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Current perspectives on the genetic causes of neural tube defects

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Abstract Neural tube defects (NTDs) are a group of severe congenital abnormalities resulting from the failure of neurulation. The pattern of inheritance of these complex defects is multifactorial, making it difficult to identify the underlying causes. Scientific research has rapidly progressed in experimental embryology and molecular genetics to elucidate the basis of neurulation. Crucial mechanisms of neurulation include the planar cell polarity pathway, which is essential for the initiation of neural tube closure, and the sonic hedgehog signaling pathway, which regulates neural plate bending. Genes influencing neurulation have been investigated for their contribution to human neural tube defects, but only genes with well-established role in convergent extension provide an exciting new set of candidate genes. Biochemical factors such as folic acid appear to be the greatest modifiers of NTDs risk in the human population. Consequently, much research has focused on genes of folate-related metabolic pathways. Variants of several such genes have been found to be significantly associated with the risk of neural tube defects in more studies. In this manuscript, we reviewed the current perspectives on the causes of neural tube defects and highlighted that we are still a long way from understanding the etiology of these complex defects.

Keywords Neural tube defects (NTDs) · Neurulation · Genetic risk factors · Planar cell polarity (PCP) pathway · Folate metabolism

Abbreviations NTDs: Neural tube defects · AED: Antiepileptic drug · CRs: Cysteine-rich domains · BMP: Bone morphogenetic protein · FGF: Fibroblast growth factor · FGFR: Fibroblast growth factor receptor ·

IGF: Insulin-like growth factor · DV: Dorsoventral · AP: Anteroposterior · RA: Retinoic acid · Shh: Sonic hedgehog · b-HLH: Basic helix-loop-helix · RARs: Retinoic acid receptors · PCP: Planar cell polarity · MHP: Median hinge point · DLHPs: Dorsolateral hinge points · GCPS: Greig cephalopolysyndactyly syndrome · HPE: Holoprosencephaly · BM: Body mass · Hcy: Homocysteine · THF: Tetrahydrofolate · LDL: Low-density lipoprotein · PKC: Protein kinase C

Introduction

Neural tube defects (NTDs) are a group of birth anomalies resulting from failure of fusion of the neural tube around the 28th day after conception, at a time when most women do not know they are pregnant. NTDs are known to occur in 1 out every 1,000 pregnancies in the United States, with varying rates reported among the world's populations [1]. The most common NTDs is anencephaly, which results from failure of fusion of the cranial neural tube, and myelomeningocele (commonly called spina bifida), which results from the failure of fusion in the spinal region of the neural tube. Failure of closure that involves the entire body axis is known as craniorachischisis, which is an additional, relatively rare, form of dysraphism. Anencephaly and myelomeningocele are referred as "open" NTDs because the affected region is exposed to the body surface. There are also a number of closed or skin-covered conditions that involve the neural tube, including: encephalocele, meningocele, lipomeningocele, also referred to as spina bifida occulta, and sacral agenesis. All infants with anencephaly are stillborn or die shortly after birth, whereas many infants with spina bifida survive, usually as a result of extensive medical and surgical care. However, affected individuals are at risk for a range of physical and developmental disabilities (abnormal innervation beneath the level of lesion, varying degrees of muscle weakness, and sensory impairment, neurogenic bladder, and bowel). The majority of NTDs (approximately 70%) occur in isolation and show multifactorial inheritance.

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Several lines of evidence suggest a genetic component of NTDs: firstly, NTDs are associated with known genetic syndromes, trisomies 13 and 18, and various chromosome rearrangements [2]; secondly, the estimated recurrence risk in siblings is 2–5%, representing up a 50-fold increased risk over that observed in general population [3]; and finally, the presence of family history in a number of affected ones [4]. There is a recent epidemiological evidence suggesting that genetic factors related to NTDs may be transmitted preferentially from the mother's side of the family [5]. Despite extensive efforts, no one single major gene has been implicated as a direct causal agent of these human defects, a common result in genetic studies of complex diseases.

Overview of human nervous system development

In human embryos, neurulation occurs in two phases: primary and secondary neurulation. Primary neurulation concerns the transformation of the flat ectodermal neural plate into the cylindrical neural tube. Secondary neurulation is limited to the tail bud and occurs by proliferation and condensation of stem cells that subsequently cavitate. The cavitation results in the formation of a tube making contact with the central canal of the portion of the neural tube formed during primary neurulation. The two processes have been reviewed elsewhere [6–8].

The closure of neural tube in the human embryo has been initially described as a continuous process that begins at the level of the future cervical region and proceeds both rostrally and caudally [9]. However, multiple initiation sites of neural tube closure have been demonstrated in mice and other species. In the mouse, neural tube closure begins at the boundary between the hindbrain and the cervical region (closure 1), with closure spreading from this site rostrally into the hindbrain, as well as caudally into the spinal region. A second point of *de novo* initiation of neural tube closure is in the vicinity of the forebrain–midbrain boundary (closure 2), and a third initiation site is at the rostral extremity of the neural plate (closure 3) [10]. Although the location of closures 1 and 3 appears to be uniform between mouse strains, the site of closure 2 is polymorphic and in some mouse strains (e.g., SELH/Bc) does not occur at all [11]. When closure site 1 fails, the entire neural tube from the midbrain to the lower spine remains open, which is a condition known as *craniorachischisis*. Embryos in which closure 2 is disrupted have *exencephaly*. The failure of closure 3 leads to *anencephaly* that is confined to the forebrain region, often in association with *split-face malformation*. When the caudal spread of fusion from closure 1 fails to be completed, the posterior neuropore remains open which results in *open spina bifida* or *myelomeningocele*. Based on a study of the type and frequency of human NTDs, Van Allen et al. [12] proposed a model in which five closure sites exist in human embryos. According to their model, closure 1 occurs in the cervical region and extends bidirectionally. Closure 2 takes place at the junction between prosencephalon and mesencephalon

and also extends bidirectionally. Closure 3 initiates at the rostral tip of the neural groove and proceeds caudally to meet closure 2. Closure 4 covers the rhombencephalon and completes the closure of cranial neural tube. Closure 5 initiates from the caudal end of the neural groove and spreads cranially (Fig. 1). Although this model was attractive to explain human defects, examination of histological sections of human embryos leads to different models of neural tube closure. In fact, a study by Nakatsu et al. [13] described three sites of apposition, while O'Rahilly and Muller [14] found only two regions of fusion in humans, the first one extending bidirectionally from the rhombencephalic region and the second one that proceeding caudally from the prosencephalic region. The human closure events found by O'Rahilly and Muller have striking resemblance to mouse closures 1 and 3. Therefore, multisite neural tube closure may be a universal phenomenon, although the process appears to be not the same in the human and the other species. This implies, as remarked by Nakatsu et al. [13], that “care should be taken when extrapolating embryological data from laboratory animals to the human”.

Molecular genetics of neurulation

Our ability to understand the pathological mechanisms leading to NTDs depends on the extent to which we understand the normal processes that take place during neurulation. Unfortunately, our current knowledge of these processes is limited, although this situation is changing rapidly because of the growing interest of biologists in neural development at a number of different levels: cellular studies of neurulation, studies of mutant mouse, and studies of the interactions responsible for inducing and patterning of neural plate and tube. This review dissects neurulation into distinct processes that, in turn, are further dissected at the molecular level. Moreover, we present the results of genetic analysis of human homologues of genes causing NTDs in animal models.

The earliest step in the formation of the nervous system is neural induction, the process by which ectodermal cells adopt a neural identity. Concomitantly with neural induction, the induced neural plate becomes patterned along the craniocaudal, dorsoventral, and mediolateral axes. While regional patterning is occurring, the neural plate undergoes morphogenesis: neural folds arise, approach one another in the dorsal midline, and fuse.

Neurulation is driven by redundant mechanisms both at the tissue and cellular level, as well as the molecular level of organization [7]. Nevertheless, even with both intrinsic and extrinsic forces acting redundantly, disruption of neurulation does occur, resulting in NTDs [7].

Neural induction

The amphibian embryo provides an excellent system for studying how the central nervous system is formed in a

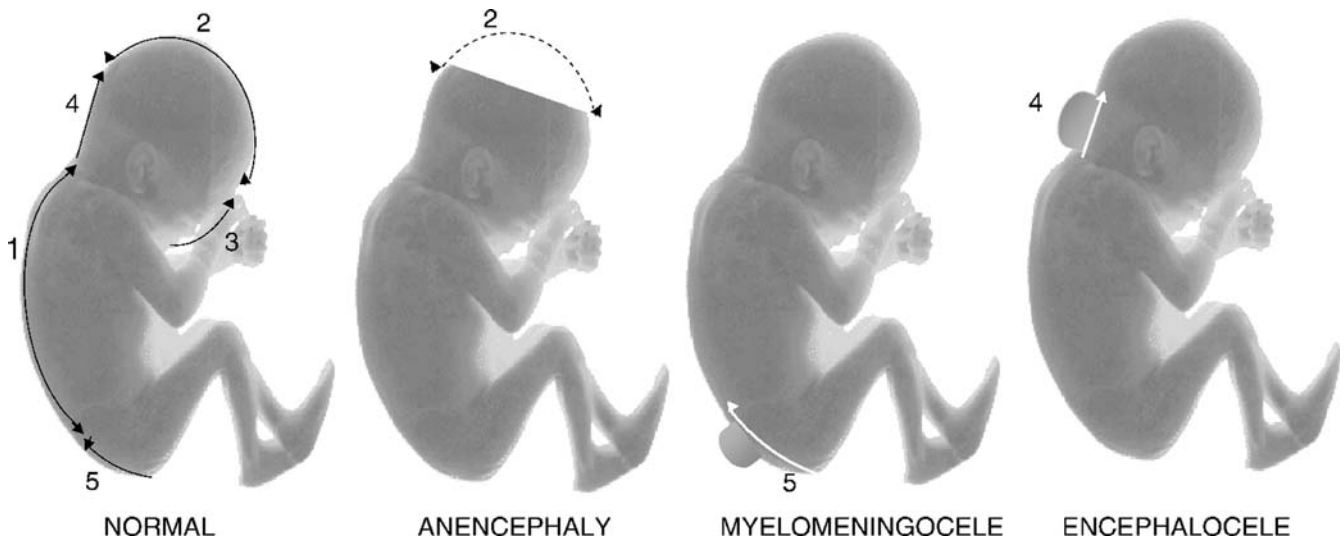


Fig. 1 Multisite closure of the neural tube in the human embryo based on the model proposed by van Allen et al. [12]. According to this model, five closures (four in the head and one in the lumbar region) exist in the neural tube of human embryos. The *arrows* indicate the direction of closure. The various types of human NTDs

