

mBtd is required to maintain signaling during murine limb development

Dieter Treichel,^{1,3} Frieder Schöck,²
Herbert Jäckle,² Peter Gruss,¹ and
Ahmed Mansouri^{1,4}

¹MPI für biophysikalische Chemie, Abt. Molekulare Zellbiologie, Am Fassberg, 37077 Göttingen, Germany;

²MPI für biophysikalische Chemie, Abt. Molekulare Entwicklungsbiologie, Am Fassberg, 37077 Göttingen, Germany

buttonhead (*btd*) encodes an SP1-like transcription factor required for the generation and specification of *Drosophila* head segments. We identified a murine *btd* homolog, termed *mouse Btd* (*mBtd*), which can support *btd*-dependent head development in transgenic fly embryos. Functional studies show that *mBtd*-deficient mice develop to term and die at birth. They exhibit brain malformations, posterior axial skeleton truncations, and shortened limbs. We present evidence that *mBtd* is required during early limb development to maintain, but not to initiate Wnt/ β -catenin-dependent FGF, Shh, and BMP-mediated signaling. The data indicate that *mBtd* represents a novel key player mediating proximodistal outgrowth of the limb.

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buttonhead (*btd*), *empty spiracles* (*ems*), and *orthodenticles* (*otd*) are required for anterior head development during *Drosophila* embryogenesis (Cohen and Jürgens 1991; Finkelstein and Boncinelli 1994). The three genes are expressed in overlapping domains at blastoderm stage. *btd* is required for development of the mandibular, *btd* and *ems* for the intercalary, and the combination of *btd*, *ems*, and *otd* for the antennal segment. *ems* and *otd* encode homeodomain transcription factors, and *btd* encodes an *Egr*-like zinc finger transcription factor (Wimmer et al. 1993).

Homologs of *ems* and *otd* have been identified in mouse. Functional analysis revealed that they are required for patterning processes during early embryonic brain development (Simeone 2002). A vertebrate homolog of *btd* has not yet been identified. However, sequence-related genes with a high degree of similarity were isolated. This includes human and mouse *Sp1*

(Wimmer et al. 1993; Schöck et al. 1999a) and the *btd*-like gene *bts1* of zebrafish (Tallafuss et al. 2001). Furthermore, BTB and SP1 proteins are capable of binding to the same DNA sites in vitro, share most biochemical properties, and regulate transcription via the same interacting factors (Wimmer et al. 1993; Schöck et al. 1999a). However, transgenes expressing *Sp1* or *bts1* in place of *btd* failed to rescue *btd* mutant embryos. This finding implies that despite the molecular similarities, none of the known vertebrate *btd*-like genes represents a *btd* ortholog (Schöck et al. 1999b; Tallafuss et al. 2001).

Here we report the identification and the functional analysis of a murine *btd* homolog, termed *mouse Btd* (*mBtd*), showing that its activity rescues head segment formation in *btd* mutant fly embryos. Loss of *mBtd* in the mouse embryo causes severe brain defects and truncations of body structures, including the posterior axial skeleton and limbs.

We focused our attention on the requirement of *mBtd* activity on limb development, a process that is initiated through interactions between ectoderm and mesenchyme. The result of these interactions is the formation of the so-called apical ectodermal ridge (AER), a signaling center which is generated through the concerted signaling activities of fibroblast growth factors (FGFs) and Wnt/ β -catenin (Tickle 2003). We show that the initial generation of the AER by *Wnt3* is not affected in *mBtd* mutants, whereas the expression of Fgfs and limb patterning genes is altered. Lack of *mBtd* results in apoptotic cell death in both mesenchymal and ectodermal tissue of the limb bud. The data provide evidence that the transcription factor *mBtd* is required to maintain gene expression initiated by FGF and Wnt signaling necessary for proximodistal limb outgrowth.

Results and Discussion

The *btd* homolog was isolated by a PCR-based approach, using degenerated primer pairs within the *btd* zinc finger box (Treichel et al. 2001). A resulting 230-bp DNA fragment was subsequently used to screen an embryonic day (E)8.5 mouse cDNA library. Several overlapping cDNA clones were isolated which represent the entire coding sequence of the *btd*-like gene.

