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(Article begins on next page)
Jaw Transformation With Gain of Symmetry After Dlx5/Dlx6 Inactivation: Mirror of the Past?

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Summary: In modern vertebrates upper and lower jaws are morphologically different. Both develop from the mandibular arch, which is colonized mostly by Hox-free neural crest cells. Here we show that simultaneous inactivation of the murine homeobox genes Dlx5 and Dlx6 results in the transformation of the lower jaw into an upper jaw and in symmetry of the snout. This is the first homeotic-like transformation found in this Hox-free region after gene inactivation. A suggestive parallel comes from the paleontological record, which shows that in primitive vertebrates both jaws are essentially mirror images of each other. Our finding supports the notion that Dlx genes are homeotic genes associated with morphological novelty in the vertebrate lineage. genesis 34: 221–227, 2002. © 2002 Wiley-Liss, Inc.

Key words: distal-less; mouse; loss-of-function; homeosis; craniofacial skeleton

INTRODUCTION

The skull is one of the most complex parts of the vertebrate body. Anatomically it is subdivided into the neurocranium, consisting of the vault and skull base, and the viscerocranium, comprising the entire branchial arch-derived skeleton. The posterior part of the head skeleton, including part of the otic capsule, the occipital bone, part of the sphenoid bone, and the postorbital bones, is derived from somitic and cephalic mesoderm (Couly et al., 1993). Most other bones, including the entire viscerocranium, are derived from cranial neural crest cells, which originate from fore-, mid-, and anterior hindbrain regions (Couly et al., 1993). Early during embryogenesis, these cells migrate into the frontonasal process and the branchial arches (BA1-6) and give rise to the nasal capsule, upper and lower jaws, and tongue skeleton.

Cranial neural crest cells derive from two distinct areas: a rostral Hox-negative and a caudal Hox-positive domain. Correct patterning of the Hox-negative region depends on signaling factors derived from the endoderm (Couly et al., 2002). This domain contributes to the frontonasal process and BA1. The more caudal Hox-positive domain requires expression of Hox genes for correct patterning and generates the crest of the more posterior branchial arches (Köntges and Lumsden, 1996). For example, Hoxa2 is expressed up to the second rhombomere. When Hoxa2 is inactivated, the neural crest cells of BA2 behave like their Hox-negative counterpart of BA1 and form pieces of the lower jaw skeleton (Rijli et al., 1993; Gendron-Maguire et al., 1993). On the other hand, ectopic expression of Hoxa2 in BA1 causes its neural crest to adopt a second arch fate, resulting in homeosis of jaw elements (Grammatopoulos et al., 2000; Pasqualetti et al., 2000).

In insects, Distal-less (Dll) is required for correct morphogenesis of the distal portion of the legs, antennae, and mouth parts (Cohen et al., 1989; O’Hara et al., 1993). Based on sequencing comparison, it is thought that during the evolution of chordates an initial gene duplication occurred, followed by several cluster duplications and selective gene losses (Stock et al., 1996; Ruddle, 1997; Zerucha and Ekker, 2000). Dll homologs have been isolated from vertebrate species like lamprey, zebrafish, newt, Xenopus, mouse, and human (see Neidert et al., 2001, and references therein). They constitute a highly conserved family of homeobox genes, which are thought to act as transcription factors.

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In the mouse, six Dll-related (Dll) genes were isolated. They are arranged as three convergently transcribed pairs. Each pair is located in proximity of a Hox cluster (Dll1 and -2 near HoxD, Dll3 and -7 near HoxB and Dll5 and -6 near HoxA). During murine craniofacial development, Dll1, Dll2, and Dll3 are expressed in the mesenchyme of the first and second branchial arches beginning at E9.5. Mice in which Dll1 and -2 are inactivated have abnormalities in the proximal first and second arch-derived structures (Qiu et al., 1995, 1997). Dll5 and Dll6 are expressed in all four branchial arches from around E9.0 onwards. While in BA1 strong expression is detected in the mandibular process with an onset at E9.0, no expression is observed in the maxillary process up to E10.5. Later, both the maxillary and mandibular processes strongly express Dll5 and Dll6 (Acampora et al., 1999; Depew et al., 1999; Charité et al., 2001). Dll5 homozygous mutants have inner ear defects and many abnormalities in the craniofacial skeleton (Acampora et al., 1999; Depew et al., 1999).

