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Myogenin can substitute for Myf5 in promoting myogenesis but less efficiently

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SUMMARY

The myogenic basic Helix-Loop-Helix transcription factors, including Myf5, MyoD, myogenin (myg) and MRF4, play important roles in skeletal muscle development. The phenotypes of mutant mice deficient in either gene are different, suggesting that each gene may have a unique function in vivo. We previously showed that targeting *myogenin* into the *Myf5* locus (*Myf5$^{myg\text{-}ki}$*) rescued the rib cage truncation in the Myf5-null mutant, hence demonstrating functional redundancy between Myf5 and myogenin in skeletal morphogenesis. Here we present the results of crossing *myogenin* knock-in (*myg-ki*) mice with either MyoD-null or myogenin-null mutants. The *Myf5$^{myg\text{-}ki}$* allele rescued early myogenesis, but *Myf5(myg-ki/myg-ki);MyoD(−/−)* mutant mice died immediately after birth owing to reduced muscle formation. Therefore, myogenin, expressed from the *Myf5* locus, is not able to completely replace the function of Myf5 in muscle development although it is capable of determining and/or maintaining myogenic lineage. *Myf5(myg-ki/myg-ki);myg(−/−)* mutant mice displayed the same phenotype as *myg(−/−)* mutants. This indicates that the earlier expression of *myogenin* cannot promote myogenic terminal differentiation, which is normally initiated by the endogenous myogenin. Thus, our results are consistent with the notion that Myf5 and myogenin are functionally interchangeable in determining myogenic lineage and assuring normal rib formation. Our experiment revealed, however, that some aspects of myogenesis may be unique to a given myogenic factor and are due to either different regulatory sequences that control their temporal and spatial expression or different functional protein domains.

Key words: Myf5, myogenin, MyoD, knock-in, redundancy, myogenesis, mouse

INTRODUCTION

During vertebrate embryogenesis, somites are formed from the segmental mesoderm in a rostral-to-caudal direction. The ventral part of the somite becomes the sclerotome, which differentiates into skeletal structures, such as the vertebrae and ribs. Simultaneously, the dorsal part develops into the dermatome, which contributes to dermis, and the myotome, which differentiates into skeletal muscle (Sassoon, 1992). Skeletal muscle formation involves two steps: (1) commitment of mesodermal progenitors to myoblasts, and (2) terminal differentiation of committed skeletal myoblasts into myotubes. Both steps are regulated by the myogenic basic Helix-Loop-Helix (bHLH) transcription factors, including Myf5, MyoD, myogenin and MRF4 (Rudnicki and Jaenisch, 1995; Olson and Klein, 1994; Buckingham, 1994). In tissue culture, Myf5 and MyoD are expressed in proliferating myoblasts, and myogenin and MRF4 are only detected in differentiating myoblasts or myotubes. However, forced expression of each of these myogenic bHLH genes can convert non-muscle cells into myoblasts and eventually into myotubes (Weintraub et al., 1991; Olson, 1990). In addition, embryonic stem cells deficient in both Myf5 and MyoD are able to differentiate into skeletal muscle (P. Schegelsberg, P. Klemm and R. Jaenisch, unpublished observations). These observations suggest that all of the myogenic bHLH factors are capable of regulating both steps of myogenesis and therefore may be functionally interchangeable.

It is known that the axial muscle and the limb muscle are derived from the dorsal-medial half and the ventral-lateral half of the somite, respectively (Christ et al., 1978; Ordahl and Le Douarin, 1992). Also, it has been shown that all four myogenic bHLH genes have different expression patterns in early mouse embryos. *Myf5* is expressed in the somites at embryonic day 8.0 (E8.0) (Ott et al., 1991), followed by *myogenin* at day E8.5, *MRF4* at day E9.0 and *MyoD* at day E10.5 (Sassoon et al., 1989; Bober et al., 1991; Hinterberger et al., 1991). Moreover, some of the factors are expressed in different compartments of the myotome. While Myf5 and MyoD are initially expressed in the dorsal-medial half and the ventral-lateral half of the myotome, respectively, myogenin and MRF4 are expressed in the whole myotome (Smith et al., 1994). The distinct expression pattern of each gene implies they may play different roles during skeletal muscle development. Indeed, the phenotypes of mice deficient in each of the four myogenic bHLH genes suggest that they function at different points in the myogenic pathway. MyoD-null mice generated by homologous recombination were viable with apparently normal skeletal muscle development (Rudnicki et al., 1992), although a recent study indicated that the adult

