# Molecular Genetics of Axis Formation in Zebrafish

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## **Key Words**

gastrulation, mesoderm, endoderm, ectoderm, Nodal, Bmp, FGF, Wnt, retinoic acid

#### **Abstract**

The basic vertebrate body plan of the zebrafish embryo is established in the first 10 hours of development. This period is characterized by the formation of the anterior-posterior and dorsal-ventral axes, the development of the three germ layers, the specification of organ progenitors, and the complex morphogenetic movements of cells. During the past 10 years a combination of genetic, embryological, and molecular analyses has provided detailed insights into the mechanisms underlying this process. Maternal determinants control the expression of transcription factors and the location of signaling centers that pattern the blastula and gastrula. Bmp, Nodal, FGF, canonical Wnt, and retinoic acid signals generate positional information that leads to the restricted expression of transcription factors that control cell type specification. Noncanonical Wnt signaling is required for the morphogenetic movements during gastrulation. We review how the coordinated interplay of these molecules determines the fate and movement of embryonic cells.

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### INTRODUCTION

Over the past 25 years, the zebrafish has become a powerful model system for investigation of vertebrate development, physiology, and disease mechanisms. Recognizing important attributes such as high fecundity, a three-month generation time, and accessibility of the embryo, Streisinger introduced the zebrafish as a model system, developed methods for constructing haploid and gynogenetic diploid fish, and identified the first few ze-

brafish mutants (308). Exploiting the optical transparency of the embryo, Kimmel established essential embryological tools, including time-lapse imaging, lineage-tracing, and cellular transplantation, which are now widely used in analyses of wild-type and mutant embryos (reviewed in 154). In the mid-1990s, the Nüsslein-Volhard and Driever groups conducted two large-scale genetic screens that identified genes with essential functions in a wide array of biological processes, ranging

from early embryonic patterning to organogenesis (68, 104). The 1990s also witnessed the advent of key resources for the molecular analysis of zebrafish mutations, including genetic maps, radiation hybrid maps, and largeinsert genomic libraries (91, 130, 164, 244). These areas have all progressed rapidly, and the zebrafish field continues to be invigorated by the identification of new mutants in screens targeted for specific phenotypes and by the development of new tools and resources (e.g., 26, 194, 349). Examples of other important advances include retroviral insertional mutagenesis, in vivo analysis of gene expression with GFP (green fluorescent protein) transgenes, the use of morpholino oligonucleotides and target-selected mutagenesis approaches for reverse genetic studies, and a concerted effort to obtain the genome sequence (88, 190, 223, 340). Because of these experimental advantages, the zebrafish system has yielded important insights into many areas of vertebrate biology; especially noteworthy among these is the genetic control of embryonic axis formation, the subject of this review.

## OVERVIEW OF ZEBRAFISH DEVELOPMENT

Only 10 h post fertilization (hpf), the zebrafish embryo has clearly recognizable anterior-posterior and dorsal-ventral axes (**Figure 1**). Moreover, the embryo is exquisitely patterned so that the precursors for different regions and cell types of the embryo can be recognized using molecular markers. To generate this basic body plan, the embryo undergoes rapid developmental and morphogenetic changes (reviewed in 155). Upon fertilization, cytoplasmic streaming generates a large blastodisc on top of the yolk. During the following 3 h of development, rapid, synchronous cleavage divisions occur within the blastodisc to generate a blastula embryo consisting of  $\sim$ 1000 cells, initially arranged in a pile (blastoderm) atop the volk. During cleavage, the volume of the embryo remains essentially constant, so that the divisions produce

a larger number of smaller cells. The cells in the blastoderm form the embryo proper, whereas the yolk is an extraembryonic structure. Cell cycles lengthen and become asynchronous during the mid-blastula transition (MBT). The MBT begins at the 512-cell stage (2.75 hpf), when cell division has increased the DNA:cytoplasm ratio to a critical threshold (58, 136). The MBT also marks the time when zygotic transcription begins (although a few genes may be transcribed prior to the MBT), so that the zygotic genome begins to govern embryonic development. Also around the time of the MBT, cells at the blastoderm margin collapse into the yolk and form the yolk syncytial layer, a thin, multinucleate structure at the interface of the blastoderm and the yolk (157).

At about 4 hpf, cellular rearrangements begin to reshape the blastoderm into a characteristic vertebrate body plan (reviewed in 298) (Figure 2). In the process of epiboly, cells intercalate radially, thereby thinning the blastoderm and spreading over the yolk. By the end of gastrulation, epiboly movements have spread the blastomeres so that the blastoderm covers the entire volk cell; the extent of volk cell coverage (measured as "percent epiboly") provides a convenient way to determine an embryo's developmental stage. Three other movements contribute to the formation of the axis. Beginning at 5 hpf, cells at the margin internalize and form the so-called hypoblast, the precursors of the mesoderm and endoderm (this usage of the term hypoblast is different from that in mouse and chick, where it denotes extraembryonic tissue). By 6 hpf, convergence and extension movements have begun, resulting in the dorsal accumulation of cells moving from lateral and ventral regions of the blastoderm (convergence). Concomitantly, converging cells intercalate with dorsal blastomeres, spreading them along the animal-vegetal axis, leading to a lengthening of the anterior-posterior axis (extension). Convergence of cells toward the dorsal side of the embryo marks the first clearly apparent break in radial symmetry and forms the Anterior-posterior axis: the line from head to tail

Endoderm: the inner germ layer, which gives rise to the gastrointestinal tract and associated structures

Gastrulation: the process by which blastoderm cells are specified and move to generate an embryo with three germ layers and anterior-posterior and dorsal-ventral polarity

Mesoderm: the middle germ layer, which gives rise to bone, muscle, connective tissue, urogenital and circulatory system

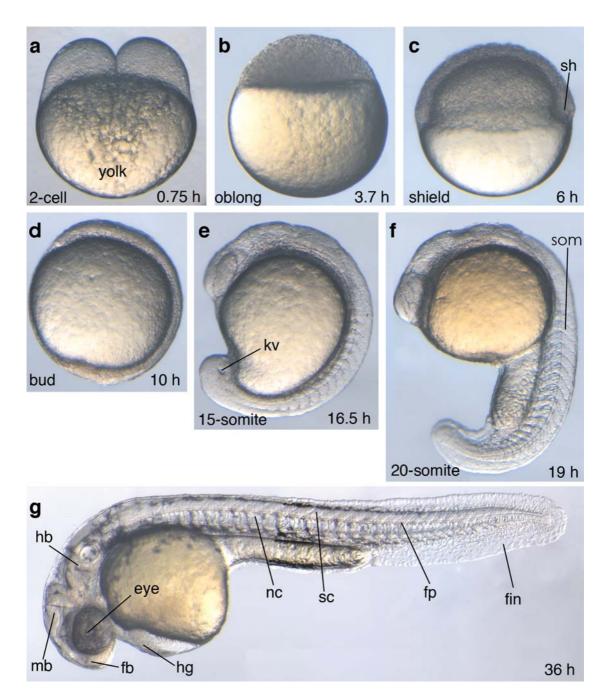


Figure 1

Zebrafish embryogenesis. Living zebrafish embryos are shown at the indicated developmental stages. Approximate developmental ages in hours postfertilization (h) are shown. Embryos are oriented: (a,b) animal pole to top; (c) animal pole to top, dorsal to the right; (d-f) anterior to the top, dorsal to the right; (g) anterior to the left, dorsal to the top. Abbreviations: sh, embryonic shield; kv, Kupffer's vesicle; som, somite; hg, hatching gland; fb, forebrain; mb, midbrain; hb, hindbrain; nc, notochord; sc, spinal cord; fp, floor plate. For further details see Reference 155.

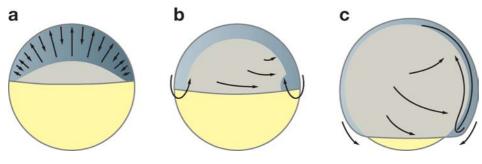


Figure 2

Gastrulation movements. (a) Dome stage. Cells intercalate radially, contributing to epiboly. (b) Shield stage. Cells at the margin internalize and migrate toward the animal pole. Cells converge dorsally, with lateral mesodermal cells starting convergence at later stages than cells closer to the shield (282). (c) 90% epiboly stage. Epiboly, internalization, convergence and extension continue. Modified from Reference 138.

shield, a thickening at the dorsal blastoderm margin that is the teleost equivalent of the amphibian Spemann-Mangold organizer (266, 286).

# FATE MAPS AND ORGANIZING CENTERS

A fate map demarcating the position of precursors for different tissues and organs is apparent at the onset of gastrulation (6 hpf), although different progenitor territories are not sharply demarcated and progenitors are intermingled (161) (Figure 3). Because embryological manipulations and mutations in the genes described below alter this fate map, it is important to take a closer look at the arrangement of tissue progenitors. The precursors of the different germ layers are arranged along the animal-vegetal axis, with ectoderm located animally, mesoderm more marginally, and endoderm, intermingled with mesoderm, at the margin itself. Precursors for different mesodermal cell types are arranged along the so-called dorsal-ventral (DV) axis, with dorsal corresponding to the site of the shield. Cells located most dorsally give rise to the axial mesoderm of notochord and prechordal plate. More laterally located cells give rise to trunk somites and heart. Blood and pronephros are derived from marginal blastomeres more distant from the shield, the so-called ventral re-

gion. Most of the posterior mesoderm (tail somites) also derives from this ventral territory. Different endodermal progenitors are also located in different dorsal-ventral positions, with pharynx located most dorsally, and stomach, intestine, and liver located more laterally and ventrally (i.e., more distant from the shield) (334). Nonneural ectoderm (epidermis) derives from the animal-ventral territory. Forebrain and midbrain progenitors are found animally and dorsally, whereas hindbrain and spinal cord precursors are located closer to the margin and more laterally and ventrally, respectively (345). Hence, precursors for different anterior-posterior regions in the nervous system do not simply align with the animal-vegetal axis. Similarly, precursors of anterior somites are located more dorsally than posterior somite progenitors. Moreover, prechordal plate precursors are located more vegetally than notochord precursors (101). Because of complex gastrulation movements, there is no completely generalizable connection between dorsal-ventral or animal-vegetal location at early gastrula stages and later anterior-posterior position. This is most clearly exemplified by prechordal plate and forebrain forming the most anterior region of the head but lying at opposite positions of the animal-vegetal axis at the onset of gastrulation. Similarly, posterior notochord and posterior somites together form the tail

**Dorsal-ventral axis:** the line from back to belly

Ectoderm: the outer germ layer, which gives rise to epidermis, nervous system and sense organs

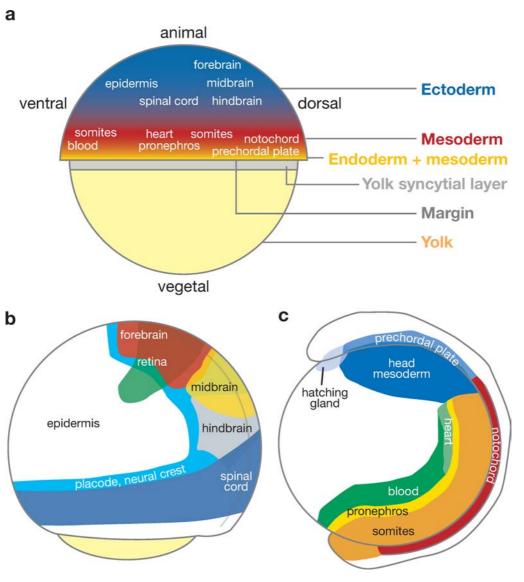


Figure 3

Zebrafish fate maps. (a) Fate map at 50% epiboly stage, the onset of gastrulation. Lateral view, dorsal to the right, animal pole to the top. Germ layers are arranged along the animal-vegetal axis. Different mesodermal and ectodermal fates are arranged along the dorsal-ventral axis. For details see References 66, 101, 145, 161, 345. For distribution of endodermal fates see Reference 334. No precise boundaries are depicted because cell fates are often intermingled. Modified from Reference 267. (b) Fate map of ectoderm at 90% epiboly. Lateral view, dorsal to the right, animal pole and anterior to the top. Modified from Reference 345; position of spinal cord territory is inferred from Reference 172. (c) Model fate map of mesoderm at early somite stage. Lateral view, dorsal to the right, animal pole and anterior to the top. Note that no precise fate map has been established at this stage. Therefore, regions shown here are approximations derived in part from the expression patterns of marker genes (ZFIN.org). The posterior region of the tail bud will continue to extend and give rise to different mesodermal and ectodermal fates. Modified from Reference 138.

mesoderm, but are derived from opposite ends of the DV axis.