Deletion of the coding and intergenic regions of Dll5 and Dll6 with a single targeting event in the mouse results in perinatal death and in a limb malformation reminiscent of the human ectrodactyly, Split Hand Foot Malformation type 1 (Merlo et al., 2002; Robledo et al., 2002). In this study, we describe the craniofacial lesion present in Dll5/6 double mutant mice. This is characterized by a homeotic-like transformation of the lower jaw into an upper jaw and in gain-of-symmetry of the snout. A suggestive parallel comes from the paleontological records, which show that in primitive bony snout. A suggestive parallel comes from the paleontological records, which show that in primitive bony fishes and early land vertebrates the upper and lower jaws are essentially mirror images of each other (Romer, 1940). Our findings support the notion that Dll5 and -6 are homeotic genes essential for anteroposterior patterning of BA1 in modern mammals.

RESULTS

Generation of Dll5/6 Double Mutants

We have deleted the coding and intergenic regions of Dll5 and Dll6 in the mouse with a single targeting event (Merlo et al., 2002). Homozygous mutant mice die shortly after birth. They have hindlimb malformations and exencephaly or anencephaly together with a unique craniofacial lesion. Both upper and lower jaws are severely affected and seem mirror-images of each other, causing their snouts to be symmetric both along the right-left and antero-posterior planes (Fig. 1a). Strikingly, whiskers pads with vibrissal follicles are visible both on the upper and the lower jaws (Fig. 1b,d). Bmp4 expression, a marker for the dermal papillae, confirms this observation in E12.5 control and double mutant embryos (Fig. 1c,d; St-Jacques et al., 1998). Moreover, structures resembling palatine rugae, a series of ridges associated with the inner surface of the palatal shelves, are present on the inner surface of both upper and lower jaws (data not shown).

FIG. 1. BA1 phenotype of Dll5/6 double mutants. Whole-mount view of Dll5/6 double mutant snouts at birth (a) and at E12.5 (b). In situ hybridization with Bmp4 probe on E12.5 normal (c) and Dll5/6 mutant (d) embryos. Note the presence of whisker pads (b) and Bmp4-expressing dermal papillae (c,d) both in the upper and in the lower jaw of the mutant (arrows in b and d).

Gradual Transformation of the Lower Jaw Into an Upper Jaw Depending on Dll5/Dll6 Gene Dosage

To study the skeletal phenotype of Dll5/6 double mutants we performed skeletal stainings on E14.5 and newborn Dll5 and -6 single and compound mutant mice. Cartilage skeletal preparations of E14.5 embryos (Fig. 2a–d) show that in Dll5/6 homozygous double mutants Meckel’s cartilage is almost totally absent, yet in some embryos a small rudiment of a Meckel’s cartilage-like structure can be found in the distalmost part of the lower jaw. Skeletal staining of newborn mice lacking two (Dll5+/−/Dlx6−/− and Dlx5+/−/Dlx6−/−), three (Dll5+/−/Dlx6−/−), or four (Dll5−/−/Dlx6−/−) alleles of the cluster and dissection of their jaw regions shows that, besides being strongly malformed, the maxillae and mandibles gradually acquire a near to identical shape, depending on the gene dosage (Fig. 3). Loss of two Dlx alleles (either in Dlx+/−/Dlx6−/− or Dlx5+/−/Dlx6−/−) leads to the loss of the coronoid process, to a reduction of the angular process and to a shortening of the mandible. Removal of three alleles leads to the complete loss of the coronoid, condylar, and angular processes and to a severe shortening of the mandible. Finally, in mutants lacking all four alleles (Dll5−/−/Dlx6−/−), the general structure of the maxillary group of bones remained identifiable, albeit profoundly distorted. In contrast, the mandible became unrecognizable and was transformed in a structure indistinguishable from the deformed maxillary bone complex. This symmetry is particularly evident when the snout skeleton of Dll5−/−/Dlx6−/− newborn mice is observed from the front (Fig. 3b). Moreover, the transformed lower jaw seemed to articulate with structures.
that may be interpreted as distorted and duplicated pterygoid processes, rather than with the squamosal bone in normal skeletons.

