presynaptic terminals. This notion is supported by the observation that NRG1 increases depolarization-evoked GABA release from synaptosomes, which are isolated from any neural networks, and decreases paired-pulse ratios of evoked inhibitory postsynaptic potentials (IPSCs) in response to two consecutive stimulations, suggesting that NRG1 might facilitate vesicle release that is evoked by neuronal activation¹¹². These results identify a novel function for NRG1–ErbB4 signalling: NRG1, through activity-dependent GABA release, regulates signal integration by pyramidal neurons. The final output of pyramidal neurons depends on glutamatergic and GABAergic inputs that are both regulated by NRG1. This function of NRG1 could have implications for working-memory deficits in patients with schizophrenia and in people with neurological disorders such as epilepsy¹¹² (Fig. 6c).

Long-term plasticity

It is widely accepted that long-term plasticity, such as late-phase LTP, requires new protein synthesis. There is evidence to support the notion that NRG1 regulates long-term plasticity in the brain. First, NRG1 has been shown to stimulate the expression of receptors for key neurotransmitters, including glutamate, GABA and ACh^{64, 106, 107, 108, 109, 131}; it could

thus potentially regulate excitatory and/or inhibitory neurotransmission. Importantly, protein synthesis is necessary for the NRG1-mediated increase of GABA-induced currents in cerebellar granule cells⁶⁴, the decrease of miniature IPSC amplitudes in CA1 hippocampal neurons¹⁰⁸ and the increase in the peak amplitude of the ACh-induced current in hippocampal GABAergic neurons¹⁰⁶. In addition, NRG1 stimulates the expression of Ca²⁺-activated K⁺ channels in parasympathetic neurons^{132, 133}. Considering the distinct synaptic localization of ErbB4, it is tempting to speculate that NRG1 might regulate local protein synthesis at synapses. Finally, expression and processing of NRG1 are regulated by neuronal activity^{24, 25, 26, 27}, so the increased neurotransmission that is induced by NRG1 and the subsequent production of more NRG1 are likely to contribute to long-term synaptic plasticity.

NRG1 and ErbB signalling in neuronal survival

In vitro studies indicate that NRG1 can be neurotrophic and neuroprotective for cortical neurons¹³⁴, motor neurons¹³⁵, dopaminergic neurons¹³⁶, cochlear sensory neurons¹³⁷ and PC12 cells¹³⁸; it also protects neurons following ischaemia^{139, 140, 141}. How this effect relates to schizophrenia awaits further investigation.

NRG1 and ErbB4 as susceptibility genes

Mutations in NRG1 and ERBB4 that are associated with schizophrenia

Schizophrenia has a strong genetic component, and several susceptibility genes for schizophrenia have been identified³. Meta-analyses of whole-genome linkage scans identified 8p as a susceptibility locus for the disorder^{142, 143}. Extensive fine-mapping of the 8p locus and haplotype-association analysis of affected families in Iceland narrowed the region to 8p12–8p21, and *NRG1*, which lies in this region, was identified as a candidate gene for schizophrenia¹¹⁰ (Fig. 7a). The original ‘core at-risk haplotype’ (hereafter referred to as the ‘deCODE haplotype’) consisted of five single-nucleotide polymorphisms (SNPs) (SNP8NRG221132, SNP8NRG221533, SNP8NRG241930, SNP8NRG243177 and SNP8NRG433E1006) and two microsatellites (478B14–848 and 420M9–1395) in a region spanning the 5' end of *NRG1* and extending into the second intron. The association of SNP8NRG221533 and two other SNPs, rs3924999 and rs2954041, in *NRG1* was soon reported in an independent study of Chinese Han schizophrenia family trios (consisting of the father, the mother and the affected offspring)¹⁴⁴. The genetic association between *NRG1* and schizophrenia has been confirmed in follow-up studies in multiple populations in Scotland, Ireland, the United Kingdom, the Netherlands, Korea and China^{145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155}. Most of the 80 schizophrenia-associated SNPs are localized to the 5' region^{110, 146, 149, 152, 153, 154, 155} and 3' region^{149, 150, 152, 155, 156} of *NRG1*.

Evidence suggests that the 5' SNPs regulate *NRG1* expression in patients with schizophrenia^{157, 158, 159}. The risk allele SNP8NRG243177, which is part of the original deCODE haplotype, is associated with decreased activation of frontal and temporal lobe regions, increased development of psychotic symptoms and decreased premorbid IQ¹⁶⁰. Together, these results provide strong evidence that *NRG1* is a schizophrenia-susceptibility gene in many populations, although studies of Japanese, Irish and Spanish cohorts showed poor association^{161, 162, 163}.

Of note are SNPs that generate changes in the coding region of *NRG1*. A missense mutation (Val to Leu) was identified in the transmembrane region of the NRG1 protein¹⁶⁴. The change from Val to Leu is a conservative mutation that lengthens the aliphatic side chain of the amino acid by only a single hydrocarbon. The functional implication of this *NRG1* mutation remains unclear. Interestingly, the rs3924999 mutation (Arg to Gln) in the Type-II-NRG1-specific region is significantly associated with deficits in pre-pulse inhibition, a measure of attentional processes and sensorimotor gating¹⁶⁵ (although the rs10503929 mutation (Met to Thr) was

not associated with changes in prepulse inhibition¹⁶⁵). The rs3924999 mutation is also associated with an increased score on the Perceptual Aberration Scale (PAS) but not on the Schizotypal personality Questionnaire (SPQ)¹⁶⁶. These results suggest that the rs3924999 mutation might have a role in causing the prepulse inhibition deficits and schizotypal personality in patients with schizophrenia.