Dye labeling experiments at early cleavage stages indicate that the planes of the first cell divisions do not predict the future dorsal-ventral axis (1, 120, 160). In addition, these experiments revealed that there is extensive cell mixing during epiboly such that a cell's position during early cleavage stages does not determine the fates of its descendants, although cells at more vegetal positions tend to contribute more marginal progenitors at the onset of gastrulation. The first lineage restrictions to emerge separate embryonic blastomeres from the extraembryonic blastomeres of the yolk syncytial layer and the enveloping layer, which forms a flattened epithelium that covers the blastoderm. Single embryonic blastomeres at the 1000to 2000-cell stage can still give rise to several tissue types, and most individual blastomeres are not restricted to particular fates until the early gastrula stage (158). Progenitors of different germ layers begin to occupy definable and distinct positions after the 1000cell stage, when, for example, ectodermal and mesendodermal progenitors are largely separated, with the exception that some muscle progenitors are intermingled with hindbrain and spinal cord progenitors (161). Although individual blastomeres adopt particular fates that are predictable based on their positions at the early gastrula stage, transplantation experiments show that most individual cells are not committed to particular fates until the midto late-gastrula stages (126).

As described in detail below, embryological manipulations have identified regions in the embryo that are required or sufficient to induce specific fates in neighboring cells (reviewed in 267) (**Figure 4**). The dorsal margin is the source of factors that can induce dorsal, anterior and lateral cell types and repress ventral and posterior fates (266, 286). The yolk syncytial layer is the source of mesoderm and endoderm inducers (44, 213), and the ventral margin can induce posterior structures (4, 346).

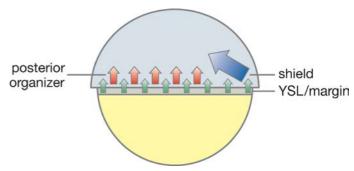


Figure 4

Zebrafish organizing centers. Lateral view, dorsal to the right, animal pole to the top. Yolk syncytial layer (YSL) can induce mesendodermal fates upon transplantation (*green arrows*). Posterior organizer is located at the ventral and lateral margin and can induce tail, posterior trunk, and hindbrain tissue upon transplantation (*red arrows*). Shield corresponds to Spemann-Mangold organizer and can induce dorsal and anterior structures upon transplantation (*blue arrow*).

# DORSAL-VENTRAL PATTERNING: MATERNAL FACTORS

The mature zebrafish oocyte is radially symmetric about the animal-vegetal axis, and no dorsal-ventral asymmetry is evident prior to fertilization. During fertilization, the sperm enters the egg through a specialized structure, the micropyle, at the animal pole (344). Thus it seems that the sperm entry point itself cannot be the cue that breaks symmetry in zebrafish, in contrast to the situation in amphibians (reviewed in 336), but the possibility remains that an activity of the sperm after fertilization is somehow involved in establishing the dorsal-ventral axis. Although the first five cleavage divisions occur in a stereotyped alternating orthogonal pattern, these cleavage planes do not correlate with the eventual dorsal-ventral axis (1, 120, 160). Nevertheless, embryological experiments show that events important for the formation of dorsalventral asymmetry are occurring even before the first cleavage division. Embryos are ventralized by removal of the vegetal region of the volk before the first cell division, and the frequency of ventralized embryos rapidly diminishes when the operation is performed at later stages (212, 232). Similarly, treatment with nocodazole, an inhibitor of microtubule polymerization, causes the loss of dorsal axial structures when applied within 10 min after fertilization, but not after the first cell division (133). Drawing on parallels between these results and previous work on dorsal-ventral axis formation in *Xenopus*, it has been proposed that the dorsal side of the zebrafish embryo is established by a dorsal determinant initially located at the vegetal pole that is translocated along microtubules to the future dorsal side before the first cleavage division occurs (133). This is an intriguing model, but certain key predictions remain untested. For example, directed movement from the vegetal pole toward the dorsal side of the early embryo has not been observed. Likewise, it has not been shown that the vegetal pole contains a determinant sufficient to determine dorsal identity or rescue a ventralized embryo in a transplantation experiment. Thus many questions remain about the mechanisms that establish the earliest dorsal-ventral asymmetries in the zebrafish. The analysis of recently identified maternal-effect mutants with ventralized phenotypes will define important players that act at early stages to establish the dorsal-ventral axis (147, 228, 330).

#### $\beta$ -catenin

Evidence suggests that maternal  $\beta$ -catenin acts to establish the dorsal-ventral axis in zebrafish.  $\beta$ -catenin protein acts as a transcriptional effector in the canonical Wnt signaling pathway and also has a function in cell adhesion (reviewed in 129, 188). A complex containing APC, axin, and GSK3 $\beta$  and other components targets  $\beta$ -catenin protein for degradation, thereby allowing only a low level of  $\beta$ -catenin to accumulate. Activation of the canonical Wnt signaling pathway inhibits the  $\beta$ -catenin degradation complex, stabilizing  $\beta$ -catenin and allowing it to enter the nucleus, where it activates transcription of canonical Wnt target genes.

In the zebrafish embryo,  $\beta$ -catenin accumulates specifically in nuclei of dorsal margin

blastomeres as early as the 128-cell stage (66, 274). This asymmetric nuclear localization of  $\beta$ -catenin is an early marker of the dorsalventral axis (Figure 5). As in the amphibian embryo, overexpression of  $\beta$ -catenin leads to axis duplication (148). Moreover,  $\beta$ -catenin seems to be required for dorsal axis formation, as overexpression of proteins that inhibit  $\beta$ catenin's action as a transcriptional activator (cadherin or a dominant negative form of Tcf3 that binds  $\beta$ -catenin but not DNA) reduces dorsal gene expression and produces ventralized embryos (238). In addition, the maternal effect mutations ichabod and tokkaebi, whose molecular bases are not known, disrupt the nuclear localization of  $\beta$ -catenin and lead to ventralized embryos (147, 228).

Soon after the mid-blastula transition,  $\beta$ -catenin activates the expression of a number of zygotic genes, including *bozozok* (*boz*, also known as *dbarma* and *nieuwkoid*), *cbordin*, *dick-kopf1* (*dkk1*), *squint* (*sqt*) and FGF signals (63, 66, 75, 79, 87, 113, 147, 165, 247, 261, 263, 292, 324, 353). As detailed below, these  $\beta$ -catenin targets act to inhibit the action of ventralizing factors or, in the case of Sqt, induce mesendodermal fates at the dorsal margin.

Recent work suggests that asymmetric localization of Wnt11 triggers the accumulation of  $\beta$ -catenin in dorsal blastomeres in Xenopus (314). Zebrafish wnt11 mutants (silberblick) have defects in morphogenetic movements during gastrulation (see below), but formation of the dorsal-ventral axis is normal, even in embryos lacking maternal and zygotic wnt11 (119). Moreover, Xenopus but not zebrafish wnt11 mRNA is localized to the vegetal pole. There is another wnt11 gene in the zebrafish genome (90), and further work is needed to determine if this gene functions in the establishment of the dorsal-ventral axis or if the wnt11 duplicates might have redundant functions in this process.

Although the asymmetric distribution of  $\beta$ -catenin has not been observed during the first few cleavages, one study suggests that dorsal-ventral asymmetry is evident even in the two-cell embryo (83). Activation of the

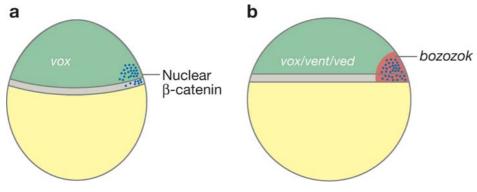


Figure 5

Transcriptional interactions patterning the dorsal-ventral axis. Lateral view, dorsal to the right, animal pole to the top. (a)  $\beta$ -catenin is stabilized on the dorsal side during cleavage stages. Soon after mid-blastula transition, vox is expressed ubiquitously. (b)  $\beta$ -catenin activates bozozok (boz), which represses vox, vent, and ved expression in dorsal blastomeres.

map kinase p38, assessed with an antibody specific for the doubly phosphorylated form of p38, occurs in the region of the embryo that will eventually become the dorsal side. Despite its early dorsal activation, p38 does not apparently act to specify dorsal fates, and expression of dorsal-specific genes occurs in embryos expressing dominant negative versions of p38. Instead, p38 is required specifically on the dorsal side to control the rate of cell division in dorsal blastomeres, so that there are fewer, larger blastomeres on the dorsal side in embryos expressing dominant negative p38. Activation of p38 does not occur in embryos ventralized by inhibition of microtubules or vegetal volk depletion, indicating that p38 is regulated by the same factors that establish dorsal-ventral asymmetry and that p38 acts in parallel to the genes that specify dorsal identity (83).

# DORSAL-VENTRAL PATTERNING: ZYGOTIC FACTORS

In recent years, the default model for dorsalventral patterning has gained widespread acceptance (reviewed in 121). This model, first formulated to explain dorsal-ventral patterning in frog, holds that the Spemann-Mangold organizer induces dorsal fates by inhibiting the action of ventralizing and posteriorizing signals such as Bmp2/4/7 and Wnt8. According to this view, development of dorsal and anterior fates is a "default" state, such that dorsalizing factors act to block the influence of ventralizing signals rather than to actively trigger pathways that specify dorsal fates. Analysis in zebrafish has confirmed certain key predictions of this model, identified genes with essential roles in dorsalventral patterning, and advanced the understanding of dorsal-ventral patterning by explaining events that are not wholly accounted for by the simplest version of the default model.

# **Bmp Signaling**

Members of the Bmp family of TGF- $\beta$  signals induce ventral fates (reviewed in 219, 327). Secreted Bmp ligands bind the extracellular domains of type I and type II Bmp receptors, which are transmembrane proteins with intracellular serine/threonine kinase domains. The closely related Smad family transcription factors Smad1/5/8 are phosphorylated by ligand-bound receptors, allowing these proteins to translocate to the nucleus and regulate target gene expression together with the

nonreceptor-regulated Smad protein Smad4, and other DNA binding cofactors, such as the zinc finger protein Oaz. A large number of inhibitory proteins function to regulate Bmp pathway activity at different levels: for example, Chordin, Noggin, and Follistatin are secreted Bmp antagonists, the transmembrane protein Bambi functions as a decoy receptor, and inhibitory Smads Smad6/7 interfere with Smad1/5/8 phosphorylation (reviewed in 219).

Mutational analysis has demonstrated that a number of Bmp pathway components are essential for formation of ventral cell types in zebrafish (Table 1), including the Bmp ligands, Bmp2b and Bmp7, the type I receptor Alk8, the transcriptional effector Smad5, and the protease Tolloid, which cleaves the Bmp antagonist Chordin (22, 49, 60, 124, 162, 209, 226, 272). Although these mutations define components of the same pathway, the mutant phenotypes span a range from weakly dorsalized and viable to strongly dorsalized and lethal in the first day of development (218). Soon after the MBT, bmp2b and bmp7 are widely expressed, but their expression becomes restricted to approximately the ventral half of the embryo by the onset of gastrulation (60, 162, 198, 272) (Figure 6). Swirl/bmp2b mutants and wild-type embryos overexpressing Chordin or Noggin are strongly dorsalized, with dorsoanterior structures greatly expanded at the expense of ventroposterior structures (162, 218, 219b, 226). In the ectoderm, neural fates including forebrain, midbrain, and hindbrain are expanded to encompass the most ventral regions of the embryo, whereas epidermis, neural crest, and Rohon-Beard sensory neurons are lacking in swirl/bmp2b mutant embryos. A similar fate transformation is evident in the margin region of swirl/bmp2b mutants, in which anterior (trunk) somites and anterior endoderm are expanded, whereas ventrolateral and posterior fates such as blood, heart, pronephros, pancreas, and tail are reduced or missing. Axial mesoderm is largely unaffected in swirl/bmp2b and the other bmp pathway mutants, indicating that other factors act to restrict the most dorsal fates to the appropriate territories. Complete loss of snh/bmp7 function also produces a strongly dorsalized phenotype, indicating that both bmp2b and bmp7 are required for normal dorsal-ventral patterning, despite the fact that the expression of these genes largely overlaps (60, 272). It is possible that the active ventralizing signal in vivo is a Bmp2b-Bmp7 heterodimer (272). Bmp7, however, can induce ventral cell types when overexpressed in bmp2b mutants, showing that high levels of Bmp7 are sufficient to specify ventral identity even in the absence of its putative heterodimer partner Bmp2b. Using an inducible dominant negative Bmp receptor, it has been shown that Bmp signaling is required for global dorsalventral patterning decisions during early gastrulation, whereas Bmp signals regulate tail development from mid-gastrulation through early somitogenesis (246).