Abnormalities in Vaults, Skull Base, and Hyoid Skeleton of Dlx5/6 Double Mutant Mice

Besides the abnormalities in the first arch-derived skeleton, also second and third arch-derived structures were affected in Dlx5/6 homozygous double mutants. In double mutants at E14.5 and at birth, fusions were detected between the hyoid bone and the pterygoid processes of the sphenoid bone and the superior horns of the thyroid; the stylohyoid ligament was often chondrified. Additional craniofacial abnormalities were detected in the skull plates, which were virtually absent, and in the anterior skull base. The basisphenoid bone was distorted and severely bent to allow articulation of the pterygoid process with the transformed lower jaw. The presphenoid was strongly reduced and the alisphenoids were duplicated: the two copies lie on different planes and are connected, as illustrated for its precursor, the ala temporalis, in E14.5 skeletons in Figure 2e. The occipital bone, which is derived from presomitic mesoderm, remained relatively unaffected by the mutation.

In conclusion, most affected craniofacial structures are neural crest-derived. This correlates well with the expression patterns of Dlx5 and -6 in neural crest-derived mesenchyme in all branchial arches. Malformation of cephalic or presomitic mesoderm derived cranial structures most likely is secondary to the failure of neural tube closure or to the primary skull defects in the viscerocranium. Table 1 is a summary of the cranial structures affected by this mutation.

Transformation of the Mandibular Process Is First Visible Around E10.5/E11.0 and Is Confirmed by Expression of Mandibular Marker Genes

The striking morphological similarity of the upper and the lower jaw of Dlx5/6 double mutants suggests a transformation of the mandibular process into a maxillary process early during craniofacial development. To determine the time point of onset of the branchial arch abnormalities in Dlx5/6 double mutant embryos, we isolated E9.5 to E14.5 embryos. While the exencephalic phenotype was already clearly present at E9.5, the branchial arch abnormalities become first visible around E10.5–11.0. At this stage Dlx5 and Dlx6 are normally predominantly expressed in the mandibular process of BA1. In E10.5–11.0 Dlx5/6 double mutant embryos the mandibular processes have failed to fuse and are somewhat increased in size. This defect becomes even more evident in later stage double mutant embryos (see Fig. 4e,f for an E11.5 embryo).

To determine the molecular identity of the mandibular process of Dlx5/6 double mutant embryos, we analyzed the expression of marker genes with an asymmetric anteroposterior distribution in BA1 (Fig. 4). In E10.5 embryos, PitX1 is normally expressed in the mesenchyme of the mandibular process and in the ectoderm of the stomodeum (Lanctôt et al., 1997). In E10.5 and E11.0 double mutant embryos, PitX1 expression was present in the ectoderm of the mandibular and the maxillary process, but was completely absent from the mandibular mesenchyme (see Fig. 4a–c), suggesting that it may be a Dlx5/6 downstream target gene during patterning of the mandibular process. Moreover, dHAND, which in E10.5 pharyngeal regions is usually expressed in the mandibular process and is activated by Dlx6 (Charité et al., 2001), is almost silenced in the branchial arch of the double mutant (Fig. 4d). Finally, whereas in normal E11.5 embryos Dlx1 is uniformly expressed in the maxillary process and only proximally in the mandibular process, in the Dlx5/6 double mutant the expression domain of Dlx1 in the mandibular process has extended to more distal regions, causing a “mirror-image pattern of expression” in the upper and lower jaws (Fig. 4e,f; Qiu et al., 1995, 1997). These molecular data corroborate the hypothesis that the mandibular process has acquired a maxillary identity.

DISCUSSION

The simultaneous inactivation of Dlx5 and Dlx6 in the mouse results in severe malformations in the skull vault and base and in all branchial arch derivatives. Most strikingly, in these mice lower jaws are gradually transformed into upper jaws, depending on the gene dosage...
and resulting in a symmetric snout in mutants lacking all four alleles. Their mandibular processes gives rise to a structure, which is the mirror image of that derived from the maxillary portion of BA1.

