






RESEARCH ARTICLE

A bovine CD18 signal peptide variant with increased binding activity to *Mannheimia haemolytica* leukotoxin [version 1; peer review: 3 approved]

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Abstract

Background: *Mannheimia haemolytica* is the major bacterial infectious agent of bovine respiratory disease complex and causes severe morbidity and mortality during lung infections. *M. haemolytica* secretes a protein leukotoxin (Lkt) that binds to the CD18 receptor on leukocytes, initiates lysis, induces inflammation, and causes acute fibrinous bronchopneumonia. Lkt binds the 22-amino acid CD18 signal peptide domain, which remains uncleaved in ruminant species. Our aim was to identify missense variation in the bovine CD18 signal peptide and measure the effects on Lkt binding.

Methods: Missense variants in the integrin beta 2 gene (*ITGB2*) encoding CD18 were identified by whole genome sequencing of 96 cattle from 19 breeds, and targeted Sanger sequencing of 1238 cattle from 46 breeds. The ability of different CD18 signal peptide variants to bind Lkt was evaluated by preincubating the toxin with synthetic peptides and applying the mixture to susceptible bovine cell cultures in cytotoxicity-blocking assays.

Results: We identified 14 missense variants encoded on 15 predicted haplotypes, including a rare signal peptide variant with a cysteine at position 5 (C₅) instead of arginine (R₅). Preincubating Lkt with synthetic signal peptides with C₅ blocked cytotoxicity significantly better than those with R₅. The most potent synthetic peptide (C₅ PQLLLLAGLLA) had 30-fold more binding activity compared to that with R₅.


Conclusions: The results suggest that missense variants in the CD18 signal peptide affect Lkt binding, and animals carrying the C₅ allele may be more susceptible to the effects of Lkt. The results also identify a potent class of non-antibiotic Lkt inhibitors that could potentially

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protect cattle from cytotoxic effects during acute lung infections.

Keywords

Cattle, CD18, integrin beta 2, missense mutation, signal peptide variants, bacterial leukotoxin, bovine respiratory disease, shipping fever, Mannheimia haemolytica

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Introduction

Mannheimia haemolytica is the major bacteria associated with bovine respiratory disease, a heterogeneous complex of highly infectious pathogens that are the primary cause of morbidity, mortality, and economic loss affecting beef and dairy cattle industries^{1,2}. *M. haemolytica* is a commensal bacterium found in tonsillar crypts and the upper respiratory tracts of healthy cattle^{3,4}. Exposure to environmental stresses or co-infection with other viral or bacterial pathogens can impair host defenses allowing *M. haemolytica* to proliferate and colonize the lungs where infection causes acute fibrinonecrotic pleuropneumonia^{2,5,6}. This bacterium expresses a variety of virulence factors that contribute to disease pathogenesis in the lungs. However, leukotoxin (Lkt) is the primary virulence factor contributing to the clinical signs and severe lung damage observed following infection^{7,8}. Within hours of bacterial colonization of the lung, large numbers of polymorphonuclear leukocytes (PMN) infiltrate the airways^{2,9}. Lkt binds to the bovine CD18 subunit of the heterodimeric integrins on the surface of PMN causing cell lysis and the release of pro-inflammatory cytokines, proteolytic enzymes, and reactive oxygen intermediates that intensify local inflammation^{6,10-13}. Experimental depletion of PMN prior to infection¹⁴, or infection with a Lkt-deletion mutant of *M. haemolytica*^{7,8}, results in decreased morbidity and reduced lung lesions in calves. Thus, the interaction between the toxin and its receptor is critical to the pathogenesis of *M. haemolytica* infection and is a potential intervention point for the prevention of disease.

