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Review

Induction and specification of cranial placodes

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Abstract

Cranial placodes are specialized regions of the ectoderm, which give rise to various sensory ganglia and contribute to the pituitary gland and sensory organs of the vertebrate head. They include the adenohypophyseal, olfactory, lens, trigeminal, and profundal placodes, a series of epibranchial placodes, an otic placode, and a series of lateral line placodes. After a long period of neglect, recent years have seen a resurgence of interest in placode induction and specification. There is increasing evidence that all placodes despite their different developmental fates originate from a common panplacodal primordium around the neural plate. This common primordium is defined by the expression of transcription factors of the *Six1/2, Six4/5*, and *Eya* families, which later continue to be expressed in all placodes and appear to promote generic placodal properties such as proliferation, the capacity for morphogenetic movements, and neuronal differentiation. A large number of other transcription factors are expressed in subdomains of the panplacodal primordium and appear to contribute to the specification of particular subsets of placodes. This review first provides a brief overview of different cranial placodes and then synthesizes evidence for the common origin of all placodes from a panplacodal primordium. The role of various transcription factors for the development of the different placode is addressed next, and it is discussed how individual placodes may be specified and compartmentalized within the panplacodal primordium. Finally, tissues and signals involved in placode induction are summarized with a special focus on induction of the panplacodal primordium itself (generic placode induction) and its relation to neural induction and neural crest induction. Integrating current data, new models of generic placode induction and of combinatorial placode specification are presented.

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Introduction

Vertebrates are distinguished from other deuterostomes by their specialized head with an elaborate brain encased in a cartilaginous or bony skull and with complex paired sense organs such as nose, eyes, and ears. Many of these evolutionary innovations of the vertebrate head originate from only two embryonic tissues, the neural crest, and the cranial placodes, which probably evolved in early vertebrates when these ceased to be filter feeders and adopted a new life style as active predators (Northcutt and Gans, 1983; Gans and Northcutt, 1983; see also Northcutt, 1996, 2005; Baker and Bronner-Fraser, 1997a; Holland and Holland, 1999, 2001; Meulemans and Bronner-Fraser, 2004; Schlosser, 2005).

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Neural crest and placodes are specialized domains of the embryonic ectoderm which develop similarly in several respects. Both are very versatile embryonic tissues that give rise to multiple non-epidermal cell types including neurons, glia, and secretory cells. Moreover, the development of both tissues involves cell shape changes; these allow placodal and crest cells to migrate and/or to participate in various morphogenetic movements. Finally, both neural crest and placodes develop from populations of cells near the border of the neural plate.

Beyond these similarities, however, cranial placodes develop in a peculiar fashion quite distinct from the neural crest (reviewed for example in Webb and Noden, 1993; Northcutt, 1996; Baker and Bronner-Fraser, 1997a, 2001; Le Douarin and Kalcheim, 1999; Hall, 1999; Kalcheim, 2000; Santagati and Rijli, 2003; Meulemans and Bronner-Fraser, 2004; Huang and Saint-Jeannet, 2004). First, placodes develop exclusively from cranial ectoderm, whereas the neural crest develops in both

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head and trunk. Second, placodes comprise a quite heterogeneous assembly of structures, which form as focal thickenings of the cranial ectoderm at various stages of embryonic development (mostly after neural tube closure) and later invaginate and/or give rise to a subpopulation of migratory cells. The neural crest, in contrast, is an entirely migratory population of cells, which leaves the neural plate border region prior to or during fusion of the neural folds. Third, the developmental potential of placodes is more restricted than of neural crest. While both tissues give rise to secretory cells, neurons, and glia, only neural crest cells can form cartilage and bone, smooth muscle, and pigment cells. And fourth, with few exceptions, neural crest and placodes express different sets of transcription factors indicating that their development is controlled by different gene regulatory networks.

Compared to the neural crest, which has attracted much attention for its versatility and morphogenetic capacity and has been intensely studied ever since its discovery (reviewed in Baker and Bronner-Fraser, 1997b; Le Douarin and Dupin, 2003; Le Douarin and Kalcheim, 1999; Hall, 1999; Mayor and Aybar, 2001; Mayor et al., 1999; Kalcheim, 2000; Aybar and Mayor, 2002; Knecht and Bronner-Fraser, 2002; Santagati and Rijli, 2003; Meulemans and Bronner-Fraser, 2004; Huang and Saint-Jeannet, 2004), placodal development has long been neglected. The last couple of years, however, have seen a resurgence of interest in placode development, spurred by the discovery of many transcription factors with placode-specific expression and by increasing evidence for a common developmental origin of all placodes from a panplacodal primordium (for reviews, see Baker and Bronner-Fraser, 2001; Schlosser, 2002a, 2005; Streit, 2004; Brugmann and Moody, 2005).

The present review focuses on early aspects of placode development addressing in particular the origin of different placodes from such a panplacodal primordium. After providing an overview of different cranial placodes, I review the evidence for their common origin from a panplacodal primordium. Next, I address the role of various transcription factors for placodal development. I then discuss how different placodes may be specified within this primordium and how the latter is finally divided into distinct placodes. Finally, I consider tissues and signals involved in placode induction, concentrating on generic steps of placode induction and their relation to the induction of neural plate and neural crest. Evolutionary implications of our current view of placode development will not be covered but are reviewed elsewhere (Schlosser, 2005).

Development and derivatives of cranial placodes—an overview

Placodes were first discovered as transitory thickenings of cranial ectoderm (van Wijhe, 1883; Froriep, 1885; von Kupffer, 1891, 1895). The cranial placodes, as understood here, include the adenohypophyseal, olfactory, lens, trigeminal, and profundal placodes, a series of epibranchial and hypobranchial placodes, an otic placode, and a series of lateral line placodes (Fig. 1) (reviewed in Webb and Noden, 1993; Northcutt, 1996; Baker and Bronner-Fraser, 2001; Schlosser, 2002a, 2005; Streit,

2004). Most of these placodes are present in all vertebrates. However, the neurogenic hypobranchial placodes have only been found in amphibians (Schlosser, 2003; Schlosser and Northcutt, 2000; Schlosser et al., 1999), and the number of epibranchial and lateral line placodes differs for different taxa, with lateral line placodes being completely lost repeatedly, for instance, in amniotes (reviewed in Northcutt, 1992, 1993a,b, 1997; Schlosser, 2002b).

All placodes are specialized areas of the cranial non-neural ectoderm (i.e. ectoderm outside of neural plate and neural crest), where cells undergo pronounced cell shape changes (which may result in thickening, invagination, and/or cell delamination) and which give rise to various non-epidermal cell types. As I have discussed elsewhere (Schlosser, 2002a), placodes are often recognizable as thickenings (regions of columnar epithelium), but this is not always the case. It should be noted that there are some other ectodermal areas-including the amphibian hatching gland and cement gland (Drysdale and Elinson, 1992; Sive and Bradley, 1996) as well as the primordia of teeth, feathers, and hairs (Pispa and Thesleff, 2003)-which also give rise to specialized cell types but are not considered as placodes here because they apparently do not share a common developmental origin or bias (see below) with cranial placodes in the strict sense as enumerated above. Hatching and cement glands, for example, develop from the superficial layer of the bilayered amphibian ectoderm (Drysdale and Elinson, 1992; Sive and Bradley, 1996), while cranial placodes arise from its deep layer (Northcutt and Brändle, 1995; Northcutt et al., 1994; Schlosser and Northcutt, 2000).

There are several generic aspects of placode development shared by different placodes and reflected in the coexpression of many genes in different placodes (see below and McCabe et al., 2004). First, placodes are regions of increased cell proliferation compared to the epidermis (Saka and Smith, 2001; Washausen et al., 2005). Second, the development of placodal derivatives often involves cell shape changes and morphogenetic movements (reviewed in Noden, 1991; Webb and Noden, 1993; Northcutt, 1996; Baker and Bronner-Fraser, 2001), allowing placodes to develop into columnar epithelia, to invaginate, and/or to give rise to various types of migratory cells (neuronal, endocrine, or glial precursor cells or lateral line primordia). And third, all placodes with the exception of adenohypophyseal and lens placode are neurogenic (e.g. D'Amico-Martel and Noden, 1983; Ma et al., 1998; Fode et al., 1998; Schlosser and Northcutt, 2000; Andermann et al., 2002; Begbie et al., 2002). The absence of neurogenesis in these two placodes may be due to its active suppression in ectoderm originally biased for a neuronal fate judged by the initial expression and subsequent downregulation of Xenopus Ngnr-1 in the prospective lens and adenohypophyseal ectoderm (Schlosser and Ahrens, 2004).

Aside from these similarities, however, different cranial placodes develop differently and give rise to different sense organs and ganglia, each with a distinct set of derivative cell types. These are briefly summarized in the following paragraphs and in Fig. 1, which also shows the location of cranial placodes in chick and *Xenopus* embryos.

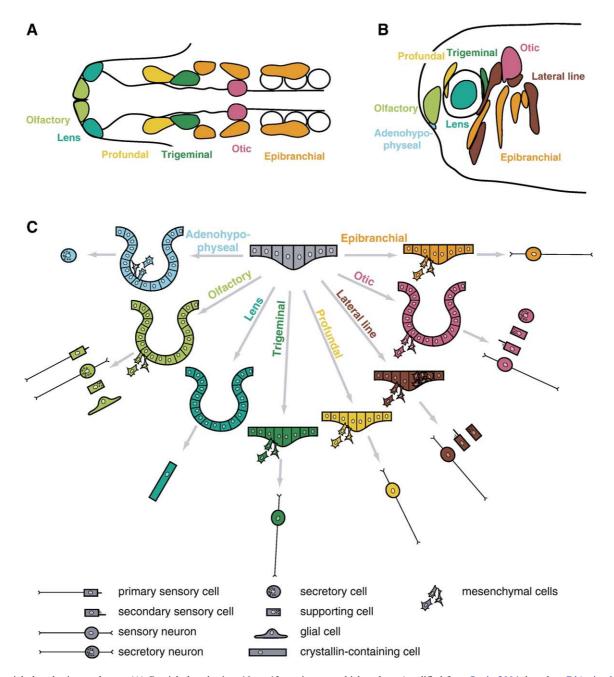


Fig. 1. Cranial placodes in vertebrates. (A) Cranial placodes in a 10- to 13-somite-stage chick embryo (modified from Streit, 2004; based on D'Amico-Martel and Noden, 1983; Bhattacharyya et al., 2004). In amniotes, profundal and trigeminal placode are commonly referred to as ophthalmic and maxillomandibular placode of the trigeminal nerve, respectively. (B) Cranial placodes in a tailbud stage *Xenopus* embryo (modified from Schlosser and Northcutt, 2000). (C) Schematic summary of morphogenesis and cellular derivatives of various cranial placodes. Invagination occurs in adenohypophyseal, olfactory, lens, and otic placodes. Moreover, in all placodes except the lens placode, some cells migrate away from the placodal epithelium as mesenchymal cells to form sensory neurons, secretory cells, or glial cells. In lateral line placodes, another subset of cells migrates along the basement membrane and forms the lateral line primordia (modified from Schlosser, 2005).

Adenohypophyseal placode

The adenohypophyseal placode forms the adenohypophysis, i.e. the anterior lobe of the pituitary gland (Couly and Le Douarin, 1985; Eagleson et al., 1986, 1995; Kawamura and Kikuyama, 1992; El Amraoui and Dubois, 1993a,b; Kouki et al., 2001; Sasaki et al., 2003; Herzog et al., 2003; Uchida et al., 2003; Chapman et al., 2005). The mode of adenohypophysis development differs for different vertebrates, but in most gnathostomes (except teleosts), it involves invagination of the

placode (which thereby forms Rathke's pouch) from the stomodeum. The adenohypophysis is of central importance for the hormonal control of multiple body functions and contains six types of endocrine secretory cells: corticotropes (ACTH), melanotropes (MSH), gonadotropes (LH and FSH), thyrotropes (TSH), lactotropes (prolactin), and somatotropes (somatotropin) (reviewed in Dubois et al., 1997; Kawamura and Kikuyama, 1998; Sheng and Westphal, 1999; Kioussi et al., 1999a; Dasen and Rosenfeld, 2001; Scully and Rosenfeld, 2002; Asa and Ezzat, 2004; Ooi et al., 2004).

Olfactory placode

The olfactory placode is one of the most versatile placodes and is the only one, which retains stem cells capable of forming various differentiated cell types throughout life (reviewed in Crews and Hunter, 1994; Calof et al., 1998; Schwob, 2002; Beites et al., 2005). It invaginates to form the epithelia of the olfactory and vomeronasal organs (e.g. Mendoza et al., 1982; Klein and Graziadei, 1983; Couly and Le Douarin, 1985; Hansen and Zeiske, 1993; Zeiske et al., 2003; reviewed in Brunjes and Frazier, 1986; Farbman, 1994; Reiss and Burd, 1997; Buck, 2004). These epithelia contain secretory cells such as supporting cells and mucus-producing cells as well as primary sensory cells (possessing an axon). The latter are chemoreceptive cells carrying odorant and pheromone receptors and their axons form the olfactory and vomeronasal nerves, respectively. In addition, the olfactory placode is the only placode, which has been demonstrated to give rise to glial cells (Couly and Le Douarin, 1985; Chuah and Au, 1991; Norgren et al., 1992; Ramón-Cueto and Avila, 1998). These include Schwann cells, which ensheath the axons of the olfactory nerve and migrate along this nerve into the olfactory bulb.

Finally, the olfactory placode is believed to give rise to a diverse population of secretory cells releasing neuropeptides such as Neuropeptide Y, FMRFamide, and gonadotropinreleasing hormone (GnRH), which migrate along the olfactory and vomeronasal nerves towards and into the brain (Schwanzel-Fukuda and Pfaff, 1989; Wray et al., 1989; El Amraoui and Dubois, 1993a,b; Murakami and Arai, 1994; Northcutt and Muske, 1994; Yamamoto et al., 1996; Dellovade et al., 1998; Bless et al., 2005; reviewed in Tarozzo et al., 1995; Daikoku, 1999; Wray, 2002). One subpopulation of the placodally derived GnRH cells forms the terminal nerve (reviewed in Muske and Moore, 1988; Demski, 1993; Von Bartheld, 2004), a distinct ganglionated cranial nerve with neuromodulatory effects on various neurons and neuroendocrine cells including the olfactory receptor cells itself (Eisthen et al., 2000; Abe and Oka, 2000; Park and Eisthen, 2003). Another subpopulation of placodal GnRH cells populates a group of septo-preoptic nuclei and later controls the release of gonadotropins (LH, FSH) from the adenohypophysis (reviewed in Muske, 1993; Parhar, 2002; Somoza et al., 2002; Wray, 2002).

Recent lineage tracing experiments in zebrafish have cast doubt on the olfactory origin of GnRH cells and suggest instead that the septo-preoptic subpopulation originates from the adenohypophyseal placode next to the anteromedial boundary of the olfactory placode, while the terminal nerve subpopulation originates from neural crest cells adjacent to the posterolateral boundary of the olfactory placode (Whitlock et al., 2003; see also Whitlock, 2005). However, due to the close apposition of the olfactory placode to both neural crest and adenohypophyseal placode at the stage when these experiments were performed, inadvertent labeling of olfactory placodal cells cannot be ruled out, and further studies are needed to unequivocally clarify the origin of GnRH cells.

Lens placode

The lens placode is the only placode besides the adenohypophyseal placode that does not form neurons. Instead, it invaginates to form the lens vesicle, which gives rise to the crystallin-accumulating cells of the lens (reviewed in McAvoy, 1980; Piatigorsky, 1981; McAvoy et al., 1999; Cvekl and Piatigorsky, 1996; Ogino and Yasuda, 2000; Chow and Lang, 2001; Lovicu and McAvoy, 2005).

Profundal and trigeminal placodes

The profundal and trigeminal placodes give rise to neuronal precursors, which migrate away from the placode and congregate in the adjacent mesenchyme. Together with neural crest cells, they will form the sensory neurons of the ganglia of the profundal and trigeminal nerves, respectively (Knouff, 1927, 1935; Hamburger, 1961; Ayer-LeLièvre and Le Douarin, 1982; D'Amico-Martel and Noden, 1983; Artinger et al., 1998; Schlosser and Northcutt, 2000). In many gnathostomes, these two nerves are distinct and have separate cranial ganglia (e.g. Allis, 1897; Norris, 1925; Norris and Hughes, 1920; Song and Northcutt, 1991; Northcutt, 1993a; Northcutt and Bemis, 1993; Piotrowski and Northcutt, 1996), but these ganglia fuse during development in amphibians (Northcutt and Brändle, 1995; Schlosser and Roth, 1997). In amniotes, there is only a single ganglion known as the trigeminal or Gasserian ganglion. The latter has, however, an ophthalmic and maxillomandibular subdivision. These subdivisions develop by the coalescence of neural crest cells with an ophthalmic and maxillomandibular placode (Hamburger, 1961; Ayer-LeLièvre and Le Douarin, 1982; D'Amico-Martel and Noden, 1983; Begbie et al., 2002). These placodes are most likely homologues of the profundal and trigeminal placodes of anamniotes, respectively, based on their position and gene expression patterns (for detailed discussion, see Schlosser and Ahrens, 2004; Schlosser and Northcutt, 2000). The sensory neurons derived from the profundal and trigeminal placodes have either free nerve endings or supply receptors of non-placodal origin such as Merkel cells (reviewed in Saxod, 1996) and monitor somatosensory information (touch, temperature, pain) from the oral cavity and the rostralmost face (e.g. Noden, 1980a,b).

Otic placode

The otic placode invaginates to form the otic veside, which gives rise to the inner ear and to neuron precursors, which migrate away from the epithelium of the otic vesicle and form the sensory neurons of the vestibulocochlear ganglion nearby (reviewed in Torres and Giráldez, 1998; Fritzsch et al., 1998, 2002; Whitfield et al., 2002; Fekete and Wu, 2002; Noramly and Grainger, 2002; Riley and Phillips, 2003; Barald and Kelley, 2004). The inner ear contains many different specialized epithelial cells including the endolymph-producing secretory cells of the stria vascularis, supporting cells and the mechanosensory hair cells (reviewed in Müller and Littlewood-Evans, 2001; Gao, 2003; Frolenkov et al., 2004; Coffin et al., 2005).

The latter are secondary sensory cells (that is, they do not possess an axon), which are innervated by the sensory neurons of the vestibulocochlear ganglion. Hair cells and supporting cells are concentrated in several distinct sensory areas, which vary in number and position between taxa (see reviews by Fritzsch and Neary, 1998; Bryant et al., 2002; Fritzsch et al., 2002). They are committed to the detection of gravity (utricular and saccular maculae in mammals), angular acceleration (cristae of the semicircular canals), and sound (cochlear organ of Corti in mammals).

Lateral line placodes

The lateral line placodes give rise to all peripheral components of the lateral line system, a sensory system for detection of water movements and electric fields. These components comprise the mechanoreceptive (neuromasts) and electroreceptive receptor organs (ampullary organs or tuberous organs) and the sensory neurons of the lateral line ganglia supplying them (reviewed in Winklbauer, 1989; Northcutt, 1992, 1997; Smith, 1996; Schlosser, 2002a; Ghysen and Dambly-Chaudiere, 2004; Gibbs, 2004). After leaving the placodal epithelium, the neuron precursors congregate in the nearby mesenchyme to form sensory neurons of the lateral line ganglia, while the remaining placodal cells become lateral line primordia. The latter elongate or migrate between surface ectoderm and basement membrane (all the time being closely tracked by outgrowing neurites from the lateral line ganglia) and finally break up into the primordia of receptor organs. Similar to the sensory areas of the ear, lateral line receptor organs are composed of secondary sensory cells (e.g. hair cells in neuromasts) and secretory supporting cells (reviewed in Flock, 1967; Russell, 1976; Blaxter, 1987; Gibbs, 2004; Coffin et al., 2005). Various numbers of lateral line placodes develop in different vertebrate taxa both rostrally and caudally to the otic placode. Six lateral line placodes were probably primitively present in gnathostomes (Northcutt, 1992, 1993a,b, 1997), but the lateral line system has been reduced to various degrees several times independently in different gnathostome lineages, resulting for example in the loss of subsets of lateral line placodes, loss of receptors of a particular modality (e.g. electroreceptors in frogs), or the complete loss of the entire lateral line system (e.g. in amniotes) (reviewed in Fritzsch, 1989; Northcutt, 1992, 1997; Schlosser, 2002b).