ERBB4, which spans 1.15 Mb on chromosome 2q34, has also been suggested to be a susceptibility gene for schizophrenia in populations of Ashkenazi Jews, Caucasians and African Americans^{155, 158, 159, 167, 168} (Fig. 7b). This gene was among several that were identified as being disrupted by microdeletions or microduplications in patients with schizophrenia¹⁶⁹. In a case-control association analysis of Ashkenazi Jews, three SNPs of *ERBB4* showed a highly significant association with the disease¹⁵⁸. A 46 kb core at-risk haplotype comprising three SNPs (rs707284, rs839523 and rs7598440) that surround exon 3 was identified by allele, genotype and haplotype frequency analysis¹⁵⁸. A separate mutation screen identified an additional 15 SNPs in *ERBB4* that are associated with schizophrenia¹⁶⁷. The SNP in intron 12, rs4673628 (intervening sequence 12–15 C>T), shows a significant genetic interaction with the original *NRG1* 'Icelandic' schizophrenia-associated haplotype. The nature of the interaction seems to be an excess of rs4673628 heterozygotes among patients with schizophrenia who carry the Icelandic *NRG1* risk haplotype. One open question is how the mutations might be pathogenic. A recent study indicated that abnormal expression of the CYT-1 isoform of *ERBB4* (Fig. 3) might be caused by mutations at rs4673628, at the three intronic risk SNPs surrounding exon 3 and at a core-risk haplotype¹⁵⁹. This would implicate abnormal PI3K/Akt signalling in the pathologic mechanisms.

Behavioural studies of mice with hypomorphic *NRG1* and *ERBB4*

It has been challenging to generate convincing animal models for abnormal behaviours that are unique to humans, such as the positive and negative symptoms in schizophrenia¹⁷⁰. In rodents, positive symptoms are thought to be modelled by hyperactivity in response to novelty and hypersensitivity to psychostimulants, whereas negative symptoms are modelled by impaired social interaction and anhedonia. By contrast, cognitive deficits are not uniquely human and can thus be measured in rodents.

Studies of *Nrg1*- and *ErbB4*-mutant mice have provided support for the potential role of mutations in these genes as risk factors for schizophrenia. *Nrg1*- and *ErbB4*-hypomorphic or conditional-knockout mice showed 'schizophrenic-like' deficits, whereas *ErbB2*- and *ErbB3*-heterozygote-null mice seem to be behaviourally normal^{31, 171}. *Nrg1*(ΔEGF)^{+/-} and *Nrg1*(ΔTM)^{+/-} mice are generally hyperactive in a number of tests, including the novel open-field test and the alternating-Y maze^{31, 110, 172}. Interestingly, the hyperactivity of *Nrg1* hypomorphs can be reversed by clozapine, an atypical antipsychotic that is used to treat schizophrenia, at a non-sedating dose. Hypomorphs of *Nrg1*(ΔIg)^{+/-} mice (which have a heterozygous deletion in the Ig domain) are impaired in latent inhibition but exhibit normal activity in open-field and running-wheel tests in comparison with control littermates¹⁷³. However, they display behaviours that are thought to indicate a schizophrenia-like phenotype, such as clozapine-induced suppression of open-field and running-wheel activity. Mice with an *ErbB4* mutation that was generated specifically in the brain did not seem to have altered motor behaviour¹⁷⁴. However, a more detailed analysis of these mutant mice revealed that they were more active than control animals at the initial stage of the behavioural evaluation but became less active than controls in longer, more comprehensive evaluations at older ages¹⁷¹. Deletion of the gene that encodes the *NRG1*-cleavage enzyme BACE generates similar 'schizophrenic' phenotypes to those that are observed in *Nrg1*^{+/-} mice¹⁷⁵, supporting the model that disruption of *NRG1* signalling might participate in the pathogenesis of schizophrenia.

Recently, *Nrg1*-hypomorphic animals were shown to exhibit a selective disruption in their behavioural response to social novelty and increased aggression towards a conspecific¹⁷². These mice, however, were apparently normal in measures of emotionality/anxiety, spatial learning and working memory. The relatively mild phenotypes of *Nrg1* heterozygous mutants might be due to functional redundancy supplied by NRG2 and/or NRG3, mutations in the genes of which have been associated with schizophrenia¹⁵⁵. Finally, transgenic female mice expressing DN-ErbB4 in hypothalamic astrocytes exhibited delayed onset of puberty and reproductive development¹⁷⁶. These observations demonstrate that *Nrg1*- and *ErbB4*-mutant mice exhibit behaviours that are similar to those of established rodent models of schizophrenia¹⁷⁷.

NRG1 hypotheses of schizophrenia

Consistent with the ‘abnormal neural development’ model of schizophrenia^{44, 115, 178}, NRG1–ErbB signalling is evidently involved in important processes of brain development. Loss of function of NRG1 or ErbB4 or perturbation of NRG1 signalling can cause deficits in the migration of pyramidal and GABAergic neurons, neurite outgrowth and axon projection, the myelination of axons and synapse formation. The resulting anatomical abnormalities could underlie the altered neurotransmission and cortical function that leads to psychotic symptoms and cognitive impairments. In addition, NRG1 has acute effects on both glutamatergic and GABAergic pathways, and it thus contributes to a second mode of action. Evidence from *Nrg1*-hypomorphic and *ErbB4*-mutant mice supports the idea that mutations in *NRG1* and *ERBB4* have a role in the aetiology of schizophrenia.