A 13-amino acid sequence in the CD18 signal peptide has been identified as the site which binds to bacterial Lkt¹⁰. The 22-amino acids that comprise the CD18 signal peptide remain uncleaved in leukocytes of ruminant species due to a conserved cleavage-inhibiting glutamine residue at position 18 (Q₁₈) of the propeptide¹⁰. In non-ruminant species, such as human and murine, leukocytes are naturally resistant to Lkt because their CD18 signal peptides undergo cleavage due to a glycine residue at position 18 (G₁₈). However, when murine cell lines were transfected with bovine *ITGB2*, the gene which encodes CD18, they became susceptible to Lkt. When site-directed mutagenesis of *ITGB2* was used in the same murine cell lines to change the bovine Q₁₈ residue to G₁₈, the bovine CD18 signal peptide was cleaved and the murine cells once again became resistant to Lkt-induced lysis¹⁰. This strategy was taken further with gene-editing, showing that leukocytes isolated from a cloned bovine fetus, homozygous for CD18 G₁₈, were unaffected by Lkt exposure because the signal peptide was cleaved and unavailable for Lkt binding¹⁵. Thus, retention of the ruminant CD18 signal peptide appears to be the cause of Lkt sensitivity in leukocytes.

Naturally occurring CD18 amino acid sequence variation can also interfere with Lkt cytotoxicity. In Holstein dairy cattle, a CD18 substitution of glycine for aspartate at polypeptide position 128 in the extracellular I-like domain of CD18 causes bovine leukocyte adhesion deficiency (BLAD) in homozygous animals^{16,17}. These calves do not express functional CD18 on the surface of their leukocytes and have significantly reduced sensitivity to Lkt compared to control calves^{18,19}. We hypothesized that other variation in the CD18 polypeptide sequence, if it exists,

may alter the Lkt-CD18 binding interaction or cell signaling and result in differences in lymphocyte sensitivity to *M. haemolytica* Lkt. Thus, the goals of this study were to identify CD18 protein variants encoded by *ITGB2* in U.S. cattle breeds, and evaluate the effects of signal peptide variants on Lkt binding. We report the identification of 15 predicted protein variants, including one with enhanced Lkt binding.

Methods

Ethics statement

All animal procedures were reviewed and approved by the U.S. Department of Agriculture, Agricultural Research Service, U.S. Meat Animal Research Center (USMARC) Institutional Animal Care and Use Committee (IACUC project number 2.2).

Panels of cattle DNA used for missense mutation discovery

Two panels of DNAs were used to determine *ITGB2* genotypes from U.S. cattle. The first was a previously described panel of 96 unrelated beef cattle from 19 popular U.S. beef breeds that had already been characterized by whole-genome sequencing²⁰. This identified predicted coding changes throughout the *ITGB2* gene. The second panel included a non-overlapping set of 1142 unrelated cattle from 46 breeds, on which targeted Sanger sequencing was performed to identify any predicted coding changes in the signal peptide region and the region containing the D128G variant causing BLAD (*ITGB2* exons 2, 3, and 5). Briefly, the first panel of 96 beef cattle (USMARC Beef Cattle Diversity Panel version 2.9 [MBCDPv2.9]) was based on commercially-available purebred registered sires. Pedigrees were obtained from leading suppliers of U.S. beef cattle semen and analyzed to identify unrelated individuals for inclusion. The number of sires representing each breed (four, five, or six) was based on their numbers of registered progeny circa 2000: Angus (n = 6), Hereford (n = 6), Charolais (n = 6), Simmental (n = 6), Red Angus (n = 6), Limousin (n = 6), Gelbvieh (n = 6), Brangus (n = 5), Beefmaster (n = 5), Salers (n = 5), Shorthorn (n = 5), Maine-Anjou (n = 5), Brahman (n = 5), Chianina (n = 4), Texas Longhorn (n = 4), Santa Gertrudis (n = 4), Braunvieh (n = 4), Corriente (n = 4), and Tarentaise (n = 4). On the basis of the number of registered progeny, the breeds were estimated to represent greater than 99% of the germplasm used in the US beef cattle industry, contain more than 187 unshared haploid genomes, and allow a 95% probability of detecting any allele with a frequency greater than 0.016²¹.