Epibranchial and hypobranchial placodes

The epibranchial placodes derive their name from their position dorsal and slightly caudal to the pharyngeal pouches. They give rise to neuronal precursors, which migrate away from the placodal epithelium to form the sensory neurons of the distal ganglia of the facial (geniculate ganglion), glossopharyngeal (petrosal ganglion), and vagal nerves (nodose ganglia). The neurons in these distal ganglia are viscerosensory and have either free nerve endings or innervate various visceral sensory receptors of non-placodal origin including taste buds (reviewed in Northcutt, 2004). The proximal ganglia of the facial, glossopharyngeal, and vagal nerves, in contrast, harbor neural crest-derived somatosensory neurons (Yntema, 1937, 1943, 1944; Naravanan and Naravanan, 1980; Aver-LeLièvre and Le Douarin, 1982; D'Amico-Martel and Noden, 1983; Couly and Le Douarin, 1990; Kious et al., 2002). In amphibians, recently, another type of neurogenic placode was discovered, which develops ventrocaudal to the pharyngeal pouches and has accordingly been termed hypobranchial placodes (Schlosser, 2003; Schlosser and Northcutt, 2000; Schlosser et al., 1999). They give rise to small hypobranchial ganglia of unknown function. However, the development of both epibranchial and hypobranchial placodes from a larger placodal area in the branchial region suggests that hypobranchial placodes may be essentially ventrally displaced epibranchial placodes generating viscerosensory neurons (Schlosser, 2003). Neurogenic hypobranchial placodes or ganglia have not been found in other vertebrates, but a recent study suggests that placodal thickenings ventral to the pharyngeal pouches form also in mammals and are later eliminated by apoptosis (Washausen et al., 2005).

Origin of all placodes from a panplacodal primordium

The spatiotemporal pattern of cranial placode development during embryogenesis has been described for many taxa in the classical embryological literature (e.g. van Wijhe, 1883; Froriep, 1885; von Kupffer, 1895, 1900; Landacre, 1910, 1912, 1916, 1926, 1927; Landacre and Conger, 1913; Stone, 1922; Knouff, 1935; Damas, 1944; Romanoff, 1960; Bancroft and Bellairs, 1977; Verwoerd and van Oostrom, 1979; Northcutt and Brändle, 1995; Northcutt et al., 1994; Schlosser and Northcutt, 2000; reviewed in Ariëns-Kappers, 1941; Baker and Bronner-Fraser, 2001). These descriptions continue to be valuable sources of information today. However, the reliance on thickenings as the sole indicators of the presence and extent of placodes necessarily puts some limitations on the usefulness of these accounts for elucidating the earliest stages of placode development. Consequently, it has long been disputed whether all cranial placodes arise by the subdivision of a common primordium (e.g. Platt, 1894; Knouff, 1935; Nieuwkoop, 1963, 1985; Jacobson, 1966; Torres and Giráldez, 1998; Baker and Bronner-Fraser, 2001; Schlosser, 2002a; Streit, 2004) or whether they are essentially unrelated structures which form as individually distinct thickenings at various positions of the head (Stone, 1922; Northcutt and Brändle, 1995; Graham and Begbie, 2000; Begbie and Graham, 2001).

As emphasized before (Schlosser, 2002a, 2005; Schlosser and Ahrens, 2004; Streit, 2004), a panplacodal primordium only exists if two conditions are met. First, all cranial placodes must in fact originate from a contiguous precursor region or preplacodal region. And second, the pre-placodal region must be biased towards the development of generic placodal properties (shared by the different placodes). Generic placodal bias here must be distinguished from the mere competence to respond to placodal inducers and requires that the pre-placodal region has an autonomous tendency to develop generic placodal properties (without being necessarily already fully specified), for example, due to the expression of transcription factors promoting proliferation, morphogenesis, or neurogenesis in all placodes.

Fate maps suggest that all placodes originate from a common pre-placodal region

Concerning the first condition, fate maps of early teleost (Kozlowski et al., 1997; Whitlock and Westerfield, 2000; Dutta et al., 2005), amphibian (e.g. Vogt, 1929; Röhlich, 1931; Carpenter, 1937; Fautrez, 1942; Jacobson, 1959; Eagleson and Harris, 1990; Eagleson et al., 1995), and amniote (Couly and Le Douarin, 1985, 1987, 1990; Streit, 2002; Bhattacharyya et al., 2004) embryos indeed suggest that all cranial placodes originate from a horseshoe-shaped pre-placodal region in the outer neural folds and the immediately adjacent ectoderm (Fig. 2), which borders the anterior neural plate rostrally and the cranial neural crest laterally. In teleost and chick embryo, it has been shown that, at late gastrula or early neural plate stages, the areas of origin for particular placodes within this pre-placodal region still show considerable overlap (Figs. 2A, B) and segregate only later (Kozlowski et al., 1997; Whitlock and Westerfield, 2000; Streit, 2002; Bhattacharyya et al., 2004; Dutta et al., 2005). It remains to be seen whether this is also true in Xenopus, where, unfortunately, no detailed fate maps of non-neural ectoderm at neural plate stages are currently available.

The pre-placodal region appears to be biased for placode development and, thus, constitutes a panplacodal primordium

Whether the second condition is also met is more controversial. In classical studies, the presence of a common thickening, from which various placodes develop, has often been considered as evidence for a uniform placodal bias of the pre-placodal region. However, this purely morphological criterion has tended to confuse rather than to clarify the question of placodal origins for several reasons. Most importantly, such common thickenings can be identified only in some vertebrate taxa such as teleosts, anurans, and mammals but not in others such as birds, while the condition in urodeles is debated (discussed in detail in Schlosser, 2002a; Schlosser and Northcutt, 2000). Moreover, several thickenings such as the "primitive placodal thickening" described in anuran embryos by Knouff (1935) correspond to a transitional zone between the highly columnar epithelium of the neural plate/neural crest and the flat, squamosal epithelium of the epidermis. This transitional zone extends throughout head and trunk levels and, thus, cannot be equated with the cranial pre-placodal region (even though it covers parts of it).

More convincing evidence for the presence of a generic placodal bias in the pre-placodal region comes from the recent identification of transcription factors, which are initially expressed within this horseshoe-shaped domain, later continue to be expressed in some or all cranial placodes, and have experimentally verified roles for placode development (reviewed in Baker and Bronner-Fraser, 2001; Riley and Phillips, 2003; Streit, 2004; Schlosser, 2005; Schlosser and Ahrens, 2004; Brugmann and Moody, 2005). Many of these transcription factors are either confined to some subregion of the pre-placodal region or extend into ectoderm beyond its limits. However, genes of the Six1/2 and Six4/5 subfamilies and of the Eya family are expressed in a horseshoe-shaped pattern matching the preplacodal region at neural plate stages and subsequently continue to be expressed in all cranial placodes (Fig. 3) (Six1/2 and Six4/5genes: Oliver et al., 1995a; Seo et al., 1998a; Ohto et al., 1998; Esteve and Bovolenta, 1999; Kobayashi et al., 2000; Pandur and Moody, 2000; Ghanbari et al., 2001; Ozaki et al., 2001, 2004; Laclef et al., 2003a; Zheng et al., 2003; Li et al., 2003; McLarren et al., 2003; Schlosser and Ahrens, 2004; Bessarab et al., 2004; Zou et al., 2004; Eya genes: Abdelhak et al., 1997; Xu et al., 1997a, 1999, 2002a; Kalatzis et al., 1998; Duncan et al., 1997; Mishima and Tomarev, 1998; Sahly et al., 1999; David et al., 2001; McLarren et al., 2003; Schlosser and Ahrens, 2004; Zou et al., 2004). Perturbations of these genes in mutants or by experimental manipulation result in a similar spectrum of

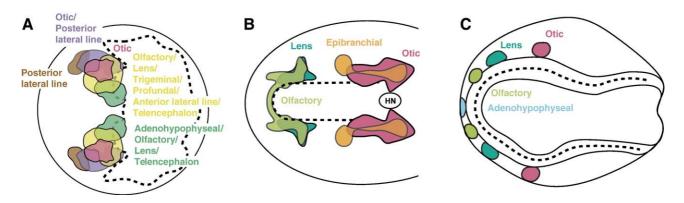


Fig. 2. Fate maps of cranial placodes at late gastrula or neural plate stages. The boundary of the (prospective) neural plate (here defined as the precursor of the entire neural tube, which includes the inner but not the outer neural folds) is indicated by a broken line. All placodes originate from a pre-placodal region in the non-neural ectoderm within and immediately adjacent to the outer neural folds. (A) Fate map of late gastrula zebrafish embryos with substantial overlap between ectodermal regions giving rise to different placodes (modified from Kozlowski et al., 1997). (B) Fate map of neural plate stage chick embryo (0–1 somite stage) with extensive overlap between various prospective placodes (based on data from Streit, 2002; Bhattacharyya et al., 2004). (C) Fate map of neural plate stage salamander (*Ambystoma*) embryo (based on Carpenter, 1937). Recently, otic and lateral line placodes in *Ambystoma* were reported to originate from the outer neural folds themselves and, thus, from slightly more medial positions than depicted here (Northcutt, 1996). HN: Hensen's node.

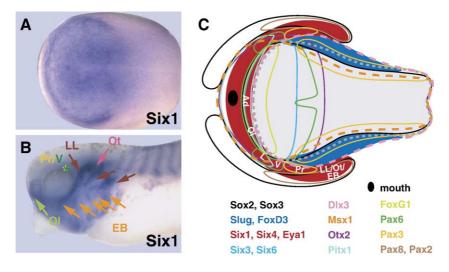


Fig. 3. *Six1*, *Six4*, and *Eya1* define a panplacodal primordium as illustrated for *Xenopus*. (A) *Six1* is first expressed in a horseshoe-shaped domain around the neural plate. (B) At tailbud stages, *Six1* expression continues in all placodes. The position of the fused profundal and trigeminal ganglia is indicated by asterisks (the respective placodes are already disappearing at this stage). (C) Position of the panplacodal primordium (red) relative to the neural plate (gray) and neural crest (blue). The gray broken line indicates the border of the neural plate proper (i.e. the entire ectoderm, which will become incorporated into the neural tube). Solid colored lines enclose areas of expression of various transcription factors, while the broken lines (*Dlx3* and *Msx1*) enclose areas, from which expression is excluded. Note that the region of the outer neural folds immediately peripheral to the hatched gray line is occupied by neural crest cells laterally but by the panplacodal primordium anteriorly. Although no fate map is available, gene expression patterns suggest that placodes arise approximately from the following regions as indicated by white letters: the preoral ectoderm gives rise to the stomodeum with the adenohypophyseal placode and to the olfactory placodes; the lateral domain of *Pax6* expression gives rise to the posterior placodal area, from which otic, lateral line, and epibranchial placodes develop. Expression data are based on the following sources: Bang et al. (1997), Bellefroid et al. (1998), Zygar et al. (1998), Heller and Brändli (1999), Feledy et al. (2001), Schweickert et al. (2001), Schlosser and Ahrens (2004). Abbreviations: Ad: adenohypophyseal placode; EB: epibranchial placodes; L: lateral line placode; CI: olic factory placode; Pr: profundal placode; V: trigeminal placode.

deficiencies in all placodes, including reductions in cell proliferation and survival and failure of morphogenetic movements and neuronal differentiation as will be discussed in more detail below. *Six1/2*, *Six4/5*, and *Eya* genes are, therefore, currently the most promising candidates for genes biasing the pre-placodal region towards the development of generic placodal properties.

Moreover, many transcription factors involved in regulating some aspect of placode development (including genes of the *Pax, Sox, Fox, Irx, Pitx,* and *Tbx* families) are expressed in multiple placodes in a complex pattern of partially overlapping domains. Such a pattern, which will be described in more detail below, is also easier to reconcile with a model according to which different placodes become step by step individualized from a common primordium and may even use some kind of combinatorial code for their specification (Torres and Giráldez, 1998; Schlosser and Ahrens, 2004) than with the alternative model according to which each placode develops completely independently of the others.

To confirm the presence of generic placodal bias in the preplacodal region experimentally, it has to be shown that development of a normal and positionally appropriate placode from a particular region of the pre-placodal region (e.g. the prospective olfactory region) is more likely when ectoderm in this region is replaced by ectoderm from another part of the preplacodal region (e.g. the prospective otic region) rather than by ectoderm from outside the pre-placodal region. While this has not yet been explored in a systematic way, experimental evidence in amphibians indeed suggests that, at late neural fold stages, one part of the pre-placodal ectoderm can substitute to some degree for another, while at least some ectodermal regions outside of the pre-placodal region cannot (for exceptions see, however, Yntema, 1933; Schlosser and Northcutt, 2001). For example, when the prospective olfactory or lens placodes are replaced by prospective otic placodes at these late stages, olfactory and lens placodes form from the replacing ectoderm, while otic placodes form in the reverse experiment (Yntema, 1933; Ikeda, 1937, 1938; Haggis, 1956; Reyer, 1958; Jacobson, 1963a; Henry and Grainger, 1987; Gallagher et al., 1996; Grainger et al., 1997). This suggests that the replacing ectoderm had already acquired some generic bias for placode development in its original position.

Another line of evidence comes from the formation of ectopic placodes after experimental overexpression of transcription factors implicated in development of specific placodes. Such ectopic placodes are often localized exclusively to cranial ectoderm in the vicinity of other placodes, suggesting that proper placode development requires cooperation of these transcription factors with generic placodal factors expressed specifically within the pre-placodal region. For example, overexpression of Pax6, Six3, or Sox3 (each expressed in the lens placode in addition to several other placodes) results in the formation of ectopic lenses only in cranial ectoderm (Oliver et al., 1996; Altmann et al., 1997; Loosli et al., 1999; Chow et al., 1999; Köster et al., 2000; Lagutin et al., 2001). On the other hand, however, ectopic otic marker gene expression as well as the formation of ectopic otic vesicles after overexpression of FoxI1 (Solomon et al., 2003a), Sox3 (Köster et al., 2000), or

components of various signaling pathways (Gutknecht and Fritzsch, 1990; Lombardo and Slack, 1998; Vendrell et al., 2000; Koebernick et al., 2003) is also found in the trunk and is not cranially restricted, although it is always confined to dorsal ectoderm. The latter findings per se argue neither for nor against a generic placodal bias of the pre-placodal region because it remains currently unclear, whether they are associated with the posterior expansion or ectopic induction of ectoderm with generic placodal bias in these experimental situations or rather reflect the possibility of placode formation independent of generic placodal transcription factors.

Six1/2, Six4/5, and Eya: transcription factors promoting generic aspects of placode development

The panplacodal distribution of *Six1/2*, *Six4/5*, and *Eya* genes and their known effects on development of multiple placodes make these genes the most promising candidates for regulators of generic placodal properties and suggest that their early expression in the pre-placodal ectoderm provides this ectodermal domain with a generic placodal bias. Here, I briefly review how these genes interact and what evidence supports their role in promoting generic placodal properties.

The Six-Eya-Dach-Pax network

Six genes encode homeodomain transcription factors, which bind directly to DNA (reviewed in Relaix and Buckingham, 1999; Kawakami et al., 2000; Wawersik and Maas, 2000; Hanson, 2001; Epstein and Neel, 2003; Kardon et al., 2004; Brugmann and Moody, 2005). Out of the three metazoan subfamilies of *Six* genes (Kawakami et al., 2000; Bebenek et al., 2004), only *Six1/2* and *Six4/5* but not *Six3/6* subfamily genes exhibit panplacodal expression in vertebrates although details of expression differ between species.

Eya genes encode protein tyrosine phosphatases, which act as transcriptional coactivators of *Six* genes (reviewed in Relaix and Buckingham, 1999; Wawersik and Maas, 2000; Hanson, 2001; Epstein and Neel, 2003; Kardon et al., 2004; Rebay et al., 2005). Due to gene duplication, there are four *Eya* genes in vertebrates, whereas invertebrates have only a single *Eya* gene (Xu et al., 1997a; Zimmerman et al., 1997; Duncan et al., 1997; Borsani et al., 1999; Mazet et al., 2005). All *Eya* genes except *Eya3* are widely expressed in cranial placodes, with each placode expressing at least one *Eya* gene, although the distribution of the different paralogues among placodes differs for different species.

In *Drosophila*, it has first been shown that *sine oculis* and *eyes absent*—homologues of the vertebrate *Six1/2* and *Eya* genes, respectively—form a regulatory network essential for compound eye development together with the nuclear protein *dachshund* and the *Pax6* homologue *eyeless* (reviewed in Gehring and Ikeo, 1999; Relaix and Buckingham, 1999; Wawersik and Maas, 2000; Kumar and Moses, 2001a; Pappu and Mardon, 2004; Rebay et al., 2005). Mutants in any of these genes disrupt compound eye development (Cheyette et al., 1994; Serikaku and O'Tousa, 1994; Bonini et al., 1993, 1997;

Mardon et al., 1994; Pignoni et al., 1997; Rayapureddi et al., 2003; Tootle et al., 2003). Conversely, these genes synergize in promoting ectopic eye formation after misexpression (Bonini et al., 1997; Pignoni et al., 1997; Chen et al., 1997; Shen and Mardon, 1997; Halder et al., 1998; Niimi et al., 1999). Because the same set of genes is also coexpressed elsewhere in the embryo, a similar regulatory network may operate in other developmental contexts, although this has not been rigorously analyzed yet (Cheyette et al., 1994; Serikaku and O'Tousa, 1994; Bonini et al., 1993, 1998; Pignoni et al., 1997; Suzuki and Saigo, 2000; Kumar and Moses, 2001b; Fabrizio et al., 2003).

In vertebrates, Six and Eva genes are also coexpressed with Dachshund (Dach) and Pax genes (including Pax6 but also members of other Pax subfamilies such as Pax2) in various tissues. These include the kidney, somites, retina, and several placodes (reviewed in Relaix and Buckingham, 1999; Kawakami et al., 2000; Wawersik and Maas, 2000; Hanson, 2001; Baker and Bronner-Fraser, 2001; Kardon et al., 2004; Streit, 2004). Furthermore, some regulatory interactions between these genes as discovered in Drosophila appear to be preserved in the vertebrate expression domains, although there are also important differences (reviewed in Relaix and Buckingham, 1999; Kawakami et al., 2000; Wawersik and Maas, 2000; Hanson, 2001; Kardon et al., 2004; Rebay et al., 2005). Most importantly, while in Drosophila, the Pax6 homologue eyeless acts as an upstream transcriptional regulator (although subject to feedback regulation) of eya, sine oculis, and dach (Bonini et al., 1997; Halder et al., 1998; Niimi et al., 1999; Bui et al., 2000; Punzo et al., 2002; Pappu et al., 2005), in many tissues of vertebrates including the otic placode Pax genes are not upstream of initial expression of these other genes (Xu et al., 1999; Zheng et al., 2003; Ozaki et al., 2004; Purcell et al., 2005; but see Xu et al., 1997a).

At the core of the network are direct physical interactions between Six and Eya proteins (with conflicting reports for Six3/ 6 subfamily members) and between Eya and Dach (Chen et al., 1997; Pignoni et al., 1997; Heanue et al., 1999; Ohto et al., 1999; Ikeda et al., 2002; Li et al., 2003; Silver et al., 2003; Purcell et al., 2005). The binding of Eya to Six proteins is required for the translocation of Eya into the nucleus where Eya then acts as a transcriptional cofactor of Six (Ohto et al., 1999). Dach acts as another cofactor of Six, although it also appears to be able to bind DNA directly (Ikeda et al., 2002; Kim et al., 2002; Li et al., 2003).