The fly orthologue of the ventralizing Bmps, Decapentaplegic (Dpp), acts as morphogen, and it has been proposed that graded action of Bmp signals directly specifies fates of tissue progenitors across the dorsal-ventral axis in vertebrates (64, 176a, 225, 343). In zebrafish, the evidence for this is best in the ectoderm, where graded inactivation of Bmp signals leads to striking modulations of DV patterning (21, 226). Null mutations in bmp2b eliminate epidermis, placodes, neural crest, and Rohon-Beard sensory neurons, whereas forebrain, midbrain, and hindbrain fates are expanded to encompass the most ventral regions of the embryo. When Bmp activity is reduced but not eliminated, as with hypomorphic mutations or overexpression of intermediate concentrations of a Bmp antagonist in wild-type embryos, neural crest and placodal fates are expanded relative to wild type. These seemingly paradoxical results can be explained if the perturbations change the slope of a Bmp gradient. According to this view, a larger region of the DV axis falls within, for example, the neural crest specification threshold when the Bmp gradient is shallower than in wild type. This can account for expansion of

Table 1 Genes essential for zebrafish axis formation and patterning

Mutation	Gene product	Function	Phenotype	Reference
Bmp signaling				
swirl	Bmp2b	Bmp signal	Severely dorsalized	(162)
snailhouse	Bmp7	Bmp signal	Severely dorsalized	(60, 272)
lost-a-fin	Alk8	Type I Bmp receptor	Severely dorsalized	(22, 209)
somitabun	Smad5	Transcription factor	Weakly (zyg.) or strongly (mat.) dorsalized	(124)
morpholino	Twisted Gastrulation	Bmp agonist	Dorsalized	(186, 350)
minifin	Tolloid	Metalloprotease for Chordin	Weakly dorsalized	(49)
chordino	Chordin	Bmp inhibitor	Ventralized	(277)
ogon	Sizzled	Bmp inhibitor	Ventralized	(199, 351)
norpholino	Radar/Gdf6a	Bmp signal	Dorsalized	(293)
*	Kheper	Zinc finger/homeodomain	Reduced neuroectoderm	(220)
_	_		Reduced ventral ectoderm	, ,
morpholino	ΔNp63	Transcriptional repressor		(16, 177)
morpholino	ADMP	Divergent Bmp signal	Dorsalized	(180, 341)
Canonical Wnt sign	naling			
wnt8	Wnt8	Wnt signal	No ventral and posterior structures	(72, 179)
masterblind	Axin	Scaffolding protein	No eyes and telencephalon	(117)
beadless	Tcf3	Transcription factor	No forebrain and midbrain	(153)
norpholino	Tlc SFRP	Wnt antagonist	Reduced telencephalon	(127)
chabod	?	$\beta$ -catenin localization?	Variably ventralized	(147)
tokkaebi	?	$\beta$ -catenin stability?	Variably ventralized	(228)
norpholino	Sp5 and Sp5-like	SP1 Zn Finger	Anteriorized and dorsalized	(337)
_	opr man opr and	22		(,)
Nodal signaling	O OT 11)	NT 11: 1	0.1.:	(115 252
yclops	Cyc (Nodal)	Nodal signal	Cyclopia	(115, 252, 265)
squint	Sqt (Nodal)	Nodal signal	Cyclopia, dorsal mesoderm defects	(79)
morpholino	Southpaw (Nodal)	Nodal signal	Loss or randomization of LR asymmetry	(191)
cyclops;squint			No endoderm and head/trunk mesoderm	(79)
one-eyed pinhead	EGF-CFC	Nodal co-receptor	No endoderm and head/trunk mesoderm	(102)
schmalspur	FAST1/FoxH1	Transcription factor	Dorsal mesoderm defects	(243, 295)
bonnie and clyde	Mix homeodomain	Transcription factor	Reduced endoderm	(243, 293) $(151)$
morpholino	Lefty1 and Lefty2	Antagonist of Nodal signaling	Increased mesoderm and endoderm	(3)
morpholino	Dapper2	Antagonist of Nodal signaling	Increased mesoderm and endoderm	(362)
morpholino	Charon	Antagonist of Nodal signaling	Loss of LR asymmetry	(114)
FGF signaling				
acerebellar	Fgf8	FGF signal	Ventralized with loss of chordin	(87, 253)
morpholino	Fgf24	FGF signal	Loss of posterior structures with loss of fgf8	(67)
				(Continu

Table 1 (Continued)

Mutation	Gene product	Function	Phenotype	Reference
norpholino	Sef	Antagonist of FGF signaling	Dorsalized	(84, 323)
norpholino	Sprouty2	Antagonist of FGF signaling	Dorsalized	(87)
norpholino	MKP3	Antagonist of FGF signaling	Dorsalized	(324)
etinoic acid signal	ing			
eckless	Raldh2	RA synthesis pathway	Anterior spinal cord reduced, myocardial progenitors increased	(24, 144)
iraffe	Cyp26a1	RA degradation	Anterior spinal cord expanded	(70, 172)
ranscription factor	rs			
ozozok	Boz homeodomain	Transcriptional repressor	Variable loss of dorsal mesoderm and forebrain	(75)
ox/vent	Vox, Vent homeodomain	Transcriptional repressor	Severely dorsalized in double mutants	(131)
norpholino	Ved homeodomain	Transcriptional repressor	Severely dorsalized with vox/vent	(290)
ugelig	Cdx4 homeodomain	Transcription factor	Reduced tail and blood	(56)
norpholino	Prdm1/Blimp1	Transcriptional repressor	Dorsalized	(342)
ominant negative	Iro3	Transcriptional repressor	Reduced dorsal mesoderm	(171)
oiel ohne grenzen	Pou2/Oct4	Transcription factor	Strongly reduced endoderm in maternal-zygotic mutants	(193, 254)
ust	Gata5 Zinc finger	Transcription factor	Reduced endoderm and heart	(255)
asanaova -	HMG domain	Transcription factor	Strongly reduced endoderm	(61, 150)
norpholino	Mezzo homeodomain	Transcription factor	Reduced dorsal mesoderm and endoderm with bon	(245)
o tail	Ntl T-box	Transcription factor	Loss of notochord and tail	(106, 278)
loating head	Flh homeodomain	Transcription factor	Loss of notochord	(312)
padetail	Spt T-box	Transcription factor	Loss of paraxial and lateral mesoderm	(99, 156)
Epiboly				
alf-baked	E-cadherin	Cell adhesion	Strongly reduced epiboly	(137)
lominant negative	Eomesodermin T-box	Transcriptional activator	Strongly reduced epiboly	(32)
norpholino	Mtx2 homeodomain	Transcription factor	Disrupted epiboly during gastrulation	(32)
tat3 pathway				
norpholino	Stat3	Transcription factor	Reduced prechordal plate migration and CE	(354)
norpholino	Liv1	Zinc transporter	Reduced prechordal plate migration and CE	(355)
norpholino	Snail1	Zinc-finger transcription factor	Reduced prechordal plate migration	(355)
lanar cell polarity	signaling			
lberblick	Wnt11	Wnt signal	Reduced CE	(119)
ipetail	Wnt5	Wnt signal	Reduced CE	(249)
nypek	Glypican4	Wnt co-receptor?	Reduced CE	(320)
rilobite	Strabismus	Transmembrane protein	Reduced CE	(132)

(Continued)

Table 1 (Continued)

Mutation	Gene product	Function	Phenotype	Reference
morpholino	Frizzled2	Wnt receptor	Reduced CE	(236, 309)
morpholino	Flamingo1a and 1b	7TM protocadherin	Reduced CE	(82)
morpholino	Prickle1	Regulates Fz/Dsh	Reduced CE	(37)
morpholino	Diversin	Ankyrin repeat protein	Reduced CE	(279)
Others				
morpholino	$G\alpha 12/13$	G protein subunit	Reduced CE	(184)
morpholino	Quattro	Rho GEF	Abnormal prechordal plate migration and CE	(51)
morpholino	CAP1	Regulates actin distribution	Abnormal prechordal plate migration and CE	(51)
dominant negative	Rok2	Kinase	Reduced CE	(197)
dominant negative	Rac1	Small GTPase	Reduced CE	(17)
inhibitor	Phosphoinosite 3-kinase	Kinase	Abnormal prechordal plate migration and CE	(216)
morpholino	Hyaluronan synthase 2	Polysaccharide synthesis	Reduced CE	(17)
landlocked	Scribble1	LRR/PDZ domain protein	Reduced CE	(329)

Abbreviations: LR, left-right; CE, convergence and extension; TM, transmembrane; for more extensive references see text.

fates specified by intermediate Bmp levels in partial loss-of-function situations, and still explain how these fates are lost when Bmp levels are reduced below the relevant thresholds.

Among the genes acting downstream of Bmp signals to pattern the ectoderm are  $\Delta Np63$  and *kheper*, both of which encode transcriptional repressors (15, 16, 177, 220). The ventrally expressed  $\Delta Np63$  gene is required for development of the epidermis and is directly activated by Bmps. *Kheper*, a zinc fingerhomeobox gene expressed in the neural plate, is repressed by Bmp signaling and dorsalizes the ectoderm when overexpressed.

An interesting exception to the neural expansion seen after inactivation of the Bmp pathway is that posterior spinal cord fates are lost rather than expanded in *swirl/bmp2b* mutants. In contrast to other neural progenitors, the tail spinal cord precursors are located on the ventral side of the embryo just above the marginal zone, and it seems that specification of these cells requires ventralizing Bmps, and perhaps other signals such as FGFs (167, 170, 172, 257).

It has also been proposed that graded action of Bmp patterns fates along the dorsal-ventral axis of the mesendoderm (52, 224, 227, 273). Bmps are clearly required for formation of ventrolateral margin fates such as blood, heart, pronephros, and tail somites, but the case for direct action of a Bmp morphogen in patterning different mesodermal fates is weaker than for ectoderm. "Allelic series" experiments have not provided evidence of expansion of intermediate territories as described for the ectoderm above. Thus other signals, including Wnt8 and FGF, are probably involved in patterning these marginal progenitors.

Despite the evidence for DV patterning by a Bmp activity gradient, the postulated gradient has not been directly visualized. Widespread overexpression of synthetic *bmp* mRNA can rescue *bmp* mutants, suggesting that ventral restriction of *bmp* expression is not the only mechanism that operates to form the postulated Bmp activity gradient (226). Instead, it seems that the action of modulators of Bmp signaling ensures the proper levels

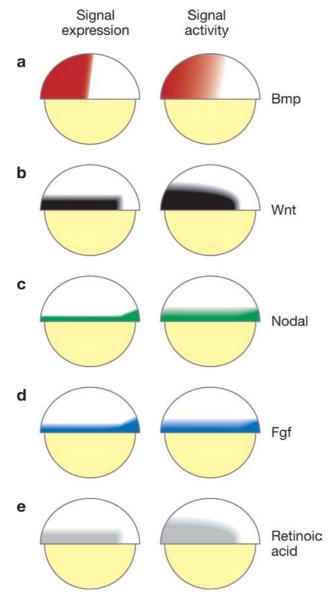


Figure 6

Signals patterning the embryo. Late-blastula stage, lateral view, dorsal to the right, animal pole to the top. Signal expression is based on published reports, but signaling activities are speculative and based on the potential range of signals and the expression pattern and range of antagonists. For example, Bmp signaling activity is inhibited dorsally by antagonists such as Chordin and Noggin. Wnt signaling activity is inhibited by antagonists such as Dickkopf1. Retinoic acid distribution indicates the site of synthesis by RALDH, and activity is inhibited by Cyp26-mediated hydrolysis of retinoic acid dorsally and at the animal pole. Nodal and FGF signals are concentrated on the dorsal side soon after the mid-blastula transition (not shown), but these signals are more uniform across the dorsal-ventral axis by the late-blastula stage that is represented in the figure.

of Bmp signaling activity across the dorsalventral axis.

# Bmp Signaling is Modulated by Extracellular Factors

Extracellular modifiers of Bmp signals include Chordin, Ogon/Sizzled, Tolloid, and Twisted gastrulation (reviewed in 219, 352) (Figure 6). Mutational analysis demonstrates an essential role for Chordin in antagonizing ventralizing Bmps and thereby promoting the development of dorsal fates. Chordin mutants have a ventralized phenotype characterized by expansion of blood and tail fin, and a reduction of anterior neural territories (81, 109, 277). Analysis of marker gene expression indicates that DV pattern is disrupted during gastrulation, when ventral territories are expanded at the expense of presumptive neural and paraxial domains. Genetic studies support the biochemical evidence that Chordin acts to inhibit ventralizing Bmp signals: bmp2b;chordin double mutants are dorsalized, indicating that chordin is not needed for dorsal development if *bmps* are inactivated by mutation (110, 241).

Genetic studies suggest that ogon acts in concert with chordin to inhibit ventralizing bmps (351). Mutants for ogon have a ventralized phenotype very similar to chordin mutants (109, 208). The ogon gene encodes Sizzled, a member of the secreted frizzled related protein family (SFRP) (199, 351). Although SFRPs, which are related to the Wnt receptor Frizzled, were initially recognized as antagonists of Wnt signals, Ogon/Sizzled instead seems to antagonize ventralizing Bmp signals. The ogon mutant phenotype can be suppressed by overexpression of Chordin (or Noggin, another secreted Bmp antagonist). Overexpression of Ogon/Sizzled dorsalizes wild-type embryos but has no effect in chordin mutants, indicating that the dorsalizing activity of Ogon/Sizzled requires Chordin. The mechanism of Ogon/Sizzled action is not clear, but it seems that Sizzled augments the activity of Chordin, perhaps by inhibiting an inhibitor

of Chordin, by directly making Chordin more active, or by modulating Bmp signals so that they become more susceptible to Chordin inhibition.