The second panel of 1142 cattle consisted of samples from male and female registered purebred cattle with diverse pedigrees from 46 breeds. Samples were from semen, blood, or hair follicles, depending on gender and availability²². Where possible, animals within breed were chosen so they did not share parents or grandparents, and none were closely related to the 96 sires in the MBCDPv2.9. The breeds used in the second panel were: Angus (n = 24), Ankole-Watusi (n = 20), Ayrshire (n = 24), Beefmaster (n = 24), Belgian Blue (n = 24), Blonde d'Aquitaine (n = 24), Brahman (n = 23), Brahmousin (n = 24), Brangus (n = 24), Braunvieh (n = 24), Brown Swiss (n = 26), Charolais (n = 24), Chianina (n = 24), Corriente (n = 24), Devon (n = 23), Dexter (n = 22), Gelbvieh (n = 23), Guernsey (n = 23), Hereford (n = 24), Highland

(n = 24), Holstein (n = 81), Indu-Brazil (n = 25), Jersey (n = 29), Limousin (n = 24), Maine-Anjou (n = 24), Marchigiana (n = 24), Mini-Hereford (n = 24), Mini-Zebu (n = 24), Montbeliard (n = 24), Murray Grey (n = 20), Nelore (n = 24), Piedmontese (n = 25), Pinzgauer (n = 23), Red Angus (n = 23), Red Poll (n = 24), Romagnola (n = 24), Salers (n = 24), Santa Gertrudis (n = 24), Senepol (n = 23), Shorthorn (n = 23), Simmental (n = 23), Tarentaise (n = 24), Texas Longhorn (n = 23), Texas Longhorn, Cattlemen's Texas Longhorn Registry (CTLR, n = 19), Tuli (n = 23), and Wagyu (n = 22).

DNA sequencing and single nucleotide polymorphism (SNP) genotyping

Unless otherwise indicated, reagents were molecular-biology grade. DNA from whole blood samples was extracted by use of a solid-phase system incorporating either spin-columns or 96-well microtitration plates according to the manufacturer's instructions (Qiagen Inc., Germantown, MD, USA). DNA from liver, muscle, skin, or hair samples was extracted by standard procedures²². Briefly, minced tissue (35 mg) or hair follicles (100 trimmed bulbs) were suspended in 2.5 mL of a lysis solution containing 10 mM TrisCl, 400 mM NaCl, 2 mM EDTA, 1% wt/vol sodium dodecyl sulfate, RNase A (250 µg/ml; Sigma-Aldrich, St. Louis, MO, USA), pH 8.0. The solution was incubated at 37°C with gentle agitation. After 1 hour, 1 mg proteinase K was added (Sigma-Aldrich) and the solution was incubated overnight at 37°C with continued agitation. The solution was transferred to 15 ml tube containing 3 ml of a phase-separation gel (high-vacuum grease, Dow Corning Corporation, Midland, MI, USA) and extracted twice with 1 vol of phenol:chloroform:isoamyl alcohol (25:24:1), and once with 1 vol of chloroform before precipitation with 2 vol of 100% ethanol. The precipitated DNA was washed once in 70% ethanol, briefly air dried, and dissolved in a solution of 10 mM TrisCl, 1 mM EDTA (TE, pH 8.0).

DNA from commercial bull semen was extracted similarly, with slight modification²³. Briefly, three 0.5 ml straws of commercial semen from a single animal were pooled, and the cells were collected by centrifugation for 5 min at 1000 x g. The cell pellet was washed three times in 1 ml of a wash solution (TE with 100 mM NaCl, TNE) and suspended in 1 ml of the same solution with 1% wt/vol sodium dodecyl sulfate, 1 mg proteinase K (Sigma-Aldrich), and 40 mM dithiothreitol (DTT). This 1 ml lysis solution was incubated overnight at 37°C, transferred to a 15 ml tube containing 1.5 ml of TNE with 40 mM DTT, and 3 ml of a phase-separation gel, extracted twice with 1 vol of phenol:chloroform:isoamyl alcohol (25:24:1), and once with 1 vol of chloroform before precipitation with 0.1 vol of 3 M sodium acetate (pH 5.2) and 2 vol of 100% ethanol. The precipitated DNA was washed once in 70% ethanol, briefly air dried, and dissolved in a solution TE.