MyoD mutants had deficit in muscle regeneration (Megeney et al., 1996). Similarly, muscle formation was normal in newborn mice deficient in *Myf5*. Nevertheless, the Myf5 mutants died perinatally due to a rib cage truncation (Braun et al., 1992). *Myf5* is the first expressed myogenic bHLH gene (Ott et al., 1991), and the Myf5-positive cells formed early in the myotome may provide a permissive environment for the differentiation of adjacent skeletal precursor cells from which the ribs are derived. Therefore, the rib defect in Myf5 mutants may be due to the loss of those Myf5-positive myogenic cells and other later expressed myogenic factors may not substitute for the role of Myf5 in rib development. Consistent with this speculation, the initial expression of muscle-specific markers in the myotome was delayed by 2 days in Myf5 mutants (Braun et al., 1992). Normal muscle formation in either Myf5 or MyoD mutants suggests that these two myogenic factors have overlapping functions in skeletal muscle development. Indeed, this notion was supported by the observation that no skeletal muscle was formed in mutant mice lacking both *Myf5* and *MyoD* (Rudnicki et al., 1993). In contrast, mice lacking myogenin had normal numbers of myoblasts but very few muscle fibers (Hasty et al., 1993; Nabeshima et al., 1993), indicating the role of myogenin in myogenic terminal differentiation instead of myogenic lineage determination. Furthermore, MRF4 mutant animals had normal muscle formation but displayed a 5-fold elevation of *myogenin* expression, suggesting myogenin may compensate for the absence of MRF4 (Zhang et al., 1995). The severe phenotypes of two other *MRF4* mutants (Patapoutian et al., 1995; Braun and Arnold et al., 1995) probably resulted from down-regulation of the *Myf5* expression caused by the MRF4 mutations through a positional effect (Olson et al., 1996). On the basis of phenotypes observed in mice deficient in one or two myogenic factors, a simplified myogenic pathway was postulated: Myf5 or MyoD is required for establishing and/or maintaining myoblasts, while myogenin and MRF4 are responsible for the differentiation of myoblasts into myotubes (Weintraub, 1993). Furthermore, we demonstrated previously that the expression of myogenin from the *Myf5* locus ($Myf5^{myg\text{-}ki}$) rescued the rib cage truncation in Myf5-null mutants (Wang et al., 1996). This experiment suggested that myogenin can replace the role of Myf5 in rib cage formation and argued that the different phenotypes of mice deficient in either Myf5 or myogenin were due to the distinct developmental expression pattern of the respective gene.

To investigate whether $Myf5^{myg\text{-}ki}$ alone is sufficient for normal muscle formation, we crossed the *Myf5(myg-ki/myg-ki)* mutation into the *MyoD(–/–)* background to generate double homozygous mutants. The mutant mice died at birth due to reduced muscle formation. This result suggests that myogenin, when expressed in the same temporal and spatial pattern as *Myf5*, is able to replace the role of Myf5 in myogenic lineage determination, but is not as potent as Myf5 in promoting normal muscle formation. However, when the *Myf5(myg-ki/myg-ki)* mutation was introduced into the *myg(–/–)* background to produce double mutants, the earlier expression of *myogenin* did not rescue the phenotypes of the myogenin-null mutant. These findings demonstrate that Myf5 and myogenin are functionally interchangeable to some extent, and that regulatory sequences guiding developmental activation may be responsible for some of their unique roles in skeletal muscle development.

MATERIALS AND METHODS

Animal breeding

Myf5(myg-ki/myg-ki) mice were crossed with MyoD(–/–) mice to generate Myf5(+/myg-ki);MyoD(+/–). Myf5(myg-ki/myg-ki);MyoD(–/–) and Myf5(+/myg-ki);MyoD(–/–) were recovered by interbreeding Myf5(+/myg-ki);MyoD(+/–) double heterozygotes.

Similarly, *Myf5(+/myg-ki);myg(+/–)* double heterozygotes were produced by crossing *Myf5(myg-ki/myg-ki)* mice with *myg(+/–)* mice. Subsequently, those double heterozygotes were interbred to generate *Myf5(myg-ki/myg-ki);myg(–/–)* and *Myf5(+/myg-ki);myg(–/–)*.

The genotyping for each gene was performed as described (Rudnicki et al., 1992; Wang et al., 1996; Hasty et al., 1993).

RNA isolation and RT-PCR

RNA was isolated (Chomczynnski and Sacchi, 1987) from the carcasses of newborn mice, in which the internal organs and heads were removed. The PCR primers used for detecting muscle-specific genes were described previously, and a different quantitative PCR condition was used for each set of primers (Zhang et al., 1995; Patapoutian et al., 1995) and tested to ensure the amplification was in a linear range. The ribosomal *RPL7* was used for normalizing the RT-PCR. The PCR products were then loaded on 1% agarose gel for Southern blot analysis by various probes.

Skeleton preparation and histological analysis

Newborn pups were skinned, eviscerated and stained with alizarin red and alcian blue (Zhang et al., 1995). For histological analysis, newborn mice were fixed in 4% paraformaldehyde, dehydrated with ethanol and embedded in paraffin. Tissue sections were stained with both hematoxylin and eosin. Immunofluorescence was performed on frozen sections with a monoclonal antibody against striated muscle-specific actinin (1:400 dilution; mouse IgG1; Sigma).

Immunostaining of primary myoblast cultures

Primary myoblasts were isolated from both wild-type and the mutant neonates and cultured according to Freshney (1987). To induce myogenic differentiation, 2% horse serum in DMEM was used. Immunostaining was performed by anti-skeletal myosin heavy chain (MF-20) and FITC-conjugated antibody to mouse IgG on fixed muscle cells.