Tolloid is a conserved extracellular metalloproteinase that promotes Bmp signaling by cleaving and inactivating Chordin (28, 240). Several homologs of Tolloid, originally identified as an activator of Dpp/Bmp signaling in *Drosophila*, are present in vertebrates (287). Modified Chordins that are resistant to cleavage by Tolloid have more potent dorsalizing activity than wild-type Chordin in overexpression assays, showing that Tolloid activity limits the function of Chordin in the embryo (350). The tolloid gene is disrupted in zebrafish minifin mutants, which lack ventral tail structures but have normal DV patterning through the end of gastrulation (49). Chordin is cleaved in tolloid mutants, suggesting that the lack of an early phenotype in mfn/tolloid mutants reflects the action of redundant proteases during gastrulation (350).

Twisted gastrulation (Tsg) is a conserved extracellular protein that binds Bmps and has been implicated as both an agonist and an antagonist of ventralizing Bmp signaling (40, 234, 262, 280). The initial morpholino study in zebrafish reported that tsg morphants (embryos injected with antisense morpholino oligonucleotides for tsg) have some characteristics of ventralized embryos, supporting a role for Tsg in the antagonism of Bmp signaling (262). In contrast, two studies show that tsg morphants are dorsalized and that loss of tsg function can partially suppress the ventralized phenotypes of chordin and ogon/sizzled mutants (186, 350). This provides strong evidence that the predominant function of Tsg in the early zebrafish embryo is to promote Bmp signaling. Overexpressed Chordin accumulates at higher levels in tsg morphants than in wild type, suggesting that Tsg promotes Bmp signaling, at least in part, by reducing the level of Chordin (350). Tsg's mechanism of action in not clear, but one model proposes that the action of Tsg depends on the nature of Chordin, that is, whether Chordin is full-length or fragmented by Tolloid cleavage (174). Tsg, however, must have functions independent of Chordin and its fragments, because loss of Tsg function reduces Bmp signaling activity even in the absence of Chordin. Both overexpression and inhibition of tsg dorsalize embryos, indicating that too much or too little Tsg activity can inhibit Bmp signals (186, 350). One proposal that accounts for these phenotypes is that Tsg links Bmp proteins to another, as-yet unidentified, cofactor, such that BMP-Tsg-X complex does not form in tsg morphants and that inactive BMP-Tsg and Tsg-X complexes form in the presence of excess Tsg (186).

The antidorsalizing morphogenetic protein (ADMP) is a divergent member of the Bmp family that is expressed on the dorsal side of the late blastula and in the axial mesoderm and anterior neuroectoderm during gastrulation (180, 341). Overexpression of *admp* causes ventralization and a reduction of the organizer, whereas injection of morpholino oligonucleotides against *admp* causes a moderate expansion of dorsal mesoderm. The action of *admp* is not well understood, but it may function as part of a negative feedback system to limit the size of the organizer region, perhaps in concert with *bmp2b* and *bmp7*.

# Maternal Bmps Activate Expression of Zygotic Bmps

There is evidence from the analysis of *smad5* mutants that maternal Bmp signaling is required for the activation of zygotic *bmp7*. Mutations that eliminate or disrupt the C-terminal domain of Smad5 exhibit a characteristic maternal-zygotic inheritance pattern, which results from a dominant negative function of these mutant Smad5 proteins (124). Homozygotes for a *smad5* null mutation are weakly dorsalized, but *smad5*<sup>-/-</sup> females produce strongly dorsalized progeny (referred to as maternal *smad5*, or *Msmad5*, mutants) (168). The dorsalized phenotype of *Msmad5* mutants is apparent before the zygotic *bmp* mutant phenotype, suggesting

that the Msmad5 phenotype reflects more than a simple function as a transcriptional mediator of zygotic bmp2b and bmp7 (168). The identity of the putative maternal Bmp signal is not clear, but Gdf6a/Radar is one candidate (293). Maternal Radar, however, may not be the signal acting upstream of maternal Smad5, because the radar morphant phenotype is different from and weaker than the Msmad5 phenotype (293). Bmp4 and bmp7 are also expressed during oogenesis (168), suggesting that they may act maternally in parallel with radar, but there is no evidence that either gene is required maternally for an early patterning function (60, 272).

## Wnt Signaling

Signaling through the canonical Wnt pathway is essential for the specification of ventral and posterior fates (reviewed in 129). Wnt signaling through a Frizzled-Lrp receptor complex and a number of cytoplasmic proteins including Dsh, GBP, Axin, Ccd1, APC, and GSK3 stabilizes  $\beta$ -catenin, allowing it to accumulate in the nucleus and activate target gene expression (reviewed in 188). There are several secreted antagonists of Wnt signaling, including SFRPs, Cerberus, and Wnt inhibitory factor (WIF), which act by binding to Wnt proteins, and Dickkopf (Dkk), which binds the LRP subunit of the receptor (reviewed in 143).

Genetic studies in zebrafish show that Wnt8 signals are essential for the establishment of ventral and posterior fates (72, 179). During gastrulation, wnt8 mRNA and strong activity of a Wnt/ $\beta$ -catenin responsive reporter are evident at the ventrolateral margin (63, 149) (**Figure 6**). Deletion or morpholinoinhibition of both ORFs of the bicistronic wnt8 gene produces a severe loss of ventroposterior structures, with a concomitant expansion of dorsal fates (179). Simultaneous reduction of Wnt3a and Wnt8 activities results in a stronger expansion of dorsoanterior fates, indicating that these genes have overlapping functions (288). This zygotic role of canonical Wnt signaling in ventral and posterior patterning is opposite to its earlier role in dorsal patterning by maternally provided  $\beta$ -catenin described above.

Wnt signals have a role in repressing dorsal mesodermal fates that is distinct from the action of Bmp signals. In contrast to the bmp pathway zygotic mutants, the axial mesodermal territory in wnt8 mutants is expanded along with the paraxial mesodermal and neural domains. In addition, anterior neural fates are expanded in embryos with reduced wnt8 function, supporting a role for Wnt8 in posteriorizing the neuroectoderm (72, 179). Furthermore, mutations that inactivate repressors of Wnt signaling lead to an expansion of posterior neural fates at the expense of more anterior territories (62, 117, 153). Embryological and genetic evidence also indicates that the position of the midbrain-hindbrain boundary is established by Wnt8 signals, possibly acting as morphogens, emanating from the blastoderm margin during gastrulation (259, 346, 347).

Among the target genes of Wnt8 and Wnt3a are the homeobox gene *cdx4/kugelig*, which is essential for tail development and the regulation of posterior *box* genes (56, 94, 288), the T-box gene *tbx6* (311), and the Sp1 class zinc finger gene *Sp5-like* (337). In addition to these functions during gastrulation, experiments with low doses of morpholinos suggest that *wnt8* and *wnt3a* function during segmentation to maintain presomitic mesoderm in the tail bud (319).

The roles of Wnt antagonists have not been extensively studied in zebrafish, but dkk1, an early target of maternal  $\beta$ -catenin, is expressed early in the dorsal margin and dorsal yolk syncytial layer and during gastrulation in the developing prechordal plate, where it could function to counteract the ventralizing and posteriorizing effects of canonical Wnt signaling (113, 292).

The SFRP protein Tlc is expressed at the anterior neural border, a region required for induction of anterior neural fates (127, 128). Telencephalic fates are reduced in *tlc* morphant embryos, and it has been proposed

that Tlc acts locally within the neural plate to promote anterior identity by inhibiting Wnt8b signals from the midbrain-hindbrain boundary.

# Boz and Vox/Vent Transcriptional Repressors

Inactivation of the redundant homeodomain transcriptional repressors Vox (Vega1) and Vent (Vega2), by deletion, coinjection of morpholino oligonucleotides for both genes, or injection of a vent MO into a vox point mutant, leads to a severe loss of ventroposterior structures including blood, pronephros, and tail (131, 139, 140, 204). The loss-offunction phenotype is strain dependent, such that AB strain embryos lacking vox/vent are essentially wild type (131). Inactivation of a third gene encoding a homeodomain transcriptional repressor, ved, along with vox and vent, is sufficient to strongly dorsalize even AB strain embryos (290). Although embryos lacking vox/vent resemble the Bmp pathway mutants, important phenotypic differences are that dorsal mesodermal fates are strongly expanded in embryos lacking vox/vent, and anterior neural fates are shifted more toward the margin and less toward the ventral side than in bmp pathway mutants such as swirl/bmp2b (131). The dorsalized phenotypes of vox/vent and wnt8 mutants are very similar, and there is evidence that wnt8 activates vox and vent expression, thereby repressing dorsal genes (248). chordin is a key target of Vox and Vent, and these proteins also repress other dorsal genes including boz, goosecoid, floating head (flb), and dkk1.

Mutants for the homeodomain transcriptional repressor Boz have a variable phenotype characterized by cyclopia, reduction of dorsal mesoderm, and, in the most severe cases, reduction of forebrain coupled with an expansion of hindbrain (75, 166, 291, 294, 300). Maternal  $\beta$ -catenin activates *boz* expression in dorsal blastomeres soon after the MBT (263, 353) (**Figure 5**). Beginning shortly thereafter, *boz* expression is confined

to the dorsal yolk syncytial layer until boz mRNA is no longer detectable at the midgastrula stage. Studies with fusion constructs containing the Boz homeodomain and potent transcriptional activator or repressor domains indicate that Boz acts as a transcriptional repressor (290). Although boz is predominantly expressed in the yolk syncytial layer, it can act nonautonomously to dorsalize overlying blastomeres, presumably by repressing a ventralizing signal expressed in the volk syncytial layer (353). Key targets of Boz include bmp2b, wnt8, and vox/vent/ved (76, 96, 131, 182). Thus Boz specifies dorsal fates by repressing the expression of ventralizing factors rather than directly activating dorsal gene expression (Figure 5). For example, dorsal mesoderm is expanded in boz;vox;vent triple mutants, demonstrating that boz is not needed to promote dorsal mesoderm gene expression when the ventralizing repressors are inactivated by mutation (131).

Two additional transcriptional repressors, Prdm/Blimp1 and Iro3, are expressed at the dorsal margin. In contrast to Boz, Prdm1 represses *chordin* expression and antagonizes dorsal fates when overexpressed, and knockdown of Prdm1 function weakly dorsalizes the embryo (342). At later stages, Prdm1 is required for slow muscle development and patterning of cell types at the edge of the neural plate (23, 123). Iro3 appears to act as a repressor of *bmp* transcription (171). These observations indicate that depending on their target genes, dorsally expressed repressors can have opposite roles in DV patterning.

## A Model for Dorsal-Ventral Patterning

The detailed analysis of mutants that affect Bmp and Wnt signaling and several transcription factors suggests the following model for DV patterning. Soon after the onset of zygotic transcription, ventralizing genes, including *bmp2b* and *vox*, are widely expressed in the embryo, including in the most dorsal territories (139, 182) (**Figures 5** and **6**).

The maternal pathways inducing the expression of vox and bmp2b are not known, but Bmp signals likely have a role (168, 293). It seems that bmp2b and vox are activated in parallel, because zygotic bmp and vox/vent are not required for each other's expression until the late-gastrula stage (131). In contrast, Wnt8 regulates vent expression and mesodermal vox expression (248). At the same time, maternal  $\beta$ -catenin protein activates dorsalizing genes, including boz among others, specifically in dorsal blastomeres and, soon thereafter, dorsal nuclei in the yolk syncytial layer (353). Hence, the earliest zygotic regulators of DV patterning act downstream of maternal factors to establish a two-state pattern, in which cells express either dorsal and ventral genes or only ventral genes.

After a short lag, presumably reflecting the time needed for Boz protein to accumulate to sufficient levels, Boz represses transcription of *bmp2b*, *vox*, and other ventralizing genes at the dorsal margin (75, 139, 182). This allows for expression of dorsal genes, such as *chordin*, *dkk1*, and *goosecoid*, which would otherwise be repressed by *vox/vent/ved* (131, 290). Thus as the first wave of zygotic genes becomes active, cells have gene expression patterns characteristic of either dorsal cells (e.g., *boz*, *goosecoid*, *chordin*, *dkk1*) or ventrolateral cells (e.g., *bmp2b*, *bmp7*, *vox*, *vent*, *ved*, *wnt8*).

Through the action of Bmp and Wnt8 signals and their antagonists, the simple pattern of mid-blastula stage embryos becomes much more elaborate, with many different groups of tissue progenitors fated to arise from different regions of the early gastrula embryo. As Bmps, Wnt8, and other signals elaborate and refine the pattern of the early gastrula, the regulatory interactions among DV-patterning genes change. For example, vox/vent and bmp2b/swirl are initially expressed independently of each other's action. As embryogenesis proceeds, however, expression of vox/vent and bmp2b/swirl genes becomes interdependent, apparently through a positive feedback loop established during gastrulation (131, 139, 140, 204). At mid-gastrulation, zygotic

Bmp signals are required for normal levels of vox and vent expression. Conversely, vox and vent act to promote bmp2b/swirl and bmp4 expression by inhibiting the expression of chordin, which blocks a positive autoregulatory activity of BMP signals (110, 277). Although the primary function of vox/vent/ved is to repress dorsal genes rather than to induce ventral genes, interruption of this vox/ventbmp2b positive feedback loop is responsible for a reduction of ventral gene expression in embryos lacking *vox* and *vent* at mid-gastrulation. Thus the *vox/vent-bmp2b* positive feedback loop maintains ventral positional identity during gastrulation, and the participation of the extracellular factors Chordin and Bmp incorporates flexibility and sensitivity to the cellular environment into the mechanism that maintains dorsal-ventral identity. For example, a cell moving from ventral to dorsal territories during gastrulation would reduce its expression of vox and vent in response to increased levels of Chordin and reduced levels of Bmp activity. The reduction of Vox and Vent levels would, in turn, permit the expression of dorsal genes appropriate for the cell's new environment.