It is worth pointing out that most of the genetic variations or SNPs in both *NRG1* and *ERBB4* are either intronic or synonymous exonic substitutions or are located in 5' or 3' non-coding regions⁸. It therefore remains unclear how these changes affect disease susceptibility. One plausible hypothesis is that the genetic variations are regulatory and that they thus affect disease susceptibility by altering the expression or splicing of *NRG1* and *ERBB4* or by altering NRG1 or ErbB4 mRNA stability. Recent studies have provided some evidence for this hypothesis. For example, brain samples from patients with schizophrenia showed increased mRNA for Type I NRG1 (Refs 157, 158, 179) and abnormal expression of ErbBs^{158, 180, 181}. Specifically, mRNA levels of Type I NRG1 were elevated both in the PFC and in the hippocampus^{157, 171}. However, mRNAs of the JMα/CYT-1 isoform of ErbB4 were upregulated in the PFC but not in the hippocampus^{158, 159}, suggesting that changes in the expression of *ERBB4* isoforms are not secondary to *NRG1* abnormalities and do not result from the general effects of illness state or medication. Whether NRG1 and ErbB4 protein levels are also altered has been a subject of controversy¹⁸², although a recent study showed that NRG1-ICD and ErbB4 protein levels were increased in the PFC of patients with schizophrenia¹⁸³. This might be due to differences in the study participants’ ages or to differences in the experimental particulars, such as the antibodies that were used.

Gain-of-function and hypoglutamatergic function in schizophrenia

Altered ErbB4 levels might change the balance of ErbB4 homo- and heterodimers and their downstream signalling pathways. Thus, an increase in the CYT-1 isoform of ErbB4 would be expected to stimulate PI3K (alterations in which have previously been implicated in schizophrenia¹⁸⁴) and subsequently Akt. Indeed, evidence of increased NRG1 signalling and/or function was found in the PFC of patients with schizophrenia¹⁸², including an increase in the PSD95–ErbB4 interaction that can further enhance NRG1 signalling¹¹⁸, activation of both ERK and Akt, and NRG1-induced suppression of NMDA receptor activation. These findings are exciting and, together with studies of NRG1 and ErbB4 expression in the schizophrenia brain, provide important links between the susceptibility genes and schizophrenic pathology. Based on the limited results, we propose a gain-of-function hypothesis of NRG1–ErbB4

signalling as a potential mechanism in the pathogenesis of schizophrenia: increased expression of Type I NRG1 and CYT-1 ErbB4 and/or increased NRG1 signalling in the PFC stimulates GABA transmission, which is anticipated to reduce the firing rate of glutamate-dependent pyramidal neurons. This would lead to hypofunction of the glutamatergic pathway, consistent with the reduced glutamatergic transmission and plasticity that is found in the brains of patients with schizophrenia^{114, 116, 117}.

The activity of glutamic acid decarboxylase (GAD) and the staining of parvalbumin, a Ca²⁺-binding protein that is expressed in a subset of GABAergic interneurons, are reduced in the PFC of patients with schizophrenia¹⁸⁵. In view of the newly identified function of NRG1–ErbB4 signalling as a potentiator of GABAergic transmission, it is possible that elevated NRG1–ErbB4 expression and signalling compensate for reduced GAD activity. Conversely, GAD activity and parvalbumin expression might be repressed in an effort to compensate for elevated NRG1–ErbB4 expression and signalling. Settling this uncertainty will require a thorough assessment of the changes in GAD activity, parvalbumin staining and the relative expression and activity of distinct NRG1–ErbB4 isoforms in schizophrenia patients of different ages.

Conclusions and perspectives

Recent studies have provided compelling evidence that the NRG1–ErbB4 signalling pathway is involved in the pathogenesis of schizophrenia. Novel functions of NRG1 and ErbB4 have been identified in both neural development and synaptic plasticity. These advances have also raised many questions. Schizophrenia is most commonly viewed as a disorder of development⁴⁴. Can a dysfunction in the NRG1–ErbB4-mediated regulation of neurotransmission be a mechanism of schizophrenia? The effect of NRG1 on both excitatory and inhibitory neurotransmission in adult-brain slices, including those of *Nrg1*-mutant mice, suggests that alterations in the NRG1–ErbB4 signalling pathway might result in dysfunctional regulation of synaptic plasticity in an already abnormally developed mature brain. Future studies will be facilitated by animal models that control NRG1–ErbB signalling in space and time to dissect developmental and post-developmental mechanisms. In particular, gain-of-function models that increase NRG1–ErbB4 signalling in the adult brain to mimic pathological findings in patients might be useful.

In addition to *NRG1* and *ERBB4*, many other genes have been associated with schizophrenia, including those that encode catechol-O-methyl transferase (*COMT*), dysbindin (*DTNBP1*), regulator of G-protein signalling 4 (*RGS4*), disrupted-in-schizophrenia 1 (*DISC1*) and metabotropic glutamate receptor 3 (*GRM3*, also known as *MGLUR3*)^{3, 186}. NRG1 activates various intracellular pathways. Does it regulate the expression of these susceptibility genes and/or their function? Conversely, is NRG1–ErbB signalling regulated by any of these genes? These are questions that remain to be addressed in the near future. The answers to these questions, however, could be complicated by recent studies that suggest that NRG2, NRG3 and EGFR might also serve as risk factors for schizophrenia — all of these proteins can stimulate ErbB kinases¹⁵⁵. Nevertheless, these are exciting times for schizophrenia research. We anticipate that an improved understanding of the pathogenic mechanisms that are associated with the identified disease-associated genes might eventually lead to the development of more effective therapeutics.

