The PDGFα receptor is required for neural crest cell development and for normal patterning of the somites

Philippe Soriano
Division of Basic Sciences, Fred Hutchinson Cancer Research Center, 1100 Fairview Avenue North, Seattle, WA 98109, USA (e-mail: psoriano@fhcrc.org)

SUMMARY

Platelet-derived growth factors (PDGFs) have been implicated in the control of cell proliferation, survival and migration. Patch mutant mice harbor a deletion including the PDGFα receptor gene and exhibit defects of neural crest origin which affect pigmentation in heterozygotes and cranial bones in homozygotes. To verify the role of the PDGFαR gene during development, mice carrying a targeted null mutation were generated. No pigmentation phenotype was observed in heterozygotes. Homozygotes die during embryonic development and exhibit incomplete cephalic closure similar to that observed in a subset of Patch mutants. In addition, increased apoptosis was observed on pathways followed by migrating neural crest cells. However, alterations in mutant vertebrae, ribs and sternum were also observed, which appear to stem from a deficiency in myotome formation. These results indicate that PDGFs may exert their functions during early embryogenesis by affecting cell survival and patterning.

Key words: PDGFαR, somite, neural crest, growth factor, mouse, Patch, cell proliferation, cell migration, apoptosis

INTRODUCTION

Over the years a number of classical and targeted mutations have been accumulated in the mouse that affect neural crest derivatives or skeletal development (Grüneberg, 1963). Neural crest cells migrate from the dorsal neural tube and give rise to an astounding variety of cell types, including neurons, glia, pigment cells and facial bones (for reviews, see Bronner-Fraser, 1995; Le Douarin et al., 1993). In the trunk, these cells need to migrate around or through blocks of paraxial mesoderm, the somites. In time, somites give rise to sclerome, myotome and dermatome, the precursors of bones, muscle and dermis, respectively. Genetic studies as well as cell biological evidence have shown that the molecular pathways underlying normal development or proper patterning of these cell types include control of cell proliferation and survival, as well as migration along extracellular matrices or guidance by chemotactic or repulsive cues.

Many growth factors may be involved in controlling these processes. Platelet-derived growth factors (PDGFs) have been shown to regulate not only cell growth and survival, but also various aspects of cell morphology and movement, such as scattering, chemotaxis or deposition of extracellular matrix (for a review, see Claesson-Welsh, 1994; Kazlauskas, 1994). These factors derive their name from their original isolation from platelets and have been shown to have an important role in vascular biology, but they are also known to stimulate the proliferation of many other cell types during development and in the adult (Ross et al., 1986). PDGFs are disulfide-bonded homodimers or heterodimers of two polypeptide chains, A and B. Their receptors are two tyrosine kinases, PDGFαR (αR) and PDGFβR (βR), which can also homodimerize or heterodimerize upon binding of the ligand (Seifert et al., 1989). Previous work has shown that the βR, which binds only PDGF BB with high affinity, is required for normal development of the kidney and the microvasculature (Soriano, 1994), but PDGFR functions earlier in development may be masked by the presence of the αR, which can bind all PDGF isoforms. Further information on the role of PDGF receptors during development has been obtained from studies in Xenopus embryos, where the introduction of a dominant negative PDGF receptor leads to abnormal gastrulation (Ataliotis et al., 1995), and mutations in the PI3 kinase binding sites in the receptor lead to abnormal spreading of mesodermal cells (Symes and Mercola, 1996).

A deletion encompassing the αR gene, found in Patch (Ph) mutant mice, has been interpreted as a model of αR deficiency. Ph mutant mice, initially studied by Grüneberg and Truslove (1960), exhibit defective melanocyte migration in heterozygotes leading to a white patch in the trunk. The phenotype of the homozygous mutants depends on their genetic background: on a C57BL6/J background, homozygotes die by E10.5 and exhibit multiple defects including reduced growth, dilation of the pericardium, subepidermal blebs, a wavy neural tube and defects in the yolk sac (Orr-Urtreger et al., 1992). However, when backcrossed to CBA or Balb/C background, about a third of the embryos survive until E16-17 and exhibit a cleft face and spina bifida (Grüneberg and Truslove, 1960; Schattenman et al., 1992). The cleft face phenotype has been associated with a defect in the migration of cranial neural crest cells (Morrison-Graham et al., 1992), although it remains unclear if this defect
is on their migration pathway or associated with the neural crest cells themselves.