# MESODERM AND ENDODERM FORMATION: MATERNAL FACTORS

The progenitors of the different germ layers are arranged along the animal-vegetal axis, with mesendoderm progenitors residing at and next to the margin and ectodermal progenitors located more animally (161, 334) (**Figure 3**). The animal-vegetal axis, in contrast to the DV or left-right axes, is already formed during oogenesis (281, reviewed in 237). The egg thus has an animal-vegetal polarity that is highlighted by morphological and molecular markers such as the position of the germinal vesicle and the localization of maternal mRNAs (18, 195). It is unknown how this polarity is generated during oogenesis, but maternal-effect mutants such as bucky ball might provide insights into this process (65).

mRNAs that are localized animally or vegetally in wild type fail to do so in *bucky ball* mutants, and cytoplasmic streaming occurs in multiple directions. This phenotype suggests an animal-vegetal polarity defect of the egg.

The animal-vegetal polarity of the egg has to be translated into the induction of mesendoderm at the margin. The molecular basis of this process remains elusive, but several lines of evidence indicate that the volk cell, and specifically the yolk syncytial layer, contains signals that can induce mesendodermal markers (Figure 4). First, transplantation of the yolk cell onto the animal region of the blastoderm can ectopically induce genes that are normally expressed at the margin (212, 213, 232). Second, injection of RNase into the yolk syncytial layer blocks the expression of ventral and lateral mesendodermal markers (44). Dorsal markers are still expressed, probably due to the dorsal determinant  $\beta$ -catenin in dorsal blastomeres. The maternal factors that establish the yolk syncytial layer as a signaling center are unknown. In Xenopus the transcription factor VegT has been implicated as a maternal factor that can activate mesoderm inducers (360). Xenopus VegT mRNA is localized vegetally and required for mesendoderm induction. In zebrafish spadetail is a related T-box gene, but neither its expression nor mutant phenotype suggest any functional similarity to Xenopus VegT (99, 156). Maternal eomesodermin mRNA is localized vegetally in zebrafish eggs, but there is no evidence that this T-box gene might act in a VegT-like fashion (33). No maternal mutant has been isolated yet that blocks mesoderm and endoderm induction in zebrafish.

# MESODERM AND ENDODERM FORMATION: ZYGOTIC FACTORS

# **Nodal Signaling**

Members of the Nodal family of TGF $\beta$  signals are essential inducers of mesoderm and endoderm in vertebrates (reviewed in 268).

Nodal signals are received by EGF-CFC coreceptors and type I and II Activin receptors, which function as serine/threonine kinases. Receptor activation leads to phosphorylation of the transcription factors Smad2 and Smad3. This results in their binding to Smad4, nuclear translocation, and association with additional transcription factors such as FoxH1 and Mixer to regulate target genes. Nodal signaling is antagonized by feedback inhibitors such as Lefty proteins, which are divergent members of the TGF $\beta$  family and block EGF-CFC coreceptors (41, 48), and Dapper2, which enhances the degradation of type I Activin receptors (362, but see 335).

Mutant screens in zebrafish have identified several components of the Nodal signaling pathway (**Table 1**). These include the Nodal signals Cyclops (Cyc) and Sqt, the EGF-CFC coreceptor One-eyed pinhead, and FoxH1 [schmalspur (sur)] and Mixer [bonnie & clyde (bon)] (31, 71, 79, 108, 115, 118, 151, 173, 243, 251, 252, 265, 270, 271, 295, 300, 306, 322, 361). In addition, molecular studies have led to the isolation of zebrafish Lefty and Dapper2 homologues and TARAM-A, a putative Nodal type I receptor (27, 239, 258, 316, 335, 362). In the case of the Leftys and Dapper2, but not TARAM-A, morpholino experiments have revealed essential roles for these proteins (3, 11, 46, 77, 362). Below we summarize the role of Nodal signaling in mesendoderm formation in zebrafish. Recent reviews provide more general discussions of the Nodal signaling pathway and its role during vertebrate development (reviewed in 268, 269).

Absence of Nodal signaling in cyc;sqt double mutants or maternal-zygotic one-eyed pin-bead mutants results in embryos that lack all endoderm and mesoderm, with the exception of a few somites in the tail (79, 102). Mutants also lack trunk spinal cord, but develop forebrain, midbrain, hindbrain, and tail spinal cord. These phenotypes are already presaged before gastrulation by the aberrant expression of genes marking presumptive mesendoderm progenitors in wild type. Consequently, the fate and morphogenetic movement of

marginal cells is affected. Marginal cells do not internalize, and dorsal marginal cells acquire neural fates instead of dorsal mesodermal fates, while ventral and lateral marginal cells contribute exclusively to the tail (36, 78). Conversely, increasing Nodal signaling by loss of Lefty1 and Lefty2 or overexpression of Cyc or Sqt results in the fate transformation of ectodermal cells into mesoderm or endoderm (3, 45, 46, 71, 77, 79, 101, 251, 252, 265).

How does the interplay of cyc, sqt and leftys control mesendoderm formation? Before gastrulation cyc, sqt, lefty 1 and lefty 2 are expressed in the 1-3 cell tiers closest to the margin, overlapping with and vegetally to mesendodermal progenitors (27, 46, 66, 71, 79, 101, 207, 251, 252, 265, 316) (**Figure 6**). In addition, *sqt* is expressed in the yolk syncytial layer (71, 79). Mutant and misexpression studies have suggested a scenario for Nodal-mediated mesendoderm induction (46, reviewed in 268). The sqt and cyc genes are transcribed in cells closest to the margin, leading to the local generation of Sqt and Cyc proteins. Sqt can move away from the source and induce mesendodermal gene expression in cells at a distance (45). In contrast, Cyc only acts at a short range and induces mesodermal markers locally (45). Nodal signaling also induces the expression of lefty1 and lefty2, which block the Nodal signaling pathway both locally to restrict the expression of sqt and at a distance to restrict the response to Sqt (46, 77). Hence, the interaction of Sqt, Cyc, and Leftys determines the extent of mesendoderm formation in zebrafish.

The strongest evidence for this model comes from the analysis of *bhikhari*, a marker for Nodal signaling expressed in 6–10 tiers from the margin. *cyc;sqt* double mutants lack *bhikhari* expression, and in the absence of *squint*, *bhikhari* is expressed only in the first few tiers (45). In contrast, the absence of only *cyc* initially does not affect the extent of *bhikhari* expression. This has suggested that Sqt might act at a long range to induce mesendodermal genes, whereas Cyc has only

short-range activity. In support of this model, ectopic clones of Sqt-expressing cells can induce downstream genes in distant cells. In contrast, Cyc-expressing clones only induce downstream genes at a short range (45). Two observations indicate that the long-range effect of Sqt is direct and not mediated via a relay mechanism. First, the activation of the Nodal signaling pathway in a clone of cells induces downstream genes cell autonomously. Second, Sqt can be made in nonresponding cells and apparently move through a field of nonresponding cells to activate gene expression in distant cells (45). These results provide support for a direct long-range effect of Sqt. It is unclear why Sqt is long-range and Cyc short-range, but studies on mouse Nodal indicate that the stability of the mature ligand might be a major determinant of range (178).

Leftys appear to restrict the range of Nodal signaling by two mechanisms (46). First, Leftys dampen Nodal autoregulation, thus limiting the generation of more Nodal. For example, in the absence of Leftys, sqt expression extends animally away from the margin and is maintained for a longer time than in wild type. Second, Leftys can act at a long range to inhibit Nodal signaling in distant cells. For example, ectopic expression of Leftys at the animal pole can block Nodal signaling at the margin of the zebrafish embryo. Moreover, depletion of Leftys extends the range of Sqt activity even in the absence of sqt autoregulation.

Although the above model accounts for the regulation of Nodal-regulated markers such as *bhikhari*, interactions between *cyc* and *sqt* provide additional complexity. Specifically, Sqt induces the expression of *cyc* on the dorsal side (66). Hence, *sqt* mutants lack Squint and have less Cyc on the dorsal side. The dorsal side is therefore more sensitive to loss of Nodal gene dosage than the lateral and ventral sides. In addition, despite their different ranges, both Cyc and Sqt can induce most mesendoderm derivatives on their own. While *cyc;sqt* double mutants lack all head and trunk mesoderm and endoderm, *cyc* mutants

display only minor defects in prechordal plate formation (66, 115, 317), and *sqt* mutants have quite mild defects in axial mesoderm and endoderm formation (66, 79, 118, 294). Hence, both short- and long-range Nodals can orchestrate most aspects of mesendoderm formation in zebrafish.

Nodal signaling not only induces the extent of mesendoderm, but also seems to pattern it. Partial reduction of Nodal signaling leads to the loss of cell types derived from marginal-most tiers. For instance, at the dorsal margin, high levels of Nodal signaling are required for prechordal plate (anterior axial mesoderm) specification, whereas lower levels are essential for notochord (posterior axial mesoderm) specification (101). Analogously, at the lateral margin where precursors for the myocardium (heart muscle) reside, high levels of Nodal signaling promote ventricular fates whereas lower levels are sufficient to induce atrial fates (145). This has led to the proposal that there might be a gradient of Nodal signaling activity at the margin, leading to the fine patterning of mesodermal and endodermal precursors (101). This conclusion is also supported by fate map studies of sqt/sqt and sqt/sqt;cyc/+ mutants that demonstrate a vegetal shift of cell fates that in wild type are located more animally (66). These mutant combinations also revealed that dorsal mesoderm requires higher levels of Nodal function than ventral and lateral regions; however, differential Nodal signaling does not pattern the mesoderm along the DV axis. In particular, dorsal margin cells are not transformed toward more lateral fates in sqt/sqt;cyc/+ mutants embryos, but dorsal expression of cyc requires Nodal-dependent autoregulation. The specification of endoderm, which derives from blastomeres that are located most marginally, also requires high levels of Nodal signaling (6, 260, 271). These observations suggest that there might be a Nodal activity gradient along the animal-vegetal axis, with the highest levels at the margin inducing endoderm, prechordal plate, and ventricular progenitors, lower levels inducing notochord and other mesodermal fates, and the absence of Nodal signaling allowing neural and tail specification (101, 315). Experiments that block or activate Nodal signaling at different times have suggested that marginal-most cells require sustained Nodal signaling before the onset of gastrulation, whereas cells more distant from the margin require shorter windows of Nodal signaling (10, 101). It is thus conceivable that Nodal signaling induces different fates using both temporal and spatial gradients.

Nodal signaling induces the phosphorylation of Smad2 and Smad3 (reviewed in 268). Smad2 or Smad3 mutants are not available in zebrafish, but mutations in FoxH1 (sur) and Mixer (bon), transcription factors that can bind to phosphorylated Smad2, have been identified (31, 151, 173, 243, 270, 295, 300, 322). bon mutants have severe defects in endoderm formation, whereas maternal-zygotic sur mutants have mild defects in axial mesoderm formation (151, 243, 295). Loss of both bon and sur results in a severe phenotype characterized by absence of prechordal plate, cardiac mesoderm, endoderm, and ventral neuroectoderm (173, 322). Some Nodal-regulated genes are regulated by either Bon or Sur, and others by both Bon and Sur (173). The phenotypes seen upon loss of both Bon and Sur are milder than those seen upon complete loss of Nodal signaling, indicating that additional Smad-associated transcription factors that act as components of the Nodal signaling pathway remain to be identified.

## Nodal Signaling and Left-Right Axis Development

Most organs in vertebrates are formed and positioned asymmetrically along the left-right axis. The analyses of *one-eyed pinhead* and *sur* mutants and of morphants for a third Nodal gene, *southpaw*, have established a requirement for Nodal signaling in zebrafish left-right axis formation (43, 191, 356). *southpaw* is expressed in the left lateral plate mesoderm, whereas *one-eyed pinhead* and *sur* are expressed bilaterally (191, 243, 295, 361). Loss

of late *one-eyed pinhead* or *sur* activity, and knock down of *southpaw* lead to a loss or randomization of organ asymmetries (43, 191, 356). For example, the consistent looping of the heart to the right side is randomized or lost in these embryos.

How genes such as southpaw, lefty, and pitx2 are specifically activated on the left side is still unclear. Notch signaling and rotating cilia have been implicated in this step of leftright patterning in several vertebrates (235, reviewed in 250). In zebrafish, these cilia are located in Kupffer's vesicle, a specialized organ lined by the descendants of the dorsal forerunner cells (50, 73, 74, 142, 169). Disruption of Kupffer's vesicle development or cilia formation and function results in the randomized activation of left-side specific markers (73, 142, 169). Based on studies in the mouse, it is thought that cilia rotation leads to a leftward flow that results either in the specific activation of mechanoreceptors or the accumulation of a signal on the left that initiates left-side-specific gene expression. Both southpaw and the Nodal antagonist charon are first expressed symmetrically around Kupffer's vesicle before southpaw expression becomes restricted to the left lateral plate mesoderm (114, 191). Inhibition of charon expression results in the bilateral activation of southpaw in the lateral plate (114). These results suggest a model wherein cilia-mediated flow and charon activity bias southpaw activation toward the left.

