# WWM-MYOBLAST PROLIFERATION AND GENE EXPRESSION IN DOUBLE MUSCLED AND NORMAL CATTLE GERRARD\*, A. L. GRANT AND M. D. JUDGE

A. L. GRANT AND M. D. Journal of Animal Sciences, Purdue University, West Lafayette, IN 47907 address: Department of Food Science and Nutrition, University of Missouri-Columbia, Columbia, MO 65211 MARY: Utilizing double muscled cattle as a model for studying myoblast proliferation and differentiation has revealed differences <sup>MY: Utilizing</sup> double muscled cattle as a model for studying myoblast proliferation and differentiation has to be a model for studying myoblast proliferation and differentiation has to be a model for studying myoblast proliferation and differentiation has to be a model (NM) and double muscled (DM) fetuses in serum mitogenic activity and tissue insulin–like growth factor–II (IGF–II) and double muscled (DM) fetuses in serum mitogenic activity muscle hypertrophy. <sup>aumal</sup> (NM) and double muscled (DM) fetuses in serum mitogenic activity and task <sup>typression</sup>. These differences may play a role in the development of cattle with muscle hypertrophy.

MODUCTION: Double muscled cattle possess nearly 40% more muscle fibers than normal cattle (MacKellar, 1968). Fetal blood-<sup>bowth</sup> factors modulate myoblast proliferation and differentiation in vitro (reviewed by Florini et al., 1991). The type and amount <sup>buth</sup> factors modulate myoblast proliferation and differentiation in vitro (reviewed by Florini et al., 1991). The operation of factor changes with time in the serum of developing mammalian fetuses (Moses et al., 1980; Daughaday et al., 1982). <sup>kai</sup>ons in serum growth factor profiles have been assessed by several researchers using myoblast cultures as a bioassay (Kotts et al., White and Browth factor profiles have been assessed by several researchers using myoblast cultures as a bioassay (Kotts et al., White et al., 1988, 1989; Gerrard et al., 1992a).

<sup>Auc et al.</sup>, 1988, 1989; Gerrard et al., 1992a). <sup>Aug</sup> tissue <sup>Aug</sup> t and tissue concentrations of IGF-II fluctuate dramatically throughout gestation. Studies by Florini et al. (1991) suggest that <sup>the Itssue</sup> concentrations of IGF-II fluctuate dramatically throughout gestation. Studies by Floring et al. (2000) <sup>the production</sup> of IGF-II is required during myoblast differentiation. Changes in the expression of a growth factor closely tied to <sup>the site</sup> man because the objectives of this study were to compare the <sup>Production</sup> of IGF-II is required during myoblast differentiation. Changes in the expression of a growth the expression of a gro

enesis may be responsible for muscle fiber hyperplasia in DM cattle. Therefore, the objectives of the objective of the objective of the objective of the objective objective of the objective objective of the objective objective objective of the objective obje

<sup>courc</sup> activity and the expression of IGF-II in liver and sketchar model. <sup>courc</sup> and METHODS: Fetal blood samples from sixty beef or dairy (NM) fetuses of various ages were collected from <sup>courc</sup> shared and METHODS: Fetal blood samples from sixty beef or dairy (NM) fetuses of various ages were collected from the isochium to the <sup>NAL</sup> and METHODS: Fetal blood samples from sixty beef or dairy (NM) fetuses of various ages were structured in the solution of the solution o <sup>vows</sup> slaughtered in a commercial slaughter plant. Double muscled fetal blood was taken from twerve tenated in the schium to the <sup>bloc</sup>td<sub>e</sub> cranine. <sup>vows</sup> slaughtered in the Purdue University abattoir. Fetal age was recorded by crown-rump length (CRL; measured from the ischium to the <sup>vow</sup>the cranine. <sup>vows</sup> slaughtered in the schium to the <sup>vows</sup> slaughtered in the Purdue University abattoir. Fetal age was recorded by crown-rump length (CRL; measured from the ischium to the <sup>vows</sup> slaughtered in the Purdue University abattoir. Fetal age was recorded by crown-rump length (CRL; measured from the ischium to the <sup>vows</sup> slaughtered in <sup>aud</sup> in the Purdue University abattoir. Fetal age was recorded by crown-rump length (Cros, and the cranium) and fetuses were assigned to a CRL representing time of gestation (<25, 26–50, 51–75, >75 cm).