The putative protein sequence of the *btd*-like gene (Fig. 1A) reveals an SP1-like zinc finger (dark green) and buttonhead (light green) domain. Thus, *btd*-like gene is a member of the SP1 family of transcription factors, such as SP1 and SP4 in mouse and human, D-SP1 and BTB in *Drosophila* (Wimmer et al. 1993, 1996; Schöck et al. 1999a), and BTS-1 in zebra fish (Tallafuss et al. 2001). The highly conserved zinc finger domain (>90% sequence identity) is insufficient to reconstruct the evolutionary relationship of the *btd*-like gene to other members of this gene family. Therefore, a comparison of the entire proteins was undertaken. As shown in Figure 1B, the putative protein contains a serine/threonine domain (red) followed by an alanine-rich sequence (yellow) similar to D-SP1 and BTB. It also contains a glycine-rich domain (blue), which is found in D-SP1, the paralog of BTB. In contrast, the glutamine-rich sequence (purple) found in BTB, D-SP1, SP1, SP4, and BTS1 is absent in the putative protein. This domain in BTB and D-SP1 cannot account for an evolutionary link to BTS1, as this se-

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³Present address: Max-Planck-Gesellschaft, Hofgartenstr. 8, 80539 München, Germany.

⁴Corresponding author.

E-MAIL amansou@gwdg.de; FAX (551) 201-1504.

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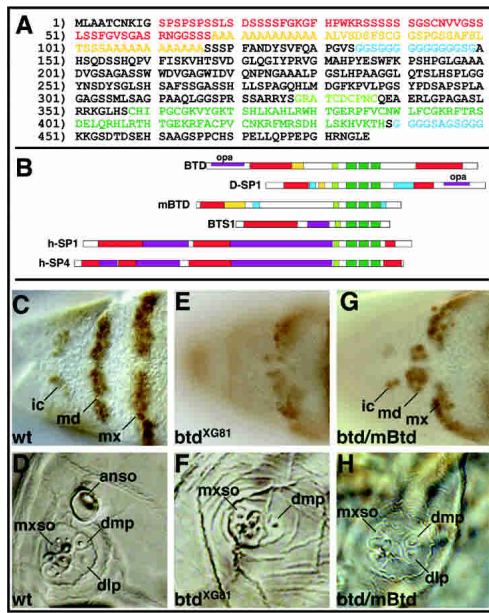


Figure 1. Cloning of *mBtd* and rescue experiment in *Drosophila*. (A) Complete amino acid sequence of the *mBtd* protein. Functional domains are highlighted in different colors. (B) Schematic comparison of the protein structure of the BTD, D-SP1, mBTD, BTS1, SP1, and SP4 proteins. Domains shown are as follows: zinc finger (dark green); *btd* domain (light green); serine/threonine-rich (red); alanine-rich (yellow); glycine-rich (blue); glutamine-rich (purple). (*opa*) Glutamine-rich *opa*-elements. (C–H) *mBtd* rescues *btd*-dependent aspects of *Drosophila* embryo head development. (C) Dorsal view of head segments in wild-type embryos visualized by anti-Engrailed antibody staining. The intercalary (ic), mandibular (md), and maxillary (mx) stripes are visible. (D) Antennomaxillary complex of a wild-type larva. Note the maxillary sense organ (mxso) of the maxillary segment, the dorsolateral papilla (dlp) of the intercalary segment, the antennal sense organ (anso) of the antennal origin, and the dorsomedial papilla (dmp) of the ocular (oc) segment. (E) *btd*^{XG81} mutant embryo lacking the antennal, intercalary, and mandibular segments (anti-Engrailed antibody staining). (F) In *btd*^{XG81} mutant larvae, corresponding sense organs are absent. (G) *btd*^{XG81} mutant embryos bearing one copy of the *btd*-*mBtd* transgene show rescue of mandibular and intercalary segments. (H) *btd*^{XG81} mutant larva showing the corresponding sensory organs. Anterior is to the left.

quence rather represents a typical *opa*-element, which is found in nonhomologous genes in *Drosophila*. Accordingly, we propose that *Bts1* is an ortholog of *Sp1* and *Sp4*, whereas the newly identified gene represents an ortholog of *D-Sp1* and *btd*.