can be explained by failure of fusion of one of the site closures. Anencephaly results from the failure of closure 2; sacral myelomeningocele results from failure of closure 5; occipital cephalocele results from incomplete membrane fusion of closure 4

vertebrate embryo. Back in 1924, Spemann and Mangold [15] showed that grafts of the dorsal lip region (“organizer”) of *Xenopus* embryos were able to induce twinning of neural tissue when transplanted into an ectopic site. Extensive screens for organizer-specific genes have been performed and lead to the identification of genes that encode secreted proteins expressed specifically in Spemann’s organizer [16]. Chordin is one of the most abundant proteins secreted by organizer tissue at the gastrula stage, reaching concentrations of 6–10 nM in the extracellular space. When microinjected into *Xenopus* embryos, chordin mRNA is able to induce twinning and neural induction, recapitulating Spemann’s experiments [17, 18]. Chordin is a secreted protein with four cysteine-rich domains (CRs) of about 70 amino acids each. Each CR domain constitutes a bone morphogenetic protein (BMP)-binding module [19]. The chordin loss-of-function phenotype can be rescued by knockdown of BMPs, underscoring that chordin is a dedicated BMP antagonist [20]. BMPs normally prevent embryonic ectoderm from executing its natural “default” tendency to differentiate into neural tissue and instead instruct cells to form epidermis [21, 22]. Lack of BMP signaling in turn leads to the dorsalization of mesoderm and to the neuralization of ectoderm [23] (Fig. 2). Other BMP inhibitors include follistatin, noggin, cerberus, Xnr3 (*Xenopus* nodal-related 3), and TSG (twisted gastrulation) [21, 24–27]. Recent findings indicate that the neural ectoderm is specified in the blastula, before the Spemann’s organizer even forms [28]. Fibroblast growth factor (FGF) signaling is required at this stage to enable later neural differentiation [29, 30]. FGFs are a large class of secreted diffusible glycoproteins that bind to four classes of extracellular receptors (FGF receptors, FGFR) to mediate their effects [31]. These transmembrane receptors consist of an extracellular FGF-ligand-binding domain, a transmembrane

domain, and an intracellular signaling domain [31]. It has been demonstrated that overexpression of dominant negative forms of FGF receptors, which contain the FGF-binding domain but lack the intracellular domain, blocks the generation of neural tissue [32].

Canonical Wnt signaling has also been implicated in the selection of neural or epidermal fate in *Xenopus*. Wnt signaling molecules are a large class of highly conserved secreted glycoproteins, which participate in multiple developmental events during embryogenesis [33]. In *Xenopus*, Wnt signaling activates a transcriptional corepressor of the iroquois family (*Xiro1*), which in turn downregulates BMP expression [34].

Recently, the insulin-like growth factor (IGF) family has also been shown to act as neural inducer in *Xenopus* ectodermal explants [35]. IGFs signal through receptor tyrosine kinases; the phosphorylation and the consequent inhibition of a transcription factor called Smad1 leads to neural induction [36]. As proposed by Pera et al. [36], IGFs and BMP antagonists induce neural tissue by a common mechanism mediated by low levels of Smad1 activity.

Loss of function of noggin, chordin, follistatin, or cerberus 1 in the mouse does not lead to defects in neural induction [37–40]. Double homozygous mutants of chordin and noggin show loss of the prosencephalon [40]. In the zebrafish, loss of chordin in the *chordino* mutants leads to a decrease in the size of the neural plate [41]. By contrast, targeted null mutations in the mouse *Bmp2*, *Bmp4*, or *Bmp7* genes do not lead to changes in size of neural plate [42–45]. Mice lacking either Smad1 and Smad5 activity, two intracellular mediators of BMP signal-transduction components, die early in embryogenesis, but these mutations have no effect on neuroectodermal fate specification [46, 47]. Evaluation of *BMP4* gene and its inhibitor *Noggin* (*NOG*) has also been investigated as

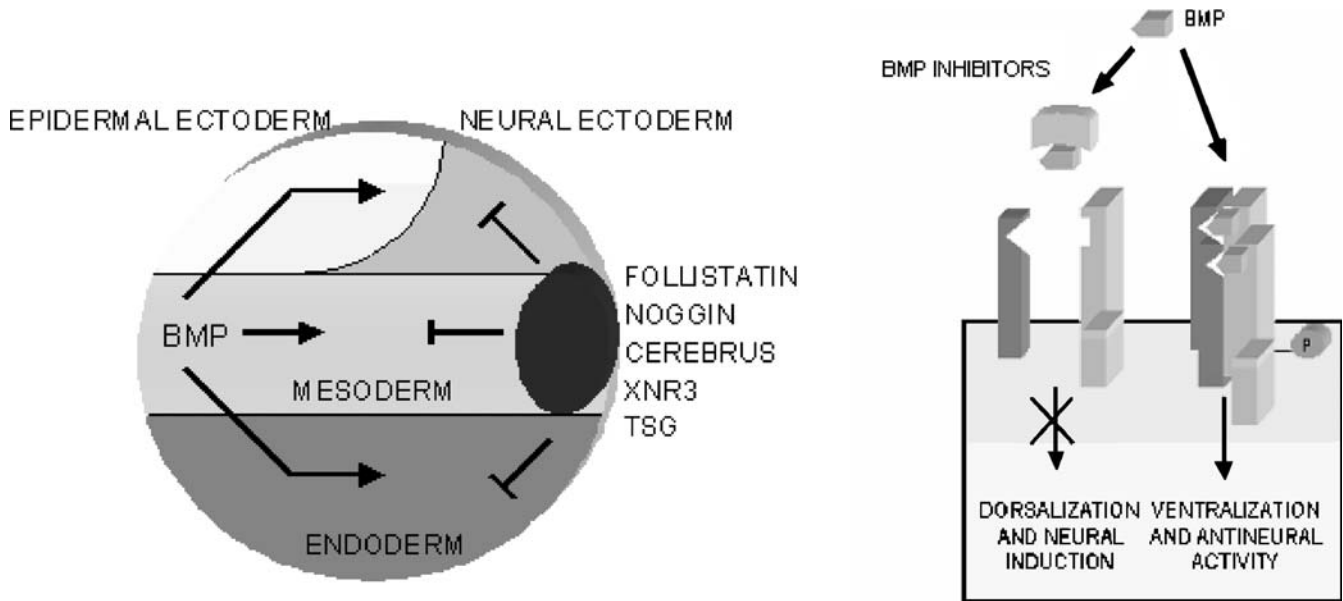


Fig. 2 Neural induction. Signals from the Spemann's organizer induce ectoderm to become anterior neural tissue. Secreted bone morphogenetic protein (BMP) causes ectodermal cells to become epidermis and prevents ectoderm from executing its natural "default" tendency to differentiate into neural tissue. Chordin,

folliculin, noggin, cerberus, Xnr3, and TSG (produced by Spemann's organizer) block BMP signaling leading to the dorsalization of mesoderm and to neuralization of ectoderm. *Xnr3*, *Xenopus nodal-related 3*; *TSG*, twisted gastrulation

candidates in human NTDs. Four missense mutations in *BMP4* and one in *NOG* were found, but it is likely that these mutations act together with other gene variants in independently segregating loci [48].

Neural plate shaping

Increasing evidences suggest that the main driving force for neural plate shaping is convergence extension, a medially directed movement of the cells, with intercalation in the midline, which leads to narrowing and lengthening of the neural plate. In *Xenopus*, misexpression of *dishevelled* (*Xdsh*) produces disruption of convergence extension and NTDs because the broadened midline results in neural folds that are too far apart to meet [49]. These defects result from the failure of the planar cell polarity (PCP) pathway, which is instrumental in governing the polarization of cells within the plane of a cell sheet. PCP signals control cell polarity during convergent extension (CE), an essential process for vertebrate neural tube closure [49–55]. Very recently, Ciruna et al. [56] demonstrated a novel role for PCP signaling during neurulation. These authors demonstrated that PCP signaling polarizes neural progenitors along the AP axis. This polarity, which is transiently lost during cell division in the neural keel, is reestablished as daughter cells reintegrate into the neuroepithelium. The PCP pathway is also referred to as the noncanonical Wnt pathway, in contrast to the canonical Wnt pathway that acts via stabilization and nuclear translocation of armadillo (Arm, β -catenin in vertebrates) (Fig. 3). Members of Frizzled (Fz), a family of seven-transmembrane receptors, and Dishevelled (Dsh/Dvl), a cytoplasmic transducer

protein, are essential for both the canonical and non-canonical PCP pathway [57, 58]. *Drosophila* genetics revealed several other signaling components that are specific to the PCP pathway, including Flamingo (Fmi), Strabismus (Stbm)/Van Gogh (Vangl), Prickle (Pk), Diego, RhoA, and Rho kinase [59–65]. A recent study has shown that the PCP pathway might also be associated with cilia morphogenesis. Disruption of *Xenopus laevis* orthologs of two fly PCP effector proteins, Inturned and Fuzzy, leads to defective neural tube closure [66]. The mutant embryos (Xint and Xfy) show failure of ciliogenesis as a consequence of microtubules incorrectly orienting themselves. Moreover, accumulation of Dsh and Int near the basal apparatus of cilia suggests that these proteins regulate ciliogenesis through a conserved PCP pathway [66]. The relationship between ciliary function and closure of the neural tube has been demonstrated in humans by the identification of two genes (*MSK1* and *MSK3*) responsible for Meckel syndrome, one of the major contributors to syndromic NTDs, and potentially involved in the formation of the cilia apparatus [67, 68].