The Ph mutation, however, represents a large deletion that involves more than one gene and for which both breakpoints have not been mapped (Brunkow et al., 1995; Nagle et al., 1994; Smith et al., 1991; Stephenson et al., 1991). In particular, the deletion extends towards, but does not include, the neighboring c-kit gene, which is involved in migration of a number of different cell types including melanocytes. Moreover, the domain of expression of kit is altered in Ph heterozygotes (Duttlinger et al., 1995; Wehrle-Haller et al., 1996), raising the possibility that this may be responsible for the pigmentation defect. In this work, I have generated mice carrying targeted mutations in the PDGFRα gene and discuss the mutant phenotypes in comparison with Ph and in light of roles that this receptor may play in cell survival during development.

MATERIALS AND METHODS

Derivation of mutant mice

The PDGFRα locus was isolated from a 129Sv genomic library using a full-length cR cDNA plasmid (provided by Dan Bowen-Pope and Chuck Stiles). The targeting construct used to derive the cR1 strain was constructed using a neo expression cassette (PGKneoBP; Soriano et al., 1991) to replace a 0.5 kb EcoRI- SpeI fragment encompassing part of the first immunoglobulin domain, flanked by 7 kb (SacII-EcoRI) and 1.1 kb (SpeI-Xbal) genomic sequences derived from a 129Sv library. The targeting construct used to derive the cR2-4 strains was constructed in PGKneoex2DTA, a plasmid containing a neo gene flanked by lox sites, a negative selection cassette (PGK-DTAbpA) and polylinker sites for the insertion of flanking sequences. This targeting vector replaces a 6.5 kb BamHI-Smal fragment (corresponding to the signal peptide, first and second immunoglobulin domain) with the neo cassette and includes 5.2 kb (SacII-BamHI) and 2.7 kb (Smal-EcoRV) of 5’ and 3’ sequences, respectively. The constructs were linearized, electroporated into 129Sv-derived AK7 ES cells (A. Imamoto and P. S., unpublished data), and colonies were selected with G418. Homologous recombination events were screened by PCR as described (Soriano et al., 1991), using primers from the neo gene and genomic sequences outside of the targeting construct. Southern blots were done using cR cDNA probes (EcoRI-PstI 614 bp fragment for the cR1 strain; EcoRV-NcoI 239 bp fragment for the cR2-4 strains). The blots were rehybridized with neo to show that there was only a single insertion of the vector and with plasmid to verify the absence of a concatemer. Tissue culture and blastocyst fragment for the there was only a single insertion of the vector and with plasmid to procedures. No upregulation of expression level was observed on whole embryo extracts using antibodies specific to the signal peptide, first and second immunoglobulin domain. A second targeting construct (cR16) carries a larger deletion (~0.5 kb) corresponding to the signal peptide, as well as the first and second Ig domains. Following electroporation into ES cells, 7/56 (cR6) and 18/384 (cR16) G418 clones identified by PCR had undergone homologous recombination and were subsequently verified by Southern blot analysis (Fig. 1B). One clone derived from an 06 targeting event and three clones derived from cR16 targeting events were used to derive germ-line chimeras and gave rise to the cR1 and cR2-4 mutant strains, respectively. Heterozygous offspring had normal agouti pigmentation and did not display the white patch observed on the trunk of Ph mice. Moreover, no defect in the migration of melanocytes could be detected in E10-E13 homozygous embryos by in situ hybridization, using a TRP2 (tyrosinase related-protein 2) probe as a marker of melanocytes (Fig. 2).

RESULTS

Derivation of mutant mice

Two different mutations were introduced into the cR gene (Fig. 1A). The first targeting vector (cR6) generates a small (~0.5 kb) deletion corresponding to the first immunoglobulin (Ig) domain. A second targeting construct (cR16) carries a larger deletion (~6.5 kb) corresponding to the signal peptide, as well as the first and second Ig domains. Following electroporation into ES cells, 7/56 (cR6) and 18/384 (cR16) G418 clones identified by PCR had undergone homologous recombination and were subsequently verified by Southern blot analysis (Fig. 1B). One clone derived from an 06 targeting event and three clones derived from cR16 targeting events were used to derive germ-line chimeras and gave rise to the cR1 and cR2-4 mutant strains, respectively. Heterozygous offspring had normal agouti pigmentation and did not display the white patch observed on the trunk of Ph mice. Moreover, no defect in the migration of melanocytes could be detected in E10-E13 homozygous embryos by in situ hybridization, using a TRP2 (tyrosinase related-protein 2) probe as a marker of melanocytes (Fig. 2).