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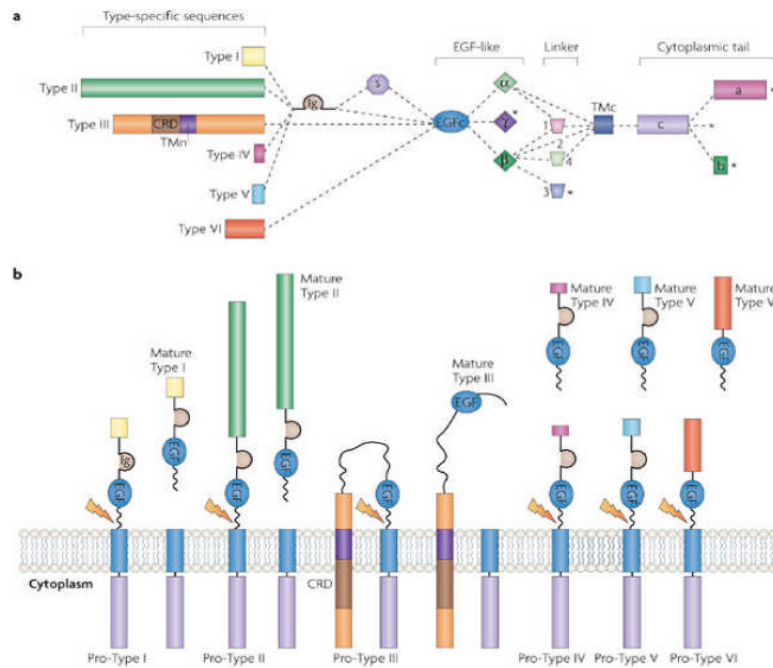
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**Fig. 1.**

a | The six types of neuregulin 1 (NRG1) isoforms are classified according to their distinct amino-terminal sequences. In the type III isoforms, this sequence contains a cysteine-rich domain (CRD) that has a transmembrane domain (TMn). All six types of NRG1 isoforms have an epidermal growth factor (EGF)-like domain. Types I, II, IV and V have an immunoglobulin (Ig)-like domain between the N-terminal sequence and the EGF domain, with or without the spacer region (S), whereas the N-terminal-specific region of types III and VI is connected directly to the EGF domain. Variants are also generated by splicing in the linker regions and the C-terminal regions. Between the two regions is a C-terminal transmembrane domain (TMc).

b | Most NRG1 isoforms are synthesized as transmembrane precursor polypeptides (pro-NRG1s) with the EGF domain located in the extracellular region, but in Type III NRG1 both the N- and the C-terminal regions are located inside the cell. Cleavage by tumour necrosis factor- α converting enzyme, β -site of amyloid precursor protein cleaving enzyme or meltrin β (indicated by the lightning arrow) generates mature NRG1s that are soluble, except in the case of Type III NRG1, which is thought to function in a manner that requires cell contact. The processing of Type IV, Type V and Type VI pro-NRG1s is less well-characterized but is thought to resemble that of Type I and Type II.

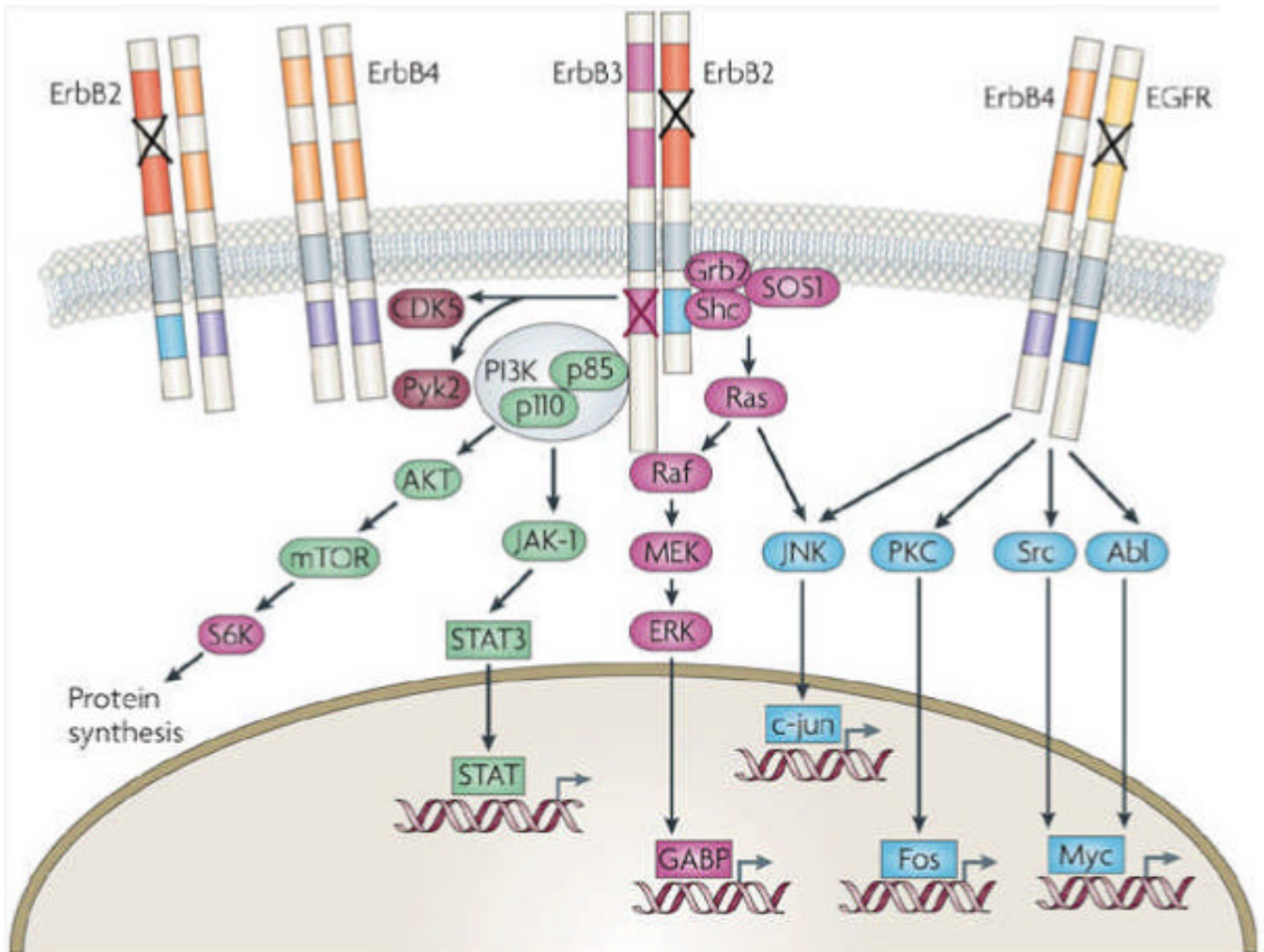


Fig. 2.