Mutations in the mouse orthologs of the *Drosophila* PCP genes result in the failure of neural tube closure. Five mouse mutants, *loop-tail* (*Lp*), *circle-tail* (*Crc*), *crash* (*Crsh*), *PTK*, and *dishevelled1/dishevelled2*, harbor defects in PCP genes and fail to undergo closure 1, which leads to craniorachischisis [69–73]. The *Lp* gene, *Vangl2* (also known as *Lpp1* or *Ltap*), has been shown to encode a protein homologous to *Drosophila* strabismus [74]. *Vangl2* is expressed broadly in the neuroectoderm throughout early neurogenesis [75]. This and the fact that the gene was altered in two independent *Lp* alleles identified it as the likely basis for the *Lp* phenotype. The *Crsh* mouse harbors

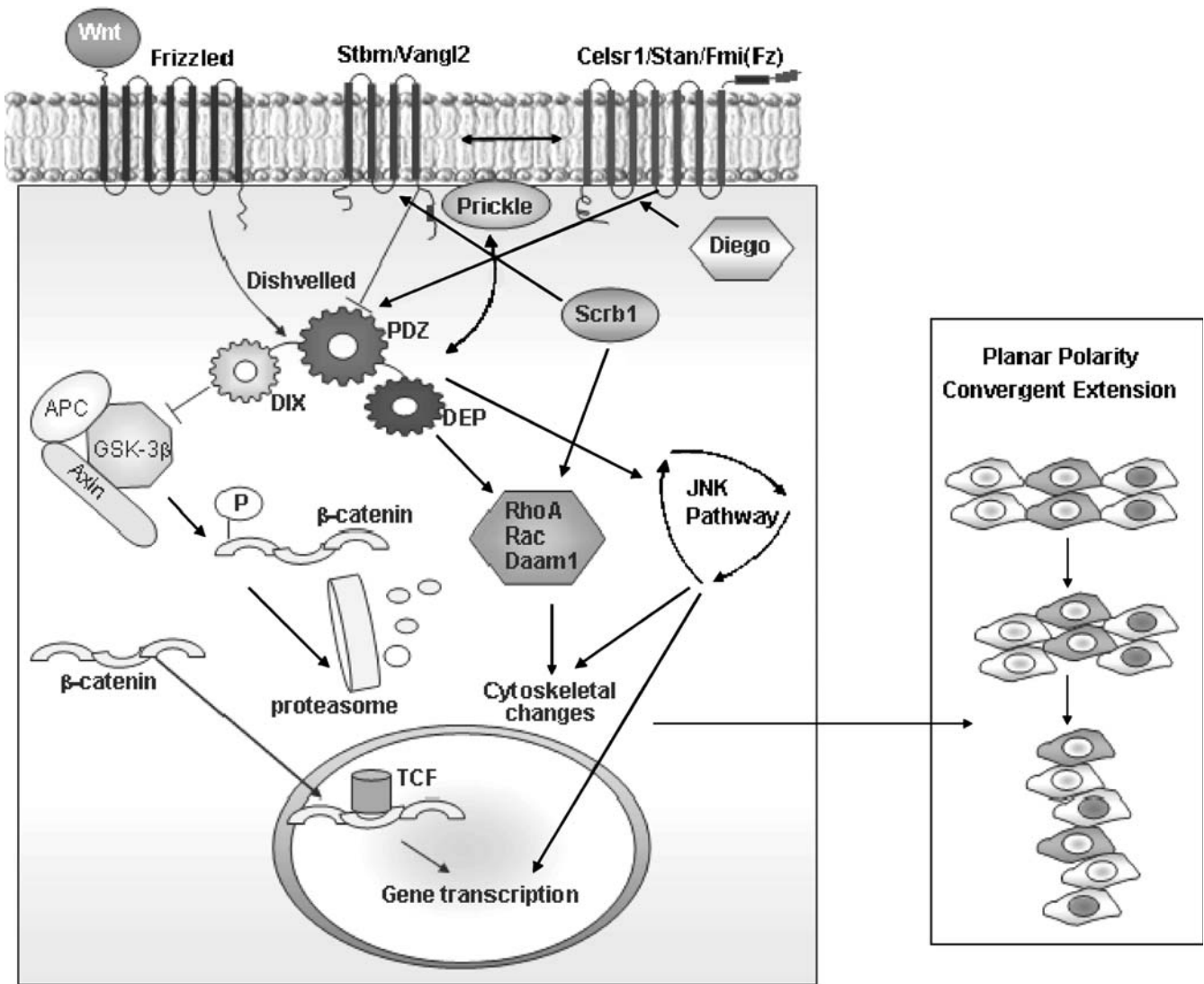


Fig. 3 Canonical (Wnt/ β -catenin pathway) and noncanonical (PCP pathway) Wnt signaling. Both pathways require the receptor Frizzled (Fz) and the cytoplasmic transducer Dishevelled (Dsh/Dvl). Dsh contains three conserved domains: the DIX, which is required for canonical Wnt signaling, the PDZ domain, and the DEP domain, required for Dsh localization during PCP signaling. Canonical Wnt signaling is crucial in developmental processes, cell fate specification, and proliferation. In the absence of Wnt signals, a cytoplasmic protein complex, consisting of glycogen synthase kinase 3- β (GSK3- β), adenomatous polyposis coli (APC), and Axin, marks β -catenin for ubiquitin-dependent degradation. In response to a Wnt ligand, this degradation complex is inactivated, and stabilized β -catenin translocates to the nucleus, where it combines with the T-cell factor (TCF), and stimulates target gene

expression. In contrast, the PCP pathway signals are transduced to the cytoskeleton through the activation of small Rho GTPases (RhoA/Rac/Daam1) and c-Jun N-terminal kinase (JNK). The PCP pathway requires a number of conserved proteins, including Flamingo, Strabismus, Diego, and Prickle whose interactions have not been defined. Scribble (Scrb1), a member of the LAP protein family, is implicated in the PCP pathway potentially by interaction with Vangl2 and with RhoA. In vertebrate embryos, similar molecular requirements have been established for convergent extension (CE) movements and neural tube closure. The CE movements involve convergence of cells toward the dorsal midline, mediolateral cell intercalations in the notochord, and neural tube leading to extension of the body axis

a mutation in *Celsr1*, a seven-pass transmembrane receptor that encodes a protein orthologous to *Drosophila* Flamingo, also known as *starry night* [71]. Like *Vangl2*, this gene also functions in the PCP pathway. In the *Crc* mouse, a point mutation was identified introducing a stop codon into the apical cell polarity gene *scribble* (*Scrb1*), a PDZ domain-containing gene that is the ortholog of *Drosophila scribble* [76]. *Scribble* was not known to be a PCP component in *Drosophila*. However, a polarity defect is

observed in the inner ear of *Crc* mice, suggesting that *Scrb1* does function in establishment of polarity in vertebrates [77]. A mutation in the *protein tyrosine kinase 7* (*PTK7*) gene, which encodes a conserved transmembrane protein with tyrosine kinase homology, disrupts neural tube closure and stereociliary bundle orientation and shows genetic interaction with *Lp* [72]. These findings identify *PTK7* as a regulator of the PCP pathway. Embryos that are double null homozygous for both *dishevelled1* and *dishevelled2*

(*Dsh1^{-/-}/Dsh2^{-/-}*) also exhibit NTDs that closely resemble the craniorachischisis phenotype of *Lp* and *Crc* [73].

Components of the PCP pathway provide an exciting new set of candidate genes for the analysis of human NTDs. Combinations of mutations may act together to provide the genetic risk for human defects. Collectively, these data point to the need to conduct a full analysis of PCP genes to establish a role in the human population. Very recently, Doudney et al. [78] analyzed the coding and splice site regions of human *VANGL1* and *VANGL2* genes in a collection of 66 patients with NTDs. These included 21 patients with craniorachischisis, 24 with spina bifida, and 21 with anencephaly. Only the 346G→A variant in *VANGL1* resulted in a nonsynonymous change (A116T). This variant was found in craniorachischisis and spina bifida patients at a similar frequency with respect to European controls. An elevated frequency was observed in the anencephalic patients, although this is unlikely to be functionally significant. Overall, the data suggest that *VANGL* gene mutations are not a major cause of the severe human NTDs phenotypes.

Dorsoventral (DV) patterning of the neural tube

The neural tube of vertebrates develops a distinct DV pattern, with different cell types arising at different positions along the dorsoventral axis, including floor-plate cells at the ventral midline, motor neurons in ventral regions, and sensory neurons and neural crest in dorsal regions. The generation of DV pattern in the developing spinal cord takes place after neural induction. It has been recognized that the surrounding and underlying mesoderm is the major determinant of the DV structure of the neural tube, rather than it being due to an intrinsic self-organizing capacity (reviewed by Holtfreter and Hamburger [79]). Four classes of secreted factors have been implicated in the DV patterning: FGFs, retinoic acid (RA), sonic hedgehog (Shh), and BMP (Fig. 4). Firstly, FGFs, which are expressed by the caudal mesoderm, must be switched off [80]. Secondly, RA that is produced in the paraxial mesoderm diffuses into the neural tube where it induces differentiation in the neuroepithelium and inhibits FGF signaling [81, 82]. RA induces ventral genes such *Pax6*, *Irx3*, *Dbx1*, and *Dbx2*, a group of homeodomain transcription factors [82]. Thirdly, Shh acts both locally and distally in the control of cell fate in the ventral neural tube. Ectopic expression of Shh in vivo and in vitro can induce the differentiation of floor-plate cells, motor neurons, and ventral interneurons [83, 84]. Conversely, elimination of Shh signaling from the notochord by antibody blockade in vitro [83, 84], or through gene targeting in mice [85], prevents the differentiation of floor-plate cells. Recent studies have provided evidence that a group of homeodomain proteins expressed by ventral progenitor cells acts as intermediary factors in the realization of graded Shh signaling [86–88]. The differential expression of five class I (Shh-repressed) proteins, *Pax7*, *Irx3*, *Dbx1*, *Dbx2*, and

Pax6, and two class II (Shh-induced) proteins, *Nkx6.1* and *Nkx2.2*, subdivides the ventral neural tube into five cardinal progenitor domains [88–90]. Subsequently, cross-repressive interactions that occur between class I and class II proteins refine the initially imprecise pattern of homeodomain protein expression initiated by graded Shh signals [88].

Finally, neuronal patterning in the dorsal half of the spinal cord requires the inductive activities of BMPs produced in the overlying ectoderm and roof plate [91, 92]. BMP provides positional information in dorsal and intermediate regions by setting borders of expression of target genes, in a similar fashion to Shh [92, 93]. Initially, BMPs act in conjunction with Shh to set expression boundaries for the *Pax* genes. The *Pax6* expression boundary that marks the border between dorsal and intermediate cells is refined by the BMP-mediated activation of *Msx1* in dorsal cells, which in turn represses *Dbx2*, a *Dbx* homeodomain protein that is expressed in the intermediate region of the neural tube [94]. This generates two pools of progenitor cells (intermediate and dorsal) with distinct developmental potentials. In intermediate cells, BMPs contribute to the generation of overlapping patterns of homeobox protein expression; their regulation of *Dbx1*, *Dbx2*, and *Pax7* generates at least three distinct populations of progenitor cells [94]. In dorsal cells, the patterning information is provided in part by mutually exclusive expression of members of the basic helix-loop-helix (b-HLH) family of proteins (*Math*, *Mash*, and *Ngn*) and LIM homeodomain proteins (*Lbx* and *Lmx*) [94, 95] (Fig. 4).