Six transcription factors can function either as transcriptional activators or as transcriptional repressors depending on which cofactors they interact with. Upon binding of Eya to Six, the phosphatase activity of Eya is able to turn Dach from a corepressor to a coactivator of Six (Li et al., 2003), thereby converting Six from a transcriptional repressor into an activator (although there are probably additional mechanisms of Six–Eya synergy; see reviews of Epstein and Neel, 2003; Rebay et al., 2005). In addition, the transcriptional activity of at least Six1/2 and Six3/6 subfamily members can also be modulated by binding to other cofactors including members of the Groucho family of corepressors (some of which are also panplacodally expressed; see, for example, Molenaar et al., 2000) (Kobayashi

et al., 2001; Zhu et al., 2002; López-Rios et al., 2003; Silver et al., 2003; Brugmann et al., 2004). It has therefore been suggested that the mode of action of Six transcription factors is determined by the relative levels of available activating or repressive cofactors (Brugmann et al., 2004; Brugmann and Moody, 2005). The various deficiencies observed in heterozygous human and mouse *Eya* mutants due to haploinsufficiency may be partly attributed to such dependence of normal function on relatively precise protein levels (e.g. Abdelhak et al., 1997; Xu et al., 1999; Zhang et al., 2004).

Promotion of generic placodal properties by Six1/2, Six4/5, and Eya genes

Mutants in mice, humans, and zebrafish suggest an important role of the panplacodally expressed *Six1/2*, *Six4/5*, and *Eya* genes in the development of various placodes. While there is at present little information about *Six2*, *Eya2*, and *Eya3*, mutants of *Six1*, *Six5*, *Eya1*, and *Eya4* have all been associated with defects in placodally derived tissues. As detailed below, *Eya1* and *Six1* represent by far the most thoroughly analyzed cases and have a very similar spectrum of defects in various placodes as well as in other tissues (Table 1). In contrast, *Six4* mouse mutants develop nearly normal and have no obvious placodal

Table 1

Deficits of placodal and pharyngeal derivatives in *Six1* and *Eya1* mutants and morphants

Placodes	Six1	Eyal	Six1/Eya1
Panplacodal markers	+ j	$+^{k}$	
Adenohypophyseal	_	_	+ ^g
Olfactory	+ ^{e,g,h}	$+^{k}$	
Lens	_	$+^{1}$	
Trigeminal	$+^{i}$	$+^{i,k}$	
Profundal	+ ⁱ	$+^{i,k}$	
Otic	+ ^{e-i,m}	+ ^{a,b,d,i,k,n-r}	$+^{f}$
Lateral line	Not determined	+ ^{a,d,k}	
Epibranchial	$+^{f,i}$	+ ^{b,i,k}	
Pharyngeal derivatives (e.g. thymus)	+ ^{e,h,m}	$+^{c,n,o,q}$	

Sources:

- ^a (Whitfield et al., 1996) (zebrafish dogeared mutant of Eya1).
- ^b (Xu et al., 1999) (mouse *Eya1* mutant).
- ^c (Xu et al., 2002a) (mouse Eya1 mutant).
- ^d (Kozlowski et al., 2005) (zebrafish dogeared mutant of Eya1).
- e (Laclef et al., 2003a) (mouse Six1 mutant).
- f (Zheng et al., 2003) (mouse Six1 and Six1/Eya1 mutants).
- ^g (Li et al., 2003) (mouse Six1 and Six1/Eya1 mutants).
- ^h (Ozaki et al., 2004) (mouse Six1 mutant).
- ⁱ (Zou et al., 2004) (mouse Six1 and Eva1 mutants).
- ^j (Brugmann et al., 2004) (*Xenopus Six1* morpholino knockdown).
- ^k Schlosser, unpublished observations (*Xenopus Eyal* morpholino knockdown).
- ¹ (Azuma et al., 2000) (human *Eya1* mutants).
- ^m (Ruf et al., 2004) (human Six1 mutants).
- ⁿ (Namba et al., 2001) (human *Eya1* mutants).
- ^o (Abdelhak et al., 1997) (human Eya1 mutants).
- ^p (Johnson et al., 1999) (mouse Eya1 mutants).
- ^q (Chang et al., 2004) (human *Eya1* mutants).
- r (Friedman et al., 2005) (mouse Eyal mutants).

defects (Ozaki et al., 2001). This absence of placodal defects in Six4 mutants as well as the occurrence of only mild defects in some placodal derivatives of Six1 and Eya1 mutants may be due to compensation by other Six and Eya genes with redundant functions. In favor of this interpretation, recently generated Six1/Six4 double null mutants show more severe developmental defects in the musculoskeletal system and in several other tissues including placodes than each of the single mutants, although the placodal defects have not yet been characterized in detail (Grifone et al., 2005).

Eval and Six1 were both identified as genes underlying particular forms of inherited deafness in humans known as branchio-otic (BO) or branchio-oto-renal (BOR) syndrome, which are associated with branchial or branchial and renal defects, respectively (Vincent et al., 1997; Abdelhak et al., 1997; Namba et al., 2001; Wayne et al., 2001; Kemperman et al., 2002; Chang et al., 2004; Ruf et al., 2004; Zhang et al., 2004). Mutants in Eya4 lead to another non-syndromic form of late-onset-inherited deafness (Wayne et al., 2001; Zhang et al., 2004). Studies of mutant mice and zebrafish suggest that these hearing deficits result partly from middle ear defects but also from deficient development of the inner ear from the otic placode. In homozygous mutants of either Eval or Six1, only small otic vesicles develop which do not form properly organized semicircular canals or a cochlear duct. The sensory areas of the inner ear are either much smaller or completely absent and do not maintain appropriate levels of expression of neuronal determination and differentiation genes such as Neurogenin1 and NeuroD (Whitfield et al., 1996; Johnson et al., 1999; Xu et al., 1999; Laclef et al., 2003a; Li et al., 2003; Zheng et al., 2003; Ozaki et al., 2004; Zou et al., 2004; Friedman et al., 2005; Kozlowski et al., 2005). While a smaller than usual vestibulocochlear ganglion first forms, it later degenerates by apoptosis in the mouse (Zou et al., 2004; Friedman et al., 2005; Kozlowski et al., 2005).

Interestingly, other placodally derived structures also show extensive developmental deficiencies in *Eval* and *Six1* mutants. The sensory epithelium derived from the olfactory placode is reduced or missing in mouse Six1 mutants (Laclef et al., 2003a; Li et al., 2003; Ozaki et al., 2004). Number and size of neuromasts, which develop from lateral line placodes, are reduced in zebrafish dogeared (Eval) mutants (Whitfield et al., 1996; Kozlowski et al., 2005). However, cranial ganglia including those derived from lateral line and epibranchial placodes appear to be normal in dogeared zebrafish (Kozlowski et al., 2005). In mouse Eya1 and Six1 mutants, the trigeminal and profundal ganglia, which receive contributions from placodes and from neural crest, are reduced in size, whereas the geniculate, petrosal, and nodose ganglion derived from epibranchial placodes are either reduced or completely absent and fail to express the neuronal determination and differentiation genes Neurogenin2 and NeuroD (Xu et al., 1999; Zheng et al., 2003; Zou et al., 2004). Furthermore, reducing Eyal protein levels in Xenopus by injection of morpholino antisense oligonucleotides leads to reduced expression of neuronal marker genes such as NeuroD in all neurogenic placodes (Völker, Stammler, and Schlosser, unpublished observations). Similarly,

morpholino-mediated knockdown of Six1 not only reduces widely expressed placodal genes such as *Eya1* and *Sox11* in *Xenopus*, but also perturbs placodal neurogenesis (Brugmann, 2005; Brugmann et al., 2004). Overexpression of *Eya1* together with *Six1*, in contrast, promotes ectopic neurogenesis (Völker, Stammler, and Schlosser, unpublished observations).

Finally, structures derived from non-neurogenic placodes are also affected, although more mildly, in *Eya* and *Six* mutants. Lens defects (cataracts) were found in mutants of *Eya1* (human) and *Six5* (mouse) (Azuma et al., 2000; Klesert et al., 2000), whereas the adenohypophysis is almost normal in mouse single mutants of *Eya1* and *Six1* but drastically reduced in double mutants (Zheng et al., 2003).

Underlying this gamut of developmental effects, there appear to be altogether at least three developmental processes affected by Six and Eya genes, all of which contribute to distinguish the various cranial placodes from the adjacent epidermis (see above). First, placode-derived structures are generally reduced in size or absent in mutants, suggesting that Six1/2 and Eyagenes are involved in size regulation. There appear to be two ways in which size is regulated by these genes and which are deficient in mutants: promotion of cell proliferation and inhibition of apoptosis (Xu et al., 1999, 2002a; Zheng et al., 2003; Li et al., 2003; Zou et al., 2004; Kozlowski et al., 2005; Friedman et al., 2005). The pro-proliferative effect of Six1 and Eya has also been implicated in tumorigenesis and may at least partly be attributable to their stimulating effect on known cell cycle control genes such as CyclinA1 and cMyc (Ford et al., 1998; Li et al., 2003; Coletta et al., 2004; Zhang et al., 2005). The anti-apoptotic effect appears to be strongly concentrationdependent since abnormally high levels of Eya genes also promote rather than inhibit apoptosis (Clark et al., 2002).

Second, the delamination of sensory ganglion cells from neurogenic placodes and morphogenetic movements (e.g. during formation of the membranous labyrinth) are compromised in mutants. Deficiencies in other tissues in *Six1* and *Eya1* mutant mice including thymus and kidney probably also involve morphogenetic in addition to proliferative defects (Xu et al., 1999, 2002a, 2003; Laclef et al., 2003a; Li et al., 2003; Ozaki et al., 2004). This suggests that *Six1/2* and *Eya* genes are involved in the promotion of cell shape changes, which may also underlie the capacity of *Six1* to enhance the invasiveness of cancer cells, thereby promoting metastasis (Yu et al., 2004). Nothing is presently known about the mechanism by which these genes affect morphogenesis and whether it depends on or is independent of their pro-proliferative effect.

Third, certain pathways of cytodifferentiation are blocked in mutants, for instance, myogenesis in the mesoderm (Heanue et al., 1999; Laclef et al., 2003b) and the formation of neurons and sensory cells in the ectoderm indicating that Six1/2 and Eya genes promote particular pathways of cytodifferentiation. Again, the underlying mechanisms remain to be elucidated, but preliminary data indicate that overexpression of Six1 or Eya1 inhibits expression of neuronal differentiation genes in cells with high Eya1 and Six1 protein levels, while coinjection of Six1 and Eya1 promotes ectopic neurogenesis only in cells of

low Eya1 and Six1 protein levels situated immediately adjacent to cells overexpressing high levels of Eya1 and Six1 (Brugmann, 2005; Brugmann and Moody, 2005; Völker, Stammler, and Schlosser, unpublished observations). This suggests that similar to SoxB1 transcription factors (see below) high levels of Six and Eya may promote a proliferative neurogenic precursor state but may be incompatible with neuronal differentiation.

Unfortunately, beyond the few genes mentioned, we still know very little about the target genes through which *Six* and *Eya* genes exert their effects. However, the deficiencies observed in mutants and morphants indicate that *Eya* genes and *Six* genes of the *Six1/2* subfamily (and possibly also of the *Six4/5* subfamily although sufficient data are lacking) regulate proliferation, apoptosis, cell shape changes, and neurogenesis in all placodes and, thereby, promote generic placodal properties shared by different placodes. Together with the expression of *Six1/2, Six4/5*, and *Eya* genes throughout the pre-placodal region and their subsequent panplacodal expression, this suggests that these genes indeed provide the pre-placodal region with a bias towards generic placodal development thereby defining a panplacodal primordium.

It is not clear whether beyond these roles in promoting expression of a number of generic placodal target genes in all placodes, Six and Eya genes have additional and more central functions for placodal development. Six and Eya genes could, for example, also introduce panplacodal bias by defining some kind of generic placodal cell state that predisposes cells to adopt one out of several placodal fates, while preventing adoption of other ectodermal fates. Such a restriction of developmental potential could result, for example, if the positionally appropriate activation of several batteries of genes specific for the different individual placodes would require input of Six and Eya genes together with multiple other and spatially more restricted transcription factors (as discussed below for transcription factors conferring multiplacodal bias). There is presently little evidence to support such a mode of action for Six and Eya genes, but this issue requires additional study.

Other transcription factors promoting placode development

Besides the panplacodally expressed *Six1/2*, *Six4/5*, and *Eya* genes, many other transcription factors are now known to affect placode development. However, some of these transcription factors are not confined to the placodal ectoderm, while others are important for only subsets of placodes or particular placodal cell types. In this section, I will briefly review the roles that some of these transcription factors play for placode development. Due to the combination of *cis*-regulatory analyses with functional studies, we are beginning to understand how different transcription factors interact and form networks, but the emerging picture is still not very clear and I will not attempt to summarize it here. Overviews can be found in several recent reviews dealing with specific placodes, viz. the adenohypophyseal (Sheng and Westphal, 1999; Kioussi et al., 1999a; Dasen and Rosenfeld, 2001; Scully and Rosenfeld, 2002; Savage et al.,

2003; Asa and Ezzat, 2004), olfactory (Beites et al., 2005), lens (Ogino and Yasuda, 2000; Chow and Lang, 2001; Bhattacharyya and Bronner-Fraser, 2004), and otic placodes (Noramly and Grainger, 2002; Fekete and Wu, 2002; Riley and Phillips, 2003; Barald and Kelley, 2004). In a separate section below, I will, however, discuss how the spatiotemporal distribution of these transcription factors can provide important clues of how a diverse array of placodes is specified within the panplacodal primordium.

To allow for a structured overview of placodal transcription factors, they will be tentatively sorted into four functional categories here, although there are certainly no sharp dividing lines between them: (1) transcription factors promoting placodal competence; (2) transcription factors promoting placodal neural progenitors; (3) transcription factors acting as positional markers of placode identity; and (4) transcription factors promoting cytodifferentiation of various placodal cell types.

The first group of transcription factors is expressed widely in the pre-placodal region but extends beyond it and covers the entire non-neural ectoderm (here defined restrictively as all ectoderm, which does not become incorporated into either neural tube or neural crest). These genes, which include Distalless/Dlx homeobox transcription factors (in particular *Dlx3* and *Dlx5*) and some GATA class zinc finger transcription factors (*GATA1*, *GATA2*, *GATA3*), are discussed in more detail below in the section dealing with placode induction. Current evidence suggests that they may play a central role for the development of non-neural ectoderm and may mediate its competence to form various derivatives including epidermis and placodes.

Transcription factors promoting placodal neural progenitors

A second group of transcription factors is approximately expressed in the reverse pattern and besides expression in the pre-placodal ectoderm shows high expression in the neural plate but little expression in the epidermal ectoderm. This group of genes includes Sox2 and Sox3, which together with Sox1 comprise the SoxB1 subfamily of HMG box containing transcription factors, as well as homeobox transcription factors Irx1 to Irx6 (also known as Xiro or Ziro genes in Xenopus and zebrafish, respectively) related to Drosophila Iroquois (Collignon et al., 1996; Rex et al., 1997; Bosse et al., 1997, 2000; Bellefroid et al., 1998; Gómez-Skarmeta et al., 1998; Wood and Episkopou, 1999; Mizuseki et al., 1998; Kishi et al., 2000; Köster et al., 2000; Cohen et al., 2000; Cheng et al., 2001; Wang et al., 2001; Abu-Elmagd et al., 2001; Ishii et al., 2001; Schlosser and Ahrens, 2004; reviewed in Wegner, 1999; Sasai, 2001; Cavodeassi et al., 2001; Gómez-Skarmeta and Modolell, 2002; St. Amand and Klymkowsky, 2001; Kondoh et al., 2004; Pevny and Placzek, 2005). Although these genes show widespread placodal expression, they do not cover the entire pre-placodal ectoderm. In Xenopus, for example, Irx1 and Irx2 genes are absent from the olfactory placode, while Sox2 and Sox3 genes are absent from the profundal and trigeminal placodes.

In the neural plate, *SoxB1* and *Irx* genes appear to have similar functions in maintaining cells in a neural progenitor state, while at the same time preventing terminal neuronal

differentiation (Bellefroid et al., 1998; Mizuseki et al., 1998; Pevny et al., 1998; Gómez-Skarmeta et al., 1998; Kishi et al., 2000; de la Calle-Mustienes et al., 2002; Itoh et al., 2002; Bylund et al., 2003; Graham et al., 2003; Lecaudey et al., 2004; Ferri et al., 2004; Zhao et al., 2004). However, *Sox1* has also been reported to directly promote neuronal differentiation (Pevny et al., 1998; Kan et al., 2004).

The roles of these genes for placode development are less well understood but may be quite similar as concerns placodal neurogenesis. Zebrafish Irx genes are required for neurogenesis in the profundal/trigeminal placode (Itoh et al., 2002). Preliminary data also indicate that Sox3 may be similarly required for neurogenesis in at least the epibranchial placodes, while overexpression of Sox3 appears to prevent migration and differentiation of neurons from different neurogenic placodes (Abu-Elmagd et al., 2001; Scotting, personal communication; Schlosser, unpublished observations). Moreover, SoxB1 genes and probably Irx genes as well (although this requires more thorough analysis) are strongly expressed in the placodal ectoderm but downregulated as soon as placodally derived neurons migrate away and express neuronal determination and differentiation genes (Abu-Elmagd et al., 2001; Schlosser and Ahrens, 2004). Taken together, this suggests that SoxB1 and Irx genes are likely to be important for regulating placodal neurogenesis probably by promoting a neural progenitor state similar to their function in the neural plate. However, neither Irx nor SoxB1 genes are expressed in all neurogenic placodes, suggesting that neuronal progenitor states may be regulated differently in different placodes.

In addition, *Irx* and *SoxB1* genes are likely to play other and possibly more fundamental roles in placodal development, which require further investigation. As discussed in more detail below, the exclusion of some Irx genes from the rostralmost neural plate and placodes makes them attractive candidates for defining a posterior equivalence group of placodes. Irx1 was indeed shown to be required for maintaining expression of various placodal transcription factors including the panplacodal factor Six1 and transcription factors with more restricted expression (Sox2, Pax2), while overexpression of Irx1 leads to an expansion of the placodal expression domains of these genes (Glavic et al., 2004). Overexpression of Sox2 even results in ectopic expression of Eyal and Pax6 and in ectopic formation of lens and otic placodes (Köster et al., 2000). In the lens placode, SoxB1 genes have been shown to cooperate with Pax6 and L-Maf in the regulation of lens-specific cytodifferentiation including direct regulation of crystallin expression (Kamachi et al., 1998, 2001; Muta et al., 2002; Shimada et al., 2003; reviewed in Bhattacharyya and Bronner-Fraser, 2004; Cvekl et al., 2004; Kondoh et al., 2004), while in the otic placode Sox2 is required for sensory organ formation (Kiernan et al., 2005).

Transcription factors acting as positional markers of placode identity

A third, large and heterogeneous group of placodal transcription factors comprise genes which are confined to

relatively large but anteroposteriorly (and sometimes dorsoventrally) restricted subregions of the panplacodal primordium (plus possibly other parts of the ectoderm). These genes often continue to be expressed in subsets of placodes at later stages, and they are required for development of the placodes, in which they are expressed. Thus, they are candidates for positional markers involved in defining placode identity. Often, these transcription factors have a relatively broad spectrum of effects on placodal development and regulate proliferation of progenitor cells, differentiation, and morphogenesis in a positionspecific manner. Transcription factors of this category comprise various homeobox (viz. Otx, Emx, Six3/6, ANF, Pitx, and Pax genes), winged helix (Fox), and T-box (Tbx) transcription factors. As a caveat, it must, however, be pointed out that many of these genes (and Otx genes in particular) are expressed in large domains extending beyond the panplacodal primordium and often are essential for development of a number of additional tissues. Therefore, some of their documented effects on placode development may be indirect, and additional studies are needed to clearly distinguish between direct and indirect modes of action.

Otx genes

Otx homeobox genes show anteriorly restricted expression in all germ layers from gastrulation onwards. Their ectodermal expression includes the prospective fore- and midbrain and the prospective adenohypophyseal, olfactory, and lens placodes; at later stages, they are also expressed in the otic placode (Simeone et al., 1993; Pannese et al., 1995; Kablar et al., 1996). Otx genes control a multitude of unrelated target genes (including, for example, pituitary hormones; Acampora et al., 1998) and are thought to play a central role in head specification (reviewed in Acampora et al., 2000; Boyl et al., 2001; Boncinelli and Morgan, 2001; Simeone and Acampora, 2001; Simeone et al., 2002). Blocking Otx2 function in early embryogenesis results in lack of many head structures including the fore- and midbrain and the adenohypophyseal, olfactory, and lens placodes (Acampora et al., 1995; Matsuo et al., 1995; Gammill and Sive, 2001) and in deficient development of the otic vesicle (Acampora et al., 1996; Fritzsch et al., 2001).