PCR-amplified fragments of genomic DNA from *ITGB2* exons 2, 3 and 5, encoding the CD18 signal peptide sequence and the region containing the known variant causing BLAD, were produced for Sanger sequencing in 96 or 384-well plates. A standard 25 µl amplification reaction contained 2.5 µl of genomic DNA in TE (10 ng/µl), 12.5 µl of a concentrated PCR cocktail (Maxima

Hot Start, Thermo Fisher Scientific, Waltham, MA, USA), 1.25 µl each of an oligonucleotide primer stock solution (100 µM, in TE), 1 µl dimethyl sulfoxide (Sigma-Aldrich), and 6.5 µl water. The sense and antisense primer sequences for exons 2 and 3 were 5'-AGG-GAG-ACT-GAC-CTG-TGT-G-3' and 5'-CTG-GGA-AGC-AGA-GTG-ATA-GT-3', respectively (USMARC primer no. 89878 and 89880). The sense and antisense primer sequences for exon 5 were 5'-AGA-GAG-ATC-CAG-GTA-GAA-CTG-3' and 5'-GTG-CAG-AGG-TGC-AGA-GGT-G-3', respectively (USMARC primer no. 89887 and 89889). The final concentration of each primer was of 5 µM (Integrated DNA Technologies, Inc., Coralville, IA, USA). PCR was performed with either the PTC 200, the PTC 220 Dyad, or the PTC 225 Tetrad thermal cycler chassis (MJ Research, Watertown, MA, USA). Reactions were denatured at 94°C for 15 min, subjected to 45 cycles of denaturation at 94°C for 20 s, annealed at 58°C for 30 s, and extended at 72°C for 1 min. After cycling the final products were extended at 72°C for 3 min before storage at 4°C. A 5 µl portion of each amplified product was analyzed by agarose gel electrophoresis (0.8%) in buffer containing 90 mM Tris-borate (pH 8.0), 2 mM ethylenediamine tetraacetic acid, and 0.1 µg/ml ethidium bromide. A 6 µl portion of each amplified product was treated with Exonuclease I (1.4 U, New England Biolabs Inc., Ipswich, MA, USA) at 37°C for 1 hr in a 13 µl reaction volume to digest single-stranded primer oligonucleotides. The Exonuclease I was inactivated with a 65°C incubation for 20 min and the DNA was precipitated with two volumes of 100% ethanol. The plates were centrifuged at 1800 x g for 30 min, decanted, and air dried.

Sequencing reactions were accomplished by dissolving air-dried DNA pellets in 5 µl of sequencing reaction cocktail containing 0.25 µl of dye terminators (DYEnamic ET Dye terminators, Amersham Biosciences, Piscataway, NJ, USA), 1.75 µl dye terminator dilution buffer (Amersham Biosciences), 2 µl oligonucleotide primer (1.6 µM stock solution in water), and 1 µl water according to the manufacturer's instructions. The final oligonucleotide concentration was 640 nM. Reactions were denatured at 96°C for 30 s, subjected to 26 cycles of denaturation at 96°C for 10 s, annealed at 50°C for 5 s, and extended at 60°C for 4 min. After cycling the final products were stored at 4°C until the DNA was precipitated with 22 µl of 70% isopropyl alcohol. The plates were centrifuged, at 1800 x g for 30 min, decanted, and the samples were washed with 22 µl of 70% ethanol. The plates were centrifuged again, decanted, air dried, sealed with foil, and stored at -20°C until use. Sequencing reactions were resolved by capillary electrophoresis as described by the manufacturer (3730xl DNA Analyzer, Applied Biosystems, Foster City, CA, USA). Animal sequences from both strands were analyzed with **polyphred** software version 6.18²⁴ in conjunction with the **phred/phrap/consed** software version 29²⁵⁻²⁷.

Whole genome sequencing of BL3 cells

Whole genome sequencing of BL3 cells (a bovine lymphoma cell line; kindly provided by Dr. Subramaniam Srikumaran) was accomplished with methods as described elsewhere²⁰. Briefly, genomic DNA was used to make a 500 bp paired-end library and sequenced with a massively parallel sequencing machine and