To test *in vivo* for evolutionary conserved functions of *btd* homologs, different genes were expressed under the control of the regulatory region of the *btd* gene (Schöck et al. 1999a,b) in *btd* mutant *Drosophila* embryos. In these rescue experiments, the two previously identified *btd*-like genes *Sp1* and *Bts1* failed to provide any scorable rescuing activity anterior to the mandibular segment (Schöck et al. 1999b; Tallafuss et al. 2001). The expression of one copy of the newly identified gene resulted in the development of *btd*-dependent mandibular (100%) and, in addition, intercalary segments (~10%, *n* > 50; Fig. 1C–H). Therefore, the encoded protein contains functional features of BTD, which are absent from SP1 and BTS1. In analogy to the *Drosophila* gene *btd*, we termed the gene *mouse Btd* (*mBtd*).

mBtd expression pattern during mouse embryogenesis

The spatiotemporal aspects of *mBtd* expression were analyzed by whole-mount *in situ* hybridization. The results of these experiments are summarized in Figure 2.

Initial expression of *mBtd* is found between embryonic day 7.0 (E7.0) and E7.5 of gestation, with a strong hybridization signal during gastrulation in embryonic ectoderm and primitive streak (Fig. 2A). During secondary gastrulation, transcripts become restricted to the tail bud (Fig. 2D). During organogenesis, *mBtd* mRNA appears within the central nervous system (CNS) in the telencephalon, midbrain–hindbrain boundary (MHB), spinal cord, otic vesicles, and nasal placodes (Fig. 2B,D,G).

Outside of the CNS, *mBtd* activity is restricted to the limbs. It is initially observed in the entire ectoderm of the limb anlagen at E9.5, with a more abundant expression in the ventral part (Fig. 2C,F). The expression becomes progressively more prominent in the AER and is additionally detected as a clear but less prominent signal in the ventral ectoderm (Fig. 2E,G–I).

These patterns suggest a possible role of *mBtd* during gastrulation and during CNS and limb development.

Loss of *mBtd* activity causes defects at the sites of expression

To elucidate the role of *mBtd* during mouse embryogenesis, we performed knockout experiments using a ho-

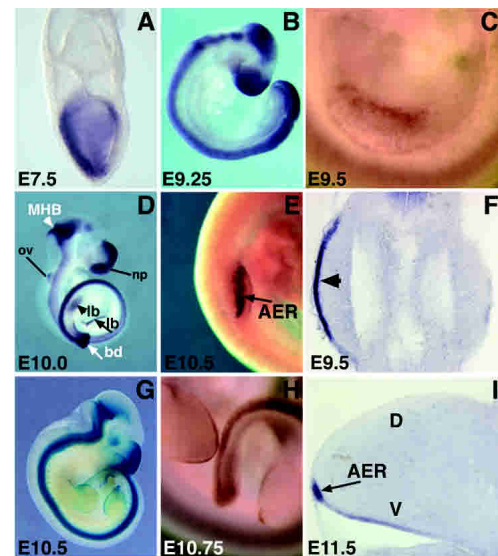


Figure 2. A highly restricted expression pattern of *mBtd* in mouse embryogenesis. Whole-mount *in situ* hybridization (A,B,C,D,E,H), LacZ staining (G), and vibratome sections of whole-mount staining (30 μm; F,I) presenting the expression of *mBtd* at different stages of development. *mBtd* is detected during gastrulation in the embryonic ectoderm and primitive streak (A). Subsequently, *mBtd* is found in the developing neural tube, in the prospective telencephalon, midbrain–hindbrain boundary, and spinal cord (B,D,G). Expression is also obvious in the otic vesicle, in the nasal placode, and tail bud (D). In the limb bud *mBtd* is shown at E9.5 in the entire ectoderm (C,F) and at E10.5, E10.75, and E11.0 in the AER (E,G,H,I) and ventral ectoderm (I). In C and H, anterior is to the left. In F, dorsal and anterior are to the top. In I, cross-section is at the level of the hindlimb. Arrows and arrowheads indicate expression domains. (D) Dorsal; (AER) apical ectodermal ridge; (bd) tail bud; (lb) limb bud; (MHB) midbrain–hindbrain boundary; (np) nasal placode; (ov) otic vesicle; (V) ventral.

mologous recombination approach in which the coding region of *mBtd* was replaced by a bacterial lacZ gene in embryonic stem cells according to Mansouri (2001; details in Supplementary Fig. 1A–C). Heterozygous *mBtd* mutant individuals develop to term. About one-third of them exhibit a slight kink at the tip of the tail (Supplementary Fig. 1E), suggesting that a reduction of the *mBtd* gene dose impairs posterior vertebra development at low but significant penetrance. Homozygous *mBtd*-deficient embryos also develop to term and die either during birth or immediately thereafter.