Given the critical role of Pax proteins in nervous system patterning, it is important to study the effect of loss-of-function mutations in *Pax* genes in both human and mice. Except *Pax1* and *Pax9*, all members of Pax family have spatially and temporally restricted expression pattern in the developing nervous system [96]. Thus far, mutations in four out of nine *Pax* genes have been associated to human diseases (*PAX1*, *PAX2*, *PAX3*, and *PAX6*). Remarkably, mutations in *Pax* genes demonstrate that they play a critical role in specification and maintenance of structures that are neural crest-derived [97]. Mutation of the *Pax3* gene causes the *Splotch* phenotype in mice (*Sp*) (reviewed by Chalepakakis et al. [98]; Gruss and Walther [99]) and Waardenburg syndrome in humans [100–102]. *Sp/Sp* mice have malformations involving neural crest-derived tissues: NTDs (exencephaly and spina bifida), limb defects, and dysgenesis of spinal ganglia and heart structures. Loss of function of the *Pax6* gene causes the *Small eye* (*Sey*) phenotype in mice and the aniridia, a congenital disorder characterized by complete or partial absence of eye structures [103]. *Pax7* null mice exhibit a loss of craniofacial structures that are neural crest-derived, whereas mutations in regulatory elements of *Pax7* can lead to muscle deficiency and rhabdomyosarcoma [104]. The role of *PAX1*, *PAX3*, *PAX7*, and *PAX9* genes in NTDs pathogenesis has been investigated in 79 sporadic and 38 familial NTDs patients. In one patient with spina bifida, a mutation in the *PAX1* gene was detected changing a conserved amino acid in the paired domain of the protein.

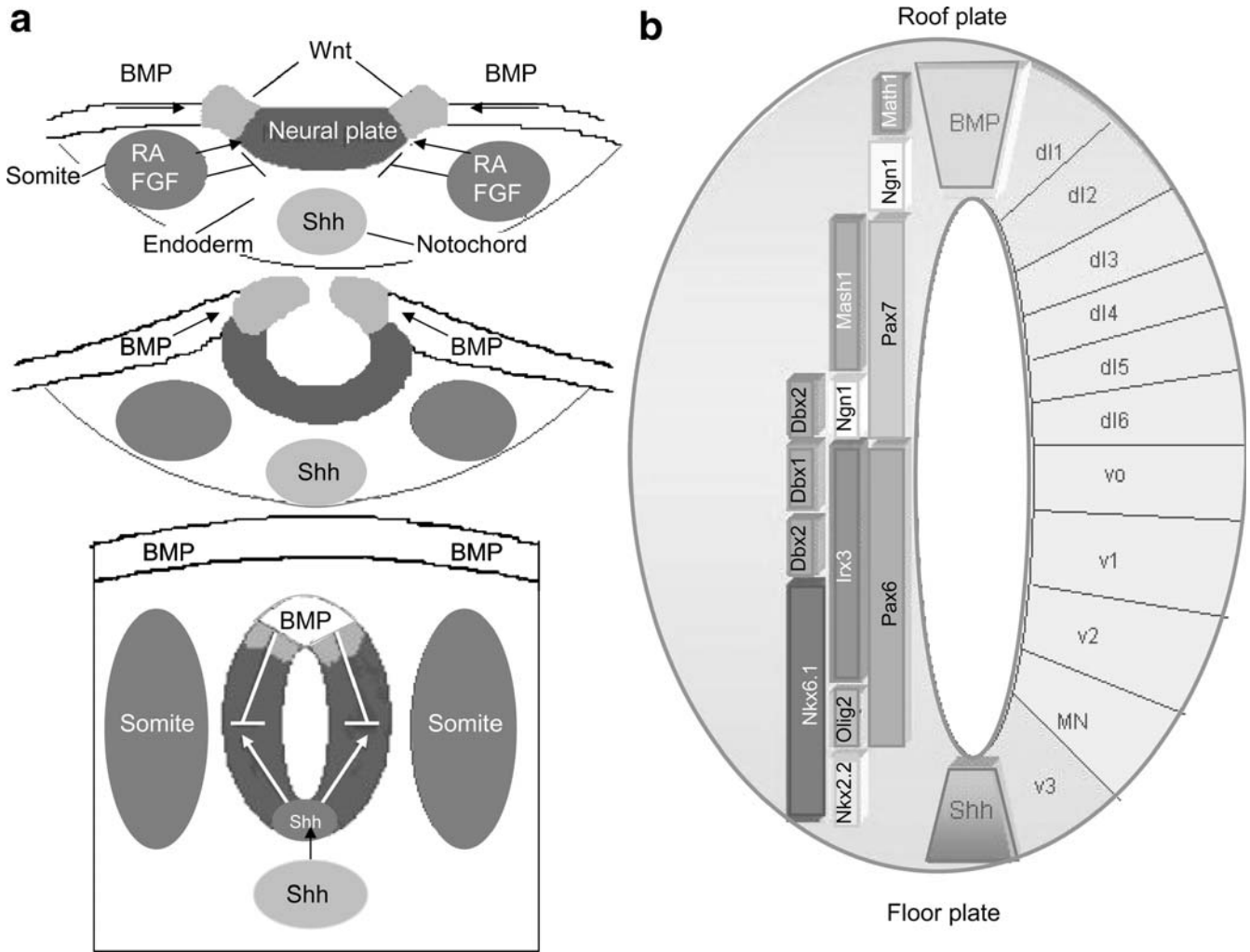


Fig. 4 Dorsal-ventral (DV) patterning of the neural tube. **a** Once the neural fate is specified, FGF (fibroblast growth factor), RA (retinoic acid), Shh (sonic hedgehog), and BMP (bone morphogenetic protein) signaling determine the DV pattern of the neural tube. FGFs from the underlying mesoderm prevent neural differentiation of the overlying neural plate. The somites express RA that antagonizes FGFs and induces a set of genes in the neural tube. The notochord differentiates and starts to express Shh. Shh is also expressed by floor-plate cells and spreads dorsally in a concentration-dependent gradient. BMP starts to be produced by the roof-

plate cells and later spreads ventrally in a concentration gradient. Another extracellular signal which is present in the roof plate involves *Wnts*. **b** The roof-plate BMP gradient and the floor-plate Shh gradient direct cells along the dorsoventral axis to specify their neuronal identity. There are six types of dorsal neurons (dl1–dl6) and five types of ventral neurons (V0–V3 and MN) in the developing neural tube. On the *left* are the protein markers which are used to identify the progenitor domains of the different DV regions

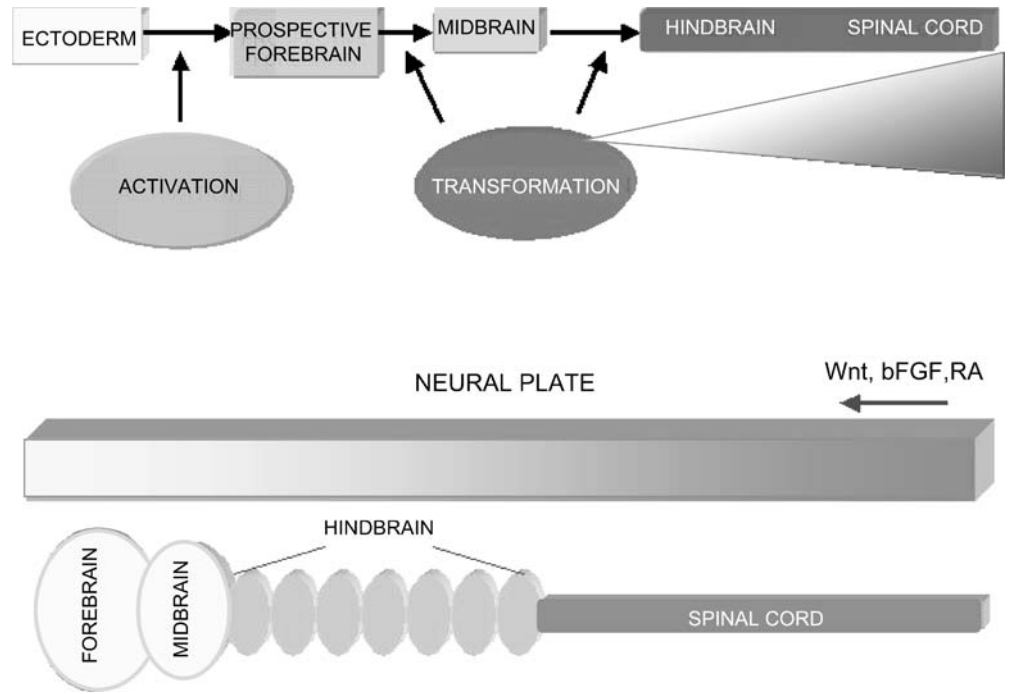
No sequence variation was observed in the paired domain of the *PAX7* and *PAX9* genes. So far, these findings do not support a major role of the *PAX* genes in the etiology of NTDs [105].

Antero-posterior (AP) patterning of the neural tube

A prevailing model for neural AP regionalization was formulated by Nieuwkoop who proposed that this process occurs in two steps: an “activation” step implying an initial induction of anterior neural structures through all presumptive neuroectoderm; subsequently, a second transforming signal is produced by posterior mesoderm [106] (Fig. 5). The major components of the activation signal are

FGF and Wnt signals that act before gastrulation to induce the organizer to secrete inhibitors of BMP signaling such as noggin, chordin, cerberus, and follistatin (reviewed by Harland [107]). In turn, these BMP antagonists induce the neuroectoderm to adopt an anterior fate. Basic FGFs (bFGFs) may act as the second signal in the two-step model for induction of the AP neural pattern [108]. Two groups tested the effect of bFGFs on animal caps of *Xenopus* embryos treated with neuralizing agents like noggin or follistatin [109, 110]. Without bFGFs, these animal caps expressed only anterior neural markers (*Otx2* in forebrain and *En-2* at mid/hindbrain border). When bFGF was also added, both anterior and posterior neural markers (*Krox-20* and *Hoxb9*) were induced. In addition to FGFs, other factors like RA are involved in the AP patterning of the