Emx genes

Emx homeobox genes show a more restricted anterior expression than Otx genes in the prospective forebrain as well as in the olfactory and otic placodes (Simeone et al., 1992; Morita et al., 1995; Kablar et al., 1996; Kawahara and Dawid, 2002). They have multiple roles in regulating proliferation, differentiation, migration, and regional subdivision of the forebrain (reviewed in Cecchi and Boncinelli, 2000; Cecchi, 2002). Placodal defects of *Emx2* mutants (Pellegrini et al., 1996; Yoshida et al., 1997) have not been well characterized, but the failure of the olfactory nerve to connect to the olfactory bulbs in such mutants is possibly due to deficient axon guidance of placode-derived olfactory receptor neurons since *Emx* proteins are known to be localized to these axons, where they regulate protein translation (Briata et al., 1996; Nedelec et al., 2004).

Six3/6 genes

In contrast to the Six1/2 and Six4/5 genes already discussed above, expression of Six3/6 is restricted to the anterior neural plate (prospective forebrain) and the immediately adjacent nonneural ectoderm including the prospective adenohypophyseal, olfactory, and lens placodes (Oliver et al., 1995b; Loosli et al., 1998; Kobayashi et al., 1998; Zuber et al., 1999; Jean et al., 1999; López-Rios et al., 1999; Zhou et al., 2000; Bernier et al., 2000). Six3/6 genes promote the development of forebrain, retina, and the rostral placodes in multiple ways: they inhibit Wnt and BMP signaling (Lagutin et al., 2003; Gestri et al., 2005); promote cell proliferation by various mechanisms including sequestering of the cell cycle inhibitor Geminin and transcriptional repression of the cell cycle inhibitor p27Kip1 (Kobayashi et al., 1998; Zuber et al., 1999; Li et al., 2002; Del Bene et al., 2004; Gestri et al., 2005); delay neuronal differentiation (Gestri et al., 2005); and bias cell fate choices (Oliver et al., 1996; Loosli et al., 1999; Bernier et al., 2000; Lagutin et al., 2001). Loss of function of either Six3 or Six6 results in loss or size reduction of forebrain, retina, and the adenohypophyseal, olfactory, and lens placodes (Zuber et al., 1999; Li et al., 2002; Carl et al., 2002; Lagutin et al., 2003).

ANF genes

The ANF homeobox genes (also known as HesX1 or Rpx in mammals) also show anteriorly restricted expression at neural plate stages in the prospective forebrain and in adjacent ectoderm of the anterior neural folds including the prospective adenohyophyseal, olfactory, and possibly lens placodes, but their placodal expression soon becomes confined to the adenohypophyseal placode (Zaraisky et al., 1992, 1995; Mathers et al., 1995; Kazanskaya et al., 1997; Ermakova et al., 1999; Hermesz et al., 1996; Thomas and Beddington, 1996). ANF genes have been implicated in both patterning and size regulation of forebrain and adenohypophysis and need to be downregulated in order to permit cytodifferentiation of neurons or of several of the adenohypophyseal neuroendocrine cell types (Ermakova et al., 1999; Dasen et al., 2001). ANF (HesX1) mutants accordingly show strong reduction or aberrant development of the forebrain, adenohypophyseal, olfactory, and lens placodes (Dattani et al., 1998).

Pitx genes

Pituitary homeobox (*Pitx*) genes are expressed (with some rather subtle differences between the different paralogues) in the ectoderm immediately rostral to the neural plate including the prospective adenohypophyseal, olfactory, and lens placodes (Semina et al., 1996; Gage and Camper, 1997; Lanctot et al., 1997; Hollemann and Pieler, 1999; Essner et al., 2000; Chang et al., 2001; Schweickert et al., 2001; Pommereit et al., 2001; Boorman and Shimeld, 2002; Uchida et al., 2003; Zilinski et al., 2005; Dutta et al., 2005). Besides their function in regulating left–right asymmetries, limb development, and craniofacial development, vertebrate *Pitx* genes play important roles for adenohypophyseal and lens development (Lamonerie et al., 1996; Szeto et al., 1996, 1999; Lin et al., 1999; Gage et al., 1999; Suh et al., 2002; Kioussi et al., 2002; Briata et al., 2003;

Shi et al., 2005; Dutta et al., 2005). They promote proliferation of different adenohypophyseal cell populations, as well as the expression of various adenohypophysis-specific transcription factors and hormones, and loss of *Pitx* genes results in reduced expression of many pituitary transcription factors, reduced numbers of adenohypophyseal cells, and in compromised lens development.

Msx genes

In contrast to the genes discussed so far, Msx homeobox genes show relatively widespread expression in the lateral neural plate, neural crest, and non-neural ectoderm including many prospective placodes with some interspecific differences (for example, Msx1 is excluded from adenohypophyseal and olfactory placodes in Xenopus but not in mice) (Hill et al., 1989; Robert et al., 1989; Mackenzie et al., 1991; Ekker et al., 1992; Maeda et al., 1997; Suzuki et al., 1997; Streit and Stern, 1999a; Feledy et al., 1999; Gong and Kiba, 1999; Onitsuka et al., 2000). As direct BMP target genes with antineural effects, Msx genes have been implicated in early ectodermal patterning (Suzuki et al., 1997; Feledy et al., 1999). In Xenopus, where Msx genes are excluded from the anterior ectoderm, they inhibit anterior development and promote epidermal development in non-neuralized ectoderm but neural crest development in neuralized ectoderm (Suzuki et al., 1997; Gong and Kiba, 1999; Feledy et al., 1999; Yamamoto et al., 2001; Tribulo et al., 2003; Monsoro-Burg et al., 2005). They are thought to exert their effects by multiple mechanisms such as preventing exit from the cell cycle and promoting apoptosis (Marazzi et al., 1997; Hu et al., 2001; Liu et al., 2004; Tribulo et al., 2004). Loss of Msx function results in complex craniofacial defects, but despite strong Msx expression in several placodes (e.g. otic placode), no severe placodal defects have been described in mutants (Satokata and Maas, 1994; Satokata et al., 2000; Houzelstein et al., 1997; reviewed in Bendall and Abate-Shen, 2000; Alappat et al., 2003) so the role of Msx for placodal development is currently unclear.

Pax genes

There are four different subfamilies of Pax genes, transcription factors with a paired-type DNA-binding domain (Dahl et al., 1997; Miller et al., 2000; Chi and Epstein, 2002). Members of the Pax2/5/8, Pax3/7, and Pax6 subfamilies, but not of the Pax1/9 subfamily, play important roles for placode development. Pax genes affect multiple developmental processes including proliferation, cytodifferentiation, cell adhesion, and signaling, and while they generally tend to maintain an undifferentiated state, they are also known to promote the formation of specific subpopulations of differentiated cells (reviewed in Mansouri et al., 1996; Dahl et al., 1997; Dressler and Woolf, 1999; Mansouri, 1998; Gehring and Ikeo, 1999; Underhill, 2000; van Heyningen and Williamson, 2002; Simpson and Price, 2002; Epstein, 2000; Chi and Epstein, 2002). Because Pax genes interact in a regulatory network with the panplacodally expressed Eva, Six, and Dach genes but are themselves expressed in a more regionally restricted manner, they were proposed to have a special role in conferring placode identity (Baker and Bronner-Fraser, 2000, 2001; Streit, 2002, 2004). However, since each *Pax* gene is still expressed in multiple placodes (see Schlosser and Ahrens, 2004), *Pax* genes alone cannot suffice to specify placode identity but must cooperate with other transcription factors (see below).

Pax6 is widely expressed in the neural plate including the prospective forebrain as well as in the adjacent rostral non-neural ectoderm that will give rise to the adenohypophyseal, olfactory, lens, and trigeminal placodes (Püschel et al., 1992a; Li et al., 1994; Grindley et al., 1995; Hirsch and Harris, 1997a; Murakami et al., 2001; Schlosser and Ahrens, 2004). Pax6 promotes the formation of rostral ectodermal structures such as forebrain, eyes, and rostral placodes (reviewed in Gehring and Ikeo, 1999; van Heyningen and Williamson, 2002; Simpson and Price, 2002; Kondoh et al., 2004; Bhattacharyya and Bronner-Fraser, 2004). For example, Pax6 directly binds to the enhancer of various lens crystallin genes and in combination with other transcription factors regulates their expression (review in Piatigorsky, 1998; Cvekl et al., 2004; Kondoh et al., 2004). While Pax6 overexpression leads to ectopic formation of lens placodes (Altmann et al., 1997; Chow et al., 1999), Pax6 mutants have reduced or missing lens and olfactory placodes due to deficient proliferation and differentiation and altered adhesive properties, which lead to the exclusion of Pax6-/- cells from placodes (Hogan et al., 1986; Hill et al., 1991; Grindley et al., 1995; Ashery-Padan et al., 2000; van Raamsdonk and Tilghman, 2000; Dimanlig et al., 2001; Collinson et al., 2001, 2003). In addition, the adenohypophyseal placode develops abnormally in Pax6 mutants due to patterning defects (ventralization resulting in decrease of lactotropes and somatotropes) (Bentley et al., 1999; Kioussi et al., 1999b).

Pax3 and Pax7 genes are expressed in the lateral neural plate (subsequently in dorsal neural tube) and neural crest as well as in the profundal placode (Goulding et al., 1991; Bang et al., 1997, 1999; Stark et al., 1997; Seo et al., 1998b; Baker et al., 1999; McCauley and Bronner-Fraser, 2002; Schlosser and Ahrens, 2004). Besides playing crucial roles in myogenesis, dorsal neural tube patterning, and at various stages of neural crest development (reviewed in Mansouri, 1998; Epstein, 2000; Chi and Epstein, 2002), Pax3 may be important for establishing neuron identity in the profundal placode (Baker and Bronner-Fraser, 2000; Baker et al., 2002). In Pax3 mutants, various cranial ganglia are strongly hypoplastic including the profundal ganglion (i.e. the ophthalmic division of the trigeminal ganglionic complex), but to what extent this is due to defects of neural crest or profundal placode development has not been determined (Epstein et al., 1991; Tremblay et al., 1995).

The three vertebrate genes of the *Pax2/5/8* subfamily (*Pax2*, *Pax5*, *Pax8*) show partly overlapping and partly distinct expression at multiple sites and are involved in the development of many different structures including the retina, kidney, thyroid, thymus, midbrain–hindbrain boundary, and spinal cord (reviewed in Dahl et al., 1997; Dressler and Woolf, 1999; Chi and Epstein, 2002). In addition, *Pax2* and *Pax8* are expressed in the posterior placodal area at neural plate stages, with expression continuing into the otic and epibranchial placodes (Püschel et al., 1992b; Rinkwitz-Brandt et al., 1996;

Heller and Brändli, 1997, 1999; Herbrand et al., 1998; Pfeffer et al., 1998; Groves and Bronner-Fraser, 2000; Streit, 2002; Lawoko-Kerali et al., 2002; Li et al., 2004a; Schlosser and Ahrens, 2004). Pax2 has been suggested to control epibranchial neuron identity (Baker and Bronner-Fraser, 2000), and Pax2 and Pax8 have crucial and partially redundant functions in otic placode development (reviewed in Whitfield et al., 2002; Noramly and Grainger, 2002; Riley and Phillips, 2003). No otic defects were reported for Pax8 mutants (Mansouri et al., 1998), but Pax2 mutants in the mouse exhibit compromised morphogenesis, sensory organ formation, and neurogenesis from the medial otic placode (Favor et al., 1996; Torres et al., 1996; Burton et al., 2004), while Pax2 mutants in the zebrafish are merely deficient in lateral inhibition during hair cell development (Riley et al., 1999). In contrast, the otic placode fails to form in zebrafish if both Pax8 and Pax2 are compromised (Hans et al., 2004; Mackereth et al., 2005).

Fox genes

Several members of the large *Fox* family of winged helix transcription factors are placodally expressed and play important roles for various aspects of placode development (review in Carlsson and Mahlapuu, 2002; Lehmann et al., 2003; Pohl and Knöchel, 2005). The *FoxE* subfamily members *FoxE3* and *FoxE4* (also known as *Lens1*) are expressed in the lens placode where they promote proliferation and prevent differentiation, which occurs prematurely in mutants (Kenyon et al., 1999; Blixt et al., 2000; Brownell et al., 2000; Zilinski et al., 2004).

The *FoxG* subfamily member *FoxG1* (previously known as *BF-1*) is expressed in the anteriormost neural plate, giving rise to the telencephalon and in all placodes and was shown to be required to maintain proliferative neural progenitors in the ventral telencephalon and olfactory placode and to affect neuronal cell fate choices (Tao and Lai, 1992; Xuan et al., 1995; Toresson et al., 1998; Bourguignon et al., 1998; Dou et al., 1999; Hatini et al., 1999; Hardcastle and Papalopulu, 2000; Ohyama and Groves, 2004; Hanashima et al., 2004; Muzio and Mallamaci, 2005; Martynoga et al., 2005).

FoxI subfamily members are expressed in various subsets of posterior placodes (with some interspecific differences) including otic, lateral line, and epibranchial placodes (Hulander et al., 1998; Pohl et al., 2002, 2005; Nissen et al., 2003; Solomon et al., 2003a,b; Lee et al., 2003; Schlosser and Ahrens, 2004). In zebrafish, overexpression of *FoxI1* induces ectopic expression of otic and epibranchial placodal markers (Lee et al., 2003; Solomon et al., 2003a), while *FoxI1* mutants are deficient in the formation of viscerosensory neurons from epibranchial placodes (Lee et al., 2003) and have severely reduced otic placodes probably partly due to the failure of otic *Pax8* induction (Nissen et al., 2003; Solomon et al., 2005). However, mouse mutants of *FoxI1* have much milder defects of otic placode development (Hulander et al., 1998, 2003).

T-box genes

Finally, several *T-box* genes (reviewed in Papaioannou, 2001; Wilson and Conlon, 2002; Showell et al., 2004; Naiche et

al., 2005) are involved in placode development. Tbx1 is expressed in the pharyngeal pouches, pharyngeal arches, and in the otic placode, and its disruption causes complex craniofacial defects (known as DiGeorge syndrome in humans) which include hypoplasia of the inner ear and reduction of its sensory areas (Bollag et al., 1994; Chapman et al., 1996; Jerome and Papaioannou, 2001; Sauka-Spengler et al., 2002; Vitelli et al., 2003; Piotrowski et al., 2003; Raft et al., 2004; Moraes et al., 2005). In the otic placode, Tbx1 has been suggested to favor sensory organ differentiation at the expense of neuronal differentiation (Vitelli et al., 2003; Raft et al., 2004). Little is known about the role of other placodally expressed *T-box* genes for placode development, such as Tbx2, Tbx3, and Eomesodermin (Chapman et al., 1996; Gibson-Brown et al., 1998; Ryan et al., 1998; Dheen et al., 1999; Ruvinsky et al., 2000; Takabatake et al., 2000, 2002; Schlosser and Ahrens, 2004).

In summary, the "positional" transcription factors discussed in this section tend to be expressed early and often in relatively large regions. They usually have multiple effects on placodal development, affecting proliferation, differentiation, and morphogenesis. Many of these transcription factors (e.g. *Six3/6*, many *Pax* and *Fox* genes) keep cells in an undifferentiated state, although they may nevertheless bias cell fate decisions. This happens usually in cooperation with other transcription factors with different spatiotemporal expression patterns allowing the spatially restricted activation of transcription factors, which are specifically dedicated to the control of particular pathways of cytodifferentiation. This latter category of transcription factors will be discussed next.

Transcription factors promoting cytodifferentiation of placodal cell types

The fourth and final group of transcription factors comprise proteins, which regulate particular pathways of cytodifferentiation. They are encoded by a large number of basic helix–loop– helix (bHLH)-related genes, LIM-, POU-, and Paired like-class homeobox genes, as well as basic leucine zipper (bZIP) genes and will be summarized here, taking the different placodal cell types in turn.

Cytodifferentiation in the lens placode

Determination and differentiation of lens fibers require many different transcription factors. However, of all transcription factors, which are essential for lens fiber differentiation, only L-Maf and several other bZIP proteins have a lens-specific expression and, thus, are thought to play a central role for lens fiber development (reviewed in Ogino and Yasuda, 2000; Chow and Lang, 2001; Reza and Yasuda, 2004; Cvekl et al., 2004; Bhattacharyya and Bronner-Fraser, 2004). In particular, these genes are known to cooperate with broadly expressed transcription factors like Pax6 and SoxB1 in the activation of various crystallins.

Cytodifferentiation in the adenohypophyseal placode

Cytodifferentiation of the various neuroendocrine cells of the adenohypophysis is likewise governed by combinations of several transcription factors (reviewed in Watkins-Chow and Camper, 1998; Sheng and Westphal, 1999; Kioussi et al., 1999a; Dasen and Rosenfeld, 2001; Scully and Rosenfeld, 2002; Savage et al., 2003; Zhu and Rosenfeld, 2004; Asa and Ezzat, 2004). Some of these transcription factors such as Six3, ANF (HesX1/Rpx), Pitx, Pax6, and the LIM homeodomain proteins Lhx3, Lhx4, and Islet1 have general roles in early development of the adenohypophysis but later show spatially restricted expression and may participate in cell type specification. Other transcription factors are more specifically required for particular subpopulations of adenohypophyseal cells. For example, the POU class homeobox transcription factor Pit1 is required for the differentiation of somatotropes, lactotropes, and thyrotropes; the zinc finger transcription factor GATA2 is required for the differentiation of gonadotropes and thyrotropes; the T-box transcription factor Tbx19 (T-pit) and the bHLH transcription factor NeuroD are required for the differentiation of melanotropes and corticotropes; and the steroid receptor FTZ-F1 (SF-1) is required for gonadotropes.

Cytodifferentiation in the neurogenic placodes

Cytodifferentiation of placodal neurons and sensory cells is now known to be under the control of transcription factors of the bHLH superfamily related to the *Drosophila atonal* and *achaete–scute* genes as is the case in the neural plate and neural crest. Some of these genes operate as neuronal determination (or proneural) genes, which are expressed in proliferative cells and initiate a cascade of transcription factors leading to neuronal specification.

Many proneural genes play a dual role in determining a generic neuronal fate and participating in the assignment of neuronal or sensory subtype identity (reviewed in Guillemot, 1999; Brunet and Ghysen, 1999; Hassan and Bellen, 2000; Bertrand et al., 2002). Consequently, specification of different placodally derived neuronal and sensory cell types depends on different proneural genes. Neurogenin1 (Ngn1) or Neurogenin2 (Ngn2), for example, are expressed in different subsets of neurogenic placodes and are essential for the determination of placodal neurons, although details differ between species (Fode et al., 1998; Ma et al., 1998, 2000; Schlosser and Northcutt, 2000; Cau et al., 2002; Begbie et al., 2002; Andermann et al., 2002; reviewed in Korzh and Strähle, 2002; Bertrand et al., 2002). In mammals, Ngn1 is involved in neuronal determination in the profundal/trigeminal and otic placodes, while Ngn2 is required for determination of epibranchial-placode-derived neurons (Ma et al., 1998, 2000; Fode et al., 1998). However, other neuronal determination genes are involved in determination of olfactory receptor neurons and otic hair cells, viz. Ash1 (e.g. Mash1 in the mouse) and Ath1 (e.g. Math1 in the mouse), respectively (Cau et al., 1997; Bermingham et al., 1999; Chen et al., 2002; Murray et al., 2003; Woods et al., 2004; reviewed in Bertrand et al., 2002; Kelley, 2002; Bryant et al., 2002; Gao, 2003; Beites et al., 2005).