Although heterozygous mice did not display a pigmentation phenotype, chimeric mice derived from the heterozygous cR ES cells gave very poor coat color chimerism (ranging from not detectable to 30% at the most), whereas chimeras made in parallel with ES cell clones in which the cR locus was not targeted, or in which the cR locus was targeted with a conditional mutation that does not eliminate cR expression (unpublished data), produced extensive (50-100%) coat color chimerism. Tail biopsies revealed extensive (over 50%) contribution of the mutant cells and test breeding of seven chimeras representing four targeted clones demonstrated in each case germ-line transmission of the mutant allele in the first litter, with progeny from six of the seven chimeras exclusively...
derived from the injected ES cells. These results suggest a dosage-sensitive, cell autonomous phenotype of the mutation on coat color pigmentation.

Heterozygous offspring were mated to derive homozygous embryos. Protein lysates from homozygotes were subjected to western blot analysis using antibodies directed against the kinase domain or the carboxy terminus of the αR. In lysates of αR1 mutant embryos, a weak low molecular weight band, migrating at about $140 \times 10^3 M_r$, (Fig. 1C), was observed. Northern blot analysis suggests that this truncated protein might be due to splicing from an exon encoding the signal peptide to an exon corresponding to the second immunoglobulin domain (not shown), which would not lead to a frameshift mutation (Wang and Stiles, 1994). A similar mutation, tested in fibroblasts, led to the formation of a receptor that was not glycosylated, did not go to the cell surface and thus did not bind the ligand (Yu et al., 1994). In contrast, western blot analysis of lysates from E12 αR2-4 embryos, using several antibodies raised against different parts of the receptor, failed to reveal any immunoreactive bands (Fig. 1C), indicating that the larger deletion leads to a null allele. Identical phenotypes were observed with both mutations indicating that the truncated molecule in the αR1 strain is unlikely to be of any physiological consequences. In addition, the similarity of the phenotype observed with both mutations argue against any effect that may have been imparted by the neo cassette or the location or size of the deletion.

**Lethality of homozygous mutant embryos**

No homozygous mutant mice were recovered from double heterozygous crosses. Timed pregnancies therefore were examined between E8 and E16 of gestation (Table 1). Close to expected numbers of homozygous embryos were recovered at various stages, on a congenic 129Sv or mixed 129Sv × C57BL/6J genetic backgrounds, as well as after four-generation backcross to C57BL/6J, but many embryos exhibited severe developmental defects. At E8, five out of six embryos had a very wavy neural tube and had not turned, one was severely retarded (headfold stage) and two had 2-4 subepidermal blebs flanking the neural tube (Fig. 3A). At E9, almost all of the embryos still displayed a wavy neural tube, and 25% of these were smaller and had not turned about their anterior-posterior axis. A few of these embryos also exhibited blebs filled with blood along the neural tube as well as on the head (Fig. 3B), or a dilated pericardium and defective yolk sac vasculature. At E10, more than half of the embryos had a very wavy neural tube, one quarter had a dilated pericardium and one quarter were very small; three embryos had not turned about their anterior-posterior axis and four exhibited subepidermal blebs. However, almost one quarter of the mutant embryos at E10 appeared normal, relative to wild-type or heterozygous embryos. At E11, more than half of the embryos were normal and the others were smaller and displayed a wavy neural tube.