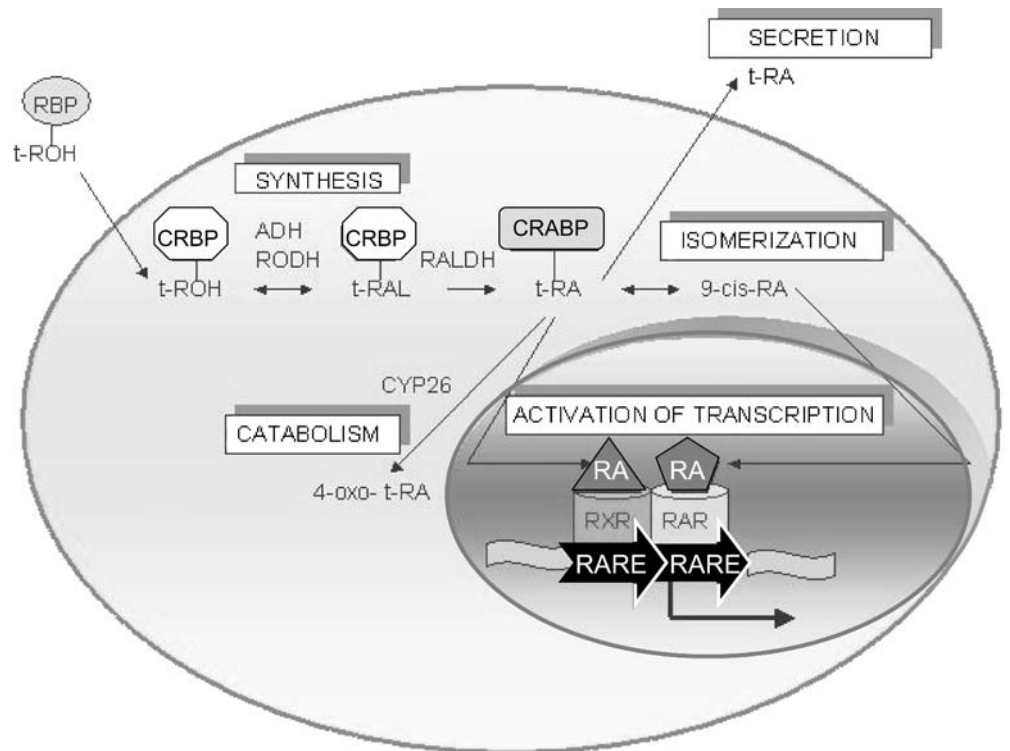
Fig. 5 Anteroposterior (AP) patterning of the neural tube. Neural AP regionalization occurs in two steps: an “activation” step implying an initial induction of anterior neural structures throughout all presumptive neuroectoderm, and a second transforming step that converts the neuroectoderm tissue to more posterior fates, including hindbrain and spinal cord. The major components of the transforming signals are Wnt, bFGF, and RA



neural tube. A series of experimental evidences show the critical role of RA signaling in positional patterning (Fig. 6). RA treatment of *Xenopus* embryos causes loss of forebrain, midbrain, and anterior hindbrain structures [111–116]. Overexpression of a dominant-negative form of RA receptors (RARs) showed that signaling through RARs is required for the RA-induced expression of the posterior markers *Hoxb9*, *N-tubulin*, and *Xlim1* [117]. Moreover, overexpression of the *Xenopus* RA hydroxylase (*Cyp26*),

which targets RA for degradation, leads to expansion of anterior structures [118, 119], whereas inhibition of *Cyp26* expression induces expansion of posterior structures [120]. Overexpression of the RA biosynthetic enzyme *Raldh2* leads to reduction of anterior structures [121], whereas *Raldh2* loss of function results to a variety of axial defects in mice, including axial shortening and loss of posterior rhombomere identity and limb buds [122]. *Cyp26A1*-null mutant mice die during mid-late gestation and show a

Fig. 6 The retinoic acid pathway. Trans-retinol (t-ROH) in the plasma is released from its carrier protein, retinol-binding protein (RBP), into the cell where it is bound by cellular retinol-binding protein (CRBP). The synthesis of retinoic acid (RA) is catalyzed by retinol dehydrogenase (RODH) and alcohol dehydrogenase (ADH) that form trans-retinaldehyde (t-RAL). This molecule is subsequently oxidized by retinaldehyde dehydrogenase (RALDH) to trans-RA (t-RA) which binds cellular retinoic acid-binding protein (CRABP). T-RA can (1) enter the nucleus and bind to retinoic acid receptors (RAR), activating transcription; (2) diffuse out of the cell (secretion); (3) isomerize to 9-*cis*-RA which binds to the RXR retinoic acid receptor; (4) oxidize to 4-*oxo*-t-RA catalyzed by the enzyme CYP26 (inactivation)



number of major morphogenetic defects: spina bifida and truncation of the tail and lumbosacral region (including abnormalities of the kidneys, urogenital tract, and hindgut) are the most conspicuous defects, leading in extreme cases to a sirenomelia phenotype. *Cyp26A1* mutants also show posterior transformations of cervical vertebrae and abnormal patterning of the rostral hindbrain, which appears to be partially posteriorly transformed [123].

It was also suggested that RA and FGF signaling can posteriorize anterior neural tissue, perhaps acting synergistically. These two pathways seem to converge on one common target gene, *Xdac3*, an homeobox gene, which has been implicated in the posteriorization pathway [124].

Because RA pathway genes have the potential for an involvement in human NTDs, human *ALDH*, *CYP26A1*, *CYP26B1*, and *CYP26C1* enzymes as well as *CRABP1* and *CRABP2* (cellular RA-binding proteins) have been studied in human NTDs cases. An association analysis using both allelic and genotypic single-locus tests revealed a significant association for NTDs risk only for three polymorphisms in the *ALDH1A2* gene [125].

A role for Wnt signaling in posteriorizing the embryonic axis has also been suggested by studies in *Xenopus* showing that overexpression of Wnt3A posteriorized anterior neuroectoderm [126, 127]. Moreover, blockade of Wnt8 signaling caused loss of posterior fates demonstrating that Wnt8 is an important transforming factor in zebrafish and *Xenopus* [128, 129]. Finally, Krumlauf and colleagues recently showed that the Wnt pathway posteriorizes *Xenopus* neural tissue via an indirect mechanism requiring FGF signaling. These findings suggest that the posteriorization pathway might be Wnt→FGF→Xcad3→posterior HOX genes [130].

Bending of the neural plate

Neural folds form at the edges of the neural plate, then elevate and fuse in the dorsal midline to create the neural tube. In birds and mammals, bending of the neuroepithelium occurs at two specific sites in the neural plate [131, 132]: at the ventral midline (the median hinge point; MHP) and at paired lateral bending sites near the junction of the neural plate and surface ectoderm (the dorsolateral hinge points; DLHPs). Midline and dorsolateral bending are regulated by mutually antagonistic signals from the notochord and surface ectoderm.

Shh pathway is critical to neural tube bending (Fig. 7). In fact, DLHP formation is normally suppressed by Shh signaling at high levels of the spinal axis [133], although it is induced in cases of Shh deficiency [134]. Shh overexpression can produce NTDs, probably by inhibiting dorsolateral bending at levels of body axis at which it is essential for closure. Neural tube closure defects of both cranial and spinal regions are seen in mice with loss of *Patched 1* (*Ptc 1*) function [135, 136]. The *Ptc* receptor is responsible for maintaining Shh signaling in an “off” state

in the absence of Shh ligand. Consequently, loss of function of *Ptc 1* leads to constitutive Shh signaling, and like Shh overexpression, to severe NTDs. In contrast, mutations that directly or indirectly reduce the strength of Shh signaling, as seen in knockouts of *Gli1/2*, and *HNF3β* (hepatocyte nuclear factor 3β) (*Foxa2*) genes fail to develop NTDs presumably because of deinhibition of DLHP formation [137, 138]. Loss of function of *Gli3*, a negative regulator of Shh signaling in some tissues, leads to cranial NTDs in the *extra-toes* (*Xt*) mouse [139], suggesting a role for Shh signaling in cranial as well as spinal neurulation. Protein kinase A (PKA) is also known to be involved in neural tube formation, as it downregulates the Shh signaling. The PKA-deficient mouse model that retains only one functional catalytic subunit allele develops localized spinal NTDs. Decreased PKA activity causes dorsal expansion of the Shh signal through the thoracic to the sacral regions of the ventral tube, suggesting differential dependence on PKA activity along the AP axis [140].

NTDs are also seen in *Zic2*^{-/-} and in the *open brain* (*opb*) mutants [141, 142]. *Opb* disrupts the *Rab23* gene, a member of small GTPase RAB proteins (a negative regulator of Shh), whereas *Zic2* encodes a zinc finger protein with anti-Shh activity. Both *opb* and *Zic2*^{-/-} mutant embryos lack dorsal neural cell types and the ability to form DLHPs [141–143].

Mutations of genes involved in the molecular mechanisms controlling the neural plate bending have been looked for in human cases. Greig cephalopolysyndactyly syndrome (GCPS), characterized by craniofacial and limb anomalies, is associated with translocations as well as point mutations affecting one allele of the zinc finger gene *GLI3* [144, 145]. In addition to GCPS, Pallister-Hall syndrome and postaxial polydactyly type A are caused by *GLI3* mutations [146, 147]. NTDs are not a recognized feature of these syndromes. This is not surprising because NTDs in *Xt* mouse are of low penetrance, occur only in homozygotes, and are expected to be perinatally lethal [148]. A number of mutations in the *SHH* gene have been identified in cases of autosomal dominant holoprosencephaly (HPE), the most common congenital structural forebrain anomaly in humans [149, 150]. Mutations in *PATCHED-1*, the receptor for Shh, are also associated with HPE; these findings demonstrate that mutations in different components of a single signaling pathway can result in the same clinical condition [151]. A recent study identified notochord splitting and abnormal expression of *SHH* gene in the floor plate of human embryos with craniorachischisis and spina bifida [152]. A pilot study designed to identify an association between variations of the human *SHH* gene and spina bifida failed to uncover any disease-related mutation, although mutational screening was limited to the sequence encoding SHH-N protein and excluded the region coding for SHH-C protein that contains the autocatalytic cleavage site of SHH [153]. Genes encoding catalytic subunits of PKA and *ZIC1/ZIC2/ZIC3* were investigated for mutations that may predispose to NTDs with negative results [154, 155].