Morphological and histological inspection of the homozygous *mBtd* mutant individuals revealed multiple and severe developmental defects in locations where the gene normally is expressed. Exencephaly at the level of the forebrain, an acerebellar hindbrain, spina bifida, and loss of nasal and palate structures were observed in these embryos (Fig. 3I; data not shown). Most striking were truncations of the posterior axis and a reduction of both fore- and hindlimbs (Fig. 3B,D,I,K). To elucidate *mBtd* function and to explore the genetic network in which *mBtd* is involved, we focused our attention on its role in limb development.

mBtd maintains signaling in the developing limb

The truncations of both fore- and hindlimbs of mutant embryos are variable, as exemplified by the range of E17.5 skeletal phenotypes of the mutants depicted in Figure 3B and D. In most cases humerus and femur, although malformed, are generated, whereas the more distal parts of the limbs are variably affected (Fig. 3B,D; see legend for details). This phenotype is reminiscent of de-

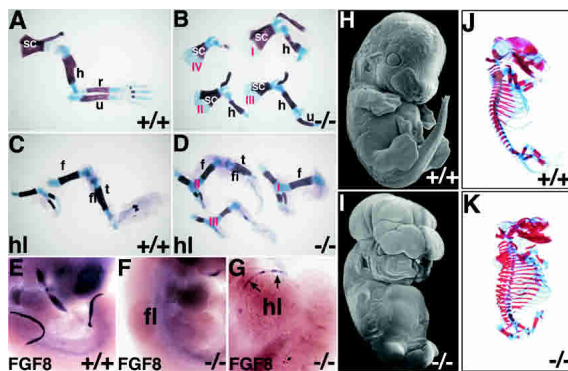


Figure 3. Severe truncations of *mBtd*-deficient limbs. Skeletal preparations at E17.5 show the severity and variability of the defects observed in the mutant limbs. Control fore- and hindlimbs are shown in A and C, respectively. Several limb truncations are presented for the fore- and hindlimbs in B and D. Some of these defects are shown, and the frequency, how often these or similar anomalies are observed. For the forelimbs: (I) 30/51; (II) 8/51; (III) 12/51; (IV) 1. For the hindlimbs (I) 20/51; (II) 7/51; (III) 24/51. The numbers label individual limb variations. Whole skeletal preparations (E17.5) of control (J) and mutant (K) embryos showing the malformations in the trunk. The expression of *Fgf8* in the AER is shown at E10.5 for control (E) and mutant (F,G) whole-mount embryos. It is obvious that at this stage of development, *Fgf8* expression is already abolished in the forelimb (F, five embryos tested), whereas a patchy expression domain is still recognizable in the hindlimb (G, five embryos). H and I represent scanning electron microscope of whole embryos at E12.5 from wild-type (H) and *mBtd*^{-/-} embryos. The arrows in G point to the patchy expression in the AER of the hindlimbs. (f) Femur; (fi) fibula; (fl) forelimb; (hl) hindlimb; (h) humerus; (r) radius; (sc) scapula; (t) tibia; (u) ulna.

fects caused by a perturbed formation of the AER (Capdevila and Izpisua Belmonte 2001; Tickle 2003). Therefore, we examined the expression of genes that are critically involved in signaling events during AER formation and its proper function.

Limb outgrowth induction is based on cross-talk between epidermal and mesenchymal tissue (Capdevila and Izpisua Belmonte 2001; Dudley et al. 2002; Tickle 2003). It is mediated by *Fgf8* and *Fgf10* (Min et al. 1998; Xu et al. 1998; Sekine et al. 1999; Lewandowski et al. 2000; Moon and Capecchi 2000; Moon et al. 2000; Sun et al. 2000, 2002). In *mBtd* mutant embryos, *Fgf8* expression is initiated but reduced in the AER area at E9.5 (Fig. 4I,J). In the AER of the hindlimbs of E10.0, *Fgf8* transcripts are still detected as a patchy pattern (Fig. 3G). However, they are absent from the forelimb bud (Fig. 3F). Similarly, mesenchymal *Fgf10* transcripts are normally expressed at E9.5, but they gradually disappear during subsequent development (Fig. 5I,J; data not shown). Furthermore, the expression of *Fgf4*, another member of the FGF gene family that is normally expressed in the AER area after stage E10, could not be detected in *mBtd* mutant embryos (Fig. 4K,L). These findings indicate that *mBtd* is not required to initiate but is required to maintain the *Fgf8* and *Fgf10* expression. The results are consistent with the observation that the *mBtd* mutant limb defects are similar to a phenotype caused by the loss of *Fgf8* and *Fgf4* activities. In the absence of *Fgf8*, the limb elements are present but malformed (Lewandowski et al. 2000; Moon and Capecchi 2000), and they are even wild type-like in *Fgf4*-deficient limbs (Moon et al. 2000; Sun et al. 2000). Loss of the combined *Fgf8* and *Fgf4* activities, however, causes more severe limb truncations than the absence of *Fgf8* only (Sun et al. 2002), and the limb truncations closely resemble the *mBtd* loss-of-function mutant limb buds shown here (Fig. 3).