RESULTS

$Myf5^{myg\text{-}ki}$;MyoD-null mice die perinatally

Double heterozygous mutant mice carrying *Myf5(+/myg-ki)* and *MyoD(+/–)* were generated by crossing mice carrying the *Myf5(myg-ki/myg-ki)* mutation to *MyoD*-null mutants and double heterozygous mutants were interbred. Nine different genotypes were expected among the offspring from the double heterozygous mutant intercrossing, with 6.25% and 12.5% expected to be *Myf5(myg-ki/myg-ki);MyoD(–/–)* and *Myf5(+/myg-ki);MyoD(–/–)*, respectively. As shown in Table 1, all genotypes were found at the expected frequency after weaning except *Myf5(myg-ki/myg-ki);MyoD(–/–)* and *Myf5(+/myg-ki);MyoD(–/–)*. To investigate lack of both mutant classes, pups were delivered by Cesarean section at term (day E18.5) or killed immediately after birth. Mice carrying all nine genotypes were observed from either the *Myf5(+/myg-ki);MyoD(+/–)* intercross or the cross between *Myf5(myg-ki/myg-ki);MyoD(+/–)* and *Myf5(+/myg-ki);MyoD(+/–)*, approximately at the expected frequency (Table 2A,B). This observation suggests that the combination

Table 1. Offspring of Myf5(+/ki);MyoD(+/–) intercrosses

Genotype		Frequency	
Myf5	MyoD	Predicted %	Observed % (No.)*
+/+	+/+	6.25	12 (7)
+/+	+/–	12.5	10 (6)
+/+	–/–	6.25	2 (1)
+/ki	+/+	12.5	22 (13)
+/ki	+/–	25	26 (15)
+/ki	–/–	12.5	0 (0)
ki/ki	+/+	6.25	7 (4)
ki/ki	+/–	12.5	21 (12)
ki/ki	–/–	6.25	0 (0)

*Data from 58 of 3-week-old mice.

of either two *Myf5*$^{myg\text{-}ki}$ alleles, or one *Myf5* plus one *Myf5*$^{myg\text{-}ki}$ allele, was unable to support the postnatal survival of MyoD-null mutants.

Myf5(myg-ki/myg-ki);MyoD(–/–) newborn mice initially appeared alive but quickly became immobile and cyanotic. They were relatively smaller (80% of their wild-type litter mates) and displayed arched spines. Dissection of these mutant pups revealed obvious skeletal muscle reduction in trunks and limbs. Slightly deformed rib cages were observed in skeletons prepared from those pups (Fig. 1). Mutant mice carrying *Myf5(+/myg-ki);MyoD(–/–)* genotype appeared normal immediately after they were born. They had normal breathing and movements initially, but their respiration gradually became intermittent. Eventually the mutants became cyanotic and died. Some pups survived for a few hours postnatally. Newborn *Myf5(+/myg-ki);MyoD(–/–)* pups were comparable to their wild-type litter mates except for slightly curved spines.

Table 2(A). Offspring of Myf5(+/ki);MyoD(+/–) intercrosses

Genotype		Frequency	
Myf5	MyoD	Predicted %	Observed % (No.)*
+/+	+/+	6.25	3 (1)
+/+	+/–	12.5	18 (7)
+/+	–/–	6.25	5 (2)
+/ki	+/+	12.5	21 (8)
+/ki	+/–	25	24 (9)
+/ki	–/–	12.5	3 (1)
ki/ki	+/+	6.25	0 (0)
ki/ki	+/–	12.5	21 (8)
ki/ki	–/–	6.25	5 (2)

*Data from 38 newborn mice.

Table 2(B). Offspring of Myf5(ki/ki);MyoD(+/–) and Myf5(+/ki);MyoD(+/–) crosses

Genotype		Frequency	
Myf5	MyoD	Predicted %	Observed % (No.)**
+/ki	+/+	12.5	14 (3)
+/ki	+/–	25	14 (3)
+/ki	–/–	12.5	9 (2)
ki/ki	+/+	12.5	18 (4)
ki/ki	+/–	25	27 (6)
ki/ki	–/–	12.5	18 (6)

**Data from 22 newborn mice.

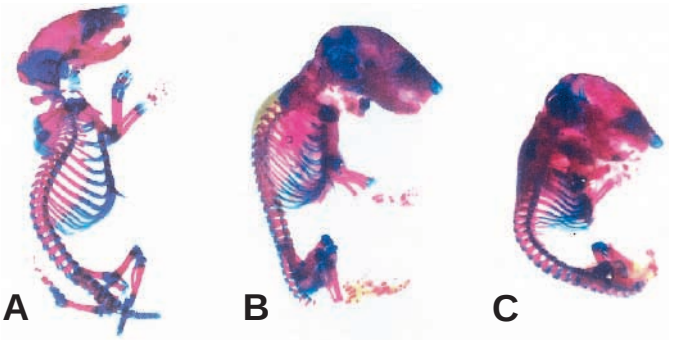

Fig. 1. *Myf5*$^{myg\text{-}ki}$ and *MyoD* double mutant mice show defects in spines. Both wild-type and mutant newborns were stained with alizarin red and alcian blue to show bones and cartilage. (A) Wild-type skeleton, (B) *Myf5(+/myg-ki);MyoD(–/–)* and (C) *Myf5(myg-ki/myg-ki);MyoD(–/–)*.