On the one hand, neuronal determination genes activate bHLH genes that control generic aspects of neuronal differentiation, such as *NeuroD* (reviewed in Lee, 1997; Cho and Tsai, 2004), which is expressed not only in various parts of the neural tube but also in all neurogenic placodes (Schlosser and Northcutt, 2000; Andermann et al., 2002). Other types of helix-loop-helix (HLH) genes, viz. the HES (hairy/enhancer of split related), Id, and COE (Collier/Olf1/EBF) genes, also have expression domains in neural tube, neural crest, and placodes (e.g. Wang et al., 1997; Garel et al., 1997; Jen et al., 1997; Dubois et al., 1998; Bally-Cuif et al., 1998; Vasiliauskas and Stern, 2000; Koyano-Nakagawa et al., 2000; Cau et al., 2000; Zheng et al., 2000; Zine et al., 2001; Pozzoli et al., 2001; Kee and Bronner-Fraser, 2001a,b, 2005; Burns and Vetter, 2002; Liu and Harland, 2003; Meulemans et al., 2003; Light et al., 2005). These genes antagonize (e.g. Hes1, Id genes; reviewed in Yokota, 2001; Bertrand et al., 2002; Tzeng, 2003; Ruzinova and Benezra, 2003) or synergize (e.g. Hes6, COE genes; reviewed in Dubois and Vincent, 2001; Bertrand et al., 2002; Liberg et al., 2002) with neuronal determination and differentiation genes.

On the other hand, neuronal determination genes activate further transcription factors that control neuronal or sensory subtype specification, but this requires cooperation with other placodally expressed transcription factors in particular LIMclass (e.g. Islet1; Korzh et al., 1993; Li et al., 2004b; Radde-Gallwitz et al., 2004) and Paired like-class (e.g. Phox2a, Phox2b; Tiveron et al., 1996; Pattyn et al., 1997; Guo et al., 1999; Begbie et al., 2002; Talikka et al., 2004) homeodomain transcription factors (reviewed in Bertrand et al., 2002; Shirasaki and Pfaff, 2002; Brunet and Pattyn, 2002; Allan and Thor, 2003). Among the latter are, for example, POU class IV homeodomain transcription factors such as Brn3a and Brn3c, which promote maturation and survival of neurons in the trigeminal and vestibulocochlear ganglia and hair cell differentiation, respectively (Erkman et al., 1996; McEvilly et al., 1996; Xiang et al., 1997, 1998; Huang et al., 1999, 2001; Eng et al., 2004; reviewed in Latchman, 1999; Bryant et al., 2002; Gao, 2003).

Specification of different placodes in the panplacodal primordium—insights from *Xenopus*

Recently, increasing availability of data on gene expression during early placode development revealed a surprising molecular complexity in the early panplacodal primordium indicating that, despite its apparent morphological uniformity and its uniform expression of transcription factors promoting generic placodal development, it is already divided into various molecularly non-equivalent subdomains. In particular, many transcription factors that are restricted to subsets of placodes at subsequent stages already show properly regionalized expression at neural plate stages (for example, the various *Pax* genes discussed above). This suggests that the panplacodal primordium is already subdivided at neural plate or early neural fold stages into subregions differentially biased for several different types of placodes.

To elucidate the potential role of various transcription factors in placode specification, it is useful to consider their spatiotemporal expression pattern in relation to the developing placodes in some detail. I will do this here focusing on Xenopus for which both a detailed description of placode development and extensive information on gene expression are available (see Figs. 3-6 and Schlosser and Ahrens, 2004; Schlosser and Northcutt, 2000). Most of the transcription factors described have also been cloned from chick, mouse, and zebrafish and, generally, have similar distributions there (see above). It must be emphasized that we still know relatively little about the precise role of many of these transcription factors during placode development and how they interact with each other. As summarized above, most of them have been shown experimentally to be required for some aspects of placode development, but, in many cases, it still needs to be clarified, which of these effects are directly due to their activity within pre-placodal and placodal cells rather than in adjacent tissues. At present, therefore, most of the transcription factors discussed should merely be considered promising candidates for factors, which probably participate at some level in the regulatory networks underlying placode specification.

Overview of placode development in Xenopus

Fig. 4 summarizes placodal development in *Xenopus* (Schlosser and Ahrens, 2004; Schlosser and Northcutt, 2000) and relates some of the molecular subdivisions of the panplacodal primordium at neural plate and fold stages (Figs. 3C, 4A, B) to the morphologically recognizable units, which become apparent after neurulation. Immediately after neural tube closure, all prospective placodes with exception of the lens are thickened. However, at early tailbud stages, the various placodal thickenings are still very closely apposed to each other (Figs. 4C, D). The olfactory placode and the stomodeal thickening, which includes the prospective adenohypophyseal placode, together form a contiguous anterior placodal area. Profundal and trigeminal placodes are fused but can be distinguished by their distinct gene expression patterns. Finally, a posterior placodal area can be recognized probably containing the prospective otic, lateral line, epi- and hypobranchial placodes. The posterior placodal area initially forms two ventral

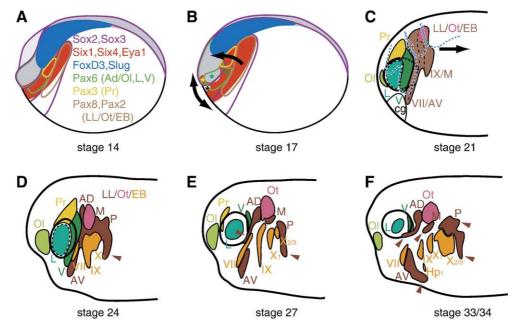


Fig. 4. Summary of placodal development in Xenopus laevis in lateral views (modified from Schlosser and Ahrens, 2004; stages after Nieuwkoop and Faber, 1967). (A, B) Gene expression domains (colored outlines) during neural plate (A) and neural fold stages (B). The panplacodal primordium (red) is apposed to the neural plate (gray) anteriorly and to neural crest (blue) laterally (see also Fig. 3C). Arrows in panel B indicate shifts of placodal expression domains due to neural fold elevation (dorsal shift) and wedge-like expansion of anterior ectoderm accompanying the formation of the optic vesicles. Green stars identify three areas of Pax6 expression that will contribute (from anterior to posterior) to adenohypophyseal and olfactory placode (light green), lens placode (blue green), and trigeminal placode (dark green). Six1 and Eya1 expressions are downregulated at neural fold stages in the regions of prospective lens placode and cement gland (black asterisk). (C-F) Development of placodes after neural tube closure until late tailbud stages. Drawings are based on reconstructions of ectodermal thickenings from serial sections (after Schlosser and Ahrens, 2004; Schlosser and Northcutt, 2000). The adenohypophyseal placode, which is located medial to the ventral part of the olfactory placode, is not shown in these lateral views. Various green colors identify placodes or prospective placodes expressing Pax6, yellow identifies the profundal placode expressing Pax3, and brown, pink, and orange jointly identify the posterior placodal area expressing Pax2 and Pax8, with pink being reserved for the subregion forming the otic placode/ vesicle and orange for the subregions forming the epibranchial placodes. At stage 21, the posterior placodal area is divided into an anterior and a posterior subregion of thickened ectoderm, separated ventrally by an indentation and dorsally by a region of thinner ectoderm (between broken black lines), while the prospective otic placode (pink) is identifiable as a particularly prominent thickening. The broken blue lines in panel C indicate neural crest streams as reconstructed from serial sections (Schlosser and Northcutt, 2000). The arrow in panel C indicates that the posterior placodal area expands posteriorly at early tailbud stages. Brown arrowheads in panels D-F indicate developing lateral line primordia. Abbreviations: Ad/OI: anterior placodal area, from which adenohypophyseal (Ad) and olfactory placodes (OI) develop; AV: anteroventral lateral line placode; cg: cement gland; Hp1: first hypobranchial placode; L: prospective lens placode (hatched outline), lens placode or lens (invagination of placode between stage 27 and 33/34); LL/Ot/EB: posterior placodal area, from which lateral line (LL), otic (Ot), and epibranchial (EB) placodes develop; M: middle lateral line placode; OI: olfactory placode; Ot: otic placode or vesicle (invagination of placode between stage 24 and 33/34); P: posterior lateral line placode; Pr: profundal placode; V: trigeminal placode; VII: facial epibranchial placode; IX: glossopharyngeal epibranchial placode; X₁: first vagal epibranchial placode; X_{2/3}: second and third vagal epibranchial placodes (fused).

References	I Gómez-Skarmeta et al. (1998): Xiro1, Glavic et al. (2004): Xiro1, Schlosser and Ahrens (2004): Xiro1	Gomez-Skarmeta et al. (1998): Xiro2	Bellefroid et al. (1998): Xiro3	N von Bubnoff et al. (1996), C Tour et al. (2001, 2002) E	Pannese et al. (1995), Kablar et al. (1996), Zygar et al. (1998)	Kablar et al. (1996)	Vignali et al. (2000)	Pannese et al. (1998)	N Bayramov et al. (2004)	Zaraisky et al., (1992, 1995), Ermakova et al. (1999), Mathers et al., (1995)	Hollemann and Pieler (1999), Chang et al., (2001), Schweickert et al. (2001)	Schweickert et al. (2001)	Pommereit et al., (2001)	Maeda et al. (1997), Suzuki et al. (1997), Feledy et al. (1999), Schlosser and Ahrens (2004)	Gong and Kiba (1999), Onitsuka et al. (2000)	N Hirsch and Harris (1997a), Zygar et al., (1998), Schlosser and Ahrens (2004)	N Bang et al. (1997, 1999), C Schlosser and Ahrens (2004)
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References	Pandur and Moody (2000), Ghanbari et al. (2001), Schlosser and Ahrens (2004)	Ghanbari et al. (2001)	Ghanbari et al. (2001), Schlosser and Ahrens (2004)	Zhou et al. (2000), Ghanbari et al. (2001)	Zuber et al. (1999), Ghanbari et al .(2001)	David et al. (2001), Schlosser and Ahrens (2004)	Molenaar et al. (2000)	Dirksen et al. (1994): XdII2, Feledy et al. (1999), Luo et al. (2001a,b), Schlosser and Ahrens (2004)	Papalopulu and Kintner (1993): Xdll3, Luo et al. (2001a,b)	Luo et al. (2001a)	Kelley et al. (1994), Walmsley et al. (1994), Read et al. (1998)	Kim et al. (2003)	Huanget al. (2005)	Mizuseki et al. (1998), Penzel et al. (1997), Zygar et al. (1998), Schlosser and Ahrens (2004)	Brugmann et al. (2004)	Spokony et al. (2002), Saint-Germain et al. (2004)	Honoré et al. (2003), Aoki et al.(2003)
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References	Ma et al. (1996), Schlosser and Northcutt (2000) Schlosser and Ahrens (2004)	Lee et al. (1995), Schlosser and Northcutt (2000)	Kim et al. (1997): their "trigeminal" expression is most likely anterior lateral line	Takebayashi et al. (1997), Burns and Vetter (2002)	Kanekar et al. (1997), Burns and Vetter (2002)	Dubois et al. (1998); COE2, Burns and Vetter (2002)	Pozzoli et al.(2001), Burns and Vetter (2002)	Zhang et al., (1995): Idlla, Liu and Harland (2003)	Wilson and Mohun (1995): Idx, Zhang et al., (1995): Idla, Liu and Harland (2003)	Liu and Harland (2003)	Koyano-Nakagawa et al. (2000)	Deblandre et al. (1999)	Turner and Weintraub (1994), Davis et al. (2001), Tsuji et al. (2003)	Pichon et al. (2002)	Bellefroid et al. (1996), Schlosser and Northcutt (2000)	Hutcheson and Vetter (2001)	Hirsch and Harris (1997b)
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extensions, which most likely give rise to the facial and glossopharyngeal epibranchial placode, the first hypobranchial placode, and an anterior subset of lateral line placodes (Fig. 4C). In contrast, the vagal epibranchial placodes, the second hypobranchial placode, and a posterior subset of lateral line placodes probably arise from a secondary posterior expansion of the posterior placodal area, which forms only at mid-tailbud stages (Fig. 4D). Separate placodes—recognizable either as distinct thickenings or as areas of disrupted basement membranes—develop from these placodal thickenings at later tailbud stages (Figs. 4E, F) and subsequently give rise to the various sensory organs and ganglia as described above.

Transcription factor expression during early Xenopus placode development

The expression pattern of a large number of transcription factors in various subregions of the panplacodal primordium at neural plate/fold stages and their subsequent expression in the different placodes a tailbud stages are summarized in Fig. 5 (which also lists the relevant references). Fig. 6 gives a schematic overview over how their expression domains are positioned relative to each other at neural plate/fold stages, whereas Fig. 3C shows this more realistically for a few important transcription factors. Although a detailed fate map of the ectoderm in neural plate stage *Xenopus* embryos is not yet available and only the approximate position of prospective placodes relative to these expression domains is known, some general patterns are evident.

Most transcription factors are expressed in multiple placodes

First, with few exceptions (e.g. *Pax3* expression in the prospective profundal placode), placodally expressed transcription factors are not restricted to a single prospective placode at neural plate stages but rather extend through larger areas, from which multiple placodes originate (Figs. 5, 6). Whereas many transcription factors are expressed in a contiguous domain covering several adjacent placodes, transcription factors specifically involved in governing neuronal differentiation (e.g. *NeuroD*, *ATH3*, *EBF2*, *EBF3*, *MyT1*, *Brn3d*) are often absent from the regions of the prospective non-neurogenic adenohypophyseal and lens placodes. Unfortunately, important details of these expression patterns, which are crucial for further

elucidating mechanisms of placode specification, are still unknown. For instance, it is largely unclear to what extent transcription factors with overlapping expression domains are in fact coexpressed at equal levels in individual cells or whether there is instead a mosaic of cells, which preferentially or exclusively express one or the other transcription factor (as has been suggested to be the case for *Dlx5* and *Pax6* expression in the rostral part of the pre-placodal region in chick embryos; Bhattacharyya et al., 2004).

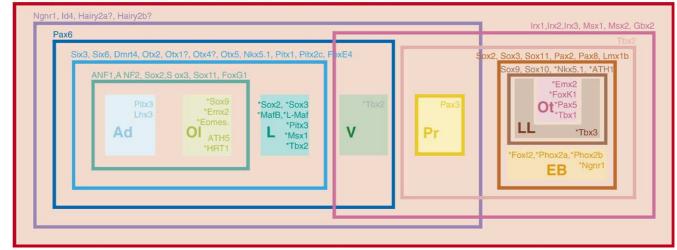
Transcription factor expression domains are centered around a rostral and a caudal focus

Second, the majority of those transcription factors, which are not panplacodally expressed, have expression domains centered around either the anterior placodal area (with prospective adenohypophyseal and olfactory placodes) or the posterior placodal area (with prospective lateral line, otic and epibranchial placodes) (Fig. 6), each of which is also apparent as a morphological unit (Schlosser and Northcutt, 2000). Only at later stages are these two areas further subdivided (see below). Beyond its implications for models of placode specification (see below), this pattern is suggestive of a particular trajectory of placode evolution, which can only be sketched here for space constraints. Briefly, it is most compatible with an evolutionary scenario, in which all placodes evolved from only two placodes, one rostrally and one caudally, in the ancestor of extant vertebrates (these in turn may have evolved from a single rostral protoplacode as discussed in Schlosser, 2005). These two placodes subsequently split into the adenohypophyseal, olfactory, and lens placodes and the otic, lateral line, and epi- and hypobranchial placodes, respectively, while the trigeminal and profundal placodes budded off at some time from either the rostral or the caudal group of placodes.

Nested and partly overlapping expression of transcription factors suggests a combinatorial mode of placode specification

Third, while most expression domains include either the anterior or the posterior placodal area or both, their spatial extension differs (Fig. 6). The resulting nested domains of transcription factors subdivide the panplacodal primordium into different areas characterized by the expression of different combinations of transcription factors. The prospective lens placode, for example, shares expression of many transcription

Fig. 5. Expression of transcription factors and cofactors in the placodal ectoderm of neural plate (stage 13–16) and tailbud (stage 24–26) stage *Xenopus* embryos (stages after Nieuwkoop and Faber, 1967). Approximate borders of prospective placodal areas at neural plate stages are indicated by gray lines, whereas borders of definite placodes at tailbud stages are indicated by black lines. Faint colors indicate weak expression. In some cases, spatial restriction of gene expression to parts of a placode is indicated by corresponding partial coloring. N, C, and E indicate that a gene is also expressed in neural plate or tube (N), neural crest (C), or epidermis (E). Question marks indicate that gene expression in a particular placode at a particular stage has either been not described or cannot be determined unambiguously from published information. Hypobranchial placodes are not listed separately but tend to share gene expression patterns with epibranchial placodes. Transcription factors that are very widely or universally expressed throughout the embryo or that are associated with particular signaling cascades (e.g. Smads or Lef/Tcf) are not included even if they have placodal area, from which lateral line, otic, and epibranchial placodes; EB: epibranchial placodes; C1: lens placode; PT: profundal placode; V: trigeminal placode. Expression domains are based on the references listed in the right column (in addition to references cited elsewhere in the text, this include Aoki et al., 2003; Bayramov et al., 2004; Bellefroid et al., 1996; Davis et al., 2001; Deblandre et al., 1999; Dirksen and Jamrich, 1995; Eagleson and Dempewolf, 2002; Halim et al., 2003; Hayata et al., 1999; Hirsch and Harris, 1997b; Honoré et al., 2003; Hutcheson and Vetter, 2001; Kanekar et al., 1997; Kim et al., 1997; Tour et al., 2001; Tsuji et al., 2002; Pohl and Knöchel, 2004; Saint-Germain et al., 2004; Spokony et al., 2004; Sont, Germain et al., 2004; S



Six1, Six2, Six4, Eya1, Grg4, Grg5, Dlx3, Dlx5, Dlx6, GATA1, GATA2, GATA3, NZFB, FoxI1, Id3, Hes6?, ESR6e

Fig. 6. Schematic summary of transcription factor expression domains in the placodal ectoderm of neural plate stage *Xenopus* embryos. Transcription factors that control neuronal determination and differentiation and are expressed in all neurogenic placodes but excluded from adenohypophyseal and lens placodes are not included. The position of various prospective placodes within the panplacodal primordium (faint red) is indicated by colored rectangles. Colored lines enclose expression domains of the transcription factors listed at neural plate stages. Listing of transcription factors without asterisk refers to their expression domains established at neural plate stages, while listing of transcription factors preceded by asterisks refers to expression domains established at later stages. Question marks indicate tentative assignments because precise domain boundaries cannot be determined unambiguously from published information. For simplicity, some details of expression are ignored (for example, *Msx1* and *Msx* 2 are strongly expressed only in the dorsal part of the indicated region). For details and references, see Fig. 5. Note that there are two foci of transcription factor expression, one centered on an anterior placodal area (with prospective adenohypophyseal and olfactory placodes), the other centered on a posterior placodal area (with prospective lateral line, otic, and epibranchial placodes). However, the spatial extension of various expression domains differs resulting in two nested hierarchies, which are overlapping in the regions of profundal and trigeminal placodes; Ot: otic placode; Pr: profundal placode; V: trigeminal placode.

factors including *Six3*, *Six6*, *Pitx1*, *FoxE4*, and *Nkx5.1* with the anterior placodal area but is distinguished from the latter by its lack of expression of other genes such as *ANF1*, *Sox2*, *Sox3*, and *FoxG1*. Moreover, some anteriorly centered transcription factors overlap with some of the posteriorly centered transcription factors in the regions, where the profundal and trigeminal placodes form. This results in unique combinations of transcription factors in each of these domains: the trigeminal placode forms, where the anterior *Pax6* domain overlaps with the posteriorly centered domains of, for instance, *Irx1*, *Msx1*, and *Gbx2*, whereas the profundal placode develops posterior to the *Pax6* domain in a region expressing *Tbx2* in addition to *Irx1*, *Msx1*, and *Gbx2*.

Even though the precise role of many of these transcription factors for placode specification remains to be elucidated, the partly nested and partly overlapping expression in the preplacodal ectoderm of such a large number of transcription factors likely to be involved in placode specification supports combinatorial models of placode specification (Torres and Giráldez, 1998). More specifically, it suggests that the expression domains of various transcription factors covering multiple prospective placodes may define nested hierarchies of multiplacodal areas-ectodermal regions biased for the development of particular set of placodes. For example, within the region expressing Six1, Six4, and Eya1 biased for generic placodal development, the ectodermal area expressing ANF and *FoxG1* genes may be biased to form either adenohypophyseal and olfactory placodes, the more comprehensive ectodermal region expressing Six3, Six6, Pitx1, FoxE4, and Nkx5.1 may be biased to form adenohypophyseal, olfactory, or lens placodes, whereas the region expressing *Pax2* and *Pax8* may be biased to form lateral line, otic, or epibranchial placodes.