Limb outgrowth defects were shown to be associated with an altered expression of *Sonic hedgehog* (*Shh*; Yang et al. 1997; Chiang et al. 2001; Kraus et al. 2001) in the posterior distal mesenchyme. In *mBtd* mutant embryos, expression of the signaling molecule *Shh* is properly initiated, but the transcripts are progressively lost (Fig. 5A,B), as observed with *Fgf8* and *Fgf10*. This is likely due to a disruption of the reciprocal feedback loop between the AER and posterior mesenchyme (polarizing region), which involves *Fgf4* and *Shh* activities (Laufer et al. 1994; Niswander et al. 1994). This argument is supported by the altered expression of the *BMP* antagonist *Gremlin*, which relays the *Shh/Fgf4* feedback loop (Zuniga et al. 1999; Te Welscher et al. 2002). In *mBtd* mutant limbs, *Gremlin* expression is initiated normally but not maintained (data not shown). Furthermore, expression of the limb mesenchyme marker genes *Gli3*, *Gbx2*, and *Hoxd12* is initiated normally (Büscher et al. 1997; Hérault et al. 1999), but their activities are progressively lost (Figs. 4E,F, 5C,D,G,H). Collectively, these findings establish that *mBtd* is specifically required to maintain signaling gene activities during early stages of limb outgrowth.

mBtd is also required for the dorsoventral limb patterning

AER formation involves a regulatory loop connecting FGF and the Wnt/ β -catenin signaling activities (Kengaku et al. 1998; Galceran et al. 1999; Kawakami et al. 2001;