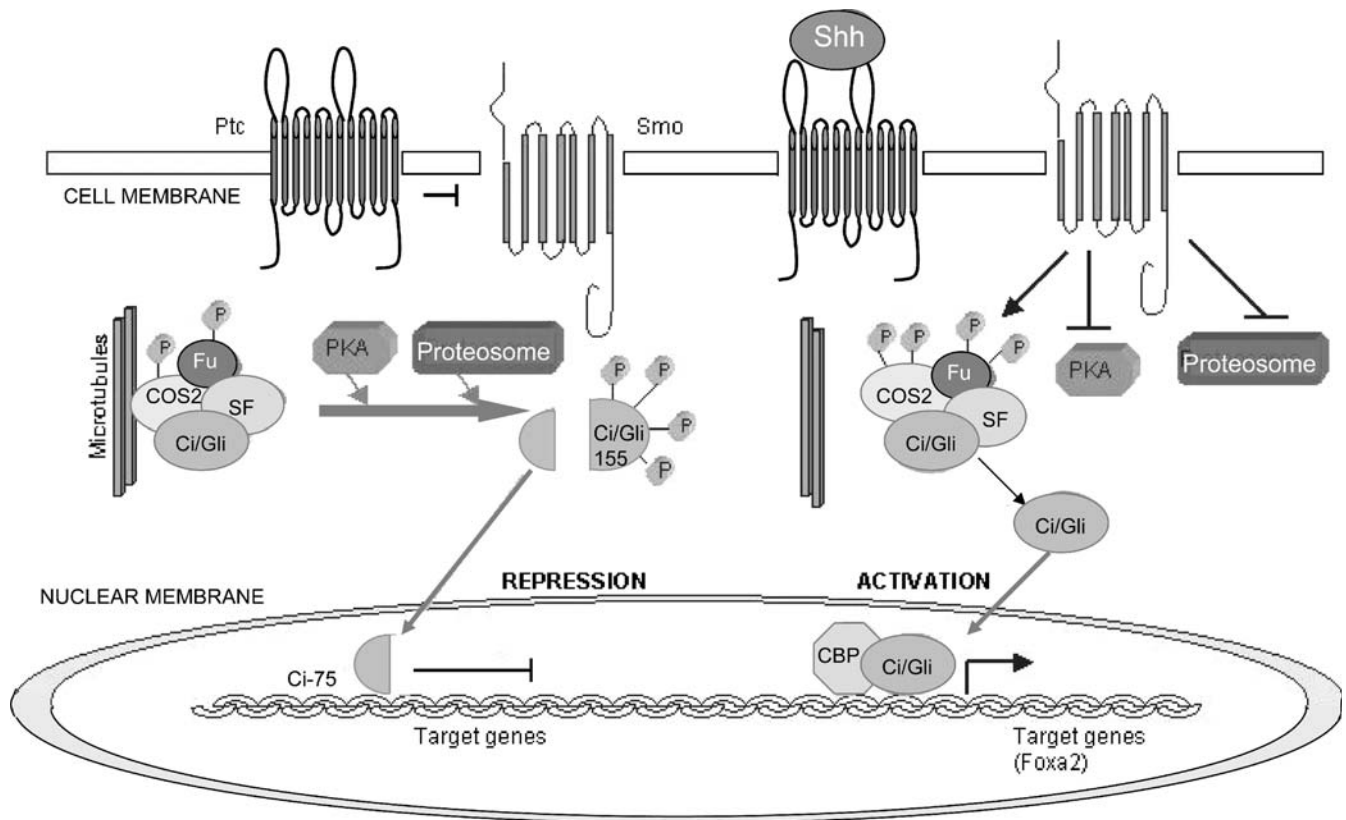


Fig. 7 Sonic hedgehog transduction (Shh) pathway. Shh binds the protein Patched (Ptc), which is a 12-pass membrane protein that acts as a receptor for Shh. In the absence of Shh, Ptc inhibits the protein smoothed (Smo), which is a seven-pass membrane protein that acts as a signal transducer. A transcription factor, called Cubitus interruptus (Ci) in *Drosophila* and Gli in vertebrates, acts as a transcriptional repressor. The nucleocytoplasmic shuttling of Ci/Gli proteins depends on a complex formed by the serine/threonine kinase Fused (Fu), suppressor of Fused (SF), and Costal 2 (COS2). Ci/Fu/SF/COS2 are bound together in a high weight molecular

complex which is attached to microtubules. In absence of Shh stimulation, Ci/Gli is cleaved into a smaller N-terminal fragment (Ci-75) which enters the nucleus and represses target genes. Once Smo is freed of the inhibitory effects of Ptc, Smo signals causing hyperphosphorylation of COS2 and Fu and inducing the complex to loosen its hold on microtubules. This leads to the stabilization of full length Ci/Gli (Ci-155) that migrates into the nucleus where it binds the coactivator CBP/p300 and activates target genes. Also involved in Shh signaling are the proteasome and protein kinase A (PKA) that phosphorylates Ci/Gli at different residues

Apical constriction

Cell shape changes and cellular movements are required for correct neural tube formation. The process that converts columnar cells into wedge-shaped cells is called apical constriction. Apical constriction is coordinated both at the cellular and molecular level. More recent findings on genetic control of these processes have been reviewed by Wallingford [156]. Only very few molecules have been identified as regulators of apical constriction in the neural plate: p190RhoGAP and Shroom. P190RhoGAP is a negative regulator of the Rho GTPase, which is in turn a regulator of actin filament dynamics. Mice lacking a functional *p190RhoGAP* gene exhibit several defects in neural development, which include abnormalities in fore-brain hemisphere fusion, ventricle shape, optic cup formation, neural tube closure, and layering of the cerebral cortex [157]. Cells of the neural tube floor plate in *p190RhoGAP* mutant mice present excessive accumulations of polymerized actin, suggesting a role for p190RhoGAP in the regulation of Rho-mediated actin assembly within the neuroepithelium [157]. The second molecule implicated in

controlling apical constriction is the filamentous (F)-actin-binding protein, Shroom. Mice lacking *Shroom* function display 100% penetrant exencephaly with loss of apically localized actin in the neuroepithelium [158]. It has been demonstrated that ectopic Shroom can elicit apical constriction in undifferentiated epithelial cells of *Xenopus* [159]. Moreover, cells expressing Shroom undergo apical constriction and increase their apical surface [159]. Loss of function of other genes that regulate actin arrangement at the cell membrane, such as the protein kinase C targets *Macs* and *Mlp*, the actin-binding *vinculin*, the nonreceptor tyrosine kinases *Abl/Arg*, the cytoskeleton-related genes *Mena (Enah)/Profilin1 (Pfn1)*, results in cranial NTDs [160–164]. These findings suggest that actin-mediated mechanisms are crucial for closure of the cranial neural tube by allowing dorsolateral bending of the cranial neuroepithelium. *MLP* and *MACS* genes have been investigated as potential candidates for human NTDs, but no evidence of linkage disequilibrium has been found for flanking markers of these genes in 43 simplex NTDs families, suggesting that these genes are not major genes for NTDs in these families [165].

Fusion of the neural folds

Molecules that mediate neural fold adhesion and fusion are little known. Biological evidence supports a role for cell adhesion in neurulation, but few specific cell adhesion molecules have been identified. Inactivation of Eph-A5, a cell surface ephrin ligand, results in NTDs [166]. Inactivation of the Eph-A7 receptor also produces NTDs [166]. Eph tyrosine kinase receptors and their membrane-bound ephrin ligands mediate cell–cell interactions and participate in several developmental processes. Both Eph-A5 and Eph-A7 are expressed in the cranial neuroepithelium before and during neurulation, but not in spinal neuroepithelium, which accounts for cranial NTDs in these mice [166].

A recent study by Lee et al. [167] adds to the complexity of ephrin signaling. The authors showed that ephrinB1 acts through components of the PCP pathway to control the migration of cells during *Xenopus* development. The activity of the PCP pathway and CE movements require polarized clustering of Dsh at the cell membrane. As Eph–ephrin interactions lead to formation of large clusters at sites of cell contact, the interaction with ephrinB1 (and Eph receptors) is predicted to lead to clustering of Dsh and, therefore, to the activation of the PCP pathway. These data suggest that Eph receptors and ephrins may both contribute to the correct migration of neuronal progenitor cells.

The neural cell adhesion molecule (NCAM) is a prototypic immunoglobulin-like adhesion molecule and may play a role in neural tube formation and closure. Two members of another cell adhesion molecule family, the cadherins, have been found to be differentially expressed during neural plate formation. N-cadherin is expressed in the neural plate but not in the surrounding ectoderm, while E-cadherin shows an inverse pattern of expression [168]. *Xenopus* embryos in which the neural tube and surface ectoderm both express N-cadherin fail to separate the two tissues and develop NTDs [169]. However, mice with null mutations in *NCAM* or *N-cadherin* (*Cdh2*) genes undergo normal neural tube closure [170, 171]. Thus, these results indicate that these cell adhesion molecules do not play a major role in the normal process of neural tube formation. The role of *NCAM1* in the risk of human NTDs has been investigated in 132 spina bifida families. This study suggests that variations of *NCAM1* may contribute to NTDs risk; in addition, the authors confirmed the expression of *NCAM1* in the surrounding and late differentiating neurons of the central nervous system of human embryos [172].

Risk factors for human NTDs

Over the years, epidemiologic studies have been instrumental in elucidating the causes of NTDs in humans. Overall, these studies have suggested that environmental and genetic factors have a joint role in the causation of NTDs. However, many of the reported associations have been weak and have not been replicated.

Environmental risk factors

Maternal diabetes has long been associated with NTDs risk, while periconceptional glycemic control has been associated with a reduction in the risk. Maternal hyperinsulinemia and hyperglycemia have also been suggested to be putative risk factors for NTDs-affected pregnancies [173]. Abnormally, high glucose levels in maternal blood, which leads to increased glucose transport to the embryo, is responsible for teratogenic effects. In addition, maternal obesity increases the NTDs risk (1.5- to 3.5-fold higher risk) in women in the highest body mass (BM) index categories as compared to women with lower BM indices [174]. There is also strong evidence that maternal hyperthermia increases the risk of having a child with an NTDs by up to twofold [175].

Some specific pharmaceutical compounds have been associated with an increased risk for NTDs. During the first and second months of pregnancy, exposure to antiepileptic drugs (AEDs) is associated with a 10- to 20-fold increase in the frequency of NTDs-affected pregnancies [176]. The teratogenic mechanism is still unknown. Valproate and other AED are folic acid antagonists due to their ability to inhibit dihydrofolate reductase and decrease folate absorption. In addition to AEDs, association with NTDs has also been found with diuretics, antihistamines, and sulfonamides [177]. To date, the results on non-AED drugs are still debated and require further studies.

Other potential extrinsic factors that require further confirmation include: food contaminated with fumonisin (a class of mycotoxin), chlorination disinfection by products in drinking water, electromagnetic fields, pesticides, hazardous waste sites, maternal stress, lack of social support, and maternal diarrhea [178–184].

The most important epidemiological finding with respect to NTDs is the protective effect of maternal periconceptional folic acid supplementation [185, 186]. These studies demonstrated that maternal folic acid supplementation of at least 4 mg/day reduces the incidence of NTDs by up to 75%. This finding has been translated into public health policies, including educational campaigns and food fortification programs. However, public campaigns promoting the voluntary daily use of folic acid have not had an appreciable impact on the prevalence of NTDs. In contrast, data from countries that have implemented fortification programs indicate a 30–50% reduction in the prevalence of NTDs after fortification [187].

The role of folate in the etiology of human NTDs

Folate supplementation provides a well-documented benefit for the prevention of developmental defects in humans, most notably of craniofacial defects and NTDs. It has been estimated that 70% of human NTDs are preventable by adequate folate intake [185, 186].