At E12 and later, the mutant phenotype was less variable and embryos displayed large blebs on their heads accompanied by a cleft (Fig. 3C,D). The embryos also displayed blebbing in multiple locations and oedema, which increased in severity by E13, but all of the embryos were still alive. At E14, several mutant embryos were dead and survivors were distended and exhibited bleeding at various locations. Most of the embryos

| Table 1. Genotype of PDGFαR null mutant embryos |
|-------------------------------|------------------|------------------|
|                               | +/+              | +/-              | −/−              |
| E8                            | 1               | 11              | 6 (33%)          |
| E9                            | 18              | 33              | 18 (26%)         |
| E10                           | 68              | 147             | 65 (23%)         |
| E11                           | 9               | 16              | 7 (22%)          |
| E12                           | 9               | 16              | 3 (11%)          |
| E13                           | 23              | 33              | 9 (14%)          |
| E14                           | 16              | 26              | 9 (18%; 3 dead)  |
| E15                           | 20              | 37              | 19 (25%; 11 dead)|
| E16                           | 19              | 30              | 6 (11%; 4 dead)  |

Fig. 1. Targeted disruption of the PDGFαR gene. (A) Map of the genomic locus. The α6 and α16 targeting vectors, used to derive the αR1 and αR2-4 strains, respectively, are shown. Arrowheads mark the position of PCR primers used to detect targeted insertions. The neo cassette (neo) in α16 is flanked with loxP sites for Cre recombinase. A, Apal; s, SacII; N, Nhel; B, BamHI; RI, EcoRI; S, SmaI; X, XbaI; RV, EcoRV. Not all restriction sites are shown. SP, I, II and III represent the approximate positions of cDNA sequences encoding the signal peptide, first, second and third immunoglobulin domain, respectively. (B) Southern blot analysis of wild-type (++) and targeted α16 (−−) ES cell DNAs digested with Apal or Nhel. Apal does not cut in the targeting vector, and the 20 kb fragment is diagnostic for normal integration of the vector on the 5’ side. The probe used to detect α16 targeted events (hatched box in A) is derived from the αR cDNA, and also hybridizes further 3’ to Nhel fragments of 1 kb (not shown) and 20 kb. (C) Western blot analysis of whole E10 αR1 (left) and E12 αR4 (right) embryos, using a polyclonal antibody (27P) to the αR, ++, wild type; −−, heterozygotes; −, homozygotes. Note the presence of a $140 \times 10^3 M_r$ fragment in lysates from heterozygous and homozygous αR1 embryos. The diffuse band of higher mobility in wild-type lysates represents the non-glycosylated form of the receptor.
Fig. 2. Normal melanocyte development in mutant embryos. (A,B) E.10.5. Melanocyte precursors, visualized by hybridization with TRP-2, can be identified as a stream of cells migrating, caudally from the otic vesicle (ot). (C,D) E13.5. Lateral views at the level of the eye and ear (e). (E,F) E13.5. Lateral views at the level of the tail (t) and hindlimb (hl). Note the normal number of melanocytes around the ear and tail, which are lacking in Patch mutant embryos (Wehrle-Haller et al., 1996).

Fig. 3. Phenotypic abnormalities in mutant embryos. (A) E 8.5. The arrows indicate subepidermal blebs flanking the neural tube. (B), E9.5. Note a bleb filled with blood. (C,D) E12.5 embryo, showing a large bleb on the head accompanied by bleeding and a cleft face. (E,F) E15.5 embryos, exhibiting significant oedema, bleeding, and a cleft face. (G,H), cross section through a wild-type (G) and mutant (H) E15.5 embryo. Note oedema, abnormal dorsal neural tube and bulging out of the liver.
Fig. 4. Skeletal abnormalities in mutant E15.5 embryos. (A) Cranial bones. wt, left; mutant, right. bb, basisphenoid bone; pb, parietal bone; fb, frontal bone; zb, zygomatic bone; nb, nasal bone. Note the failure in the mutant for the nb to fuse, and retardation or absence of other bone structures. (B) Scapula. wt, left; mutant, right. Note the poor development of the acromion (a). (C) Thoracic cavity. wt, left; mutant, right. Note the failure for the sternal bands (arrows) to meet in the mutant. (D) Side view of spinal column. wt, left; mutant, right. Note the severe arching in the mutant. (E,F) Rib fusions in mutant embryo (heavy arrowheads) and incomplete fusion of the sternal bands. s, sternal bands. (G-I) Frontal view of cervical vertebrae from wt (G) and mutant (H-I) embryos. Note different levels of vertebral fusions (arrows; also in E and F). (J) Dissected ninth thoracic vertebrae from wt (bottom) and mutant (top) embryos. Note the absence of flexure of the mutant vertebra. a, vertebral arch; vb, vertebral body. (K) Dissected first sacral vertebrae from wt (bottom) and mutant (top) embryos.