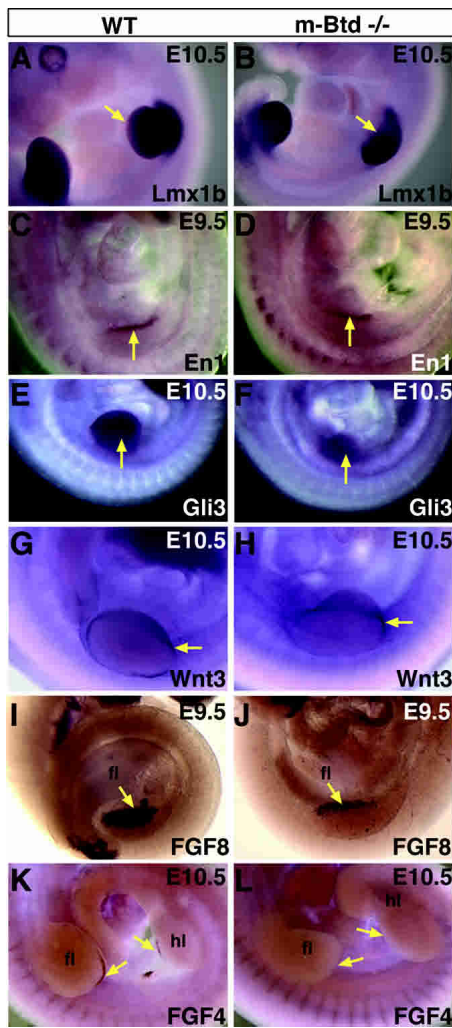


Figure 4. Analysis of the limb phenotype with molecular markers. Whole-mount in situ hybridization at E9.5 or E10.5 showing the expression pattern of molecular markers involved in limb patterning. (I,J) *FGF8* expression is detected in the forelimb of E9.5 *mBtd*^{-/-} embryos, as compared with E10.5 in Figure 3F. (K,L) The expression of *Fgf4* is not initiated (10 embryos tested). (G,H) The ectodermal *Wnt3* expression is not altered by the loss of *mBtd* activity (five embryos tested). (A,B) The expression domain of *Lmx1b* in the forelimb is extended into the ventral portion of the bud (arrows; seven embryos tested), pointing to a progressive dorsalization of the limb. (C,D) In the same embryo, the younger hindlimb still exhibits a normal dorsoventral expression pattern. Initial expression of *En1* at E9.5 is normal. (E,F) The expression of *Gli3* is not maintained in *mBtd*^{-/-} limbs. Except for A, B, and J, rostral is to the left. Arrows indicate the expression domains in the limb.

Barrow et al. 2003). In chick limb mesenchyme, Wnt/ β -catenin signaling establishes *Fgf10* expression, which in turn is necessary to initiate *Wnt3a* activity in the ectoderm. Subsequently, *Wnt3a* triggers *Fgf8* expression in AER cells that maintains *Fgf10* expression in a Wnt/ β -catenin-dependent manner in the mesenchyme (Kengaku et al. 1998; Kawakami et al. 2001). Mouse *Wnt3* was also recently shown to be critical for AER formation and limb outgrowth, possibly as a part of the regulatory loop connecting the Wnt/ β -catenin and FGF signaling pathways as established for chick limb development (Barrow et al. 2003). This assignment fits the observation

that lack of *Wnt3* or β -catenin activities causes severe outgrowth defects in the developing mouse limb (Barrow et al. 2003). In both *Wnt3* and β -catenin mutant limbs, expression of *Shh*, *En1*, and *BMP4* is abolished and limbs become progressively dorsalized (Barrow et al. 2003). Furthermore, simultaneous inactivation of *Lef1* and *Tcf1*, the mediators of the Wnt signaling pathway, abolishes *En1* expression and prevents limb outgrowth (Galceran et al. 1999).

The limb truncations observed in *mBtd* mutants are similar to those seen in *Wnt3* or β -catenin mutants. In particular, the expression of *Lmx1b*, a marker for the dorsal limb mesenchyme, is extended ventrally, as has been observed in *Wnt3* mutant limbs (Fig. 4A,B). In contrast to *Wnt3* or β -catenin mutants, the expression of genes involved in dorsal ventral patterning, such as *En1*

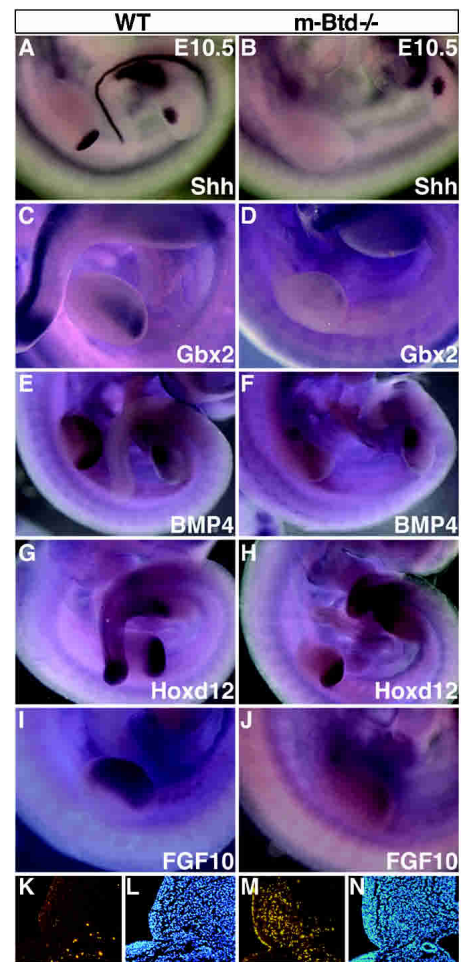


Figure 5. Expression of molecular markers and cell death analysis in the *mBtd* mutant limbs. (A,B,E,F,I,J) Sonic Hedgehog, BMP, and FGF signaling is not maintained in *mBtd* mutant limbs shown in whole-mount in situ at E10.5. Two other markers are also affected: *Gbx2* (C,D) and *Hoxd12* (G,H). In A–J, anterior is to the left. Apoptotic cell death was assayed on cross-sections of E10.5 embryos at the level of the forelimb bud by using TUNEL. (K,M) Cell death in the forelimb bud of E10.5 control and mutant embryos is shown. (M) Apoptosis is detected in the mesenchyme and ectoderm of the *mBtd*-deficient forelimb bud at E10.5. (K) There is little or no apoptosis in the control forelimb bud. L and N indicate the corresponding DAPI staining to K and M, respectively. In K–N, dorsal is to the left.