Folate metabolism

Folic acid is an inactive water-soluble B vitamin that in mammalian tissues functions as substrate in series of interconnected metabolic cycles involving thymidilate and purine biosynthesis (adenosine and guanine) and methionine synthesis via homocysteine (Hcy) remethylation (Fig. 8). Thus, folate is directly or indirectly essential for cell function, division, and differentiation. There are over 25 proteins involved in the folate pathways. Several of the corresponding genes have been examined as risk factors for NTDs, but few have been associated with NTDs risk (Table 1). The 677C→T thermolabile isoform of *MTHFR* first emerged as a possible genetic risk factor for NTDs in some populations [188–190], even if other studies failed to demonstrate an association [191–193]. A recent meta-analysis found a pooled odds ratio for cases homozygous at 677C→T (677TT) of 1.7 (95% CI 1.4–2.2), with a pooled attributable fraction of NTDs cases of 6% for homozygosity [194]. A second mutation in the *MTHFR* gene

(1298A→C) has also been associated with NTDs [195–197]. Given its important role in folate metabolism, the trifunctional enzyme methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase/formyltetrahydrofolate synthetase (*MTHFD1*) may play a role in NTDs pathogenesis. Brody et al. [198, 199] demonstrated that the polymorphism 1958G→A (R653Q) within the *MTHFD1* gene resulting in the substitution of a conserved arginine by glutamine is a maternal risk factor for NTDs. A recent study by Rothenberg et al. [200] showed that some mothers with an NTDs pregnancy produce autoantibodies that bind to folate receptors on the placental membrane and therefore block the binding of folic acid. The authors suggest that folate supplementation would bypass autoantibody formation that mediates the placental folate receptor blockage. Mutations in genes for folate receptors are very rare and have been identified in only a few patients [201]. These receptors appear to be essential during embryogenesis such that their incorrect function leads to fetal death. On the other hand, a prevalent polymorphism (A80G) in

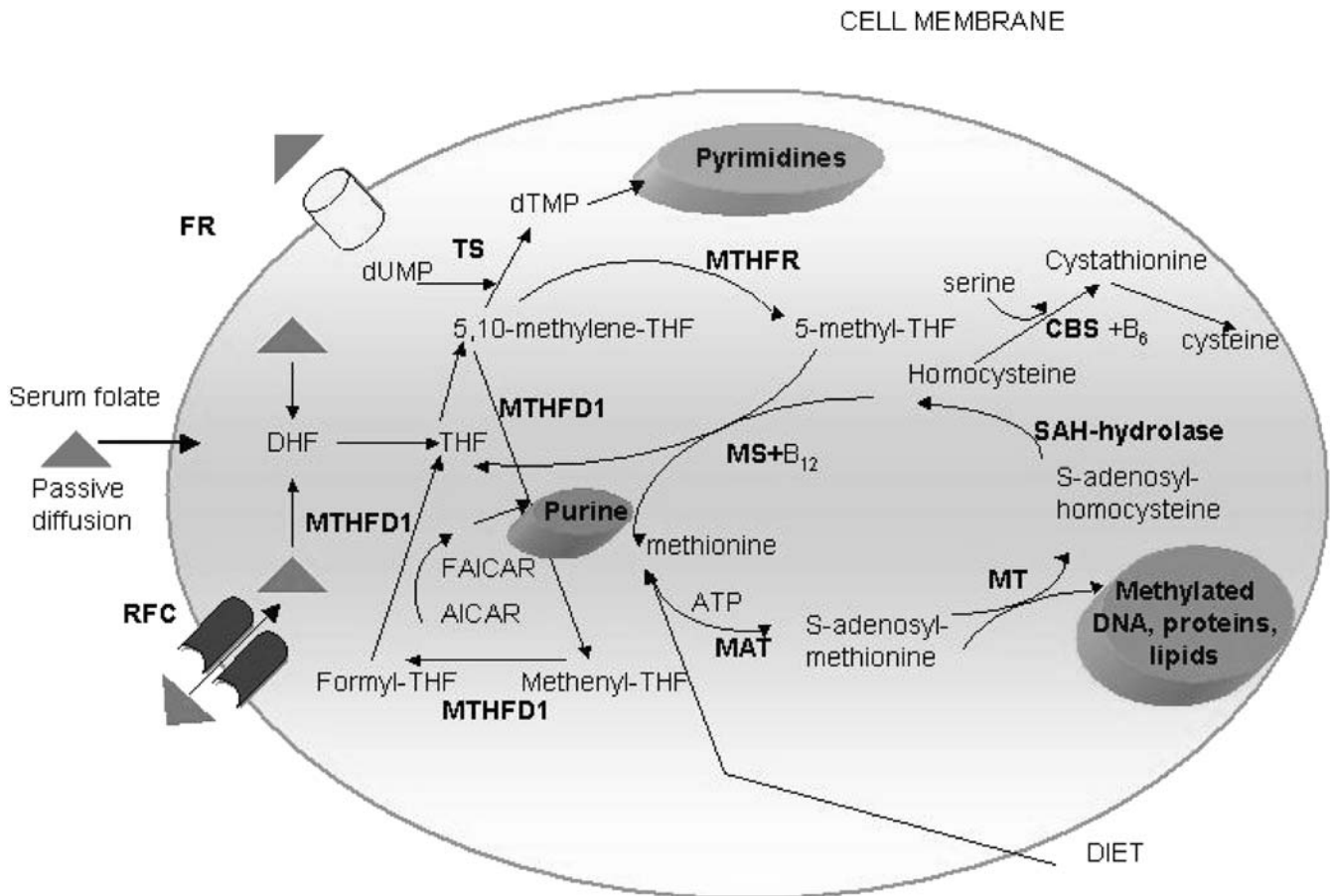


Fig. 8 Folate metabolism and the role of genes in the pathway. Foliates: *DHF* dihydrofolate, *THF* tetrahydrofolate, *5,10-methylene-THF* 5,10-methylene-tetrahydrofolate, *5-methyl-THF* 5-methyl-tetrahydrofolate. Cofactors: B_{12} vitamin B_{12} , B_6 vitamin B_6 . Folate genes (**bold characters**): *FR* folate receptor, *RFC* reduced folate carrier, *TS* thymidylate synthetase, *MTHFR* methylenetetrahydrofolate reductase, *MS* methionine synthase, *CBS* cystathionine-beta-

synthase, *MTHFD1* methylene-tetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase/formyltetrahydrofolate cyclohydrolase, *MAT* methionine adenosyltransferase, *MT* methyltransferase, *SAH hydrolase* S-adenosylhomocysteine hydrolase, *dUMP* deoxyuridine monophosphate, *dTMP* deoxythymidine monophosphate, *AICAR* 5-amino-4-imidazolecarboxamide ribonucleotide, *FAICAR* formyl-5-amino-4-imidazolecarboxamide ribonucleotide

Table 1 Candidates genes from folate/homocysteine metabolism

Human gene	Human locus	Polymorphism	Amino acid change	Association with NTDs risk
<i>MTHFR</i>	1p36.3	C677T	A222V	+/-
		A1298C	E429A	+/-
		C116T	P39P	+/-
		G1793A	R594Q	+/-
<i>MTHFD1</i>	14q24	G1958A	R653Q	+
<i>RFC-1</i>	21q22.3	G80A	R27H	+
<i>GCPII</i>	11p11.2	C1561T	H475Y	-
<i>MS</i>	1q43	A2756G	D919G	+/-
<i>MTRR</i>	5p15.2–15.3	A66G	I22M	+/-
		C524T	S175L	-
		A1049G	K350R	-
		A67G	I23V	-
<i>TCII</i>	22q12.2	G280A	G94S	-
		A701G	E234R	-
		C776G	P259R	-
		C1043T	S348F	-
		G1196A	R399E	-
<i>SHMT</i>	17p11.2	C1420T	L474F	-
<i>BHMT</i>	5q13.1–q13.2	G742A	R239Q	-
<i>CBS</i>	21q22.3	844ins68bp	Premature stop codon? ^a	+/-
<i>TS</i>	18p11.32	28 bp repeat	Promoter polymorphism	+/-

^aThis polymorphism creates an alternate splicing site, which eliminates not only the inserted intronic sequences but also the T833C mutation associated with this insertion. The net result is the generation of both quantitatively and qualitatively normal mRNA and CBS enzyme. +, Positive association; -, negative association

the gene coding for the folate carrier (*RFC-1*) has been demonstrated as a genetic risk factor for NTDs [202, 203]. Additional studies demonstrated that this variant may interact with low folate status and *MTHFR* mutations to increase NTDs risk [204].

Homocysteine and vitamin B12 metabolism

Hcy participates in three essential reactions or sequences: (a) the transsulfuration pathway that leads via cystathionine to the formation of cysteine; (b) the cycling of intracellular folates; and (c) the catabolism of choline and betaine. Hyperhomocysteinemia is correlated with an increased risk for multifactorial diseases including NTDs. Several hypotheses have been advanced to explain the toxic effects of homocysteine. Exposure of neurons to homocysteine causes DNA damage through poly(ADP-ribose) polymerase activation and p53 induction leading to programmed cell death. There is also evidence that low maternal B₁₂ levels represent risk factors for NTDs [205]. Investigation of an A-to-G transition at bp 2,756 and a C-to-A transversion at bp 5,094 of the methionine synthase (*MS* or *MTR*) gene, which converts folate and Hcy to tetrahydrofolate (THF) and methionine, yielded controversial conclusions depending on the population studied [206, 207]. Thus far, only few studies examined the role of the A66G polymorphism of the methionine synthase reductase (*MTRR*), the enzyme that activates MS. An increased

prevalence of the *MTRR* 66GG homozygous genotype in NTDs patients and their mothers was observed. In combination with low vitamin B₁₂ levels, the relative risk of the *MTRR* 66GG genotype increased by two- to fivefold in the NTDs patients and their mothers [208]. This may indicate that, especially when the cofactor of MS (vitamin B₁₂) is limited, a reduced activation of MS by *MTRR* could lead to disturbed remethylation of Hcy to methionine. However, a recent analysis of *MTRR* polymorphisms (A66G, C524T, and A1049G) in a large homogeneous Irish NTDs population did not support an important role for these variants in NTDs [209]. Two groups studied the role of some SNPs of the transcobalamin II (*TCII*) gene coding the protein involved in the transport of vitamin B₁₂ within plasma, but none of these SNPs was associated with a significantly increased NTDs risk [210, 211]. Other genes of Hcy pathways have been investigated; among them are serine hydroxymethyltransferase (*SHMT*), betaine-homocysteine methyltransferase (*BHMT*), cystathionine beta-synthase (*CBS*), and thymidylate synthase (*TS*) [212–215]. So far, the results of these studies provide no direct evidences for a role of these genes in NTDs risk.