How may a transcription factor covering multiple prospective placodes promote multiplacodal bias? One possibility is that it contributes to the activation of target genes specifically required in all of the placodes derived from a particular multiplacodal area but not in others (akin to the role of Six and Eya genes in the promotion of generic placodal properties proposed above). However, there is at present little evidence for the existence of many effector (e.g. cytodifferentiation) genes shared, for example, among lens, olfactory, and adenohypophyseal placodes to the exclusion of other placodes. An alternative and more plausible scenario is illustrated schematically in Fig. 7. A transcription factor may also introduce a multiplacodal bias in binding to *cis*-regulatory regions of target genes, each of which promotes development of a different individual placode but will only be fully activated after binding of additional transcription factors with spatially more restricted distribution. An increasing number of studies provide evidence for this type of combinatorial action of transcription factors at cis-regulatory regions of placodal target genes, among them the well-studied regulation of lens crystallins by Pax6, Sox2, and L-Maf already mentioned (reviewed in Piatigorsky, 1998; Bhattacharyya and Bronner-Fraser, 2004; Cvekl et al., 2004; Kondoh et al., 2004).

Some empirical support for the existence of mutiplacodally biased regions comes from recent studies in the zebrafish, where *pitx3* initially defines a broad anterior placodal region (similar to *Xenopus Pitx1*, *Pitx2b*, and *Pitx2c*; see Fig. 3C), giving rise to

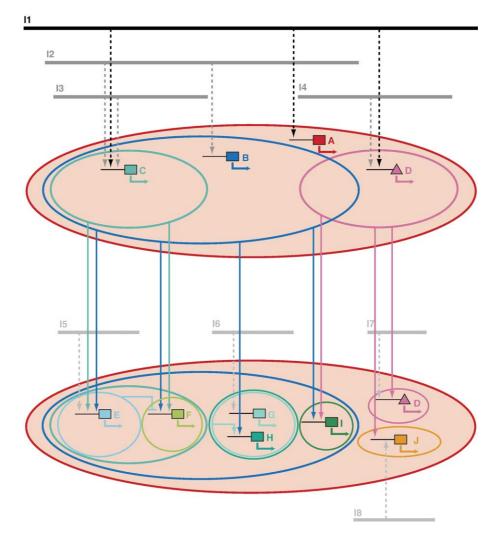


Fig. 7. Combinatorial multistep model for placode induction and specification. Expression of various transcription factor genes involved in placode specification (colored rectangles and triangles, A–J) may be regulated by particular combinations of upstream factors including inducing signaling molecules (I1–I8) as well as other transcription factors, which bind to their *cis*-regulatory region. Upstream factors may be activating (arrows; broken arrows are used for inducing signals because these act indirectly via transcription factors downstream of signaling cascades) or repressing (bars). In the hypothetical case illustrated, upstream factors are assumed to be singly necessary but only jointly sufficient for activation of the downstream gene. The expression domain of a transcription factor (enclosed by colored lines; the red area represents the panplacodal primordium) is determined by the spatial extent of the expression domains of inducers and transcription factors acting upstream (indicated by black and gray lines for inducers and colored ellipses for transcription factors). The expression of transcription factors (as illustrated for D), which show placode-specific expression at later stages, may initially be more broadly expressed but then become restricted because they require input form more localized inducers for sustained activation. This model implies that different placodes share some but not all of the inducers and transcription factors involved in their specification. Moreover, it proposes that at early stages of placode specification (upper panel) there are nested and partially overlapping regions differentially biased for development of different sets of placodes. Multiplacodal bias is introduced by transcription factors (such as B–D) which cover multiple prospective placodes and activate various placode-specific transcription factors, without being by themselves sufficient for their activation. Panplacodally expressed transcription factors such as A may, in addition, activate genes involved in

adenohypophyseal, olfactory, lens, and trigeminal placodes (Dutta et al., 2005; Zilinski et al., 2005). Moreover, pitx3 is required both for the expression of several pituitary-specific genes and for lens fiber cell specification (Dutta et al., 2005). Whether and where lens or adenohypophyseal placodes form within the pitx3-positive region appears to depend mainly on the level of hedgehog signaling with high levels of hedgehog emanating from the axial midline determining a medial position of the adenohypophyseal placode during normal development (Karlstrom et al., 1999; Kondoh et al., 2000; Varga et al., 2001; Herzog et al., 2003; Sbrogna et al., 2003). When hedgehog is

overexpressed in the prospective lens ectoderm, the latter also adopts an adenohypophyseal phenotype (Dutta et al., 2005). Blocking hedgehog signaling in the region of the prospective adenohypophyseal placode, conversely, leads to the rostromedial expansion of the lens placode at the expense of the adenohypophyseal placode (Karlstrom et al., 1999; Kondoh et al., 2000; Varga et al., 2001; Dutta et al., 2005; Zilinski et al., 2005). Taken together, this suggests that the *pitx3* expressing ectodermal domain constitutes an "equivalence domain" (Dutta et al., 2005) or a multiplacodal area, biased for the differentiation of adenohypophyseal and lens placodes (and possibly olfactory and trigeminal placodes as well, although this has not been analyzed). However, whether there is in fact a nested hierarchy of such multiplacodal areas, as the model predicts, and whether otic, lateral line, and epibranchial placodes comprise a similar multiplacodal area in the posterior still remain to be confirmed experimentally.

Dynamic changes of expression patterns result in placode-specific combinations of transcription factors

Fourth, the further differentiation of prospective placodes and the subdivision of initially molecularly equivalent areas (such as the anterior or posterior placodal area) involves various dynamic changes of gene expression after neural plate stages (Fig. 5). On the one hand, new transcription factors and other genes, which may be involved in the regulation of placodespecific processes of cytodifferentiation and morphogenesis, are upregulated in a placode-specific manner (for example, *Lhx3* in the adenohypophyseal placode, Ath5 in olfactory placodes, *MafB* in the lens placode, *FoxK1* in the otic placode, *Tbx3* in the lateral line placodes, *Phox2* genes in the epibranchial placodes; for other genes, see, for example, Baker et al., 1995; Shi et al., 1998; Vokes and Krieg, 2000; Golub et al., 2000; Novoselov et al., 2003). On the other hand, existing transcription factor domains may expand (for example, the upregulation of Sox2 and Sox3 in the lens placode or of FoxG1 in the otic, lateral line, and epibranchial placodes) or retract (for example, the exclusion of Pitx2 genes from the olfactory and lens placodes, of FoxE4 genes from the adenohypophyseal and olfactory placodes, and of Dlx3, Six1, Six4, and Eya1 from the lens placode). The latter may result either from differential local downregulation or from cell sorting. This will be discussed in more detail in the section below, dealing with individualization of placodes.

The appearance of placode-specific combinations of transcription factors is the first indication for the separation of the various multiplacodal areas into individual placodes. However, it does not imply that these molecularly distinct regions are already fully specified or even committed for a particular placodal fate because they may still require localized signals from adjacent tissues for consolidation of present or induction of additional transcription factors.

In Xenopus, molecularly distinct individual placodes appear at the following schedule. Profundal and trigeminal placodes are already molecularly distinct at neural plate stages, immediately followed by their terminal neuronal differentiation (Chitnis et al., 1995; Lee et al., 1995; Ma et al., 1996; Schlosser and Ahrens, 2004; Schlosser and Northcutt, 2000). Adenohypophyseal, olfactory, and lens placodes acquire separate identities at approximately neural fold stages (e.g. Zaraisky et al., 1995; Kenyon et al., 1999; Ishibashi and Yasuda, 2001; Burns and Vetter, 2002; Pommereit et al., 2001) but continue to require localized inductive signals for proper patterning and differentiation (reviewed in Grainger, 1996; Calof et al., 1996; Plendl et al., 1999; Kioussi et al., 1999a; Ogino and Yasuda, 2000; Chow and Lang, 2001; Dasen and Rosenfeld, 2001; Baker and Bronner-Fraser, 2001; Scully and Rosenfeld, 2002; Fisher and Grainger, 2004; Lang, 2004; Beites et al., 2005). Finally, the posterior placodal area while being already capable of forming

ectopic otic-like vesicles at neural plate stages (Gallagher et al., 1996) only subdivides into molecularly distinct otic, lateral line, and epibranchial placodes much later at mid-tailbud stages (e.g. Baker et al., 1995; Vokes and Krieg, 2000; Shi et al., 1998; Golub et al., 2000; Novoselov et al., 2003; Talikka et al., 2004; Ataliotis et al., 2005; Schlosser and Ahrens, 2004). The requirement for localized inductive signals for proper patterning of the otic vesicle into different sensory areas even persists into later tailbud stages (Kil and Collazo, 2001; see also Yntema, 1933, 1939; Harrison, 1945; Ginsburg, 1946, 1995; Detwiler and van Dyke, 1951; reviewed in Baker and Bronner-Fraser, 2001; Whitfield et al., 2002; Noramly and Grainger, 2002; Riley and Phillips, 2003; Barald and Kelley, 2004). Thus, somewhat surprisingly, placodes with very similar function such as the profundal and trigeminal placodes appear to diverge very early regarding their dependence on specific transcriptional regulators, whereas the functionally heterogeneous rostral and caudal groups of placodes appear to rely for much longer on common regulatory factors.

Individualization of placodes requires formation of stable boundaries and physical separation

The individualization of different placodes from larger fields involves the subdivision of these fields by the differential suppression of initially overlapping transcription factors in different subdomains and/or by the local upregulation of new transcription factors (e.g. in response to locally confined inducers). Consequently, mutually exclusive expression domains of certain transcription factors are established (Fig. 8A), which then control the development of placode-specific pathways of cytodifferentiation or morphogenesis. For example, the subdivision of the anterior placodal region, which initially coexpresses Pitx2c, FoxE4, and several other genes and which gives rise to adenohypophyseal, olfactory, and lens placodes, involves the exclusion of Pitx2c from the olfactory and lens and of *FoxE4* from the adenohypophyseal and olfactory territory together with the upregulation of Lhx3 in the adenohypophyseal placode, of ATH5 in the olfactory placode, and of MafB in the lens placode. Such subdivisions of a larger field of cells require mechanisms to establish stable boundaries and to keep cells with distinct identities separate from each other. The formation of stable boundaries between gene expression domains must then be accompanied or followed by processes leading to the physical separation of the individual placodes.

Formation of boundaries by switch-like cell fate decisions and compartmentalization

Two different types of mechanisms probably play a role for boundary formation: switch-like cell fate decisions and compartmentalization. Switch-like cell fate decisions abolish or prevent coexpression of transcription factors in individual cells. Sharpening of boundaries results from the differential upregulation of one but downregulation of the other transcription factor in cells located in different regions, for example due to (direct or indirect) mutual transcriptional repression (Fig. 8B). Compartmentalization

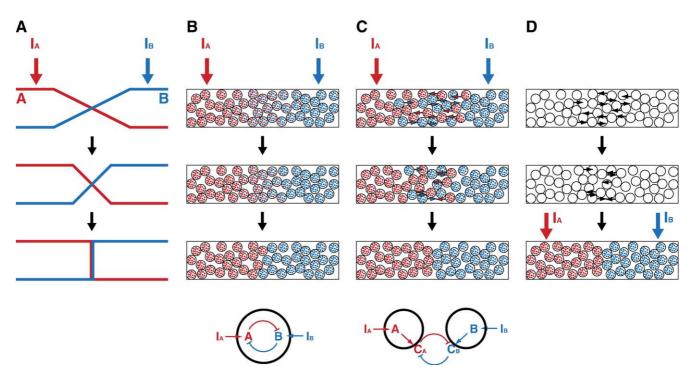


Fig. 8. Establishment of sharp boundaries between differentially specified regions by switch-like cell fate decisions or compartmentalization. (A) Transcription factors A and B, which are involved in specification of two different domains (e.g. neural crest and placodes or two different individual placodes), may be induced by two different inducers (I_A and I_B , respectively) and have initially overlapping expression domains followed by sharpening of the boundary. (B) Overlapping expression domains as depicted in panel A may be due to coexpression of A and B proteins (red and blue dots) in individual cells (circles). Sharpening of the boundary in this case involves the differential upregulation of one but downregulation of the other transcription factor in individual cells (switch-like cell fate decisions), for example, due to their direct or indirect mutual transcription factors. Sharpening of the boundary may then involve the sorting of cells by non-random cell movements (arrows) (compartmentalization), for example mediated by mutually repelling cell adhesion molecules (C_A , C_B), activated by the different transcription factors (lower panel). (D) However, occurrence of cell movements per se does not necessarily imply cell sorting as depicted in panel C since random cell movements (arrows) may also occur before ectodermal areas are differentially specified to express different transcription factors.

on the other hand abolishes or prevents intermingling of cells expressing different transcription factors. Sharpening of boundaries results from the sorting of different cells by cell movements possibly mediated by cell adhesion molecules, which are mutually repellent and activated by the different transcription factors (Fig. 8C). This may result in the formation of separate compartments, i.e. adjacent domains of cells, which are lineage-restricted and do not mix. Due to the occurrence of random cell movements in epithelia, the maintenance of stable boundaries between different adjacent epithelial domains probably always requires some sort of compartmentalization. Of course, switch-like cell fate decisions and compartmentalization are not mutually exclusive mechanisms, and they may cooperate in the establishment of stable boundaries.

Both of these mechanisms are involved in boundary formation during development of the central nervous system (CNS) and in other developmental contexts (reviewed in Dahmann and Basler, 1999; Simeone, 2000; Irvine and Rauskolb, 2001; Wurst and Bally-Cuif, 2001; Redies and Puelles, 2001; Kiecker and Lumsden, 2005), but, unfortunately, we still know very little about their role and relative importance during the formation of individual placodes from the panplacodal primordium.

At present, there is no direct evidence for the involvement of switch-like cell fate decisions in the subdivision of the panplacodal primordium. However, several transcription factors expressed in adjacent domains in the pre-placodal ectoderm have been shown to be involved in boundary formation in central nervous system development due to mutually antagonistic effects. These include Otx2 and Gbx2 (Millet et al., 1999; Broccoli et al., 1999; Katahira et al., 2000; Martinez-Barbera et al., 2002; Tour et al., 2002), Six3 and Irx3 (Kobayashi et al., 2002), as well as *Pax6* and *Pax2* (Schwarz et al., 1999, 2000; Matsunaga et al., 2000). Moreover, in the case of Pax6 and Pax2, there is evidence for direct mutual repression of these transcription factors (Schwarz et al., 2000). It is tempting to speculate that these transcription factors play a similar role during the subdivision of the panplacodal primordium. Although placodal Pax2 and Pax6 expression domains are partly separated by a Pax3 domain, Pax2 expression extends laterally around the Pax3 domain and forms a common border with Pax6 rostrally (see Fig. 3C). Otx2 and Gbx2 as well as Six3 and Irx genes, in turn, are attractive candidates for defining the boundary between an anterior multiplacodal area including adenohypophyseal, olfactory, and lens placodes and a posterior multiplacodal area including the remaining (i.e. profundal, trigeminal, otic, lateral line, and epibranchial) placodes. Experimental perturbations that lead to rostral shifts of the expression of some Irx genes in the CNS of zebrafish have indeed been shown to similarly affect their placodal expression (Itoh et al., 2002), suggesting that CNS and placodal expression domains are regulated in a similar fashion. However, additional experiments are needed to clarify the role of these genes for placode formation.

Presently, there is also no conclusive evidence for a role of compartmentalization in the subdivision of the panplacodal primordium. However, several recent studies in chick and zebrafish embryos, which have followed the fate of individually labeled cells or of small groups of cells in various subregions of the pre-placodal ectoderm, have suggested that such mechanisms may be of greater importance than previously thought (Whitlock and Westerfield, 2000; Streit, 2002; Bhattacharyya et al., 2004; Dutta et al., 2005). These studies revealed a surprising degree of mixing of cells, which later contribute to different placodes at neural plate and neural fold stages. Prospective otic placode cells are interspersed with prospective epibranchial placode cells posteriorly (Streit, 2002), whereas prospective olfactory placode cells are intermingled with prospective lens placode cells and at least in the zebrafish also with adenohypophyseal placode cells anteriorly (Bhattacharyya et al., 2004; Dutta et al., 2005). Mixing of cells destined for different parts of the inner ear has also been found within the otic placode/vesicle of Xenopus after neural tube closure, but whether precursors of different placodes are intermingled at earlier stages has not been investigated (Kil and Collazo, 2001). Extensive cell movements then lead to the segregation of precursors for different placodes at late neural fold and early neural tube stages in the chick (Streit, 2002; Bhattacharyya et al., 2004).

These fate mapping studies could, however, not establish to what degree this segregation of cells fated for different placodes involves the directed sorting of cells already specified for a specific placodal fate (Fig. 8C) or rather is due to random movement of cells, which are only specified for a particular placodal fate later (Fig. 8D). The timing of specification of various placodes in the chick was analyzed in other experimental studies involving explantation and ectopic grafts (reviewed in Baker and Bronner-Fraser, 2001). Such studies failed to provide a clear picture regarding the specification of lens and adenohypophyseal placodes, but they demonstrated that specification of the olfactory and otic placodes takes place at stages at which little or no intermingling of precursors for different placodes are seen anymore in fate mapping studies (Street, 1937; Herbrand et al., 1998; Groves and Bronner-Fraser, 2000). This does not rule out that cell sorting occurs (for instance of cells, which are already biased but not specified for a particular placodal fate), but it indicates that cell sorting may not be required to account for the segregation of cells fated for different placodes observed in recent fate mapping studies, which may instead be due predominantly to random cell movements of unspecified cells.

Additional studies are, thus, needed to firmly establish to what extent cell sorting contributes to the sharpening of boundaries between different placodes and whether individual placodes subsequently form lineage-restricted compartments. That cell sorting may at least play some role is suggested by some further recent observations. First, the overwhelming majority of cells individually labeled in the rostral placodal domain of zebrafish bud stage embryos later contributed only to a single placode despite strong mixing of adenohypophyseal, olfactory, and lens placode precursor cells in some regions (Dutta et al., 2005). Second, there is some evidence that initially overlapping but later mutually exclusive transcription factors such as Pax6 and Dlx5 in the chick are initially expressed in a mosaic-, salt-, and pepper-like pattern (although it remains to be shown that their expression is complementary), suggesting that there is in fact intermingling of cells biased or specified in a non-equivalent fashion (Bhattacharyya et al., 2004; see also Streit, 2002). Third, lens precursor cells, which ectopically overexpress Dlx5 or which lack Pax6 expression, are excluded from the lens (Collinson et al., 2000; Bhattacharyya et al., 2004), suggesting that these transcription factors mediate cell sorting, possibly via the documented ability of Pax6 and Dlx genes to promote expression of cell adhesion molecules (Chalepakis et al., 1994; Holst et al., 1997; Stoykova et al., 1997; Meech et al., 1999; Davis et al., 2003; Tyas et al., 2003; Rouzankina et al., 2004; McKeown et al., 2005).

Unfortunately, while placodes are known to be distinguished from the adjacent epidermis by the expression of several cell adhesion molecules (Thiery et al., 1982; Levi et al., 1987; Richardson et al., 1987; Miragall et al., 1989; Simonneau et al., 1992; Prouty and Levitt, 1993; Brown et al., 1998; David and Wedlich, 2000; Xu et al., 2002b; Novince et al., 2003), virtually nothing is known about differential expression of cell adhesion molecules in the pre-placodal ectoderm, which could mediate its compartmentalization into different placodes.

Finally, while the studies reviewed here have documented extensive cell movements in the posterior as well as in the anterior part of the pre-placodal ectoderm, they leave open how far anteriorly and posteriorly these movements extend. It will be a challenging task for future studies to relate cell movements in the pre-placodal ectoderm to patterns of transcription factor expression in order to establish whether any of the larger multiplacodal areas defined by molecular subdivisions of the pre-placodal ectoderm at neural plate and fold stages (for example the anterior or posterior placodal area) already forms a lineage-restricted compartment before individual placodes segregate.

Physical separation of individual placodes

Because different placodes form distinct entities at tailbud stages, which occupy widely separate positions in the head ectoderm, the initial regionalization of the panplacodal primordium by the local up- and downregulation of transcription factors and possibly by the restriction of cell movements can only be a first step in the subdivision of the panplacodal primordium into distinct placodes. This must be followed by additional steps leading to the physical separation of placodes. How this is achieved is little understood, but several different processes are likely to be involved.