Skeletons prepared from those pups displayed normal rib cage formation (Fig. 1). These results indicated that *Myf5(+/myg-ki);MyoD(–/–)* mutants might have reduced skeletal muscle, suggesting that the *Myf5*$^{myg\text{-}ki}$ allele contributes little to postnatal viability when compared to *Myf5(+/–);MyoD(–/–)* pups (Rudnicki et al., 1993).

Skeletal muscle formation in mice deficient for MyoD but carrying the *Myf5*$^{myg\text{-}ki}$ allele

To investigate muscle-specific gene expression in mutant mice carrying *Myf5(myg-ki/myg-ki);MyoD(–/–)*, RNA was isolated from the skeletal muscle of newborn pups and analyzed by RT-PCR (reverse transcriptase polymerase chain reaction). RNA from litter mates carrying wild-type or *Myf5(+/myg-ki);MyoD(–/–)* alleles was also included in the experiments for comparison. The newborn *Myf5(myg-ki/myg-ki);MyoD(–/–)* pups expressed all the skeletal muscle-specific markers tested, including myosin light chain, fetal-myosin heavy chain, muscle creatine kinase, troponin T and alpha-skeletal actin (Fig. 2A). However, the levels of expression were reduced to approximately 10% of wild type. Similar reduction in the expression of muscle-specific genes was also observed in the E9.5 mutant embryo (data not shown). These results indicate that the Myf5$^{myg\text{-}ki}$ is able to promote myogenesis and activate the downstream muscle-specific genes. However, Myf5$^{myg\text{-}ki}$ is less potent than Myf5 in promoting myogenesis.

Myf5(+/myg-ki);MyoD(–/–) mutant mice died shortly after birth despite their relatively normal appearance, Fig. 2A shows that the expression levels of muscle-specific genes in those pups were generally about 50-60% of the wild-type litter mates. This suggested that the muscle formation promoted by the *Myf5*$^{myg\text{-}ki}$ allele was much less than that by the *Myf5* allele.

The expression of the myogenic bHLH genes was also analyzed in mutant mice using RT-PCR. Both *myogenin* and *MRF4* were expressed in *Myf5(myg-ki/myg-ki);MyoD(–/–)* mice, but the levels of expression were only about 10% of that of wild type (Fig. 2B). This suggests that myogenin expressed from the *Myf5* locus is able to activate the endogenous *myogenin* and subsequently *MRF4*. The expression levels of *myogenin* and *MRF4* in *Myf5(+/myg-ki);MyoD(–/–)* were only half of that of wild type (Fig. 2B), a similar reduction as seen for muscle-specific gene

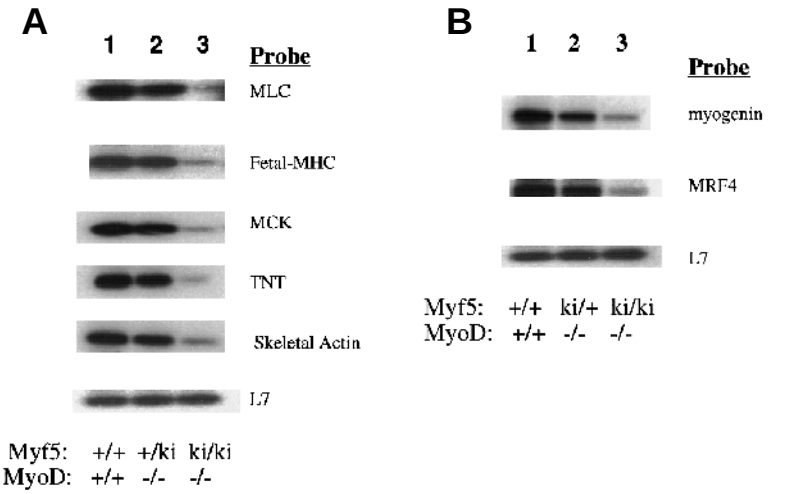

Fig. 2. Skeletal muscle-specific markers are present in Myf5$^{myg\text{-}ki}$;MyoD-null mice. Total RNA was isolated from newborn skeletal muscle and subjected to quantitative RT-PCR analysis for detecting transcripts of (A) skeletal muscle-specific markers and (B) the myogenic bHLH genes. The following genes have been analyzed: myosin light chain 1 and 3 (*MLC*); fetal-myosin heavy chain (*fetal-MHC*); muscle creatine kinase (*MCK*); troponin T (*TNT*); skeletal actin; *myogenin* and *MRF4*. The gene encoding ribosomal protein *L7* was used for normalizing the RNA input and PCR efficiency, and each PCR amplification was in a linear range.

expression (Fig. 2A). These results suggest the *Myf5$^{myg\text{-}ki}$* allele induces reduced levels of downstream bHLH genes or muscle-specific genes as compared to the *Myf5* wild-type allele.