## Downstream of Nodal Signaling: Endoderm Formation

Several genes have been identified that are regulated by Nodal signaling and mediate its endoderm-inducing activity, including the Sox gene *casanova*, the GATA gene *faust*, and the homeobox genes *bonnie&clyde* and *mezzo* (5, 42, 61, 150, 151, 245, 255, 256, 264, 302, reviewed in 231). These four genes encode transcription factors and appear to be direct targets of the Nodal signaling pathway, as suggested by experiments using cycloheximide

(245). As described above, Bon is also a component of the Nodal signaling pathway.

Of these four genes, casanova appears to be the most central and downstream player (61, 150). casanova is expressed in a subset of marginal-most cells that are thought to give rise to endoderm. Indeed, loss of casanova causes these cells to adopt an aberrant mesodermal fate. In addition, casanova is sufficient to induce cells to give rise to endoderm, and casanova can induce endoderm in the absence of Nodal signaling. Since the activities of faust, bon, and mezzo depend on casanova, the main role of faust, bon, and mezzo may be to induce and maintain casanova expression. Casanova activity and maintenance require the POU domain gene spiel ohne grenzen (pou2/Oct4) (25, 34, 193, 254). In contrast to Casanova, spiel ohne grenzen expression is not induced by Nodal, but is ubiquitous and activated both maternally and zygotically. These results suggest that endoderm formation induced by Nodal is predominantly mediated by the induction of Casanova and its interaction with Spiel ohne grenzen.

# Downstream of Dorsal Mesoderm Induction: Midline Development

As the embryonic pattern is refined during gastrulation, cells at different positions in the shield and the immediate vicinity adopt different fates, including prechordal plate, notochord, hypochord, adaxial muscle, and floor plate (175, 206, 285). The prechordal plate arises from the marginal-most cells in the shield, under the influence of the highest levels of Nodal signals (101). The cells of the developing prechordal plate specifically express the transcriptional repressor Goosecoid (301). Goosecoid may repress expression of genes that promote other cells types (80), although *goosecoid* has not been analyzed in loss-of-function studies in zebrafish.

The notochord arises from cells at slightly more animal positions within the shield (101, 206). The homeobox gene *flh* and the T-box gene *no tail (ntl)* are essential for

notochord development (106, 107, 278, 312). Both genes are expressed in all margin cells in the late blastula (276, 312). By the beginning of gastrulation, flb is specifically expressed in notochord precursors, whereas ntl is expressed in all margin cells, the developing notochord, and, at later stages, the tail bud. Fate mapping with mutant embryos showed that flb is required to prevent notochord precursors from differentiating as muscle, whereas ntl acts to prevent notochord precursors from forming floor plate (7, 105, 205, 206). A key target of flb is spadetail (spt), a T-box gene initially expressed in all marginal cells and then repressed in the notochord domain early in gastrulation (8, 99). The Xenopus ortholog of flb, Xnot, encodes a transcriptional repressor, suggesting that Flh may directly repress spt transcription (328, 357). Trunk muscle and other ventral-lateral mesodermal derivatives are reduced in spt mutants, and it has been proposed that spt both activates expression of genes required for muscle differentiation and morphogenesis (e.g., myod) and antagonizes the function of *ntl* in notochord development (7, 8, 99, 125, 156).

In addition to the interactions among these transcriptional regulators, local signaling interactions are important to allocate cells in the shield region to particular fates. For example, the Nodal signal Cyc is required during gastrulation for the formation of the medial floor plate (115, 217, 229, 233, 265, 319a, reviewed in 307). The Cyc signal antagonizes the notochord-promoting function of ntl, perhaps by inducing the expression of the transcriptional repressor Her9 (105, 176). Repression of ntl by Notch signaling and another Hairy/Enhancer of split gene, her4, allows cells lateral to the notochord domain to differentiate as hypochord (12, 13, 175). At later stages the growth factor Midkinea is expressed in the paraxial mesoderm and required for the formation of the posterior medial floor plate (266a). Hedgehog signals from the midline during gastrulation instruct the immediately adjacent adaxial cells to differentiate as slow muscle and the overlying neuroectoderm to form lateral floor plate (29, 169a, 233, 266b, reviewed in 307). These studies indicate that complex, local interactions among several signaling pathways and transcription factors specify different midline cell fates.

## **FGF Signaling**

Members of the FGF family of signals have been implicated in mesoderm formation, neural induction, DV patterning, and anteriorposterior patterning of the embryo (reviewed in 296). Data in zebrafish mainly suggest an early role for FGF signaling in repressing Bmp signaling and a later role in promoting the development of posterior structures. FGFs bind and activate receptor tyrosine kinases. Receptor dimerization leads to transphosphorylation and the recruitment and activation of a plethora of downstream effectors, including PKC and the ras/MAPK cascade. In contrast to the Nodal and Bmp signaling pathways, zygotic mutant screens have only uncovered a single mutation in a component of the FGF signaling pathway—mutations in acerebellar disrupt the fgf8 gene (30, 253). The dearth of FGF signaling mutants might be due to the overlapping roles or maternal contribution of these gene products. Hence, morpholinos, misexpression or small molecule inhibitors have been used to analyze the role of FGF signaling during embryogenesis. Such studies have identified the type I transmembrane protein Sef ("similar expression to fgf genes") as a novel feedback inhibitor of FGF signaling (84, 323).

The expression patterns of downstream targets for FGF signaling have revealed that the pathway is first active at the dorsal blastoderm margin, then along the entire margin and finally in the tail bud (87, 247, 261, 324) (**Figure 6**). Consistent with this pattern of activity, the earliest role for FGF signaling is during blastula stages, when *fgf3*, *fgf8*, and *fgf24* are expressed at the dorsal margin. Misexpression of FGF signals can inhibit the expression of *bmp2b* and *bmp7* at blastula stages

and lead to the lateralization and dorsalization of the embryo (86, 87, 324). However, blocking only FGF signaling during these stages does not result in a ventralized embryo. In contrast, blocking both Chordin and FGF signaling results in ventralization (87). These results suggest that FGF signaling, Bozozok, and Bmp antagonists such as Noggin and Chordin all contribute to blocking Bmp signaling in dorsal margin blastomeres. Conversely, inactivating the FGF signaling feedback inhibitor Sprouty2 results in the repression of Bmp expression and the dorsalization of the embryo (87). Taken together, these results establish an early role for FGF signaling in restricting Bmp expression and activity.

Following dorsal margin expression, several FGF ligands become expressed in the entire margin at the onset of gastrulation (35, 67, 85, 253). Moreover, downstream targets like pea3, erm, and sprouty4 are induced in broad domains in neighboring cells (87, 247, 261, 324). These downstream genes appear to be activated at different thresholds of FGF activity, with *sprouty4* being the target most sensitive to low levels of FGF signaling and expressed in most-distant cells (275). These results suggest that FGF signals form a vegetal-to-animal activity gradient. Indeed, tagged FGF can be detected in intracellular vesicles at a distance from the source. This localization is dependent on receptor-mediated endocytosis, which leads to the clearance of the ligand from extracellular space. As a consequence, blocking endocytosis results in an increased FGF signaling range (275).

These results suggest a long-range and graded FGF signaling activity at early gastrulation stages, but it is unclear what role this activity might have. At the onset of gastrulation mesendoderm formation and patterning are initiated correctly in the apparent absence of FGF signaling, and only at later gastrulation stages is the expression of genes such as *tbx6*, *spt*, and *ntl* lost (67, 84, 87, 98, 100, 200, 247, 323, 324). It is therefore conceivable that very early FGF signaling only has consequences at later stages of gastrulation (see below), or

that it acts redundantly with other pathways, e.g., the Nodal signaling pathway. The latter possibility is raised by double mutant studies of FGF and Nodal signaling components (100, 200). For example, partial inhibition of FGF signaling and blocking zygotic activity of One-eyed pinhead, a Nodal coreceptor, disrupts posterior development and leads to the death of dorsal mesoderm cells by the end of gastrulation. However, it remains unclear when Nodal and FGF signaling interact.

An alternative scenario is that FGF signaling during gastrulation primes and maintains cells for posterior development. For example, severe posterior truncations are generated in embryos exposed to the FGFR inhibitor SU5402, expressing a dominantnegative FGF receptor or lacking full fgf8 and fgf24 activity (67, 98, 100, 200). Tail and posterior trunk mesoderm do not form in these embryos and mesodermal markers such as the T-box genes ntl and spt cease to be expressed at later gastrulation stages. These results suggest that FGF signaling is required for the maintenance of a pool of mesoderm progenitors during gastrulation. A role for FGF signaling in the formation of posterior cell types is also seen in the nervous system (167, 170, 172, 189, 257). FGF signaling is required for the expression of posterior neural markers during gastrulation. Strikingly, this neural inducing role of FGFs is independent of the organizer or the inhibition of Bmp signaling.

# **Retinoic Acid Signaling**

Retinoic acid signaling acts during gastrula stages in the posteriorization of the neuroectoderm and the formation of myocardial progenitors (**Figure 6**). Retinoic acid binds to its receptors, members of the nuclear hormone receptor family, leading to the regulation of downstream genes. Retinoic acid is synthesized by RALDH and hydrolyzed by Cyp26/P450RA1. Studies on retinoic acid function in zebrafish have used exposure to retinoic acid, pharmacological inhibition of

retinoic acid receptors, mutations in *raldh2* or *cyp26a1*, and morpholinos against *cyp26a1* (24, 70, 97, 122, 172, 185). These studies have suggested that the expression of RALDH in the posterior mesoderm during gastrulation generates a source of retinoic acid that induces posterior hindbrain and spinal cord markers, in particular specific subsets of *Hox* genes. Conversely, *cyp26a1* is expressed in more anteriorly located precursors of the neuroectoderm and thought to generate a retinoic acid-free zone that is thus protected from retinoic acid-mediated posteriorization.

A role for retinoic acid has also been found in the mesoderm. Blocking retinoic acid signaling during gastrulation stages increases the number of myocardial progenitors (144). This is not simply due to an expansion of the myocardial progenitor region but appears to be a consequence of an increase in the density of myocardial progenitors within a normally sized field containing these precursors.

#### **MicroRNAs**

MicroRNAs are  $\sim$ 22 nucleotides long nonprotein-coding RNAs that regulate gene expression at the posttranscriptional level (reviewed in 9, 20). MicroRNAs have been implicated in many processes, but the roles of microRNAs in zebrafish embryogenesis have only been tested recently (92, 338, 339). A large-scale analysis of the expression of more than 100 microRNAs has revealed very specific patterns during embryonic and larval stages (338). Maternal-zygotic mutants for the RNaseIII enzyme Dicer cannot process microRNA precursors and thus lack mature microRNAs (92). The resulting phenotype is quite mild. Mutant embryos develop normal axes and are regionalized correctly. The major cell types are specified, and no dramatic modulation of embryonic signaling pathways has been observed. The main defects are in morphogenetic processes such as a delay in epiboly, impairment of ventricle inflation, and abnormal somite differentiation (92). These results suggest that microRNAs have subtle roles during zebrafish axis formation and might be involved in the differentiation of multiple cell types at later stages.

#### **GASTRULATION MOVEMENTS**

The movements of epiboly, internalization, convergence, and extension transform the radially symmetric blastula into the gastrula embryo with clear DV and anterior-posterior axes (333, reviewed in 2, 138, 155, 181, 215, 298) (**Figure 2**). Mutant analysis has indicated that these processes can be genetically separated, e.g., defects in internalization do not lead to an obligatory disruption of epiboly or convergence.

## **Epiboly**

Epiboly describes the process of spreading and thinning of the embryo during blastula and gastrula stages and results in the envelopment of the yolk by the embryo. Microfilament and microtubule networks in the yolk cell are thought to contribute to epiboly (47, 299, 305, 321). The cellular basis for epiboly appears to be at least in part a process of radial intercalation—deeply positioned cells move outward between more superficial cells, resulting in a thinning and spreading of the embryo (Figure 2). This process has been well documented during gastrula stages, when two cell layers can be distinguished in the epiblast. An epithelial-like exterior layer underlies the enveloping layer and an inner layer overlies the hypoblast (137). During epiboly, cells from the inner layer intercalate between cells of the outer layer and flatten to dimensions typical in that layer. Hence, both cell intercalation and cell flattening can contribute to epiboly.

Zygotic screens have isolated mutations in only a single locus that affects epiboly (135, 137, 202, 300). Mutations in the adhesion molecule E-cadherin (*half-baked*) severely affect epiboly and arrest the vegetal spreading of deep cells during gastrulation (137, 289). Mutant cells can intercalate but often deintercalate into the deeper layer and do not

flatten. These results suggest that E-cadherin is required to bind cells together so that they can form a flattened spread-out layer that envelops the yolk. How epiboly is regulated is still poorly understood, but blocking the T-box transcription factor Eomesodermin or its target *mtx2*, a homeobox gene, blocks epiboly (32).