ErbB proteins are type I transmembrane receptor tyrosine kinases. Each has an extracellular region containing two extracellular cysteine-rich domains, a transmembrane domain, a short intracellular juxtamembrane region, a tyrosine kinase domain and a carboxy-terminal tail. In response to neuregulin 1 (NRG1) stimulation, ErbB proteins become dimerized to form homo- and heterodimers, such as ErbB2–ErbB3, ErbB4–ErbB4, ErbB2–ErbB4 and ErbB4–epidermal growth factor receptor (EGFR). ErbB2 does not bind to NRG1 (indicated by the black crosses) but has an active kinase domain; ErbB3 binds to NRG1 but has an impaired tyrosine kinase domain (indicated by the purple cross). Therefore, ErbB2 and ErbB3 need to form heterodimers with each other or with ErbB4 to be functional, whereas ErbB4 homodimers can bind to NRG1 and become activated. Activation of the tyrosine kinase domains leads to auto- and trans-phosphorylation of the intracellular domains, generating docking sites for the adaptor proteins Grb2 and Shc, which activate the Raf–MEK–ERK pathway, and for the p85 subunit of PI3K (indicated in the figure for the ErbB2–ErbB3 heterodimer), which activates the PI3K pathway and subsequently mTOR-dependent protein synthesis. NRG1 activates CDK5, which is also stimulated by neuronal activity³⁶. EGFR does not bind to NRG1. Its downstream pathways include ones that involve JNK, Src, Abl, and PKC in addition to ones that involve ERK and PI3K/Akt.

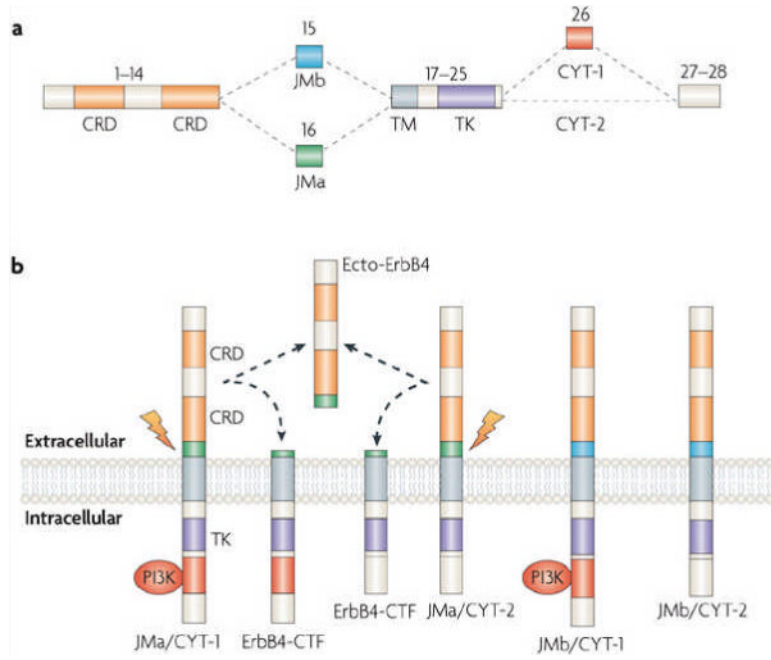


Fig. 3. **a** | Inclusion of exon 26 in the intracellular domain of ErbB4 generates CYT-1, whereas its exclusion gives rise to CYT-2 (Refs 188,189). The extracellular juxtamembrane region of ErbB4 is encoded by either exon 16 or exon 15, to generate JMa or JMb, respectively. Different combinations of CYT-1, CYT-2, JMa and JMb thus create 4 isoforms of ErbB4. Exon numbers are shown on the top of corresponding domain structures. **b** | CYT-1 contains the motif that binds to the p85 subunit of PI3K and thus activates this kinase. Thus, although both isoforms are coupled to the Raf–MEK–ERK pathway, CYT-1 but not CYT-2 activates PI3K and subsequently Akt^{188, 189, 190}. Both JMa and JMb can be activated by neuregulin 1 (NRG1) to initiate canonical signalling, but only JMa can be cleaved by tumour necrosis factor- α converting enzyme^{188, 191, 192} (indicated by the lightning arrow) to generate a soluble extracellular polypeptide, ecto-ErbB4 (which contains the NRG1 binding site), and a carboxy-terminal fragment (ErbB4-CTF). CRD, cysteine-rich domain; TK, tyrosine kinase domain; TM, transmembrane domain.