high-output kits (NextSeq500, two by 150 paired-end reads, Illumina, San Diego, CA, USA) until a minimum of 40 GB of data with greater than Q20 quality, was collected. After sequencing, the raw reads were filtered to remove adaptor sequences, contaminating dimer sequences, and low-quality reads. The DNA sequence alignment process was similar to that previously reported²⁰. FASTQ files were aggregated for each sample and DNA sequences were aligned individually to the bovine reference assembly UMD3.1²⁸ with the Burrows-Wheeler aligner (BWA) aln algorithm version 0.7.12²⁹, then merged and collated with bwa sampe. The resulting sequence alignment map (SAM) files were converted to binary alignment map (BAM) files, and subsequently sorted via SAMtools version 0.1.18³⁰. Potential PCR duplicates were marked in the BAM files using the Genome Analysis Toolkit (GATK) version 1.5-32-g2761da9³¹. Regions in the mapped dataset that would benefit from realignment due to small indels were identified with the GATK module RealignerTargetCreator, and realigned using the module IndelRealigner. The BAM files produced at each of these steps were indexed using SAMtools. The resulting indexed BAM files were made available via the USMARC WGS browser and the raw reads for the BL3 cell line were deposited at NCBI BioProject PRJNA325058, BioSample number SAMN05217649. Mapped datasets for each sample were individually genotyped with the GATK UnifiedGenotyper with arguments “--alleles” set to the VCF file (Extended Data File S1)³², “--genotyping_mode” set to “GENOTYPE_GIVEN_ALLELES”, and “--output_mode” set to “EMIT_ALL_SITES”. Lastly, some SNP variants were identified manually by inspecting the sequence with IGV software version 2.1.28^{33,34} (described in the Methods section entitled ‘Identifying protein variants encoded by *ITGB2*’). In these cases, read depth, allele count, allele position in the read, and quality score were considered when the manual genotype determination was made.

Identifying predicted protein variants encoded by bovine *ITGB2*

Aligned WGS data from 96 sires of MBCDPv2.9 were visually analyzed in the *ITGB2* coding region to identify potential CD18 protein variants. Viewing the aligned sequences and detecting variants was accomplished with the IGV software and a browser developed for this purpose. Briefly, public internet sites at the USDA, ARS, USMARC were used in combination with open source software installed on a laptop computer and recorded manually in a spreadsheet as previously described²⁰. A Java Runtime Environment (Oracle Corporation, Redwood Shores, CA, USA) was first installed on the computer. When links to the data were selected by the user, IGV software^{33,34} was loaded from a third-party site (University of Louisville, Louisville, KY, USA) and aligned DNA sequence reads were displayed in the context of the bovine UMD3.1 reference genome assembly. For viewing *ITGB2* gene variants, WGS from a set of eight animals of different breeds was loaded, and the IGV browser was directed to the appropriate genome region by entering “*ITGB2*” in the search field. The IGV zoom function was used to view the first exon at nucleotide resolution with the [show translation] option selected in IGV. An example of the alignment view for *ITGB2* codon 27 with eight animals is shown in Extended data, Figure S1³⁵.

The exon sequences were visually scanned for polymorphisms predicted to alter amino acid sequences, including missense,

nonsense, frameshift, splice site, and insertion/deletion mutations. An *in silico* analysis of other potential splice-affecting variants was not performed as there are no consensus guidelines on the selection of programs or protocols to interpret the predicted results in cattle. Once identified, the variant nucleotide position was viewed and recorded for all 96 animals. The codons affected by SNP alleles were translated into their corresponding amino acids with IGV, codon tables, and knowledge of the CD18 protein sequence (NP_786975). Haplotype phases of predicted polypeptide variants were unambiguously assigned with homozygous individuals, and those with only one variant amino acid. A maximum parsimony phylogenetic tree was manually constructed from the unambiguously phased protein variants and used to infer phases in the remaining variants with maximum parsimony assumptions.

MALDI-TOF MS genotyping of 14 *ITGB2* missense mutations

A single multiplex assay was designed for the 14 *ITGB2* missense SNPs with software provided by the manufacturer (Agena Biosciences, San Diego, CA, USA). The oligonucleotide sequences and assay conditions are provided in Table S1. After design and validation with bovine control DNAs for each SNP, the DNA from the 96 bulls in the MBCDPv2.9 diversity panel were tested in a blinded experiment. Assay design and genotyping was performed at GeneSeek (Lincoln, NE, USA) with the MassARRAY platform and iPLEX Gold chemistry according to the manufacturer’s instructions (Agena Biosciences).