A subclone (ELC5) of the rat L6 myoblast was obtained from Dr. C. Smith (Lilly Research Laboratories, Greenfield, IN) and  $bio_{absyle}$ A subclone (ELC5) of the rat L6 myoblast was obtained from Dr. C. Smith (Lilly Research Laboratories, Oreclinerating bioassy for determining serum-induced myoblast proliferation. Incorporation of <sup>3</sup>H-thymidine into cultured proliferation of <sup>3</sup>H-thymi <sup>a bioassy</sup> for determining serum-muter Mulasts was used to indication of proliferative activity.

<sup>was used</sup> to indication of proliferative activity. <sup>Muscle samples</sup> were taken from the semitendinosus muscle of fetuses ranging in CRL of 12.5 to 90 cm for estimation of <sup>the full sele file</sup> <sup>Muscle</sup> samples were taken from the semitendinosus muscle of fetuses ranging in CRL of 12.5 to 50 cm to <sup>Muscle</sup> samples were taken from the semitendinosus muscle of fetuses ranging in CRL of 12.5 to 50 cm to <sup>Muscle</sup> fiber number. Quantification of the apparent muscle fiber number was performed using an Image Analyzer (Cambridge <sup>Muscle</sup> 570, Chi-

Muscle and liver samples were also taken. Total RNA extraction by the acid guanidine thiocyanate phenol chloroform procedure by and liver samples were also taken. Total RNA extraction by the acid guanidine thiocyanate phenol chloroform procedure by Muscle and liver samples were also taken. Total RNA extraction by the acid guanidine thiocyanate phenor chronosteries in a second described by and sacchi, 1987) was performed. Northern blot analysis was conducted using muscle and liver RNA as described by the acid guanidine of selected mRNAs. The cDNAs used in this is the second described of selected mRNAs. The cDNAs used in this second described by the acid guanidine of selected mRNAs. The cDNAs used in this second described by the acid guanidine of selected mRNAs. <sup>wy2nski</sup> and Sacchi, 1987) was performed. Northern blot analysis was conducted using muscle and liver RUCL as used in this were generated to determine relative changes in abundance of selected mRNAs. The cDNAs used in this bundance of selected mRNAs. The cDNAs used in this bundance of selected mRNAs. The cDNAs used in this bundance of selected mRNAs. The cDNAs used in this bundance subjected to an abundance subject abundanc <sup>wet</sup>al. (1991). Dot blots were generated to determine relative changes in abundance of selected mRNAs. The Contract <sup>wete</sup>rat IGF-II (Dr. M. Rechler, National Institue of Health) and rat beta actin (Dr. L. Kedes, University of Southern California).

Relative mRNA abundance, tritiated thymidine uptake, mean fiber area and apparent fiber number estimates were subjected to the subjected to the subject of SAS (1988) to determine main effects of muscling and age. Differences between means were determined by the <sup>At I</sup>GF-II (Dr. M. Rechler, National Institue of Health) and rat beta actin (Dr. L. Kedes, University of Council, <sup>A</sup> procedure mRNA abundance, tritiated thymidine uptake, mean fiber area and apparent fiber number estimates were subjected to an <sup>A procedure</sup> of the subject of the subject

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(0.2)

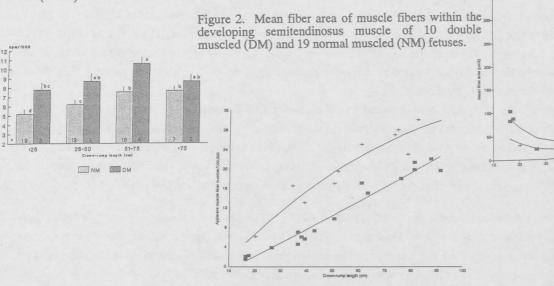
<sup>by</sup> the means of the SAS (1988) to determine the second determined determine the second determined determ With CRL for both NM and DM fetuses (Figure 1). Normal muscled fetal serum-induced thymidine incorporation in L6 With CRL for both NM and DM fetuses (Figure 1). Normal muscled fetal serum-induced thymidine uptake by L6 With CRL for both NM and DM fetuses (Figure 1). Normal muscled fetal serum-induced thymidine incorporation  $W_{as}$  greatest at CRL > 50, least at CRL  $\leq$  25 and intermediate for 26–50 cm CRL (P<.05). Thymidine uptake by L6  $W_{as}$  greatest at CRL > 50, least at CRL  $\leq$  25 and intermediate for 26–50 and 51–75 cm (P<.05) and tended to be  $w_{as}$  greatest at CRL > 50, least at CRL  $\leq 25$  and intermediate for 26–50 cm CRL (P<.05). Inymittine upton of  $w_{as}$  greatest at CRL > 50, least at CRL  $\leq 25$  and intermediate for 26–50 cm CRL (P<.05) and tended to be  $w_{as}$  greater with serum from DM fetuses than NM fetuses at CRL  $\leq 25$ , 26–50 and 51–75 cm (P<.05) and tended to be