Downregulation of placodal and upregulation of epidermal transcription factors in parts of the pre-placodal ectoderm accompanied by cell sorting is likely to play at least some role because the pre-placodal ectoderm is known to give rise not only to placodes but also to epidermal regions in the vicinity of placodes, including for example the epidermis of the pharyngeal grooves and the stomodeum (Ishii et al., 2001; Xu et al., 2002a;

Streit, 2002; Laclef et al., 2003a; Schlosser, 2003; Bhattacharyya et al., 2004; Dutta et al., 2005).

In addition, morphogenetic movements may be important. The separation of the adenohypophyseal and olfactory placodes from the remaining placodes, for example, has been suggested to be mediated by the elevation of the neural folds during neurulation (Schlosser and Ahrens, 2004). Neural fold elevation may dorsally displace the rostralmost placodes relative to the others because the rostralmost part of the pre-placodal ectoderm extends until the tip of the outer neural folds, while more posterior parts of the pre-placodal ectoderm are positioned further laterally (due to the occupation of the outer neural folds by neural crest cells; see Fig. 3C). Expansion of the anterior non-neural ectoderm (see, for example, Carpenter, 1937), associated with the bulging out of the retina, may additionally contribute to this separation. Finally, apoptosis has also been suggested to contribute to the physical separation of placodes, while increased proliferation within the placodes makes them morphologically more apparent (Washausen et al., 2005).

Induction of placodes

As detailed above, generic placodal genes such as Six1, Six4, and Eval begin to be panplacodally expressed at neural plate stages. In addition, many other transcription factors, which contribute to the development of various placodes, are expressed in partly nested and partly overlapping patterns often from neural plate stages on before placode-specific transcription factors appear later in development. Since specification of each placode appears to depend on multiple of these transcription factors, each of which is expressed in a different spatiotemporal pattern, placode induction itself is likely to be a complex multistep process, which relies on different inducers for the induction of panplacodally expressed transcription factors (generic placode induction) and for the induction of transcription factors with a more restricted distribution. Some of these restricted inductive processes are probably shared between adjacent placodes that depend on the same transcription factor, but others will be placode-specific. Moreover, the early molecular subdivision of the panplacodal primordium, as discussed here for neural plate stage Xenopus embryos, together with experimental evidence for the early specification of some placodes already during neural plate stages in frogs (Zwilling, 1940, 1941; Bando, 1930; Choi, 1931; Ginsburg, 1995; Gallagher et al., 1996), indicates that some of these more restricted inductive processes occur early and in parallel with generic placode induction.

Induction of individual placodes—a brief overview

Placode induction has been most thoroughly investigated for the adenohypophyseal, lens, and otic placode. Each of these placodes and the olfactory and lateral line placodes require early (gastrula–neural plate stage) signals from the endomesoderm, while signals from the anterior neural plate or tube are necessary for at least some and often multiple subsequent steps of placode development (e.g. Zwilling, 1940; Kohan, 1944; Raven and Kloos, 1945; Yntema, 1950; Jacobson, 1963a,b,c; Orts-LLorca and Jimenez-Collado, 1971; Henry and Grainger, 1990; Giraldez, 1998; Mendonsa and Riley, 1999; Gleiberman et al., 1999; Ladher et al., 2000a, 2005; reviewed in Jacobson, 1966; Grainger, 1996; Reiss and Burd, 1997; Kioussi et al., 1999a; Ogino and Yasuda, 2000; Baker and Bronner-Fraser, 2001; Chow and Lang, 2001; Dasen and Rosenfeld, 2001; Schlosser, 2002a, 2005; Noramly and Grainger, 2002; Scully and Rosenfeld, 2002; Riley and Phillips, 2003; Fisher and Grainger, 2004; Barald and Kelley, 2004; Streit, 2004; Lang, 2004; Bhattacharyva and Bronner-Fraser, 2004; Rizzoti and Lovell-Badge, 2005). In contrast, there is at present only evidence for a neural-plate-derived signal required for induction of the profundal placode (Stark et al., 1997) and for pharyngealpouch-derived signals required for the induction of epibranchial placodes (Begbie et al., 1999; Holzschuh et al., 2005; Nechiporuk et al., 2005), although signals from additional tissues are probably involved at least in case of the latter (Nechiporuk et al., 2005; Scotting, personal communication).

Multiple signaling pathways are involved in the induction of the different placodes. Induction of the adenohypophyseal placode initially requires hedgehog signaling from axial midline tissues and subsequently depends on Wnt, BMP4, and FGF signals from the prospective diencephalon and on sonic hedgehog from the oral ectoderm before intrinsic signaling gradients of BMP2 and Wnt4 are established, which pattern the adenohypophyseal primordium (Treier et al., 1998; Ericson et al., 1998; Takuma et al., 1998; Sbrogna et al., 2003; Herzog et al., 2003, 2004; reviewed in Sheng and Westphal, 1999; Kioussi et al., 1999a; Baker and Bronner-Fraser, 2001; Dasen and Rosenfeld, 2001; Scully and Rosenfeld, 2002; Rizzoti and Lovell-Badge, 2005).

Induction of olfactory and lens placodes, in contrast, is blocked by hedgehog signaling (Cornesse et al., 2005; Dutta et al., 2005). However, it is still unknown which endomesodermaland/or neural-plate-derived signals are positively involved in the early induction of olfactory and lens placodes. Retinoic acid, FGFs, and BMPs from the adjacent frontonasal mesenchyme (largely neural-crest-derived) and the olfactory ectoderm itself all play important roles for subsequent development of the olfactory epithelium (e.g. La Mantia et al., 2000; Kawauchi et al., 2004; reviewed in Calof et al., 1996; Plendl et al., 1999; Beites et al., 2005). BMPs (BMP4 and possibly BMP7) and FGFs from the optic cup also have been implicated in lens induction, while BMP expression in the lens placode itself may be required for subsequent stages of lens development and FGFs and IGFs appear to be essential for promoting lens fiber differentiation (Furuta and Hogan, 1998; Wawersik et al., 1999; Faber et al., 2001; reviewed in Chow and Lang, 2001; Lang, 2004; Fisher and Grainger, 2004; Lovicu and McAvoy, 2005).

Induction of the otic placode depends on an early FGF signal from the endomesoderm followed by additional FGF signals emanating from the hindbrain (which may synergize with a Wnt signal in amniotes), although the FGFs involved in these various steps differ between different vertebrates (Represa et al., 1991; Lombardo and Slack, 1998; Ladher et al., 2000a, 2005; Vendrell et al., 2000; Phillips et al., 2001, 2004; Maroon et al., 2002; Léger and Brand, 2002; Liu et al., 2003; Alvarez et al., 2003; Wright and Mansour, 2003; Wright et al., 2004; Solomon et al., 2004; reviewed in Whitfield et al., 2002; Noramly and Grainger, 2002; Riley and Phillips, 2003; Barald and Kelley, 2004). Further patterning of the otic vesicle requires additional signals including Wnt and sonic hedgehog from the adjacent notochord and neural tube (Liu et al., 2002; Riccomagno et al., 2002, 2005).

Induction of neurogenesis in the epibranchial placodes depends on both BMP and FGF signals from the adjacent pharyngeal pouch endoderm (Begbie et al., 1999; Holzschuh et al., 2005; Nechiporuk et al., 2005), while additional factors, which are most likely not endodermally derived, are required for the induction of earlier markers of the epibranchial placodes such as *FoxI1* and *Sox3* (Nechiporuk et al., 2005; Scotting, personal communication).

Because most studies of placode induction so far have focused on a particular placode, we unfortunately still know very little about inductive processes shared between different placodes or about generic placode induction, i.e. the induction of the panplacodal primordium itself. However, many of the transcription factors used as markers in studies of induction of a particular placode are also expressed in adjacent placodes, suggesting that at least some of the inductive events identified for a particular placode are in fact shared among several placodes. For example, Pax8, Pax2, and FoxI1, which have been regarded as otic placode markers, are expressed more broadly at neural plate stages in the posterior placodal area, which gives rise to otic, epibranchial, and lateral line placodes (Pax8, Pax2) or even in the entire panplacodal primordium (FoxII) (Schlosser and Ahrens, 2004). Therefore, some of the signals implicated in the early induction of the otic placode may in fact be more general inducers of the posterior placodal area, which may only later be regionalized by more localized inductive signals from the pharyngeal pouches and hindbrain, which induce transcription factors specific for epibranchial and otic placodes, respectively.

Models for generic placode induction

Concerning generic placode induction, the orderly and stereotypical positioning of the neural crest, panplacodal primordium, and epidermis around the anterior neural plate in a quasi-concentric fashion (except for the rostral absence of neural crest cells) suggests that the processes underlying induction of these four ectodermal tissues are in some way linked (Fig. 9A). Our understanding of neural and neural crest induction has made great advances in the last decade, and several excellent reviews synthesize these issues (Chang and Hemmati-Brivanlou, 1998a; Weinstein and Hemmati-Brivanlou, 1999; Streit and Stern, 1999b; Mayor et al., 1999; Harland, 2000; Wilson and Edlund, 2001; Mayor and Aybar, 2001; Aybar and Mayor, 2002; Knecht and Bronner-Fraser, 2002; Gammill and Bronner-Fraser, 2003; Meulemans and Bronner-Fraser, 2004; Wu et al., 2003; Yanfeng et al., 2003; Huang and Saint-Jeannet, 2004; Niehrs, 2004; De Robertis and Kuroda, 2004; Stern, 2005). Neural induction, essentially, occurs during gastrulation by the interplay of various signaling molecules

from the organizer including FGFs, Wnt antagonists, and BMP antagonists. While the precise mode of action of these signals is still debated and may differ somewhat for different vertebrates, in each case, a sink of BMP signaling is finally created in the dorsal midline and stable induction of the neural plate appears to require BMP signaling to be below a certain low threshold level. However, how the induction of other ectodermal cell fates is tied to neural induction is more controversial and several models have been proposed (Fig. 9A).

The first model, which I will refer to as the "Delay model", suggests that a neurally inducing signal travels slowly from the dorsal midline (e.g. via homoiogenetic induction in the ectoderm involving a relay mechanism), while the ectodermal competence to respond to it changes in a cell-autonomous fashion, resulting in the induction of an orderly progression of different ectodermal fates (Nieuwkoop et al., 1985; Albers, 1987).

The second model, here labeled the "Gradient model", proposes that a gradient of a morphogen such as BMP, which is established in the ectoderm during gastrulation, induces different ectodermal fates at different threshold concentrations (Sasai and De Robertis, 1997; Neave et al., 1997; Nguyen et al., 1998; Marchant et al., 1998; Mayor and Aybar, 2001; Mayor et al., 1999; Aybar and Mayor, 2002; Tribulo et al., 2004; Glavic et al., 2004; Brugmann et al., 2004).

The third model (which is compatible with the Gradient model, but does not require a gradient), termed the "Neural plate border state model", proposes that first a neural plate border state is induced between neural plate and epidermis. Additional signals from the underlying mesoderm as well as from neural plate and epidermis then induce neural crest medially and placodal fates laterally within this border region (Streit and Stern, 1999a; Baker and Bronner-Fraser, 2001; McLarren et al., 2003; Woda et al., 2003; Meulemans and Bronner-Fraser, 2004; Glavic et al., 2004; Brugmann et al., 2004; Litsiou et al., 2005). Different versions of this model differ regarding whether the border region is induced by a morphogen gradient (Glavic et al., 2004; Brugmann et al., 2004), by epidermal-neural interactions (Streit and Stern, 1999a; McLarren et al., 2003; Woda et al., 2003; Glavic et al., 2004), or by initial induction of a border fate throughout the dorsal ectoderm followed by induction of a proper neural plate in its central part (Morgan and Sargent, 1997; Streit and Stern, 1999a; Litsiou et al., 2005).

Finally, the fourth model, here referred to as "Binary competence model", suggests that signals from the organizerderived axial mesoderm induce a dorsal ectodermal region (the border of which may be set at a particular threshold of a morphogen gradient), which maintains competence to form neural plate and neural crest (with a neural default fate), while further ventrally ectoderm loses neural/neural crest competence to adopt epidermal or placodal fates (with an epidermal default fate). Subsequently, signals from the epidermis and paraxial or intermediary mesoderm induce neural crest at the border of the neural/neural crest competence region, whereas signals from the neural plate and dorsolateral mesoderm induce the panplacodal primordium at the border of the epidermal/placodal competence region (Ahrens and Schlosser, 2005).

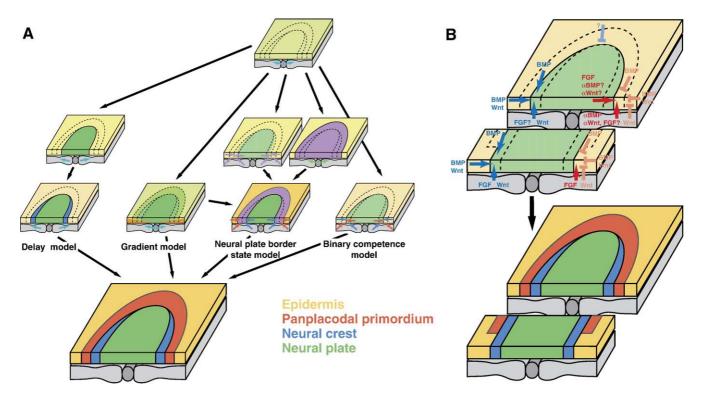


Fig. 9. Models for generic placode induction. (A) Four models have been proposed to explain the positioning of the neural crest, panplacodal primordium, and epidermis around the anterior neural plate. All models share the assumption that in a first step neural induction occurs by a signal (turquoise arrows) from the axial mesoderm (dark gray circle). The Delay model suggests that the slowly spreading neural inducer then reaches more lateral ectoderm after a time delay, during which ectodermal competence has changed in an autonomous fashion (more yellowish color). The Gradient model assumes that neural induction establishes a gradient of a morphogen (e.g., BMP; orange) followed by the specification of different ectodermal fates at different threshold concentrations. The Neural plate border state model proposes that a special neural plate border region (pink) is induced first followed by the induction of neural crest and panplacodal primordium by additional signals from adjacent ectoderm and mesoderm (blue and red arrows). Different versions of this model suggest (from left to right) that the neural plate border is established (1) by a morphogen gradient (orange), (2) by epidermal-neural interactions (pink arrows), or (3) by initial induction of a border state throughout the dorsal ectoderm followed by induction of a proper neural plate in the center (green arrows). The Binary competence model suggests that neural induction establishes a dorsal ectodermal competence region (possibly at a particular threshold of a BMP gradient), which maintains competence (light green) to form neural plate and neural crest and has a neural default fate, while ventral ectoderm cell-autonomously loses neural/neural crest competence but retains competence (light yellow) to adopt epidermal or placodal fates and has an epidermal default fate. Subsequently, additional signals from adjacent ectoderm and mesoderm induce neural crest and panplacodal primordium (blue and red arrows). (B) Summary of tissues and signals involved in induction of neural crest (left side; blue arrows and bars) and panplacodal primordium (right side, red arrows and bars) from the perspective of the Binary competence model. In addition to the cranial neural plate, its continuation into upper trunk levels is depicted. Whereas signals from prospective epidermis, neural plate border region, and paraxial mesoderm including Wnts, FGFs, and BMPs induce neural crest at the border of the neural/neural crest competence region, FGFs together with BMP and Wnt antagonists from the anterior neural plate and the cranial dorsolateral endomesoderm induce the panplacodal primordium at the border of the epidermal/placodal competence region. Because neural crest is specified earlier than the panplacodal primordium, it may escape the action of BMP and Wnt antagonists from the neural plate. Note that in this model differential ectodermal competence of the dorsal and ventral ectodermal territories defines the ventral limit of neural crest induction and the dorsal limit of generic placode induction. The ventral and posterior limits of generic placode induction are probably imposed by the extent of the signaling center producing BMP and Wnt antagonists in the cranial dorsolateral endomesoderm, which protects the overlying ectoderm from BMP and Wnt signals only in the dorsolateral head region. In contrast, the dorsal limits of neural crest induction may be set by thresholds of availability of the signals (Wnts, BMP, FGF) required for neural crest induction, while the anterior limits of crest induction are probably imposed by an unknown repressing signal that is rostrally confined.

Several recent studies have begun to shed light on the timing of generic placode induction, on the tissues and signals involved, and on the role of ectodermal competence (McLarren et al., 2003; Woda et al., 2003; Brugmann et al., 2004; Glavic et al., 2004; Ahrens and Schlosser, 2005; Litsiou et al., 2005). In combination with studies on neural and neural crest induction, these new data allow a tentative evaluation of the models just described even though much remains to be clarified.

Time window of generic placode induction

The time window of generic placode induction was determined by grafting and extirpation experiments in *Xenopus*.

These demonstrated that expression of *Six1* in the panplacodal primordium is specified at late neural plate stages and is committed at neural fold stages, while non-neural (belly) ectoderm remains competent to express *Six1* until tailbud stages (Ahrens and Schlosser, 2005). In contrast, neural plate and neural crest are specified at the end of gastrulation in *Xenopus* accompanied by a decline in competence for neural and neural crest induction in non-neural ectoderm (Kintner and Dodd, 1991; Servetnick and Grainger, 1991; Mayor et al., 1995; Mancilla and Mayor, 1996). This delay of generic placodal induction relative to neural and neural crest induction is compatible with most of the proposed models but is difficult to reconcile with a Gradient model.

Tissues involved in generic placode induction

Several tissues have been identified as signaling sources for generic placode induction. Both the anterior neural plate and the cranial dorsolateral mesoderm, which includes mesodermal precursors for the heart and pharyngeal arches (Rosenquist, 1970; Keller, 1976; Redkar et al., 2001), are required for generic placode induction in Xenopus and chick embryos, while axial mesoderm was shown to be dispensable at neural plate stages in Xenopus (Woda et al., 2003; Glavic et al., 2004; Ahrens and Schlosser, 2005; Litsiou et al., 2005). Dorsolateral endomesoderm is also able to induce several panplacodal markers (Six1, Six4, Eya2, Dach1) ectopically in the extraembryonic ectoderm of chick embryos but cannot induce Six1 in Xenopus belly ectoderm (Ahrens and Schlosser, 2005; Litsiou et al., 2005). In contrast, neural plate induces several panplacodal markers in both species (Eya1, Six1 in Xenopus belly ectoderm; Dach1, Six1 in chick extraembryonic ectoderm) but cannot induce other panplacodal genes (Eva2, Six4) in the chick (Woda et al., 2003; Glavic et al., 2004; Ahrens and Schlosser, 2005; Litsiou et al., 2005). The somewhat divergent results in frog and chick may be due to the fact that the competence of the responding ectoderm in both cases is non-equivalent, with neural competence still present in chick extraembryonic ectoderm but not in Xenopus belly ectoderm (Kintner and Dodd, 1991; Servetnick and Grainger, 1991; Litsiou et al., 2005; Ahrens and Schlosser, 2005). Alternatively, there may be interspecific differences in the inductive capacities of endomesoderm and neural plate. Additional experiments are needed to decide between these possibilities. The finding that generic placode induction depends on neural plate and dorsolateral endomesoderm but is independent of axial mesoderm strongly argues against the Delay model and is also difficult to reconcile with a simple Gradient model because it suggests that generic placode induction requires other signaling sources than the organizerderived axial mesoderm.

Signals involved in generic placode induction

Several signals from the underlying endomesoderm and the neural plate contribute to generic placode induction (Fig. 9B). First, high BMP levels inhibit induction of panplacodal genes such as Six1, while inhibition of BMP signaling adjacent to their normal expression domain promotes their expansion without inducing them ectopically (Brugmann et al., 2004; Glavic et al., 2004; Ahrens and Schlosser, 2005; Litsiou et al., 2005). In addition, Six1 is induced in animal cap ectoderm of Xenopus in response to intermediate levels of BMP4 (Brugmann et al., 2004). However, the latter experiments do not necessarily support the Gradient model postulating a requirement of intermediate BMP levels for generic placode induction. Although no strong induction of the neural plate marker Sox2 was reported at intermediate BMP4 levels, it cannot be ruled out that partial neuralization of animal caps (with weak Sox2 expression in restricted domains) occurs only at intermediate BMP4 levels, which may be a prerequisite for permitting the epidermal-neural interactions required for *Six1* induction.