To assess the morphology of skeletal muscle in mutant mice, Harris' hematoxylin and eosin (HE)-stained tissue sections were prepared from *Myf5(myg-ki/myg-ki);MyoD(–/–)* mutants, as well as wild-type litter mates at newborn stage. In *Myf5(myg-ki/myg-ki);MyoD(–/–)* mutants, apparently normal muscle fibers with normal density of nuclei were found throughout the body. However, the numbers of muscle fibers and nuclei were greatly reduced, and the reduction was more predominant in the back and limbs than in the intercostal area between ribs and the diaphragm (Fig. 3; Table 3). Also, immunofluorescent staining on tissue sections using a monoclonal antibody against striated muscle-specific actinin showed reduced numbers of skeletal muscle fibers, although they were normally stained in the mutant mice (Fig. 4A). Similarly, immunostaining of primary cultured muscle cells from both wild type and mutants revealed comparable levels of muscle-specific proteins (Fig. 4B). These findings indicate that myogenin, expressed from the *Myf5* locus, is able to activate the whole process of myogenesis but the numbers of muscle fibers and nuclei are reduced as compared to myogenesis promoted by Myf5. In *Myf5(+/myg-ki);MyoD(–/–)* mutants, HE staining revealed about 50-60% muscle fiber formation as compared to wild type (data not shown; Rudnicki et al., 1993), which is consistent with the finding by RT-PCR. This implies that the *Myf5* allele played a quantitatively more important role in muscle formation, whereas the *Myf5$^{myg\text{-}ki}$* allele was much less efficient.

The *Myf5$^{myg\text{-}ki}$* allele does not rescue the phenotype of myogenin-null mice

To ask whether myogenin expressed from the *Myf5* locus is functional in later myogenic terminal differentiation in the absence of the endogenous myogenin, double heterozygotes were produced by crossing *Myf5(myg-ki/myg-ki)* mice with *myg(+/–)* mutants, and the double heterozygotes were intercrossed to generate mutant mice that carried various genotypes.

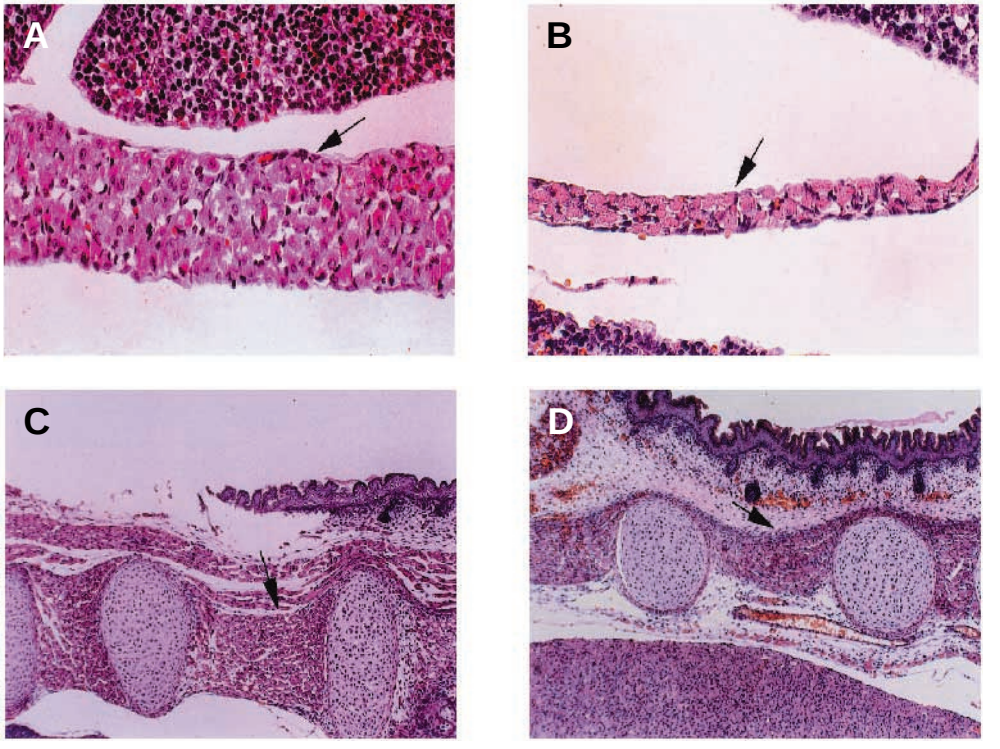

Fig. 3. Skeletal muscle formation in Myf5$^{myg\text{-}ki}$;MyoD-null mice. Hematoxylin and eosin staining was performed on the sagittal sections through the diaphragm (A,B) and intercostal muscle (C,D). *Myf5(myg-ki/myg-ki);MyoD(–/–)* mutant mice (B,D) had reduced skeletal muscle formation compared to wild type (A,C). The arrows point to the diaphragms or representative intercostal muscles. Magnification: (A,B) ×200; (C,D) ×100.

Table 3. Myf5(ki/ki);MyoD(–/–) mutant has reduced numbers of muscle fibers*

Genotype	Diaphragm	Intercostal	Back
Wild type	9.5±0.5	20.5±1.6	18.5±1.9
Myf5(ki/ki);MyoD(–/–)	2.8±0.4	9.4±1.4	2.9±0.6

*The numbers of muscle fibers were counted in HE-stained sections of wild-type and mutant newborn mice, and shown with the mean and the standard deviation.