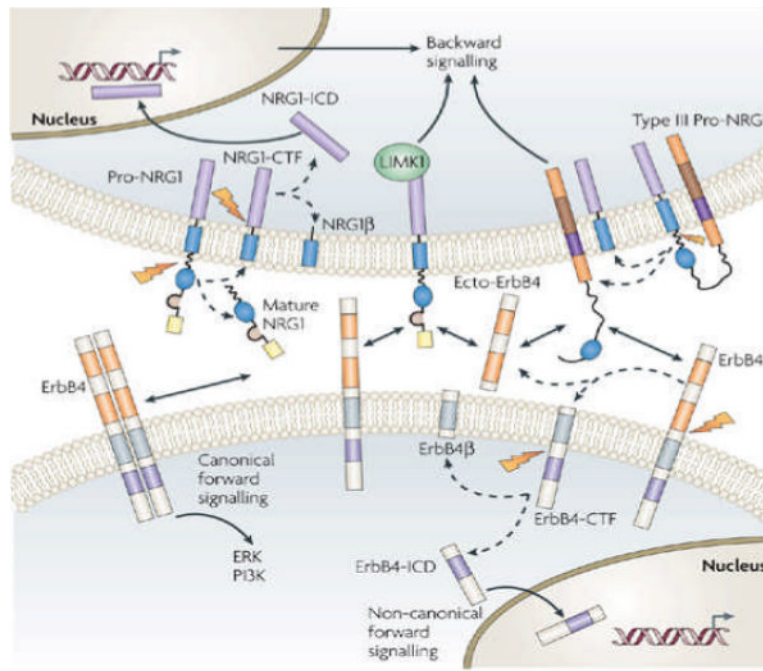


Fig. 4. In non-canonical forward signalling (bottom cell, right-hand pathway), the carboxy-terminal fragment (ErbB4-CTF) is cleaved by γ -secretase to produce ErbB4-intracellular domain (ErbB4-ICD), which can translocate to the nucleus to regulate gene expression. When it is overexpressed in transfected cells, ErbB4-ICD interacts with several transcriptional regulators, including Eto2, STAT5, Mdm2 and YAP, to mediate the transcriptional activation or repression of heterologous promoters (not shown)^{193, 194, 195, 196, 197, 198}. This interaction might require the phosphorylation of either ErbB4-ICD or the transcriptional regulator and/or the kinase activity of the ICD domain. For example, neuregulin 1 (NRG1) stimulation promotes the association of ErbB4-ICD with TAB2, an adaptor protein, in an ErbB4 kinase-domain-dependent manner⁴¹. TAB2 also interacts with the nuclear receptor co-repressor, N-CoR, to form a ternary complex that, upon translocation into the nucleus, represses the transcription of genes that are required for the differentiation of neural precursor cells into astrocytes. Backward signalling (top cell) by pro-NGR1 can proceed by two mechanisms. First, the C-terminal fragment of pro-NGR1 (NRG1-CTF), which is generated by extracellular cleavage, can be cleaved again by γ -secretase to generate NRG1-intracellular domain (NRG1-ICD), which can relocate into the nucleus to regulate gene transcription (left-hand pathway). Second, ErbB4 or ecto-ErbB4, which is released by extracellular cleavage, can serve as a ligand for pro-NGR1 or Type III NRG1, which function as receptors (right-hand pathway). It is unknown whether this interaction alters the phosphorylation of pro-NGR1 itself or whether it alters the activation of an intracellular kinase or phosphatase in pro-NGR1-expressing cells. Precisely how the signals are transduced also remains unknown. The cytoplasmic tail of pro-NGR1 interacts with the non-receptor protein kinase LIM kinase 1 (LIMK1)^{199, 200}. This kinase has been shown to regulate actin dynamics in many cell types, including neurons. Interestingly, NRG1-ICD is required for NRG1 function *in vivo*²⁰¹. Treatment of Type III NRG1-expressing neurons with a mixture of ecto-ErbB2 and ecto-ErbB4 promotes neuronal survival *in vitro* and alters the expression of several apoptotic genes²⁴ (not shown). Canonical forward signalling (bottom cell, left-hand pathway) is explained in detail in Fig. 2.