Gene–gene and gene–environment interactions

Given the interconnected nature of the folate-dependent Hcy pathway, it is possible that particular combinations epistatic of genetic variants may underlie NTDs suscepti-

bility. Multilocus analysis has investigated interactions between *MTHFR* 677C→T, *MTHFR* 1298A→C, *MTRR* 66A→G, *SHMT* 1420C→T, *CBS* 844ins68, *GCPII* 1561C→T, and *RFC-1* 80A→G. Collectively, the genes involved in folate biochemistry and their respective polymorphisms appear to produce only small increases of risk. It has been demonstrated that the penetrance of the *MTHFR* 677C→T mutation may be modified by dietary and supplemental folate [216]. Likewise, variations at the infant *RFC-1* 80A→G locus appear to modify the effects of folate supplementation on NTDs [204].

Folate supplementation in mouse models

The identification of mouse mutants with folate-sensitive NTDs greatly aids our understanding of genetic predisposition to folate-sensitive NTDs in the human population (Table 2). In mice, a number of genetic models exists in which there is an association between occurrence of NTDs and folate metabolism. In three folate-sensitive cases, the targeted or mutant gene encodes a protein that functions in transcriptional regulation: *Cart1* that encodes the homeobox gene, cartilage homeoprotein 1; *Cited 2* (known as *Mrg1/p35srj*) that encodes a member of the CITED (CBP7p300-interacting transactivators with glutamic acid (E)/aspartic acid (D)-rich C-terminal domain) family of transcriptional regulatory proteins; and *Spotch* mice that carry a mutated allele of *Pax3* [217–219]. Another folate-responsive mutant mouse model is *Folbp1*^{-/-} [220]. Because *Folbp1* (*Folr1*) is implicated in the transport of folate into cells, supplementation of the mutants corrects the cellular uptake deficiency possibly through redundant transport pathways. The NTDs in *Crooked tail* (*Cd*) mice is an excellent model of folate-responsive NTDs. Heterozygous *Cd* mice display a crooked tail whereas *Cd/Cd* animals have phenotypes that include early postimplantation lethality (20–30% of homozygotes) and exencephaly (20–30%) [221]. A missense mutation in *Cd* replaces a highly conserved amino acid in the low-density lipoprotein

(LDL) receptor-related protein, *Lrp6* [222]. *Lrp6* is an LDL coreceptor for Wnt. Identification of an *Lrp6* mutation in the *Crooked tail* mouse suggests that canonical Wnt pathway genes can be involved in folate-responsive NTDs.

Folate-resistant mouse models

Folate-resistant defects include cranial NTDs in *eph-A5* knockout mice and spinal NTDs in the *axial defects* (*Axd*) mice and *curly tail* mutants [166, 223, 224]. Spinal NTDs in *curly tail* mouse results from a defective proliferation of hindgut cells resulting in excessive ventral curvature of the caudal region of the embryo, thereby inhibiting closure of the neural folds. To date, a causative mutation in the *curly tail* mouse has not been reported; however, it has been proposed that the *curly tail* phenotype involves a mutation in the grainy head-like-3 (*Grhl3*) locus which encodes a member of the *grainy head-like* family of the transcription factors [225]. At present, the contribution of defective alleles of *Grhl3* to human NTDs has not been reported. Spinal NTDs in *curly tail* mouse can be prevented by supplementation with inositol either by administration to pregnant females or directly to embryo cultures [224]. The mechanism of action of inositol in preventing NTDs in *curly tail* mice involves protein kinase C (PKC), a family of serine/threonine kinases. The treatment of *curly tail* embryos with isoform-specific PKC inhibitors identified PKCβI and γ as essential isoforms for the normalizing action of inositol [226] (Fig. 9). These findings raise the possibility of developing novel clinical strategies for the prevention of human NTDs based on inositol. A recent study comparing the levels of myoinositol in serum from mothers that had normal pregnancies and mothers who had children with spina bifida supports the idea that inositol status may contribute to the susceptibility to NTDs. There was a 2.6-fold increased risk to have an affected child among mothers whose inositol levels were at the low end (tenth centile) of the range [227].

Table 2 Mouse models in which NTDs are preventable by exogenous agents

Mouse model	NTDs	Mechanism	Gene	Prevention by folic acid	Prevention by other agents
<i>Cart1</i> ^{-/-}	Exencephaly	Excess of apoptosis	<i>Cart1</i> ^{-/-}	Yes	–
<i>Cited2</i> ^{-/-}	Exencephaly	Excess of apoptosis	<i>Cited2</i>	Yes	–
<i>Crooked tail</i> (<i>Cd</i>)	Exencephaly	–	<i>Cd</i>	Yes	–
<i>Curly tail</i>	Spina bifida, exencephaly	Defect in the hindgut proliferation	<i>Grhl3</i>	No	Inositol
<i>Ephrin-A5</i> ^{-/-}	Spina Bifida, exencephaly	Adhesion defect	<i>Ephrin-A5</i>	No	–
<i>Axial defects</i> (<i>Axd</i>)	Spina bifida	–	<i>Axd</i>	No	Methionine
<i>Folbp1</i> ^{-/-}	Exencephaly	Folate deficiency	<i>Folbp1</i>	Yes	–
<i>Spotch</i> ^{2H}	Spina bifida, exencephaly	Excess of apoptosis	<i>Pax3</i>	Yes	Thymidine

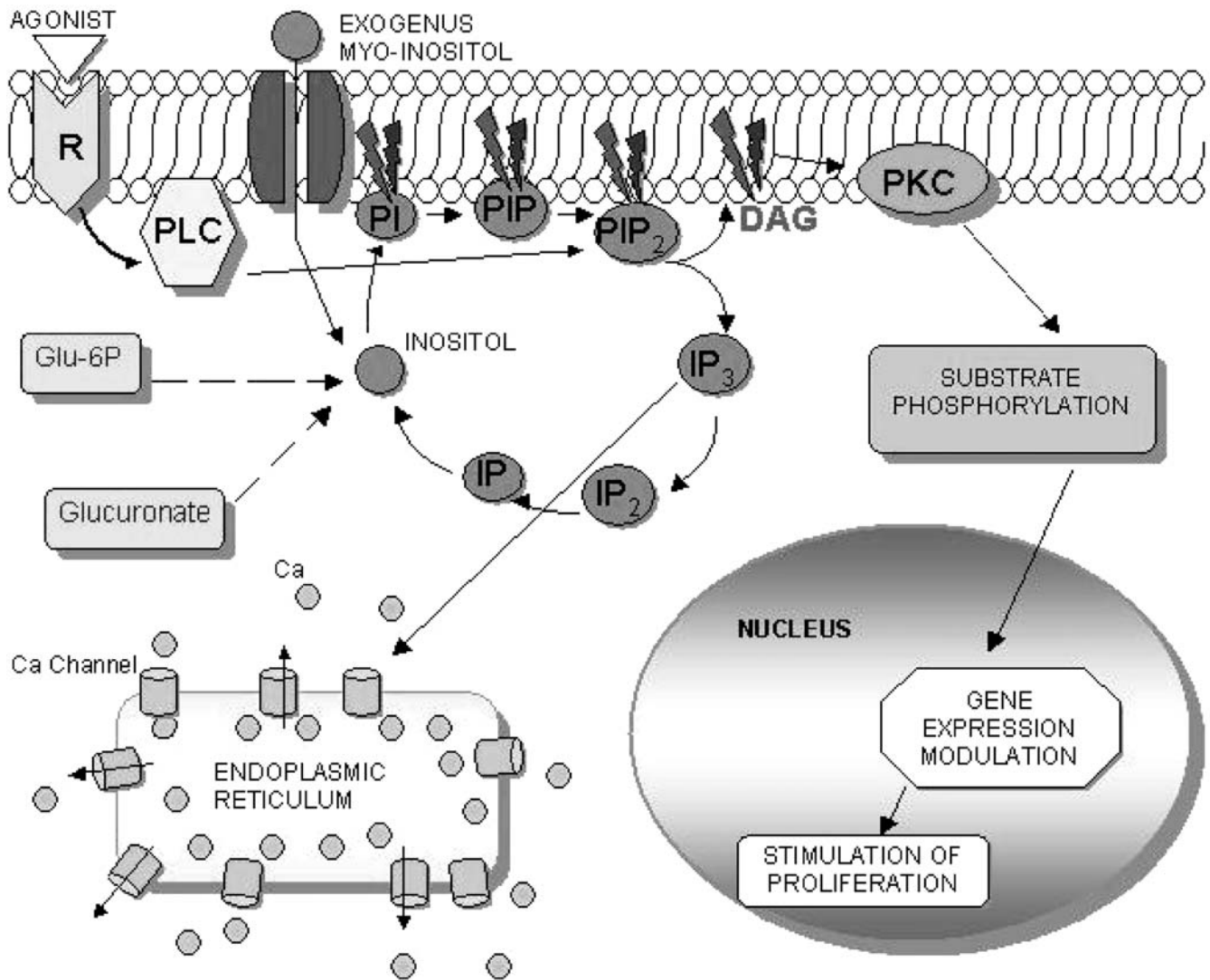


Fig. 9 Myo-inositol metabolic pathway and inositol signaling system. Exogenous myo-inositol enters the inositol phospholipid cycle and is incorporated into inositol phospholipids, including phosphatidylinositol (PI), phosphatidylinositol-4-phosphate (PIP), and finally phosphatidylinositol-4,5-bisphosphate (PIP₂). External signals, by binding to cell membrane receptors (R), induce the activation of phospholipase C (PLC) and hydrolysis of PIP₂ to diacylglycerol (DAG) and inositol triphosphate (IP₃), which are both downstream signaling molecules. IP₃ induces Ca²⁺ release from

intracellular stores. Sequential dephosphorylation of inositol phosphates leads to the release of free inositol that combines with CDP-diacylglycerol to regenerate PI. DAG induces the activation of some isoforms of protein kinase C (PKC); the subsequent phosphorylation of specific substrates results in the modulation, at nuclear level, of gene expression and in the downstream correction of cell proliferation defects, thereby normalizing neural tube closure. IP₂ Inositol bisphosphate, IP inositol monophosphate, *Glu-6P* glucose-6-phosphate, *R* cell membrane receptor

Conclusions

The identification of the relationship between folic acid and NTDs represents one of the most important successes of epidemiological research. Variants of several folate-related genes have been found to be significantly associated with the risk of NTDs. However, the identification of additional risk factors has proven to be difficult. So far, biochemical and developmental pathways as well as animal models have failed to yield definitive results. Given the multifactorial etiology of NTDs, interactions between environmental factors and target genes as well as additive or epistatic interactions should be considered. A concerted effort will be required to design adequately powered

studies and to minimize the danger of bias and spurious results.

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