Several observations in fact argue against a requirement of intermediate BMP levels for placode induction. Manipulations of BMP levels either by BMP4 injections or by mutation of BMP pathway components, which presumably lead to shallower than normal BMP gradients with broader domains of intermediary BMP concentrations, only result in expansion of neural crest domains, whereas placodal marker genes are merely displaced but not expanded contrary to the predictions of the Gradient model (Neave et al., 1997; Nguyen et al., 1998). Furthermore, when neurally competent ectoderm (e.g. animal caps) is transplanted to the pre-placodal region of neural plate stage amphibian embryos, the graft is completely neuralized and does not develop into placodal tissue (Holtfreter, 1933; Albers, 1987; Bastidas et al., 2004; Ahrens and Schlosser, 2005). This indicates that effective BMP levels in the pre-placodal region are low enough to permit neural induction in competent ectoderm. Conversely, Xenopus belly ectoderm, which has lost neural competence, is induced to express Six1, when grafted into the neural plate (Ahrens and Schlosser, 2005), where it is exposed to strong BMP inhibition from the axial mesoderm (Smith and Harland, 1992; Lamb et al., 1993; Sasai et al., 1995).

Taken together, current evidence indicates that high BMP levels are incompatible with generic placode induction without supporting a role for intermediate levels of BMP. Because BMP is strongly expressed in the pre-placodal region at neural plate stages (Fainsod et al., 1994; Hemmati-Brivanlou and Thomsen, 1995; Schmidt et al., 1995; Streit et al., 1998; Streit and Stern, 1999a; Faure et al., 2002), diffusible BMP inhibitors from the neural plate (e.g. *noggin*; Knecht and Harland, 1997) and/or the dorsolateral endomesoderm (e.g. the multifunctional BMP/Wnt/ nodal antagonist *Cerberus*; Bouwmeester et al., 1996; Chapman et al., 2002) are probably required for generic placode induction. In contrast, induction of the neural crest requires at least some BMP signaling (Liem et al., 1995; Morgan and Sargent, 1997; Nguyen et al., 1998, 2000; Marchant et al., 1998; Selleck et al., 1998; Tribulo et al., 2003).

In addition to BMP antagonists, FGF signals were shown to be required for generic placode induction. In Xenopus, FGF8most likely from the anterior neural plate—is required for Six1 induction throughout the pre-placodal ectoderm and in combination with BMP inhibitors is sufficient to induce Six1 ectopically in rostroventral ectoderm (Ahrens and Schlosser, 2005). In chick embryos, FGFs can induce some panplacodal markers (Eva2) directly but promote the induction of others (Six4) only when followed by activity of BMP and Wnt antagonists (Litsiou et al., 2005). One interpretation of these findings is that early FGF signals from organizer-derived mesoderm promote the formation of a neural plate border identity, while later FGF signals from the prospective heart mesoderm initiate expression of some panplacodal markers (Streit and Stern, 1999a; Litsiou et al., 2005). However, it is equally possible that FGF signals from the neural plate and/or the dorsolateral mesoderm (e.g. Christen and Slack, 1997; Shamim and Mason, 1999; Ahrens and Schlosser, 2005) are specifically required for the induction of panplacodal markers,

some of which need BMP and Wnt antagonists for their subsequent maintenance.

In contrast to *Xenopus*, in amniotes, *FGF8* is expressed in a restricted domain of cranial endoderm but absent from the early neural plate (Crossley and Martin, 1995; Adamska et al., 2002; Ladher et al., 2005), while in zebrafish, FGF8 is required for otic placode induction but dispensable for the induction of panplacodal genes elsewhere (Shanmugalingam et al., 2000; Léger and Brand, 2002; Solomon et al., 2004). Therefore, other FGF family members are probably involved in generic placode induction in amniotes and teleosts. Such phylogenetically flexible roles of FGFs during placode evolution were also demonstrated for FGFs involved in otic placode induction (see above). While FGFs have also been implicated in neural crest induction, different tissues (in particular paraxial mesoderm) probably serve as main sources of the FGF signal involved in neural crest induction (Mayor et al., 1997; La Bonne and Bronner-Fraser, 1998; Villanueva et al., 2002; Monsoro-Burg et al., 2003, 2005).

Finally, generic placode induction is inhibited by canonical Wnt signaling in both Xenopus and chick embryos, whereas ectopic attenuation of Wnt signaling in the trunk region in combination with BMP inhibition results in extension of panplacodal gene expression into the trunk (Brugmann et al., 2004; Litsiou et al., 2005; Huang et al., 2005). This suggests that suppression of canonical Wnt signaling in the head by Wnt antagonists secreted by the cranial endomesoderm and possibly the anterior neural plate (Bouwmeester et al., 1996; Leyns et al., 1997; Glinka et al., 1998; Piccolo et al., 1999; Duprez et al., 1999; Ladher et al., 2000b; Pera and De Robertis, 2000; Bradley et al., 2000; Chapman et al., 2002) is also required for generic placode induction. Conversely, Wnt signaling from the trunk epidermis and mesoderm (e.g. Christian and Moon, 1993; McGrew et al., 1997; Chang and Hemmati-Brivanlou, 1998b; Bang et al., 1999; Garcia-Castro et al., 2002; Schubert et al., 2002; Litsiou et al., 2005) prevents generic placode induction in the trunk. In contrast, neural crest induction requires canonical Wnt signaling, for example, from the adjacent epidermis or underlying mesoderm (Mayor et al., 1997; Chang and Hemmati-Brivanlou, 1998b; La Bonne and Bronner-Fraser, 1998; Bang et al., 1999; Garcia-Castro et al., 2002; Villanueva et al., 2002; Lewis et al., 2004; Bastidas et al., 2004; Wu et al., 2005; Sato et al., 2005; Monsoro-Burg et al., 2005). Wnt overexpression even promotes neural crest formation at the expense of the preplacodal region (Litsiou et al., 2005).

In conclusion, it is now clear that neither generic placode induction nor neural crest induction occurs simply as a corollary of dorsal midline signaling during neural induction contrary to the predictions of the Delay and Gradient models (Fig. 9A). Induction of both the panplacodal primordium and the neural crest depends instead on multiple signals from the underlying mesoderm as well as from the adjacent ectoderm, which is compatible with the Neural plate border state and Binary competence models. In order to compare these latter two models, the role of ectodermal competence for neural crest and generic placode induction needs to be considered in more detail.

Distribution of competence for generic placode induction

Importantly, when neural plate is juxtaposed with non-neural (prospective epidermal) belly ectoderm in *Xenopus*, *Six1* is only induced in the non-neural ectoderm but not in the neural plate, indicating that competence to express panplacodal genes is restricted to non-neural ectoderm but is absent from the neural plate at neural plate stages (Glavic et al., 2004; Ahrens and Schlosser, 2005). In contrast, in avian embryos, Six1 induction was observed on the neural as well as on the non-neural side of the border of anterior neural plate grafts (Litsiou et al., 2005). However, this does not necessarily imply that neural plate in avian embryos is competent to express panplacodal genes. An alternative possibility is, due to the more gradual progression of neural specification along the anteroposterior axis in avian embryos, that the posterior side of the neural plate grafts (i.e. the side oriented towards Hensen's node) may not have been fully neurally specified at the time of transplantation (stages 5-7).

Juxtaposition of neural plate and non-neural ectoderm is also known to induce neural crest cells (Rollhäuser-ter-Horst, 1979; Moury and Jacobson, 1989, 1990; Selleck and Bronner-Fraser, 1995; Liem et al., 1995; Dickinson et al., 1995; Mancilla and Mayor, 1996; Basch et al., 2000; Litsiou et al., 2005). Whereas competence for the induction of panplacodal genes appears to be restricted to the non-neural ectoderm, neural crest induction was reported to occur on both sides of the boundary between neural plate and non-neural ectoderm (Moury and Jacobson, 1990; Selleck and Bronner-Fraser, 1995; Mancilla and Mayor, 1996). However, while evidence for neural crest induction on the neural side is strong, data presented to support neural crest induction on the non-neural side are inconclusive.

In the study by Moury and Jacobson (1990), cells derived from pigmented non-neural ectoderm were reported in cranial and spinal ganglia (but never as melanocytes), and these were regarded as neural-crest-derived cells. However, it is unclear whether any of these cells were indeed neural-crest-derived since cranial ganglia also receive a placodal contribution (as the authors acknowledge), and their Fig. 7 indicates that they erroneously interpreted posterior cranial ganglia as "spinal ganglia". In the study by Selleck and Bronner-Fraser (1995), neural plates were grafted into a region of non-neural ectoderm at the border of area pellucida and opaca that is neurally competent and can be neuralized by neural plate grafts (Pera et al., 1999). Thus, the neural crest cells induced in the host ectoderm next to the graft may have formed in a neuralized portion of the host ectoderm rather than from non-neural ectoderm (as explicitly acknowledged by the authors). In the study by Mancilla and Mayor (1996), the neural plate graft was probably incompletely labeled and bigger than indicated by the authors (their Figs. 3c, d). Estimating the size of their graft by the distribution of scattered cells staining for the graft-specific fluorescent lineage tracer, which are detectable peripheral to the line supposed to demarcate the graft boundary in their published figure, the graft presumably contained all induced neural crest cells. This interpretation is in accordance with their observation that competence for neural crest formation is completely lost in non-neural ectoderm at neural plate stages (Mancilla and

Mayor, 1996). Recent experiments from my own laboratory (Ahrens and Schlosser, unpublished observations) also reveal induction of neural crest markers (*Slug*, *Foxd3*) only on the neural but not on the non-neural side after grafting anterior neural plate into belly ectoderm in early neural plate stage *Xenopus* embryos. Moreover, several studies have only reported induction of neural crest markers on the neural side of the boundary (Liem et al., 1995; Dickinson et al., 1995; Basch et al., 2000). Finally, single cell lineage studies in neural fold stage chick embryos found cells that can contribute to neural tube, neural crest, and epidermis or to neural crest and epidermis only were never found, again suggesting that neural crest cells can only be induced from neural ectoderm (Selleck and Bronner-Fraser, 1995).

Taken together, current evidence suggests that as a result of neural induction during gastrulation the ectoderm is initially divided into two territories, which differ both in default fate and competence. The dorsomedial ectoderm has a neural default fate and is competent to form neural crest cells in response to proper signals from the adjacent epidermis and underlying mesoderm, while the ventrolateral ectoderm (also referred to as non-neural ectoderm here) has an epidermal default fate and is competent to form the panplacodal primordium in response to signals from the adjacent neural plate and underlying mesoderm. This scenario supports the Binary competence model outlined above but is in conflict with models proposing that neural crest and placodes are induced from a common neural plate border state.

On the other hand, precursors for neural crest and placodal cells are still extensively intermingled at neural fold stages in chick embryos (Selleck and Bronner-Fraser, 1995; Streit, 2002), and this seems to fit better with predictions of Neural plate border state models. However, cell mixing does not necessarily imply the existence of a common neural plate border state. An alternative interpretation, which is fully compatible with the Binary competence model, is that expression boundaries between transcription factors, which promote neural/neural crest competence and those which promote epidermal/placodal competence, may be initially unsharp and overlapping due to coexpression in single cells and/or intermingling of cells before they become refined by mutual transcriptional repression and/or cell sorting (see Fig. 8). Mutual transcriptional repression has indeed been observed between placodal Six1 and the neuralcrest-specific transcription factor FoxD3 (Brugmann et al., 2004), although it is still unclear whether this is due to direct or indirect interactions. Nevertheless, more detailed analyses of how the developmental potential of single cells at the neural plate border is sequentially restricted will be necessary to conclusively decide between the Binary competence and Neural plate border state models.

Molecular basis for placodal competence in the ectoderm

The molecular mechanisms underlying differences in ectodermal competence are still poorly understood. However, some members of the *Dlx* and *GATA* families appear to be

central for the development of non-neural ectoderm and may be involved in defining its state of competence. At the end of gastrulation, Dlx3 and/or Dlx5 as well as GATA1, GATA2, and GATA3 are widely expressed in the non-neural ectoderm but are excluded from the developing neural plate (Akimenko et al., 1994; Dirksen et al., 1994; Yang et al., 1998; Depew et al., 1999; Acampora et al., 1999; Feledy et al., 1999; Pera et al., 1999; Quint et al., 2000; Luo et al., 2001a,b; McLarren et al., 2003; Schlosser and Ahrens, 2004; Walmsley et al., 1994; Kelley et al., 1994; Neave et al., 1995; Read et al., 1998; Sheng and Stern, 1999). Which Dlx gene corresponds most closely to the border of the non-neural ectoderm in the restrictive sense used here (i.e. ectoderm, which does not become incorporated into either neural tube or neural crest) differs between vertebrates. In zebrafish and Xenopus, it would be *Dlx3* but in amniotes *Dlx5*. The pre-placodal region expresses particularly high levels of Dlx3 and Dlx5 at neural plate stages, and subsequently high expression of these genes persists in olfactory and otic placodes. Although GATA2 and GATA3 genes were reported to be excluded from parts of the pre-placodal ectoderm at neural plate stages (Read et al., 1998), they are later expressed at least in adenohypophyseal, olfactory, and otic placodes (George et al., 1994; Read et al., 1998; Dasen et al., 1999; Sheng and Stern, 1999; Karis et al., 2001; Lillevali et al., 2004; Lawoko-Kerali et al., 2002).

Several lines of evidence suggest that-besides their multiple developmental functions at later stages (for a review, see Bendall and Abate-Shen, 2000; Merlo et al., 2000; Beanan and Sargent, 2000; Panganiban and Rubenstein, 2002; Patient and McGhee, 2002; Heicklen-Klein et al., 2005)-genes from both families may be critical in determining the border between a non-neural (epidermal-placodal) and neural (neural plateneural crest) competence region in the ectoderm. Canonical Wnt signaling is initially required for the exclusion of *Dlx3* from the dorsal ectoderm during early gastrulation (Beanan et al., 2000). Both GATA and Dlx genes also respond to BMP signaling, although only GATA but not Dlx genes are immediate BMP response genes (Friedle and Knöchel, 2002; Feledy et al., 1999). Consequently, during subsequent gastrulation, both Dlx and GATA genes are stably activated in a ventrally confined pattern due to dorsal inhibition of BMP signaling by the organizer (Maeno et al., 1996; Zhang and Evans, 1996; Feledy et al., 1999; Pera et al., 1999; Luo et al., 2001a,b; McLarren et al., 2003; Woda et al., 2003).

Both *Dlx* and *GATA* genes repress neural differentiation in early embryos (Xu et al., 1997b; Shibata et al., 1998; Pera et al., 1999; Feledy et al., 1999; McLarren et al., 2003; Woda et al., 2003). Conversely, these genes are required for normal development of many derivatives of the non-neural ectoderm. *GATA* factors are important for proper epidermal (Kaufman et al., 2003) and placodal development: whereas *GATA2* is required for the differentiation of gonadotropes and thyrotropes from the adenohypophyseal placode (Steger et al., 1994; Gordon et al., 1997; Dasen et al., 1999), *GATA3* is important for inner ear morphogenesis and proper differentiation of auditory neuroblasts (Karis et al., 2001; Lawoko-Kerali et al., 2004). Similarly, *Dlx3* and *Dlx5* are required for proper development of the epidermis (Morasso et al., 1996) and of the olfactory, profundal/trigeminal, and otic placodes (Acampora et al., 1999; Depew et al., 1999; Merlo et al., 2002; Solomon and Fritz, 2002; Woda et al., 2003; Long et al., 2003; Levi et al., 2003; Liu et al., 2003; McLarren et al., 2003; Solomon et al., 2004; Kaji and Artinger, 2004; Givens et al., 2005). Most importantly, the ability of belly ectoderm to ectopically express the panplacodal gene *Six1* in response to neural plate grafts is abolished if *Dlx3* activity is blocked (Woda et al., 2003). This suggests that *Dlx3* is required for making non-neural ectoderm responsive to generic placode inducers.

Gain of function studies show, however, that Dlx3 and Dlx5 are unable to activate epidermal or many placode-specific genes by themselves (less is known about GATA factors) (Feledy et al., 1999; McLarren et al., 2003; Woda et al., 2003). Taken together with the requirement of Dlx3 for responding to placode inducers, this suggests that these Dlx genes may function mainly as competence factors, which help to create a permissive environment for non-neural fates and to confer responsiveness to inducers of specialized non-neural fates such as placodes. However, after overexpression of Dlx3, Dlx5, or Dlx6, expression of the panplacodal gene Six1 is inhibited (Woda et al., 2003; Brugmann et al., 2004). This could be due to the fact that after *Dlx* overexpression the neural plate is juxtaposed with ectoderm, in which ectopic Dlx has suppressed neural fate but which otherwise is non-equivalent to normal non-neural ectoderm and does not have placodal competence. This would suggest that competence itself depends on the cooperation of several components, for example, synergy of Dlx with GATA genes, although this speculation remains to be tested.

Interestingly, juxtaposition of *Dlx*-expressing ectoderm with neural plate is also necessary for the induction of neural crest and for lateral neural plate derivatives (e.g. Rohon Beard cells), although *Dlx* expression alone is not sufficient but requires cooperation with other epidermally derived factors (Woda et al., 2003; McLarren et al., 2003; Kaji and Artinger, 2004). However, in contrast to its cell-autonomous requirement for placode induction, *Dlx* promotes neural crest and lateral neural plate fates in a non-cell autonomous fashion (McLarren et al., 2003; Kaji and Artinger, 2004), suggesting that *Dlx3* is not involved in promoting competence for neural crest induction but rather is required in the non-neural ectoderm together with other factors for the production of neural-crest-inducing signals.

In summary, current knowledge of the tissues, signals, and distribution of competence involved in generic placode induction most strongly supports the Binary competence model outlined above. It is summarized and compared with neural crest induction in Fig. 9B. During gastrulation, various signaling molecules including FGFs, Wnt antagonists, and BMP antagonists emanating from the organizer (prospective axial mesoderm) establish a dorsal ectodermal domain (possibly defined by a certain BMP threshold) competent for adopting neural or neural crest fates (neural being the default fate), whereas the remaining ventral ectodermal domain is competent to adopt epidermal or placodal fates (with epidermis being the default fate). Signals from the prospective epidermis, neural plate border region, and the paraxial mesoderm including Wnts,

FGFs, and BMPs then induce neural crest at the border of the neural/neural crest competence region at the end of gastrulation, while FGFs together with BMP and Wnt antagonists from the anterior neural plate and the cranial dorsolateral endomesoderm induce generic placodal markers such as *Six1* and *Eya1* at the border of the epidermal/placodal competence region in the head at neural plate and neural fold stages.

Conclusions

Our understanding of placode development has made significant progress in the last years. Evidence is accumulating that all cranial placodes originate from a common panplacodal primordium. We also have made great strides in elucidating the role of tissues and signaling molecules involved in the multistep induction of different placodes from this primordium as well as the role of many transcription factors involved in the specification and differentiation of placodes. However, these advances must not obscure the fact that we are only beginning to understand the intricacies of placode development.

In conclusion of this review, I want to briefly outline a few of the many important questions that remain to be tackled. First, even for the most well-studied model organisms, we still lack complete and detailed fate and specification maps of the prospective placodal ectoderm at gastrula and neurula stages. However, this information is urgently needed to understand when and how different placodes are specified. Second, we still know very little about how the different transcription factors involved in placode specification and differentiation interact and which target genes they affect. Unraveling the regulatory networks controlling placode development will require increasing integration of experimental gain and loss of function studies with cis-regulatory analyses and microarray techniques. Third, the mechanisms underlying the subdivision of the panplacodal primordium into different placodes are largely obscure. For example, what role do mutual transcriptional repression or cell sorting by differential adhesion play for the sharpening of boundaries between different placodes? And to what extent are morphogenetic movements and apoptosis involved in the subdivision of the panplacodal primordium? Fourth and finally, it is presently unclear which inductive events and subsequent pathways of specification and differentiations are unique to an individual placode and which are shared between different placodes or even between placodes and other ectodermal tissues. Addressing this important and complex question is still hindered by the narrow focus of most studies on a single placode. It is likely to be resolved only with an increasing awareness that the early developmental history of different placodes is intricately intertwined.

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