Consistent with an adhesive role for E-cadherin, more severe depletion using morpholinos instead of *hab* mutants results in the deadhesion of cells and disintegration of the embryo already during early cleavage divisions (14). An additional factor that might be involved in cell (de)adhesion, but not epiboly, is the EGF-CFC protein One-eyed pinhead. During late-blastoderm stages, *one-eyed pinhead* mutant cells appear less motile and more cohesive (332). It remains unclear how this contributes to morphogenesis and if this process is dependent on Nodal signaling.

The isolation of four maternal mutants (betty boop, poky, slow, bedazzled) suggests that many components required for epiboly are provided maternally (330). These mutants display premature constriction of the margin (betty boop) and slower or delayed epiboly (poky, slow, bedazzled).

#### Internalization

Internalization describes the process by which mesendodermal precursors located at the margin move inside, resulting in an embryo with an outer epiblast layer and an inner hypoblast layer (159, 333). There has been some debate about the exact cellular mechanism that underlies internalization (2). It was proposed that internalization is caused by involution, the inward flow of a sheet of cells, or ingression, the inward movement of individual cells (36, 53, 77, 214, 285). Imaging and embryological studies suggest that synchronized ingression underlies internalization (2). Cells move coherently toward the margin, where they begin to form protrusions, lose coherence with their neighbors, and ingress. This "flow of individuals" results in internalization.

The molecules that drive internalization are largely unknown. Complete absence of Nodal signaling blocks all internalization movements (36, 78). Conversely, upregulation of the pathway in the absence of Lefty leads to prolonged and increased internalization (77). A single cell that is mutant for the Nodal coreceptor One-eyed pinhead can initially be internalized when placed at the margin of a wild-type embryo but then it egresses (36). This result suggests that the flow of internalizing wild-type cells can carry but not keep neighboring cells inside. Activation of the Nodal pathway in a single cell can lead to the ingression of this cell even when neighboring cells do not internalize (36, 55). This effect might be caused by the differential adhesion between cells that have an active or inactive Nodal signaling pathway (214), but the Nodal downstream genes that mediate internalization are elusive.

## Convergence and Extension

Convergence and extension are defined as the narrowing of embryonic tissues mediolaterally (convergence) and their elongation anterioposteriorly (extension). These movements are driven by a number of directed and coordinated cell behaviors that lead to the accumulation of cells on the dorsal side and the formation of an axis (reviewed in 146, 222, 331). Several distinct cell behaviors underlie convergence and extension in zebrafish, including the directed migration of internalized cells toward the animal pole and toward the dorsal side and the mediolateral intercalation of dorsal and lateral cells.

Immediately after internalization, hypoblast cells move away from the margin. This has been best studied on the dorsal side, where prechordal plate (anterior axial mesoderm) precursors migrate anteriorly. It has been proposed that a  $\beta$ -catenin-Stat3-Liv1-Snail1 pathway regulates prechordal plate migration (211, 354, 355). In this model,  $\beta$ -catenin activates an unknown ligand for the JAK/STAT pathway, culminating in the phosphorylation

and consequent activation of the transcription factor Stat3. Stat3 then activates the expression of the zinc transporter Liv1. Increased levels of zinc might allow the nuclear accumulation of the zinc finger transcription factor Snail1. It has been proposed that Snail1 might promote the epithelial-to-mesenchymal transition of anterior axial mesoderm cells, but such changes in cell behavior have not been observed in wild-type embryos (2, 214). Further genetic and cell biological studies are required to more thoroughly test the  $\beta$ -catenin-Stat3-Liv1-Snail1 model.

The PDGF/PI3K/PKB pathway has also been implicated in the migration of prechordal mesendoderm precursors (216). Pharmacological block of the PDGF receptor or phosphoinositide 3-kinase inhibits the formation of polarized processes on prechordal plate progenitors and the localization of protein kinase B and F-actin to the leading edge. Despite these defects, cells maintain their directional, albeit slower, migration.

A third pathway regulating prechordal plate migration is the noncanonical Wnt signaling pathway. As discussed in more detail below, this pathway has a key role in polarizing cells in all animals (reviewed in 163). Blocking wnt11 activity during prechordal cell migration results in slower and less directed movements and the abnormal orientation of cellular protrusions (119, 325). Because the correlation of direction of movement and direction of protrusions is not absolute, it is not yet known if there is a causative link between these two wnt11-dependent processes.

The pathways described above ultimately have to regulate cell behavior by modulating cytoskeletal or adhesive properties. Indeed, two proteins implicated in actin dynamics have been implicated in the migration of prechordal plate cells (51). A cap1 homolog and quattro, which encodes a guanine nucleotide exchange factor, are expressed in the anterior mesendoderm. Quattro morpholinos disrupt the anteriorly directed convergence and aggregation of prechordal plate, and cap1 is required for the migration of the aggregated

cluster toward the animal pole. These observations identify restricted actin-regulatory molecules in the control of cell movements during gastrulation. In addition, there also appears to be a minor role for E-cadherin in the elongation and migration of dorsal hypoblast cells (214).

A hallmark of gastrulation is the polarity of cell movements and cell shapes. Some of the molecular mechanisms underlying this process appear to be conserved in all animals. In particular, components implicated in planar polarity formation in *Drosophila* are also involved in the control of cell polarization and convergence and extension movements in zebrafish and other vertebrates (reviewed in 163, 298, 331). Several components of the noncanonical Wnt signaling pathway have been identified as convergence and extension genes in zebrafish, including the Wnt signals Wnt5 (pipetail), Wnt11 (silberblick), and Wnt4; the Wnt receptor Fz2; the putative Wnt coreceptor Glypican4 (knypek); and the cytoplasmic signal transducer Dishevelled (119, 152, 201, 249, 309, 320). In addition, modulators of the pathway have been identified, including Van gogh-like 2/Strabismus (trilobite) and Prickle (37, 132, 236, 283, 326). Additional components identified in *Drosophila*, such as Flamingo and Diversin, also play important roles in zebrafish (82, 279). Downstream mediators that have been shown to play a role in zebrafish include ROK, Rac, and RhoA (17, 197, 201).

The transparency of the zebrafish embryo has been employed to great effect to study the cellular role of planar polarity genes. The main conclusion from these studies is that planar polarity proteins are required for the proper polarization of cells during directed dorsal migration and mediolateral intercalation (reviewed in 215, 222). In this process, cells intercalate between their medial and lateral neighbors, similar to the cell behavior during frog gastrulation, or migrate directionally first toward the animal pole and then toward the dorsal side, a movement not observed in frogs. Planar polarity signaling

regulates both the length-to-width ratio of cells and their orientation with respect to the embryonic axes. This polarization is also thought to be required for the persistent migration of cells. For example, both the lengthto-width ratio and mediolateral alignment of paraxial ectodermal cells is reduced in trilobite (Van gogh-like 2/Strabismus) mutants (132). Hence, cells are more rounded and more randomly oriented compared with the more elongated and more uniformly oriented wild-type cells. Concomitantly, trilobite mutant cells move with reduced net dorsal speed along less direct trajectories when compared with wild-type cells. It has thus been proposed that trilobite and other planar cell polarity genes allow for the medial-lateral cell polarization that is required for the persistent dorsal migration of cells along straight paths. The connections between cell behavior and movement are still correlative, but planar cell polarity signaling clearly controls both the shape and movement of cells.

Planar polarity signaling in zebrafish is not only required for the polarization of cells but also controls cell division orientation (95). Epiblast cells in dorsal tissues preferentially divide along the animal-vegetal axis of the embryo. Inhibition of the establishment of this animal-vegetal polarity by blocking wnt11, dishevelled, or trilobite disrupts this orientation and thus reduces the extension of the axis.

Although convergence and extension can be linked, they can also be independent. In *ntl* mutants, convergence but not extension of axial mesoderm is affected (93). In dorsalized *swirl/bmp2b* mutants, convergence of lateral cell populations is reduced, whereas their extension is normal or even increased (221). Moreover, the absence of the polysaccharide hyaluronan blocks the convergence but not the extension of lateral mesoderm (17).

In zebrafish there might also be an attractant on the dorsal side that guides cells. Specifically, misexpression of  $\beta$ -catenin on the ventral side not only induces ectopic dorsal fates

but also redirects cells ventrally. Hence, there might be  $\beta$ -catenin–regulated genes that provide the directionality of convergence and extension movements. Although components of the noncanonical Wnt signaling pathway are required for directional movement of cells, they are unlikely to act as chemoattractants in this process. For example, ubiquitous expression of wnt5 or wnt11 is able to rescue wnt11 mutants, arguing against a localized Wnt signal that controls cell polarity and migration (152). Instead, a signal regulated by Stat3 might provide polarity cues (211, 354). As described above, phospho-STAT3 accumulates specifically on the dorsal side in response to  $\beta$ -catenin stabilization. Blocking STAT3 function using morpholinos results in severe reduction of convergence and extension movement. This effect on lateral cells is non-cell autonomous. It has thus been proposed that STAT3 activates an as-yet unidentified factor that guides DV cell polarity. This interpretation is complicated by the fact that convergence and extension are also reduced in the *quattro* and *cap1* morphants described above, probably secondarily to the abnormal migration of anterior axial mesoderm (51). In this case, it might not be the absence of a signal but abnormal morphogenesis of axial mesoderm that impairs convergence and extension.

Despite the central role of planar cell polarity signaling during convergence and extension, several additional molecules have been implicated in gastrulation movements or cell polarity, including  $G\alpha 12/13$  (184), hyaluronan (17), Cyclooxygenase-1 (38), Widerborst [a B' regulatory subunit of protein phosphatase 2A (111)], Estrogen receptorrelated α (19), Scribble 1 (329), Fyn/Yes (134), Nemo-like kinase (318), Ephrins (39, 230), and Slit (359). Most of these factors have been implicated in gastrulation movements based on overexpression or morpholino analvsis. Future genetic studies will be required to firmly establish a role for these molecules and to determine how they interact with other factors controlling gastrulation.

#### THE BIOGRAPHIES OF CELLS

The previous sections discussed how the fates and movements of cells are dependent on their position in the embryo and how signaling pathways, transcription factors, and other molecules influence these decisions. We are now in a position to attempt a synthesis of these observations and describe how different cells receive and interpret these diverse inputs during early development to generate specific cell types and move to specific positions. These "childhood biographies of cells" not only allow us to integrate the findings described above, but they also serve to inform strategies in stem cell research (reviewed in 284). A major application of vertebrate embryology and genetics is to drive multipotent cells to a particular fate for therapeutic purposes. In turn, these in vitro studies provide a critical test of how completely we understand embryonic development.

# The Dorsal Margin: Making Prechordal Plate

Prechordal plate progenitors are located at the dorsal margin and become marked as dorsal when  $\beta$ -catenin is stabilized soon after fertilization (see above). After mid-blastula transition,  $\beta$ -catenin activates sqt and cyc expression in prechordal plate precursors, resulting in the full activation of the Nodal signaling pathway in these cells. In contrast, Bmp and Wnt signaling are suppressed by the  $\beta$ -cateninmediated activation of Chordin, Dkk1, and other antagonists of Bmp and Wnt signaling, and because  $\beta$ -catenin activates repressors such as Boz, which represses wnt and bmp gene expression on the dorsal side.  $\beta$ -catenin might also activate transcription factors such as Goosecoid that directly specify dorsal fates. Hence, it might be sufficient to activate  $\beta$ catenin and full Nodal signaling and block all other signaling pathways to specify prechordal plate precursors. This leads to the activation of prechordal plate-specific genes (e.g., goosecoid) and to the internalization and migration of progenitors toward the animal pole. This migration is controlled in part by the STAT3 pathway, Cap1, Quattro, Wnt11 signaling, and PDGF/PI3K signaling.

# The Dorsal Margin: Making Notochord

Like prechordal plate progenitors, notochord precursors are initially marked by  $\beta$ -catenin, which activates sqt and cyc expression next to and potentially in notochord precursors. This results in the partial activation of the Nodal signaling pathway in these cells. Hence, it might be sufficient to activate  $\beta$ -catenin and intermediate levels of Nodal signaling and block all other signaling pathways to generate notochord precursors. This leads to the induction of flb and ntl, which encode transcription factors that specify notochord identity, and the internalization, convergence, and extension of notochord progenitors. This process is regulated by ntl (convergence) and noncanonical Wnt signaling (convergence and extension). According to this model, the level or timing of Nodal signaling is the key factor that distinguishes prechordal plate and notochord progenitors.