Lkt preparation, gel electrophoresis, and protein immunoblotting

M. haemolytica strains for toxin production were isolated from cattle with severe fibrinous pleuropneumonia in feedlot environments and had complete closed whole genome sequence assemblies available at NCBI. *M. haemolytica* strain 89010807 N serotype A1 (*lktA+*) has been widely used for Lkt production for *in vitro* cytotoxicity assays and has the added advantage of being the parent strain of an isogenic leukotoxin deletion mutant (*lktA-*)^{36,37}. A second strain, *M. haemolytica* strain USDA-ARS-USMARC-183 serotype A1, was isolated from an animal that was part of a high-mortality respiratory disease outbreak in a Kansas feedlot in 1991 and represents the first strain with a complete closed genome assembly³⁸; however, it had not previously been used in *in vitro* assays.

Isolates were maintained on Brain Heart Infusion (BHI) agar (Sigma-Aldrich) frozen stocks were kept in BHI broth with 20% glycerol at -80°C. RPMI 1640 medium (without Phenol Red and L-glutamine, Sigma-Aldrich) and semi-defined medium 2 (SDM2) were used for batch culture production of Lkt. SDM2 is an amino acid-limited culture medium supplemented with cysteine, glutamine, ferric iron, and manganese and was previously shown to greatly improve Lkt production in aerobic batch culture³⁹. For Lkt production, a single, 24-hour colony isolate from BHI agar was inoculated into 5 ml BHI broth in a 10 ml culture tube and incubated overnight at 37°C in 5% CO₂ without shaking. The following morning, 1 ml of BHI liquid culture was inoculated into 100 ml of fresh culture medium in a 300 ml Delong-style Erlenmeyer flask with baffles (Corning, Inc., Corning, NY, USA) and incubated at 37°C, 250 rpm, in 5% CO₂. At intervals,

14 ml samples were removed and centrifuged at 13,100 x g for 10 min at 4°C. The clarified supernatant was decanted, flash frozen in liquid nitrogen and stored at -80°C until use.

Lkt and other proteins secreted into the growth media by *M. haemolytica* were analyzed by SDS-PAGE. Clarified supernatants were precipitated with one volume of acetone on ice for 30 min, followed by centrifugation at 20,800 x g for 5 minutes at room temperature, and air dried 30 min. Sedimented proteins were dissolved in a commercial sample buffer with lithium dodecyl sulfate and dithiothreitol and used per the manufacture instructions (Thermo Fisher Scientific). Samples were heated to 70°C for 10 minutes and loaded on 4–12% precast polyacrylamide Bis-Tris gels (Thermo Fisher Scientific) at run 160 volts for approximately 35 min in 2-[N-morpholino]ethanesulfonic acid (MES) SDS running buffer (Thermo Fisher Scientific). Proteins sorted by SDS PAGE were stained with coomassie-dye reagent (GelCode Blue, Thermo Fisher Scientific) and destained in water. Prestained protein standards (Novex Sharp, Thermo Fisher Scientific) were used to estimate molecular weights of *M. haemolytica* proteins from clarified supernatants. ImageJ software (version 1.52A) was used to estimate relative proportions of protein bands on coomassie-stained page gel⁴⁰.