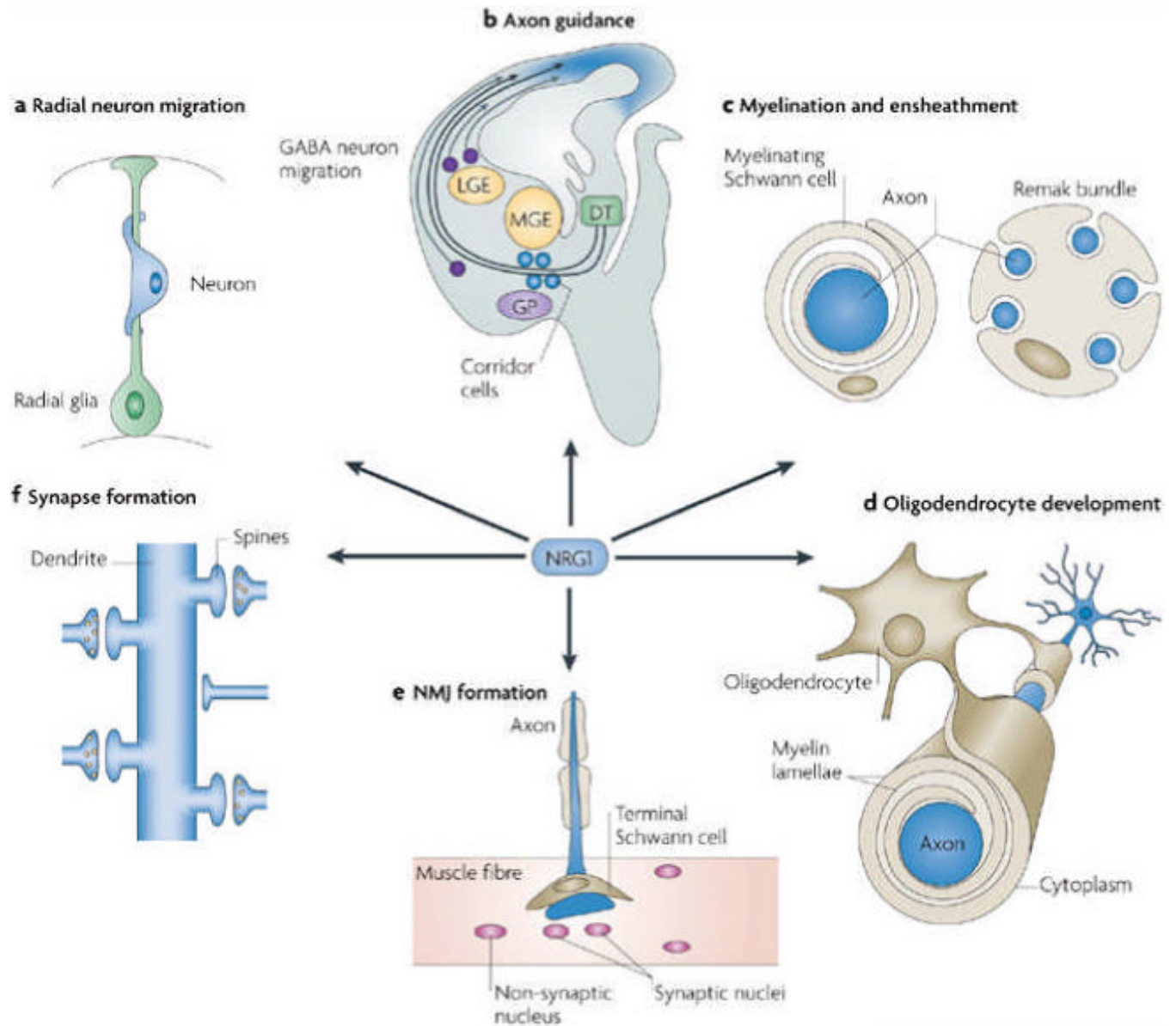
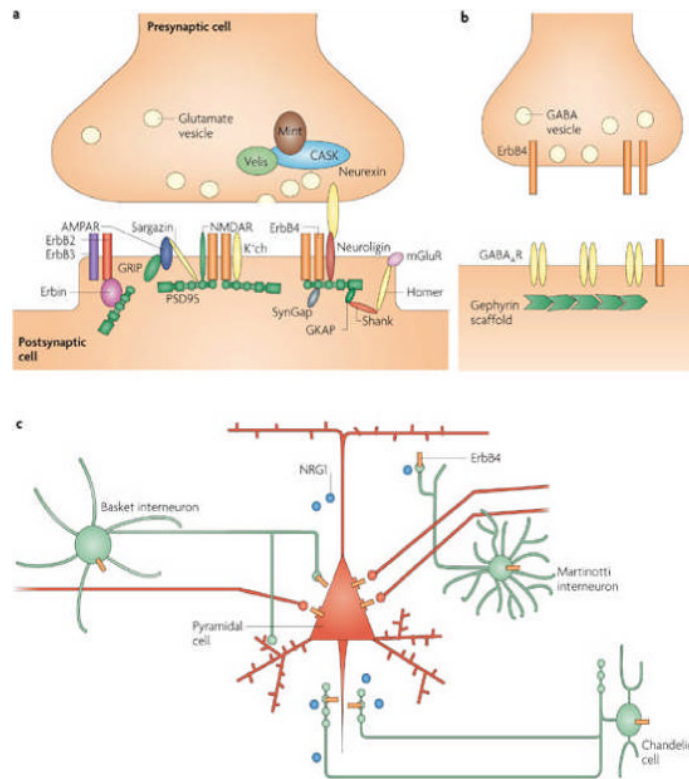


Fig. 5.

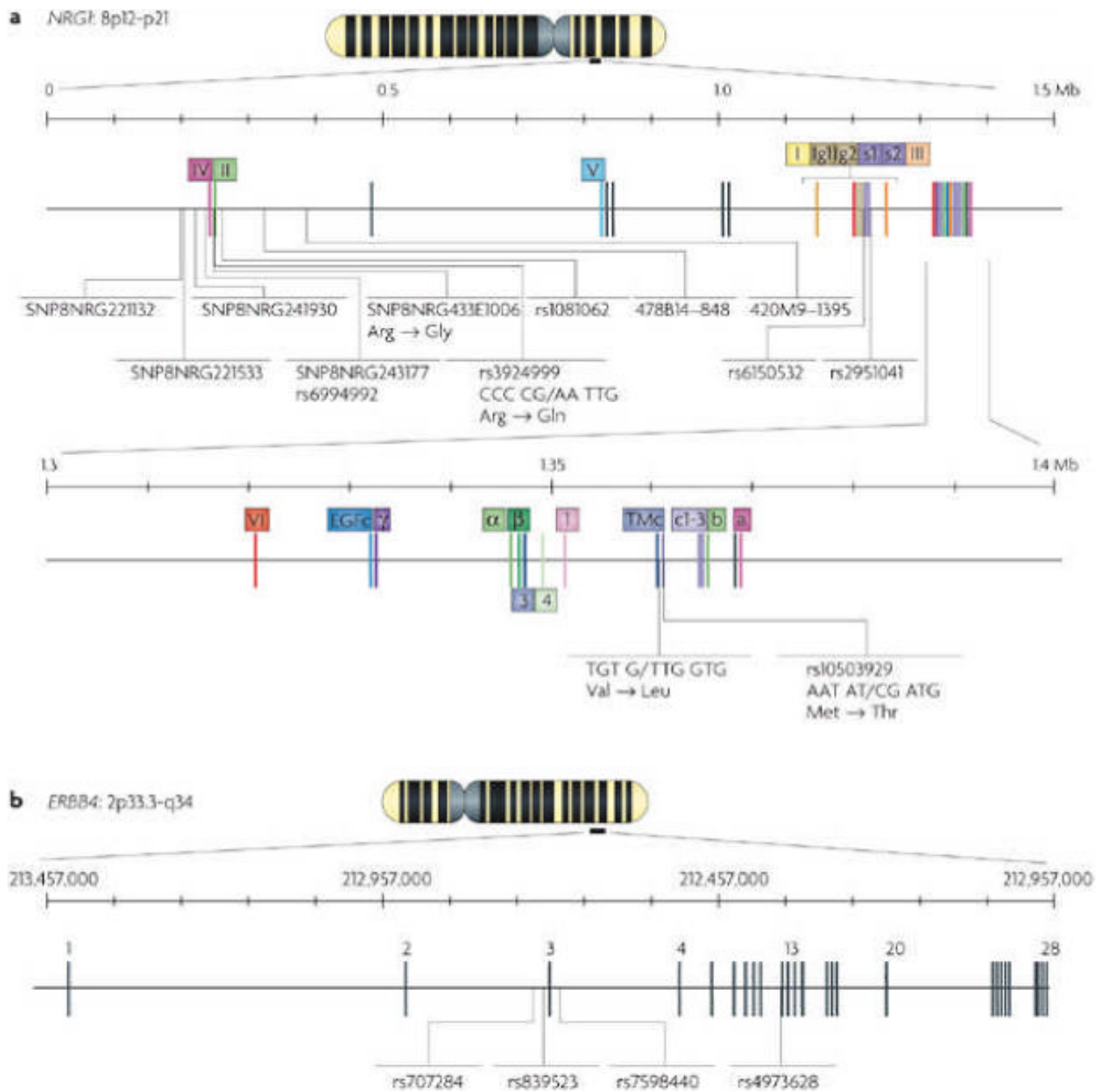
a | Neuregulin 1 (NRG1) (indicated by blue shading) is released from neurons to promote the formation and maintenance of radial glial cells, which are necessary for the radial migration of neurons from ventricular zones to the pial surface. **b** | Tangential migration of GABA (γ -aminobutyric acid)-ergic interneurons requires NRG1 in the cortical region; thalamocortical axon navigation through the diencephalon requires corridor cells that express NRG1. **c** | Myelination and ensheathment of peripheral nerves are controlled by the amounts of NRG1 produced in substrate axons. **d** | NRG1 from axons might regulate oligodendrocyte development and myelination of axons in the CNS. **e** | NRG1 is necessary for the formation of neuromuscular junctions (NMJs), probably through effects on terminal Schwann cell differentiation and survival. **f** | NRG1 stimulates CNS synapse formation. This panel shows typical excitatory synapses, formed between glutamatergic terminals and spines. DT, dorsal thalamus; GP, globus pallidus; LGE, lateral ganglionic eminence; MGE, medial ganglionic