Neither *Myf5(myg-ki/myg-ki);myg(–/–)* nor *Myf5(+/myg-ki);myg(–/–)* mutants were found among 3-week-old pups, but were recovered by Cesarean section at birth. Newborn mice carrying either genotype appeared very similar to *myg(–/–)* mutants (data not shown). To assess skeletal muscle formation in both *Myf5(myg-ki/myg-ki);myg(–/–)* and *Myf5(+/myg-ki);myg(–/–)* mutants, HE-stained tissue sections were prepared from the mutants as well as from pups carrying wild-type Myf5 but deficient for myogenin (Hasty et al., 1993; Nabeshima et al., 1993). A similar reduction in muscle fiber density was observed in all three mutants, and similar numbers of myoblasts were seen in areas normally occupied by muscle fibers (Fig. 5). These data suggest that earlier expressed myogenin did not rescue the phenotype of *myg(–/–)* mutants, thus implying that the function of the endogenous myogenin cannot be substituted by ectopically expressed myogenin.

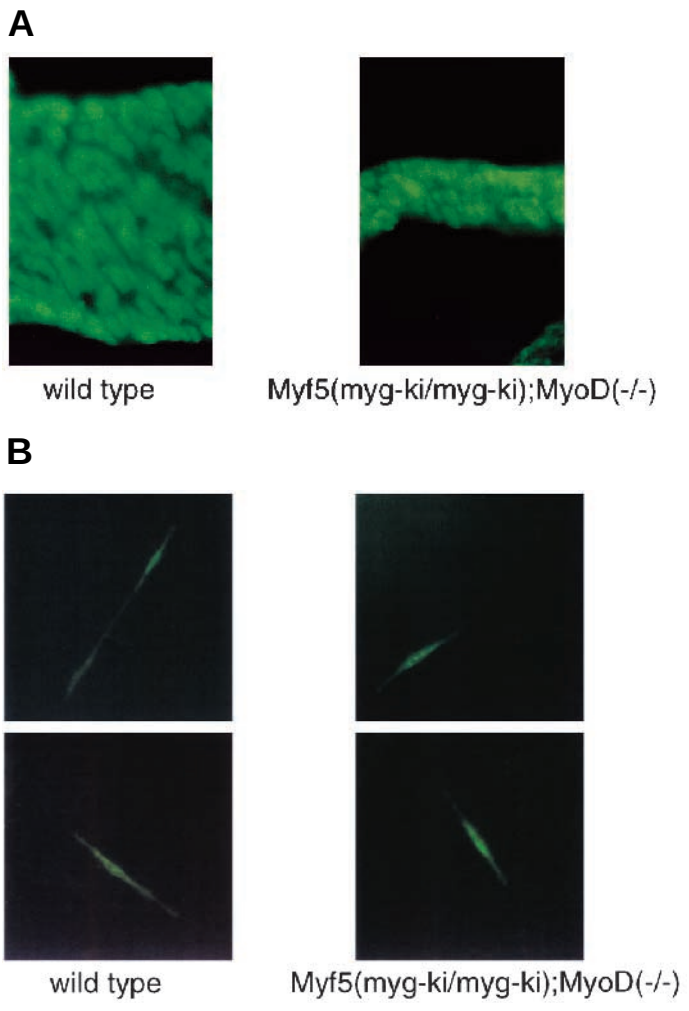

Fig. 4. The expression of muscle-specific proteins in muscle cells of both wild-type and mutant newborn mice. (A). Immunofluorescence was performed on frozen sagittal sections through the diaphragm. *Myf5(myg-ki/myg-ki);MyoD(–/–)* mutant with reduced numbers of skeletal muscles in the diaphragm (right) showing normal staining as in wild type (left). (B). Myoblasts were isolated from newborn mice with indicated genotypes and cultured in growth medium. In vitro differentiation was induced by culturing myoblasts in differentiation medium for 3 days, and the cells subsequently showed expression of muscle-specific proteins with anti-MHC antibody. Magnification: (A,B) ×400.

DISCUSSION

We have shown that both *Myf5(myg-ki/myg-ki);MyoD(–/–)* and *Myf5(+/myg-ki);MyoD(–/–)* mutants die shortly after birth, due to reduced skeletal muscle formation. These results suggest that $Myf5^{myg\text{-}ki}$ is unable to completely replace the function of Myf5 in skeletal muscle formation. Nevertheless, both RT-PCR and histological studies revealed normal skeletal muscle formation, although at a quantitatively reduced level. We have also shown that the phenotype of *Myf5(myg-ki/myg-ki);myg(–/–)* mutant mice essentially resembles that of *myg(–/–)* mutant (Hasty et al., 1993; Nabeshima et al., 1993), indicating that earlier expression of myogenin cannot promote differentiation of myoblasts into myotubes. Our investigation is relevant to the question of functional redundancy of the myogenic bHLH factors during skeletal muscle development.