Greater myoblast proliferation observed in the presence of serum from DM fetuses over NM fetuses may result from the presence of serum from DM fetuses over NM fetuses may result from the presence of serum factor which is responsible for the expression of bovine muscle fiber hyperplasia. More likely, an aberrant level the possibility of TGF-beta or FGF <sup>1/Scm.</sup> Greater myoblast proliferation observed in the presence of serum from DM fetuses over NM fetuses may result from the presence of hoving muscle fiber hyperplasia. More likely, an aberrant level <sup>the specific serum</sup> factor which is responsible for the expression of bovine muscle fiber hyperplasia. More fixer, and the served in this present during a critical stage of myogenesis. Preliminary experiments showed that the L6 myoblasts used in this served in the served of the transmission of the served of Whit factor is present during a critical stage of myogenesis. Preliminary experiments showed that the Lo myourasts and the factor is present during a critical stage of myogenesis. Preliminary experiments showed that the Lo myourasts and the factor is present during the second to two well known mitogens, FGF and TGF-beta. This does not eliminate the possibility of TGF-beta or FGF is second to two well known mitogens, FGF and TGF-beta. This does not eliminate the possibility of TGF-beta or FGF. In probably mediates the second to two wells are responsible for increased myoblast replication in this system. In <sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two well known mitogens, FGF and TGF-beta. The sub-<sup>webpond</sup> to two webponds to twebponds to two webponds <sup>the age-associated mea-</sup> <sup>the age-associated mea-</sup> <sup>the age-associated mea-</sup> <sup>the age-associated mea-</sup>

Mean fiber area decreased dramatically from 100 to 20 um<sup>2</sup> between 15 and 38 cm CRL (Figure 2). Simultaneously, a <sup>1</sup>/<sub>1</sub> increase in apparent muscle fiber number was observed at <sup>-38</sup> cm CRL (Figure 3). Swatland and Kieffer (1974) <sup>showed st</sup> increases in muscle fiber number between 10 and 42 cm CRL of fetal bovine development.

Figure 1. Means and standard errors of incorporation of  $^{3}H$ -thymidine into replicating myoblasts cultured in the presence of medium containing 10% sera from developing double muscled (DM) and normal muscled (NM) fetuses. Means bearing similar letters do not differ (P>.05).

Figure 3. Estimated apparent muscle  $_{0}^{\text{fiber}}$  the developing semitendinosus muscle  $_{0}^{\text{fiber}}$  muscled (DM) and 19 normal muscled (NM)  $_{1}^{\text{fiber}}$ 

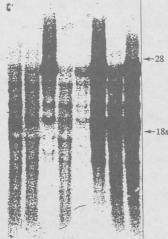


IGF-II mRNA was detected in muscle and liver tissues of both DM and NM fetuses (Figure 4). Rat IGF-II cDNA used for IGF-II was study hybridized to transcripts of 4.5, 3.6, 2.75, 2.5, 1.6 and 1.15 kb. Although multiple transcripts were observed for Infer-II was the 4.5 kb transcript was most abundant. An additional 6 kb transcript was also observed on autoradiographs with longer times. The rat beta-actin cDNA hybridized to the 2.1 kb bovine beta actin mRNA in both liver and muscle. Some cross-hybrid of the beta-actin cDNA to muscle alpha-actin mRNA occurred.

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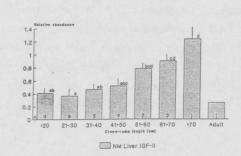
Figure 4. Autoradiogram from northern blot analysis of bovine liver and muscle tissues using a rat IGF–II cDNA (lanes 1,2,4 and 7 fetal liver; 3, 5, 6 and 8 fetal muscle).

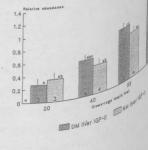
Figure 6. Means and standard errors of the abundance of IGF-II mRNA in the liver of the normal muscled (NM) fetuses. Means beams letters do not differ (P>.05).



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Figure 5. Means and standard errors of the relative abundance of IGF-II mRNA in the liver of developing normal muscled (NM) fetuses. Means bearing similar letters do not differ (P>.05).