and *BMP4* (Loomis et al. 1998; Ahn et al. 2001; Pizette et al. 2001), is normal in *mBtd*-deficient limbs, but is lost during development (Figs. 4C,D, 5E,F). This suggests that *mBtd* acts downstream of Wnt3- β -catenin signaling, implying that *Wnt3* expression is not affected in the ectoderm of *mBtd*-deficient limbs. Figure 4G and H shows that this is indeed the case. Moreover, apoptotic cell death shown to occur in *Wnt3* mutant limbs (Barrow et al. 2003) can also be detected in dorsal mesenchyme and ectoderm of the forelimbs in *mBtd* lack-of-function individuals at E10.5 (Fig. 5K–N). However, cell death also occurs in limbs lacking FGF8 or FGF8 and FGF4 function (Moon and Capecchi 2000; Sun et al. 2002). Altogether, this indicates that like in the absence of *Wnt3* and β -catenin signaling, the lack of *mBtd* function causes limbs to acquire a progressively dorsalized phenotype. Our results suggest that *mBtd* may maintain the expression of genes acting downstream of Wnt/ β -catenin signaling in the limb. However, we cannot exclude the possibility that the observed dorsalization in *mBtd* mutant limbs is related to the progressive loss of the AER. Mechanisms regulating AER formation may be linked to those establishing dorsoventral patterning (Chen and Johnson 1999). Accordingly, although our findings suggest that *mBtd* is required for the initiation of FGF4 expression in the AER, it may rather reflect the loss of AER integrity. We conclude that *mBtd* is specifically required to maintain signaling gene activities during early stages of limb outgrowth.

Does lack of mBtd activity perturb patterning and outgrowth at all sites of embryonic expression?

We have not addressed the role of *mBTD* during the development of the tail bud, midbrain–hindbrain boundary, and nasal structures. However, it appears likely that in all these tissues with related organizer functions bearing *Fgf8* expression, *mBtd* is necessary to maintain these critical intercellular signaling events during embryogenesis, as suggested by its role in limb development. Clearly, this hypothesis needs to be addressed in the future.

Materials and methods

Cloning of mouse mBtd cDNA

Using degenerated primers as described (Treichel et al. 2001), a 230-bp PCR product was amplified from mouse genomic DNA and identified by hybridization to *Drosophila buttonhead* probe. This fragment was used to screen an E8.5 mouse cDNA library (kindly provided by B. Hogan, Vanderbilt University Medical Center, Nashville, TN), from which several clones were isolated and further selected by whole-mount in situ hybridization. Five overlapping clones were used to assemble the full-length cDNA sequence (complete amino acid sequence shown in Fig. 1).

Gene targeting and chimeric mice generation

Gene targeting and chimeric mice generation were performed as described (Mansouri 2001). Targeted clones were confirmed by 5' and 3' external probes (Supplementary Fig. 1). One targeted clone produced germline chimeras. All experiments were performed on a mixed (NMR1x129Sv) background. Mice and embryos were genotyped either by genomic Southern blot or PCR.

In situ hybridization, lacZ-staining, histology, immunohistochemistry, TUNEL assay, and skeletal preparations

In situ hybridizations using digoxigenin were performed as described (Wilkinson 1992). For whole-mount in situ hybridization, a minimum of five mutant embryos was used for the analysis. For histological analysis,

embryos were fixed in 4% PFA, and paraffin sections (10 μ m) were prepared. Immunological staining of *Drosophila* embryos was performed using as primary antibodies anti- β -galactosidase (Cappel) and 4D9 anti-Engrailed/Invected together with the Vectastain ABC Elite Kit (Vector). To identify homozygous mutant embryos, blue balancers were used.

Drosophila strains

We used Oregon R as wild type, *btd*XG81, *svb*YYP17b *btd*XG81, and a homozygous line of the *btd-mBtd* transgene. The *svb btd* double mutant was used to identify *btd* mutant cuticles (Wimmer et al. 1993, 1996). Apoptosis assays were performed using the Apoptag kit (Invitrogen) according to the manufacturer's recommendations.

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