Fig. 5. Expression of sclerotome (A,B) and myotome (C-F) markers in wild-type (leftmost) and mutant E10.5 embryos. (A) Pax1 in situ hybridization. This marker is expressed normally in mutant somites, but is absent from the anterior proximal limb bud. (B) Twist is expressed normally in mutant embryos as seen by in situ hybridization. (C) Whole-mount immunohistochemistry for myosin heavy chain expression, detected following partial clearing of the embryos. Note in wild-type embryo the absence of a ventral myotome in the most rostral somites and the rounded shape of the myotome. The myotome in the rostral somites of the mutant embryo (arrow) has an elongated shape, is missing in the fifth most rostral somite and is fused between the seventh and eighth somite. (D) Dark-field photomicrograph of myogenin in situ hybridization. Note the alterations in myogenin expression in the most rostral somites (arrow) of the myotome. The abnormalities seen in C and D in the rostral myotome of mutant embryos are enlarged in E and F, respectively.
were dead by E16, but survivors exhibited accentuated phenotypes, with extensive bleeding in the head and along the vertebral column, which appeared enlarged (Fig. 3E,F). The extensive hemorrhaging observed in the mutant embryos is a likely cause of death.

Histological sections through mutant embryos confirmed the extensive edema (Fig. 3G,H). The skin was distended, and the epidermal layer was very thin and separated from any dermal layer when blebbed, perhaps similar to the phenotype observed in Ph embryos (Schattenman et al., 1992). The neural tube was abnormally thin dorsally and lacked a roof plate (arrow in Fig. 3H). Moreover, tissues such as liver were bulging from the abdominal wall musculature. Despite the extensive bleeding in the mutants, a thinning of the vasculature or cardiac defects were not immediately apparent in tissue sections or following whole-mount immunohistochemistry forPECAM-1 (Baldwin et al., 1994) and septation in the heart had proceeded normally in at least some of the surviving E15 embryos.

**Skeletal abnormalities in mutant embryos**

Skeletal preparation were made from E13-E15 embryos. This examination revealed significant defects in the skull, most conspicuous in the anterior bones (Fig. 4A). In particular, the nasal bone failed to fuse in the midline. The frontal bone and, to a lesser extent, the parietal bone exhibited incomplete fusion towards the top of the skull. The zygomatic bone, which was partially ossified by E15 in wild-type embryos, was unde-

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observed by counting labeled cells in tissue sections either at E10 or E14 (not shown). However, some tissues or cell types may be affected that were not detected. In particular, although labeling was observed throughout various bones, the shorter length of the arches in thoracic vertebrae, and the ensuing *spina bifida*, might be indicative of reduced cell proliferation.

Apoptotic cell death was examined at E9 and E10 by the ‘whole death’ procedure (Conlon et al., 1995). No significant difference between wild-type and mutant embryos was observed at E9; however, by E10, increased apoptosis in mutant embryos compared to wild type was observed in the somites, as well as in the cephalic region and the branchial arches (Fig. 6A). Sections through the labeled embryos revealed the presence of some apoptotic cells in the trunk close to the roof plate of the neural tube and within the sclerotome, reflecting the migratory pathways adopted by neural crest cells where normal cell death has been observed (Jeffs and Osmond, 1992). However, the clearest labeling was in the dermomyotome (Fig. 6B,C). Although the absolute number of apoptotic nuclei varied from experiment to experiment, there was a consistent increase in cell death in mutants in four separate experiments. The average number of apoptotic cells per somite (sectioned through rump of embryo) was 8.03±3.31 s.d. in the mutant shown in Fig. 6C (n=35 sections) versus 3.22±2.58 s.d. in a wild-type littermate (not shown). In the cranial areas, increased cell death was observed in a stream of cells flanking the otic vesicle as well as in the branchial arches (Fig. 6D-G). Again, this corresponds to the area of migration of neural crest cells (Jeffs et al., 1992). Importantly, the observed defects in the heads of the mutant embryos are consistent with the absence of neural crest cell derivatives (Morrison-Graham et al., 1992). Despite extensive cell death in this region, neuronal derivatives of cranial neural crest cells appeared to migrate properly, as observed by neurofilament expression (data not shown). These results suggest that the defects observed in *PDGFαR* mutant embryos might be due in part to increased apoptosis of a non-neuronal subset of cranial neural crest cells.