**Homeotic-Like Transformation of Lower Jaw Into an Upper Jaw in a Hox-Free Region**

Altogether, both morphological observations and molecular data support the hypothesis that combined inactivation of *Dlx5* and *Dlx6* results in a transformation of the lower jaw into an upper jaw. Using the initial definition of homeosis given by Bateson (1894) as a phenomenon in which “something has been changed into the likeness of something else,” we could interpret this as a homeotic-like transformation of the mandibular into a maxillary portion of BA1.

Both the upper and the lower jaws derive from BA1, which is colonized by neural crest cells arising from the mesencephalic neural fold and the segmented anterior hindbrain (Köntges and Lumsden, 1996; Couly et al., 1996). It has been shown that these crest cells do not express *Hox* genes and get patterning clues from the endoderm (Couly et al., 2002). Homeosis of jaw elements has previously been shown only after inactivation and forced expression of *Hox* genes in postmigratory neural crest (Rijli et al., 1998; Pasqualetti et al., 2000). Our findings support the notion that *Dlx5* and *Dlx6* can act as homeotic genes essential for anteroposterior patterning of BA1 in modern mammals. These data pave the way for further studies on the origin and molecular nature of the signals involved in BA1 patterning.

**Dlx Genes as Evolutionary Tools to Generate Morphological Asymmetry**

Apart from sharks, where the upper and lower teeth are relatively similar in shape and number, the upper and lower jaws of the extant jawed vertebrates (gnathostomes) generally differ in the shape and number of their teeth or tooth-bearing dermal bones. In bony fishes (osteichthians), and land vertebrates (tetrapods), this difference disappears as one considers early, Paleozoic groups, whose upper jaw bones are almost a mirror
image of those of the lower jaw. This curious symmetry was pointed out long ago by the American paleontologist A.S. Romer (1940) in early amphibians, but has never received any explanation other than merely functional. The generalized osteichthyan condition, in this respect, can be observed in a Devonian tristichopterid fish (Eusthenopteron), a close piscine relative to the tetrapods (Fig. 5). In living osteichthyans, this bone pattern is profoundly modified in most ray-finned fishes (actinopterygians) and, among tetrapods, in mammals, in which the lower jaw is represented by the dentary alone. But important modifications of the jaw bones, such as the loss of the maxillary or coronoids also occur in the living piscine sarcopterygians, i.e., the coelacanth and the lungfishes.

Conclusion

Our results show that Dlx5/6 gene inactivation in the mouse leads to a homeotic-like transformation of the lower jaw into an upper jaw and generates a symmetric mouth. The transformed structure is, in a sense, reminiscent of the jaw pattern of early osteichthyans, including early tetrapods. This analogy is a hint for future investigations in the evolution of an asymmetric mouth. Our findings might imply, more generally, that Dlx genes were needed to allow asymmetry when required by the rise of complex anatomical structures during evolution. Our data reinforce the concept, already present in the literature that Dlx genes are associated with the appearance of morphological novelties in vertebrates (Neidert et al., 2001).

MATERIALS AND METHODS

Locus Targeting

We previously reported the generation of mice with targeted disruption of Dlx5 and Dlx6 (Merlo et al., 2002).

Whole-Mount In Situ Hybridization

Whole-mount in situ hybridization was performed on E10.5 to E12.5 embryos essentially as described by Wilkinson (1992), with slight modifications. The Dlx1 probe comprised 720 bp of the 3’ end of murine Dlx1 cDNA and was linearized with BamHI and transcribed with T7 RNA polymerase. The Bmp4 probe, kindly provided by R. Zeller (Utrecht, The Netherlands), comprised 1.6 kb of Bmp4 cDNA sequence and was linearized using AccI and transcribed with T7 RNA polymerase. The PitX1 probe, provided by P. Briata (Genova, Italy), comprised 950 bp of the 3’ end of the PitX1 cDNA and was linearized with NcoI and transcribed with T3 RNA polymerase. The dHAND probe, kindly provided by E. Olson (Dallas, TX, USA), corresponded to 450 bp in the 3’ end of dHAND cDNA and
was linearized with EcoRI and transcribed with T7 RNA polymerase. Hybridization was detected with anti-DIG Fab and BCIP/NBT (Roche, Nutley, NJ).

**Bone and Cartilage Staining**

Cartilage staining of E14.5 embryos as well as bone and cartilage staining of newborn mice was carried out as previously described (Acampora et al., 1999).

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