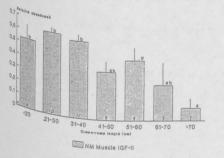


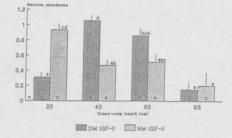


Relative hybridization intensities for the IGF-II cDNA were greater for muscle than liver tissues, possibly from dilution of liver <sup>Kelative</sup> hybridization intensities for the IGF-II cDNA were greater for muscle than liver tissues, possier, the Marka by other liver mRNAs. Figures 5 and 6 indicate liver IGF-II expression increased with CRL in both NM and DM (Perop. 1990) (Perop. 1990 (P<.05) but no differences were observed between DM and NM fetuses. Expression of IGF-II in muscle tissue of developing  $\frac{1}{100}$  but no differences were observed between DM and NM fetuses. Expression of 101–11 in induced to fall after a crown- $\frac{1}{100}$   $\frac{1}{10}$   $\frac{1}{100}$   $\frac{1}{100}$ <sup>wuges</sup> decreased (P<.05) with age post conception (Figure 7). Normal muscle IGF-II expression toneed to the point coincides with <sup>10</sup> <sup>10</sup> <sup>cm</sup> was reached. This crown-rump length represents approximately 200 d pc. Interestingly, this time point coincides with <sup>10</sup> <sup>10</sup> <sup>cm</sup> was reached. This crown-rump length represents approximately 200 d pc. Interestingly, this time point coincides with 

Bure 7. Means and standard errors of the relative Mance of IGF-II mRNA in the semitendinosus the of IGF-II mRNA in the semitentineses. The of developing normal muscled (NM) fetuses. the pot differ (P>.05). bearing similar letters do not differ (P>.05).

Figure 8. Means and standard errors of the relative abundance of IGF-II mRNA in the semitendinosus muscle of developing double muscled (DM) and normal muscled (NM) fetuses. Means bearing similar letters do not differ (P>.05).





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<sup>1</sup><sup>0</sup> reduce the possibility of confounding muscle IGF-II expression with age, NM fetuses were compared to DM fetuses with <sup>1</sup>CRL, At 20 <sup>10</sup> reduce the possibility of confounding muscle IGF-II expression with age, NM fetuses were compared to Data the possibility of confounding muscle IGF-II expression was greater (P<.05) in NM fetuses than at 20 cm CRL (approximately 100 d post-conception), muscle IGF-II expression was greater (P<.05) for DM than NM fetuses. The reason for this At 20 cm CRL (approximately 100 d post-conception), muscle IGF-II expression was greater (r<.05) in the second for this change in a second conversely, at 40 cm CRL, muscle IGF-II was greater (P<.05) for DM than NM fetuses. The reason for this since IGF-II is a mitogen of embryonic myoblasts (McFarland et al., Conversely, at 40 cm CRL, muscle IGF-II is a mitogen of embryonic myoblasts (McFarland et al., Conversely, at 40 cm CRL). <sup>And</sup> D<sub>M</sub> Cattle CRL (approximately 100 d post 200 d p <sup>1) <sup>add</sup>ge in expression of IGF-II in muscle is unknown. Since IGF-II is a mitogen of embryonic myobilasts (incention) and DM cattle develop the potential for extreme muscularity through hyperplastic muscle cell growth (Swatland and Kieffer, Ashinore et al.</sup> Ashmore et al., 1974), IGF-II may cause hyperplasia of myoblasts. Alternatively, with the compelling evidence recently shown may <sup>Ashnore</sup> et al., 1974), IGF-II may cause hyperplasia of myoblasts. Alternatively, with the compelling evidence received in the onset of the onset of terminal differentiation in the muscle of developing DM  $d_{t_{e}}$  on  $d_{t_{e}}$  (1974), IGF-II may cause hyperplastic of the onset of myogenesis, increased muscle IGF-II captures of  $d_{e}$  on  $d_{e}$  on  $d_{e}$  on  $d_{e}$  of terminal differentiation. This suggests that the onset of terminal differentiation in the muscle of developing DM delayed dots. <sup>wite</sup> onset of terminal differentiation. This suggests that the onset of terminal differentiation in the muscle of terminal differentiation. This suggests that the onset of terminal differentiation of IGF-II may allow for the onset of secondary fiber formation compared to NM fetuses. Delayed expression of IGF-II may allow for the onset of secondary fiber formation compared to NM fetuses. Delayed expression of IGF-II may allow for the onset of secondary fiber formation compared to NM fetuses. Delayed expression of IGF-II may allow for the onset of secondary fiber formation compared to NM fetuses. Delayed expression of IGF-II may allow for the onset of secondary fiber formation compared to NM fetuses. <sup>th</sup> delayed during the onset of secondary fiber formation compared to NM fetuses. Delayed and the muscle fiber production.