**DISCUSSION**

Two different mutations targeted into the *PDGFαR* gene indicate a requirement for PDGF signaling in cranial neural crest development and in the normal patterning of the somites. Several aspects of the mutant phenotype reported here differ from that observed for Ph mice, which harbor a deletion of the *αR* gene (Table 2). The first and most conspicuous difference is the absence of a pigmentation defect in heterozygotes. The close linkage between the *Ph* and *W* mutations, originally observed by Grüneberg and Truslove (1960), and the subsequent identification of the *kit* receptor tyrosine kinase gene at the W locus (Chabot et al., 1988; Geissler et al., 1988), have led to long-standing speculations that the pigmentation defect in Ph might be somehow related to *kit* misexpression. In support of this possibility, Ph heterozygous embryos exhibit an enlarged domain of expression of *kit* in the somites (Duttlinger et al., 1995; Wehrle-Haller et al., 1996). However, the lack of a pigmentation defect in *αR* mutants does not prove that altered *kit* expression is responsible for that phenotype in Ph, but merely that the *αR* is not absolutely required for melanocyte migration.

<table>
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<th>PDGFαR</th>
<th>Ph</th>
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<tr>
<td>Survival on C57BL/6J</td>
<td>Up to E16 (N4 backcross)</td>
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<tr>
<td>Trunk crest</td>
<td>No pigmentation defect</td>
</tr>
<tr>
<td>Cardiac crest</td>
<td>Septation</td>
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<tr>
<td>Cranial crest</td>
<td>Cleft face</td>
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<tr>
<td>Spina bifida</td>
<td>Fusions of cervical vertebrae and ribs; truncated acromion</td>
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*αR* mutants differed from Ph by several features other than the absence of a melanocyte migration defect. First, approximately 80% of the mutant embryos survived up to E13 following six backcross generations to C57BL/6J, whereas less than 3% of Ph embryos survive on the same background (Orr-Urütregre et al., 1992; and data not shown). In addition, many *αR* mutant embryos were recovered up to E16, even if they were often dead, whereas only one third of Ph mutant embryos made it to this stage when backcrossed onto CBA (Grüneberg and Truslove, 1960) or Balb/c (Schatteman et al., 1992) backgrounds. However, embryos homozygous for the ‘Patch extended’ mutation (an even larger deletion) occasionally survive to birth (Truslove, 1977). Taken together, these observations indicate the presence of modifier loci linked to the *αR* gene, which affect embryo survival in various mutant backgrounds. Second, although fusions of the cervical vertebrae, ribs and the defects in the sternum have recently been reported in Ph in addition to the cleft face and *spina bifida* phenotypes, some Ph embryos carry an extra rib (Payne et al., 1997). Third, *Ph* embryos exhibit a frequent defect in septum formation in the heart (Morrison-Graham et al., 1992), whereas this process appears to proceed normally in at least some *αR* mutants examined at E15. These results indicate that the *Ph* phenotype is multigenic, with some but not all features attributable to the loss of the PDGFαR.

The skeletal defects observed in the trunk are complex and include fusions of the cervical vertebrae and of the ribs, altered flexure of the thoracic vertebrae and incomplete development of the sternum. All of these bones derive from the sclerotome, which expresses the αR, whereas PDGF A is expressed in the myotome (Orr-Urütregre et al., 1992; Orr-Urütregre and Lonai, 1992). Based on these expression patterns, the observed defects might be expected to stem from an initial deficiency in the sclerotome. However, the alternate expression of the ligand and receptor in the myotome and sclerotome might indicate a signaling pathway between the two compartments required for normal sclerotome development. Surprisingly, myotome but not sclerotome markers were the ones to highlight deficiencies in the somites. At a gross level, however, muscle formation appeared normal in later stage embryos. The alterations in patterning were especially noticeable in the more rostral somites, which either showed an absence of myotome, myotomal fusions between somites or an elongated shape of the myotomal compartment. This result might indicate different requirements for growth factors or different growth factor expression patterns along the rostral-caudal axis.