The myogenic bHLH factors are a group of transcription factors that play key roles during skeletal muscle development. Functional redundancy has been suggested by the fact that each of the four myogenic bHLH factors is able to convert non-muscle cells into myocytes (Weintraub et al., 1991; Olson, 1990). The phenotypes of the mutant mice deficient in each gene have, however, allowed the placing of the factors in a myogenic pathway (Rudnicki and Jaenisch, 1995; Olson and Klein, 1994), ascribing a distinct function to each gene. While either Myf5 or MyoD is essential for determining or maintaining the myogenic lineage, Myf5 is also crucial for rib formation. In contrast, myogenin and MRF4 are important for myogenic terminal differentiation. Two hypotheses have been postulated to reconcile the in vitro and in vivo data on functions of the myogenic bHLH factors. The unique function of each myogenic bHLH factor may be due to either its distinct temporal and spatial expression pattern or to its unique transcriptional activation domain (Lassar and Munsterberg, 1994). To understand how the unique function of each myogenic bHLH factor was conferred, we previously targeted *myogenin* into the *Myf5* locus and showed that $Myf5^{myg\text{-}ki}$ rescued rib cage truncation in the absence of Myf5 (Wang et al., 1996). Here we demonstrated that $Myf5^{myg\text{-}ki}$, like Myf5 or MyoD, was able to activate the endogenous myogenin and downstream muscle-specific markers, and ultimately promoted skeletal muscle formation. Although there was a similar level of muscle-specific proteins in both wild-type and *Myf5(myg-ki/myg-ki);MyoD(–/–)* mutant muscle cells, muscle formation was reduced in *Myf5(myg-ki/myg-ki);MyoD(–/–)* mice, which is most likely due to the reduced numbers of muscle fibers and nuclei. This indicates the $Myf5^{myg\text{-}ki}$ allele is not as potent as the *Myf5* allele in recruiting muscle precursor cells into myogenic lineage and/or maintaining the lineage. We consider three possible explanations for

muscle reduction in double homozygotes. First, the expression level of *Myf5*$^{myg\text{-}ki}$ may not be as high as that of *Myf5*. This is unlikely because the only alteration in the *Myf5*$^{myg\text{-}ki}$ locus was the replacement of coding sequences of *Myf5* exon 1 by *myogenin* cDNA, leaving all other regulatory elements intact. However, RNA stability may be different. Second, translation from the *Myf5*$^{myg\text{-}ki}$ transcript may be delayed or the myogenin protein may have a higher turnover rate than Myf5. Previous studies have shown that during embryogenesis myogenin protein was, indeed, detected at least one day later than *myogenin* transcripts (Cusella-De Angelis et al., 1992; Smith et al., 1994). Since either Myf5 or Myf5$^{myg\text{-}ki}$ was hardly detected in early mouse embryo by Western blot (data not shown), we have no direct evidence indicating whether the protein level of Myf5$^{myg\text{-}ki}$ was lower than that of Myf5 in early myogenic cells. Nevertheless, we do know that the level of the myogenic bHLH factors is important in determining the number of cells being recruited into myogenic lineage. This has been suggested by the previous study in which *Myf5(+/–);MyoD(–/–)* mutants produced only half as much muscle as *Myf5(+/+);MyoD(–/–)* (Rudnicki et al., 1993). Third, myogenin may be intrinsically less potent than Myf5 or MyoD in determining myogenic lineage. Consistent with this hypothesis, a recent study showed that myogenin has only 10% of the activity of either MyoD or Myf5 in activating transcription of muscle-specific genes in repressive chromatin (Gerber et al., 1997). The transcriptional activation domains of the myogenic bHLH factors are very divergent (Olson, 1990; Weintraub et al., 1991) and they may determine the efficiency of the different factors to promote the different steps of myogenesis. It was shown that two highly conserved regions in the transcriptional activation domains shared by MyoD and Myf5 may be responsible for their greater potency in myogenic lineage determination as compared to that of myogenin (Gerber et al., 1997). In the future, switching the transcriptional activation domains among the myogenic bHLH factors would be informative for understanding the roles of those domains in myogenesis.

The importance of the expression specificity of *Myf5* and *myogenin* in determining the unique role played by the respective gene was further corroborated by the fact that the *Myf5*$^{myg\text{-}ki}$ allele did not rescue the phenotype of myogenin-null mice. Our study supports the notion that the temporal expression of each myogenic bHLH gene may be important in determining its unique role in the myogenic pathway. Moreover, our results imply that the total level of the myogenic bHLH factors may be critical in determining the different state of muscle differentiation. A certain level of the myogenic bHLH factors may be necessary for myoblast determination or maintaining myoblasts in an active proliferating state and a much higher level of the same factors may be needed for terminal differentiation. We propose that, in vivo, one of the functions of Myf5 or MyoD is to greatly increase the level of total myogenic bHLH factors by activating *myogenin*, which then promotes myogenic terminal differentiation. In other words, the level of total myogenic bHLH factors, rather than an intrinsic specificity of each protein, may be important in determining whether myoblasts undergo terminal differentiation or not. Consistent with this is that myoblasts lacking myogenin were able to undergo terminal differentiation in vitro (Nabeshima et al., 1993; Rawls et al., 1995). Alternatively, the myogenic bHLH proteins