eminence. Part **b** modified, with permission, from Ref. 69 © (2006) Elsevier Science. Part **d** modified, with permission, from Ref. 201 © (2005) Macmillan Publishers Ltd.

**Fig. 6.**

a | ErbB4 interacts specifically with the first and second PDZ domains of postsynaptic density (PSD) protein 95 (PSD95), a scaffold protein, and is localized in the PSD of excitatory synapses. The interaction with PSD95 enhances neuregulin 1 (NRG1) signalling, presumably by increasing ErbB4 homodimerization¹¹⁸. NRG1, by activating ErbB4, suppresses long-term potentiation induction and expression^{38, 118, 120, 121, 122}. The mechanisms that underlie this effect remain unclear. Through PSD95, ErbB4 signalling might regulate the properties of NMDA (*N*-methyl-D-aspartate) receptors (NMDARs), AMPA (α -amino-3-hydroxy-5-methyl-4-isoxazole propionic acid) receptors (AMPA receptors) and K^+ channels (K^+ ch)²⁰². Through the GKAP–Shank–Homer complex, ErbB4 signalling might be involved in regulating the function of metabotropic glutamate receptors (mGluRs). PSD95 might also recruit ErbB4 to the neurotigin–neurexin complex that is essential for synapse formation²⁰³. ErbB2, on the other hand, interacts with erbin, a protein that contains multiple leucine-rich domains and a PDZ domain^{204, 205}. This interaction has been implicated in regulating NRG1 signalling^{206, 207}. **b** | ErbB4 is present in the presynaptic terminals of GABA (γ -aminobutyric acid)-ergic interneurons¹¹². NRG1 stimulates presynaptic ErbB4 to enhance activity-dependent GABA release through mechanisms that have yet to be identified. **c** | A working hypothesis for how NRG1 might regulate pyramidal neuron activity. The output of pyramidal neurons in the prefrontal cortex (PFC) is regulated by excitatory glutamatergic neurons (shown in red) and various inhibitory GABAergic interneurons (shown in green). NRG1 regulates glutamatergic transmission and/or plasticity by activating PSD-localized ErbB4. There are at least three types of GABAergic interneurons in the PFC. Wide-arbor basket cells target the somata and proximal dendrites of pyramidal neurons and adjust the integrated synaptic response. Chandelier cells (or axon-targeting interneurons) terminate at or near the axon hillock of pyramidal neurons, forming vertical arrays of terminals termed ‘cartridges’, to regulate the generation and timing of action potentials. Conversely, Martinotti cells terminate on distal dendrites of pyramidal cells to influence the dendritic processing and integration of synaptic

inputs^{185, 208, 209, 210, 211}. By controlling activity-dependent GABA release, NRG1 might repress the activity of pyramidal neurons. Part **c** modified, with permission, from Ref. 185 © (2005) Macmillan Publishers Ltd.

**Fig. 7.**

a | The neuregulin 1 (*NRG1*) gene is located in a 1.5 Mb region of DNA, at 8p12–8p21. Roman numerals indicate the type-specific exons. The original deCODE hyplotype including the SNPs SNP8NRG221132, SNP8NRG221533, SNP8NRG241930, SNP8NRG243177 and SNP8NRG433E1006 and two microsatellites (478B14–848 and 420M9–1395) is shown. Exons for individual domains of *NRG1* are colour matched with the domain structure in Fig. 1a. **b** | The 1.15 Mb region of the *ERBB4* gene, at 2q33.3–2q34. The SNPs are mainly clustered around exon 3 and in front of exon 13.