A number of classical and targeted mutations have been shown to lead to deficiencies in rib formation, but those in the myogenic genes reinforce the importance of myotome-to-
sclerotome signaling. In the case of the MRF4/myf6 gene, the variability in the rib fusion phenotype between different mutant strains has been attributed to position effect interference of the neo targeting cassette (for a review, see Olson et al., 1996) with the expression of the neighboring myf5 gene, which is required for rib formation (Braun et al., 1992). Interestingly, the myf5 mutation eliminates FGF4 and FGF6 expression in the myotome, and members of the FGF and TGFβ family are able to stimulate chondrogenesis in somite micromass cultures (Grass et al., 1996), as does PDGFA (M. Tallquist and P.S., unpublished data). These results suggest that multiple growth factors may be involved in myotome-to-sclerotome signaling. Although the αR may act autonomously in the myotome if it is expressed there at low levels, its earlier expression in the undifferentiated somites rather suggests a defect in the initial formation of the myotome. It is also possible that the defect in myotome formation arises from a feedback mechanism from the sclerotome, due to the absence of the αR. Last, subepidermal blebs might lead to poor contact between the surface ectoderm and the neural tube or undifferentiated somites, and be a contributing factor preventing proper dorsalinization of the neural tube and the formation of myotome (Fan and Tessier-Lavigne, 1994; Spence et al., 1996) as well as neural crest cells (Dickinson et al., 1995; Liem et al., 1995; Selleck and Bronner-Fraser, 1995).

In the head, the observed defects were similar if not identical to those observed for Ph embryos and have been attributed to a failure of a subset of non-neuronal neural crest cells, which exhibit high levels of αR expression, to migrate to their proper destinations (Morrison-Graham et al., 1992). PDGFs are known to be involved in chemoattraction, and it is possible that such a migratory mechanism may play a role in the mutant phenotype. Conversely, the PDGFAαR has also been associated with inhibition of chemotaxis mediated by other growth factors receptors, in particular the βR (Koyama et al., 1992). Alternatively, it has been suggested that the defect in neural crest cell migration in Ph mice might be associated with an alteration in the deposition of the extracellular matrix along the cell migration pathway (Morrison-Graham et al., 1992), as PDGFs are known to be involved in ECM production.

PDGFs were initially identified as mitogens for a number of different cell types, but BrdU incorporation studies in the mutant embryos failed to detect any general decrease in cell proliferation. A more extreme view of potential roles of growth factors has been advanced by Raff and colleagues (Raff, 1992; Raff et al., 1993). According to this viewpoint, cells would normally undergo cell death if not sustained by growth factors. A role of PDGF as a survival factor is substantiated by studies of a number of cell types in culture, including oligodendrocytes (Barres et al., 1992); however, such a role in vivo might be more difficult to demonstrate and there is no direct evidence supporting a direct role for PDGF as a survival factor for neural crest cells. Increased apoptosis was noticed along the pathway of migration of cranial neural crest cells, which express high levels of the αR (M. Bronner-Fraser, personal communication). In vitro cultures of neural crest cells, grafting experiments and...
the derivation of mice carrying conditional or point mutations in the receptors may help further understand the cell autonomy and the mechanistic basis for the mutant phenotype.

The genes encoding both PDGF receptors and both PDGF ligands have now been disrupted. JR (Soriano, 1994) and PDGF B mutant embryos (Levèén et al., 1994) exhibit a generally similar phenotype, characterized by hematological and kidney defects. However, the phenotype of PDGF A mutant mice appears to vary significantly from that of the αR mutants presented here. Only a small percentage of the PDGF A mice survive past birth, where they exhibit a lung emphysema-like phenotype; and the embryos that die during development do not exhibit the skeletal abnormalities characteristic for the αR mutation (Boström et al., 1996; M. Hellström, C. Betsholtz, and P.S., unpublished observations).

Analysis of double receptor and double ligand mutants is underway, which may help further understand the requirements for PDGF during embryogenesis.

This work is dedicated to the memory of Hal Weintraub. I thank Chris Auger for careful and dedicated help with genotyping of mutant mice and embryos; Kari Lindstrum for care of the animals; Brigid Chris Auger for careful and dedicated help with genotyping of mutant mice and embryos; Kari Lindstrum for care of the animals; Brigid

REFERENCES


PDGF and skeletal development

subfamily and are differentially expressed during early mesodermal patterning in mouse embryos. Development 116, 1123-1136.


its receptor are expressed in separate, but adjacent cell layers of the mouse embryo. *Development* 115, 1045-1058.


(Accepted 9 May 1997)