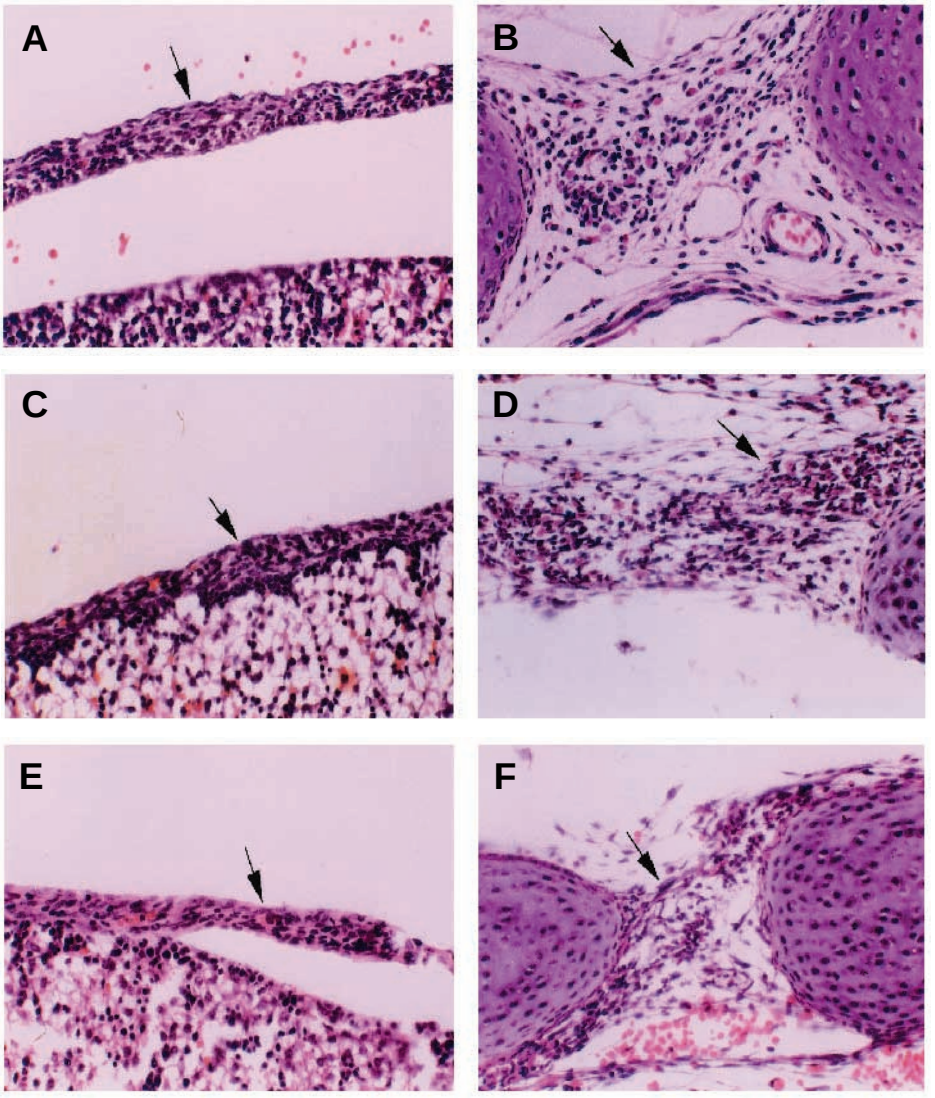

Fig. 5. Myf5$^{myg\text{-}ki}$ does not rescue myogenic differentiation in the myogenin knock-out mouse. Hematoxylin and eosin staining was performed on the sections through diaphragms (A,C,E) and intercostal muscles (B,D,F) from *myg(–/–)* mutant (A and B), *Myf5(myg-ki/myg-ki);myg(–/–)* (C,D) and *Myf5(+/myg-ki);myg(–/–)* (E,F). The arrows point to the diaphragms or intercostal areas. The numbers of muscle fibers in those mutants are largely reduced as compared to wild-type mice (Fig. 3A). Magnification: (A-F) ×200.

may have some intrinsic differences in promoting different steps of myogenesis, as was proposed by others (Gerber et al., 1997).

Our results are consistent with a model of hierarchical regulation during skeletal muscle development. Each myogenic bHLH gene may have distinct regulatory elements in its promoter, which respond to specific upstream activators. During embryogenesis, the promoters of *Myf5* and *MyoD* may be turned on by some as yet unidentified upstream transcription factors, whereas those of *myogenin* and *MRF4* may respond to the myogenic bHLH factors. Consistent with this model, the important binding site for the myogenic bHLH factors (E-box) has not been identified in either the *Myf5* or *MyoD* promoter (Patapoutian et al., 1993; Askura et al., 1995; Goldhamer et al., 1995). In contrast, E-boxes present in the *myogenin* and *MRF4* promoters are known to be essential for their proper activation (Cheng et al 1995; Yee and Rigby, 1995; Naidu et al., 1995; Black et al., 1995). The availability of more mouse mutations in myogenic genes will allow us to finally define the regulatory network operating in skeletal muscle development.

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