# The Margin: Making Endoderm

A subset of the cells that are located at the margin become endoderm (reviewed in 231). These cells are exposed to an unknown signal from the yolk syncytial layer and are also likely to contain maternally provided mRNAs encoding transcription factors of unknown identity. Before gastrulation, and shortly after the activation of sqt at the dorsal margin, all endodermal precursors express Cyc and Sqt, resulting in the full activation of the Nodal signaling pathway in these cells. Depending on the DV position, Bmp, FGF, or Wnt signaling is also activated in endodermal precursors; these pathways do not influence endodermal fate specification per se, but might modulate the type of endoderm that is formed. Hence, it might be sufficient to fully activate Nodal signaling to generate endoderm progenitors. This eventually leads to the induction of the transcription factor Casanova, which in conjunction with the transcription factor Spiel ohne grenzen might be sufficient to specify endoderm progenitors. Since high Nodal signaling is involved in both prechordal plate and endoderm specification, additional factors (e.g.,  $\beta$ -catenin and its downstream genes) might be required to specifically induce prechordal plate cells. It remains unclear why only some cells at the margin are induced to express *casanova* and form endoderm, whereas neighboring cells form mesoderm.

# The Lateral Margin: Making Heart Muscle

Cells at the lateral margin give rise to the cardiomyocytes of the heart (reviewed in 358). Nodal and Bmp signaling are required for this process, and at later stages FGF signaling is also thought to contribute to myocardium formation. These signaling pathways lead to the induction of *nkx2.5*, a marker for cells that can give rise to heart muscle, and downstream genes such as *hand2*. In contrast, retinoic acid signaling limits the number of cells in this region that are selected to form cardiomyocyte progenitors.

# The Ventral Margin: Making Blood and Tail Somites

Cells at the ventral margin give rise to multiple cell types, including blood and tail somites. Many signaling pathways are active in this region, including Wnt, Bmp, FGF, and Nodal. Both the Wnt and Bmp pathways are most active in the ventral margin region, and this coincidence is apparently required for proper expression of ventral margin genes such as *tbx6* (311). Conversely, ventral margin cells can induce an ectopic tail, and this activity can be mimicked by the local application of Bmp, Wnt, and Nodal signals (4). Despite this activity, Nodal signals are not required to make tail somites, suggesting that high-level

activity of Wnt, Bmp, and potentially FGF signaling may be sufficient to generate tail mesodermal identity. This leads to the activation of downstream transcription factors [e.g., members of the T-box and caudal-related gene families (56, 288)] and planar polarity signaling, which regulate tail morphogenesis (196).

Development of blood also requires Wnt, Bmp, and FGF signals, but in addition is dependent on Nodal signals (reviewed in 57). Indeed, Nodal signals may be a factor in determining why some ventral margin cells form blood while others form tail somites. The sqt and cyc genes are expressed at the ventral margin just prior to the onset of gastrulation, and mutational analysis shows that Nodal signals are essential for blood but not tail somites. Thus Nodal signals at certain levels or times in development may allocate a subset of ventral margin cells to a blood fate. It is not clear how Nodal signals might drive ventral margin cells toward blood fates, but they could instruct blood progenitors to involute early in gastrulation or trigger the expression of certain target genes that specify blood identity.

# Lateral and Ventral Ectoderm: Making Spinal Cord

The precursors of the spinal cord are located laterally and ventrally between the margin and the animal pole. These cells originate distant to the organizer and, in contrast to other neuronal progenitors, do not require organizer-derived inhibitors to be specified. BMP and FGF signaling promote spinal cord development, whereas Nodal signaling counteracts it. Wnt and retinoic acid signaling are also involved in this process by posteriorizing the neuroectoderm. Dorsal spinal cord and neural crest progenitors, which are located more laterally at neural plate stages, appear to be specified by higher levels of Bmp signaling than ventral progenitors, which are located more medially at neural plate stages (21, 226).

## The Animal Region: Making Forebrain and Midbrain-Hindbrain Boundary

Cells in the animal dorsal region become forebrain progenitors. It appears that forebrain specification requires the absence of all known signaling pathways. Indeed, blocking Nodal, Bmp, FGF, Wnt, and retinoic acid signaling does not affect forebrain formation and in some cases results in the expansion of forebrain territory. Absence of these signaling pathways is achieved by the absence of the signals that might suppress forebrain formation and the expression of inhibitors of these signaling pathways. For example, Dickkopf and Tlc are both inhibitors of Wnt signaling expressed in the prechordal plate underlying the forebrain territory and at the anterior border of the forebrain region, respectively. These and other factors (Tcf3, Chordin, Noggin, Lefty) inhibit signaling and allow forebrain formation. It is still controversial if forebrain formation is indeed the default state of development. For example, FGF signaling has been proposed to be required for neural induction, including the forebrain, but genetic evidence in zebrafish is not available (304).

The precursors of the midbrain-hindbrain boundary are located dorsally and at an intermediate position between the animal pole and margin. It appears that these cells are induced by lack of Bmp, Nodal, FGF, and retinoic acid signaling but require intermediate levels of Wnt signaling (259).

### **COMPARATIVE ASPECTS**

How applicable are the findings in zebrafish to other vertebrates and vice versa? Vertebrate embryos share a similar body plan, and the fate map of one species can be morphed into the one of another (298). It has therefore been expected that the underlying molecular mechanisms are also shared. The past 10 years have seen dramatic progress in our molecular understanding of zebrafish, frog, chick and mouse embryogenesis, and we can now ask if

the molecular mechanisms underlying vertebrate axis formation are conserved. At a superficial level, the answer is yes. First, the same signaling pathways and transcription factors are employed during the early embryogenesis of all vertebrates (reviewed in 59, 112, 192, 298, 303, 313). For example, the Nodal, Bmp, FGF, and Wnt signaling pathways are active in all vertebrates during blastula or gastrula stages, and transcription factors such as homeodomain and T-box proteins are widely employed. Second, interference with these regulators can result in similar phenotypes. For example, lack of Nodal signaling severely compromises mesoderm and endoderm induction (reviewed in 268), loss of FGF signaling affects posterior development (reviewed in 296), and mutations in Brachyury/ntl result in notochord defects and posterior truncations in all model vertebrates (reviewed in 297).

Despite these similarities there are also intriguing differences, in particular between frog and fish on one side and mouse on the other. For example, noncanonical Wnt signaling is required for proper gastrulation in fish and frog, but mice that lack components of this pathway display only mild posterior truncations and spina bifida (reviewed in 163, 331). However, in general, the lossof-function phenotypes of particular signaling pathways are more severe in mouse than in zebrafish or frog (reviewed in 313). For example,  $\beta$ -catenin is required for the formation of dorsal structures in fish and frog but not for mesoderm and endoderm formation (reviewed in 129). In contrast,  $\beta$ -catenin mutant mice lack anterior-posterior polarity and do not develop embryonic mesoderm and endoderm (103). Similarly, mouse wnt3 mutants do not form mesodermal and endodermal progenitors (187). In fish and frog Bmp signaling is necessary for the development of ventral structures but not for mesoderm and endoderm formation (reviewed in 219). In contrast, mouse cells mutant for Bmp receptors cannot form mesoderm and endoderm (210, reviewed in 219). Lack of FGF signaling in frog and fish results in posterior truncation in frog and fish, similar to partial loss-of-function phenotypes in mouse (reviewed in 296). However, in *fgf8* mouse mutants endoderm and mesoderm progenitors cannot gastrulate properly, resulting in the loss of these cell types (310). Hence, there are clear differences between fish/frog and mouse in the requirement for key signaling pathways.

We suggest that these differences arise from the much more pronounced role of reciprocal signaling interactions in mouse than in fish or frog. Although there is some crossregulation of FGF, Bmp, Wnt, and Nodal signaling in fish, there appears to be a striking interdependence of these signaling pathways in mouse. For example, Bmp, Wnt, and Nodal signals maintain each others' expression before the onset of mouse gastrulation (reviewed in 192, 313). Hence, interference with one pathway will affect the activity of the others, leading to more pronounced phenotypes. In fish and frog embryos, these pathways might not only be more independent but even act redundantly, suppressing potentially more severe phenotypes.

We propose that reciprocal signaling manifests itself more prominently in mouse than in fish or frog because of three major differences in the early embryogenesis of these organisms. First, mouse embryos undergo dramatic growth, whereas the volume of fish and frog embryos does not significantly change until organogenesis. In mouse, the need to coordinate growth and patterning may be met by extensive cross-regulatory interactions among various signaling pathways. This cross-regulation might explain the apparently similar phenotypes in mouse embryos that have mutations in different signaling pathways (reviewed in 313).

Second, mouse embryos require extraembryonic tissues for implantation and anterior-posterior patterning (reviewed in 192, 313). These tissues serve as signaling centers, and they are in turn regulated by different signals and their antagonists. For example, the Nodal signaling pathway patterns the extraembry-

onic (visceral) endoderm and in turn is regulated by extraembryonic ectoderm (reviewed in 192, 269). There is a role for an extraembryonic structure in the fish (the yolk syncytial layer), but it appears to be less important than mouse extraembryonic tissues and does not apparently require reciprocal signals from embryonic signaling centers. Hence, reciprocal signaling appears essential to coordinate embryonic and extraembryonic development in mouse, whereas embryonic development in fish occurs in the context of extraembryonic structures that are largely pre-established during oogenesis.

Third, fish and frog embryos strongly rely on maternal determinants to guide axis formation. The egg is already polarized, zygotic transcription is only initiated after the 500cell stage, and in frog maternal factors such as Wnt11,  $\beta$ -catenin, VegT, and Ectodermin are required for axis formation (69, 116, 314, 360). In contrast, mammals appear not to rely on localized maternal determinants and initiate zygotic transcription as early as the two-cell stage. There seem to be asymmetries during early cleavages, but they do not necessarily translate into orientations of specific axes (89, 242). Hence, the mouse embryo has to "self-organize," a process likely to require cross-regulatory interactions between patterning signals.

Taken together, these observations suggest that the dramatic growth, the importance of extraembryonic tissues, and the lack of a prepattern in mouse embryos necessitate complex cross-regulatory interactions between tissues and signaling pathways. Interference with one tissue or pathway can thus have dramatic effects on other tissues or pathways. In contrast, fish and frog eggs contain detailed patterning information, embryos grow little, and extraembryonic tissues play minor roles. In this case, the different signaling pathways are less interdependent and can specify distinct tissue types. These developmental differences might also drive the very rapid development of frog and fish embryos compared with

the relatively slow development of mouse embryos.

#### **PERSPECTIVES**

After 15 years of zebrafish molecular genetics we have attained a basic outline of the molecular bases of zebrafish axis formation, but many important questions remain. First, many of the key components involved in axis formation are not yet identified. For example, we lack any systematic knowledge of the maternal factors that contribute to vertebrate embryogenesis; RNAi experiments in other systems suggest that many modulators of specific signaling pathways are still unidentified (54); moreover, it is almost completely unknown which genes are regulated by the signals and transcription factors that set up the vertebrate body plan. Maternal or sensitized screens, reverse genetics, RNAi or morpholinos, small molecule inhibitors, and microarray experiments are likely to lead to the isolation of additional factors involved in axis formation. We speculate, however, that it is unlikely that many new signaling pathways required for axis formation will be identified. The genetic screens in zebrafish have by now reached at least 50% saturation and have not isolated any novel signaling pathways required for axis formation, although these screens did define new roles for and new modulators of known pathways (e.g., 102, 141, 348). Similarly, recent misexpression screens in *Xenopus* have not identified novel signaling pathways. It is conceivable that signaling pathways that have more subtle roles [e.g., during gastrulation movements (17, 38, 184)] remain to be discovered, but we predict that most progress will be made in the isolation of maternal upstream factors, signaling modulators, and downstream mediators.

Second, our understanding of the cell biological and molecular bases of vertebrate embryogenesis is still poor. How do signals move through the embryo? How do cells read and respond to these extracellular inputs over time? How are cytoskeletal and adhesive properties changed in response to specific signals? How is chromatin modified as cells become specified? What are the subcellular changes when progenitors become neurons, muscles, blood, and other cell types? The development of probes that allow the in vivo imaging of subcellular processes promises a detailed cell biological and dynamic view of cell movements and differentiation (reviewed in 203). The transparency of the zebrafish makes this organism particularly well suited to address these questions.

Ultimately, we need to understand how all these inputs are integrated into regulatory hierarchies and networks (reviewed in 183). It has become clear that individual cells receive multiple and diverse inputs depending on their position and history, but we are largely ignorant about how these inputs are translated into flexible but ultimately robust outcomes. This knowledge will not only provide a basis to understand human birth defects and guide our efforts in stem cell manipulations but might also uncover the regulatory logic that drives vertebrate embryogenesis.

### **SUMMARY POINTS**

- A combination of embryological, genetic, and molecular approaches has provided an outline of the molecular basis of zebrafish axis formation.
- During oogenesis the animal-vegetal axis is specified and dorsal determinants are deposited into the egg.
- 3. Nodal, FGF, Bmp, Wnt, and retinoic acid signals provide positional information and activate transcription factors that specify cell fates during gastrulation.

4. Planar cell polarity signaling is required for the gastrulation movements of convergence extension.

#### **FUTURE ISSUES**

- 1. Identify additional factors involved in zebrafish axis formation and gastrulation.
- 2. Develop in vivo probes to study the subcellular and molecular basis of zebrafish embryogenesis.
- 3. Determine how cells integrate multiple inputs to acquire specific fates and movements.

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This paper spelled out the experimental advantages and potential of the zebrafish as a vertebrate model system, inspiring other investigators to join the zebrafish field.

First description and analysis of a zebrafish mutant affecting early embryogenesis.

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