<sup>Autotic</sup> activity of myoblasts from DM fetuses which could result in greater muscle development. Mechanisms controlling the <sup>Autotic</sup> activity of myoblasts from DM fetuses which could result in greater muscle development. Mechanisms controlling the <sup>Autotic</sup> activity of myoblasts from DM fetuses which could result in greater muscle development. Mechanisms controlling the <sup>Autotic</sup> activity of an activity of myoblasts from DM fetuses which could result in greater muscle development. Mechanisms controlling the <sup>Autotic</sup> activity of an activity of myoblasts from DM fetuses a biological phenomenon worth exploiting. Muscle cell hyperplasia in <sup>Autotic</sup> an activity of activity of an activity of <sup>Nopment</sup> of an animal with 30% more muscle represents a biological phenomenon worth exploiting. Muscle cell hyperplasia in NM <sup>refetuses</sup> bouble muscled cattle provide a userul me <sup>refetuses</sup> of an animal with 30% more muscle represents a biological phenomenon worth exploiting. Muscle con appendix <sup>refetuses</sup> occurs between 85 and 210 d post-conception. Serum-induced mitogenic activity is greater in DM fetuses than in NM <sup>refetuses</sup> a time of the DM phenotype. <sup>tetuses</sup> <sup>occurs</sup> between 85 and 210 d post-conception. Serum-induced mitogenic activity is greater in Secure during a time of muscle fiber hyperplasia. Serum growth factors may play a role in development of the DM phenotype.

<sup>hge a time</sup> of muscle fiber hyperplasia. Serum growth factors may play a role in development of the Dite procession during development in bovine fetuses is consistent with myoblast culture results reported by <sup>tet</sup> al. (1991) hcreased muscle fiber hyperplasia. Serum growth factors may purple et al. (1991). Although time points prior to 13 cm CRL were not available, changes in muscle IGF-II expression during the boving of boving at the points prior to 13 cm CRL were not available. Furthermore, muscle fiber number was established by <sup>(e)</sup> al. (1991). Although time points prior to 13 cm CRL were not available, changes in muscle IGF-II expression <sup>(e)</sup> d<sub>b</sub> bovine skeletal muscle may represent different stages myogenesis. Furthermore, muscle fiber number was established by <sup>(e)</sup> bovine skeletal muscle may represent different stages myogenesis. Furthermore, muscle fiber number was established by <sup>(e)</sup> bovine skeletal muscle may represent different stages myogenesis. Furthermore, muscle fiber number was established by <sup>(e)</sup> bovine skeletal muscle may represent different stages myogenesis. Furthermore, muscle fiber number was established by <sup>(e)</sup> bovine skeletal muscle may represent different stages in the abundance of IGF-II mRNA. These data suggest that IGF-II expression in muscle <sup>Although</sup> time points prior to 13 cm CAD treat <sup>Although</sup> of bovine skeletal muscle may represent different stages myogenesis. Furthermore, muscle fiber number was com-which coincided with a significant decrease in the abundance of IGF-II mRNA. These data suggest that IGF-II expression in muscle the material the material content of the support the hypothesis that the time of IGF-II expression in muscle <sup>Me</sup> which coincided with a significant decrease in the abundance of IGF-II mRNA. These data suggest that for the master maturation of prenatal muscle tissue in vivo and support the hypothesis that the time of IGF-II expression in muscle distance of the maturation of prenatal muscle tissue in vivo and support the hypothesis at birth. These experiments support the use of the maturation of prenatal muscle tissue in vivo and support the tissue possess at birth. These experiments support the use of the maturation of prenatal muscle tissue in vivo and support the tissue possess at birth. With the maturation of prenatal muscle tissue in vivo and support the hypothesis that the time of IGF-II expression of have dictate ultimately the number of muscle fibers that bovine fetuses possess at birth. These experiments support the use of cattle cattle ultimately the number of muscle fibers that bovine fetuses possess at birth. These experiments support the use of cattle ultimately the number of muscle fibers that bovine fetuses possess at birth. <sup>thay</sup> dictate maturation of prenatal muscle tissue in vivo and support the support the support of the super support of the super support of the super support of the super <sup>thuscled</sup> cattle as an excellent model for studying myogenesis. Further work to identify the source and type of ground during the development of DM fetuses which result in increased myoblast proliferation may lead to better understanding the <sup>multing</sup> the development of Division of D

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