For protein immunoblots (western blots), proteins from SDS-PAGE gels were electrophoretically transferred to 0.2 µm polyvinylidene difluoride membranes (PVDF, Invitrolon, Thermo Fisher Scientific) with a Mini Blot Module (Thermo Fisher Scientific) per the manufacturer's instructions. PVDF membranes were wetted in 100% methanol prior to equilibrating in transfer buffer (Bolt transfer buffer, Thermo Fisher Scientific) and assembling in the blotting apparatus. Proteins were transferred to membranes for 60 min at a constant voltage of 20 V. Blots were removed from the apparatus and incubated in a blocking reagent (StartingBlock(PBS), Thermo Fisher Scientific), for 60 min at room temperature with gentle agitation. This solution was replaced with a fresh blocking reagent that had a rabbit polyclonal Ltk antibody at a concentration of 1 µg/ml (*M. haemolytica* Ltk Antibody, catalog number LS-C369014, LifeSpan, BioSciences, Inc, Seattle, WA, USA) and incubated as above for 60 min. The primary Ltk antibody was washed three times in for 10 min each in 25 mM Tris, 0.15 M NaCl, 0.05% Tween-20, pH 7.5 (TBS Tween-20, Thermo Fisher Scientific). After washing, a goat anti-rabbit IgG antibody conjugated to horseradish peroxidase (HRP) (catalog number ab97040, Abcam, Cambridge, MA, USA) was added at a concentration of 1 µg/ml in blocking reagent and incubated for 60 min at room temperature with gentle agitation. This secondary anti-rabbit antibody was washed three times for 10 min each in TBS Tween-20 prior to detection with chemiluminescent substrate (Pierce ECL Western Blotting substrate, Thermo Fisher Scientific). The immunoblot was incubated in chemiluminescent substrate for 1 min and imaged for approximately 5 min (ChemiDoc, Bio-Rad Laboratories, Inc. Hercules, CA, USA).

Cell culture and synthetic peptides

BL3 cells were propagated in RPMI 1640 medium (Gibco, Thermo Fisher Scientific) supplemented with 10% fetal bovine

serum (Atlas Biologicals, Fort Collins, CO, USA), 1x antibiotic/antimycotic (Gibco, Thermo Fisher Scientific) and 2 mM L-glutamine (Gibco, Thermo Fisher Scientific). Custom bovine CD18 signal peptides (Figure 4–Figure 7) were commercially synthesized, (Thermo Fisher Scientific) purified by preparative high-performance liquid chromatography, and lyophilized. Peptides were dissolved in dimethylsulfoxide at a concentration of 10 mg/ml, aliquoted, and stored at -20°C.

PBMC and PMN cell isolation

Primary cells were collected from two mixed breed animals (kept as part of the USMARC cattle population) that were each homozygous for the most common *ITGB2* haplotype (variant “1”). For isolation of primary bovine cells, 50 ml of blood were collected by jugular puncture using 16-gauge needles into syringes containing EDTA as an anticoagulant. PMN were isolated using a standard hypotonic lysis procedure. Briefly, blood was spun for 25 min at 1000 x g at 4°C. Plasma and buffy coat layers were removed and discarded. Sterile water was added to the red blood cell (RBC) layer to lyse RBC followed by addition of 10X PBS to restore tonicity. PMN were isolated by centrifugation for 10 min at 250 x g at 4°C. The PMN cell pellet was washed three times with 1x PBS and the final cell pellet was resuspended in RPMI 1640 medium.

Peripheral blood mononuclear cells (PBMC) were isolated essentially as described⁴¹. Briefly, PBMC were isolated over Ficoll-Paque Plus (GE Healthcare Bio-Sciences AB, Uppsala, Sweden), as per the manufacturer's instructions, with modification. Briefly, 15 ml of whole blood mixed 1:1 with PBS was underlaid beneath 14 ml of the density gradient in a 50 ml conical tube. The tubes were then centrifuged for 45 min at 900 x g at room temp and with no brake. The PBMC layer was carefully removed and brought up to 45 ml in PBS in a new 50 ml conical tube followed by centrifugation for 15 min at 400 x g at 4°C with high brake. Erythrocytes were removed using RBC lysing buffer (Sigma-Aldrich). The PBMC pellet was further washed three times with 1x PBS and the final pellet was resuspended in RPMI 1640 medium.

MTT dye-reduction cytotoxicity assay

The ability of different CD18 signal peptide variants to bind Lkt and inhibit Lkt-induced cytolysis was measured with the MTT dye-reduction cytotoxicity assay¹⁰. The BL3 cell line was selected because it is the most well-studied, readily available, immortalized cell line susceptible to Ltk-induced cytolysis. CD18 signal peptides were tested at concentrations ranging from 50 µM to 0.195 µM. CD18 signal peptides were diluted using serial 2-fold dilutions in 96-well round bottom plates containing 50 µl/well of Lkt at a 50% toxicity end point titer in colorless RPMI 1640 medium without phenol red (Sigma-Aldrich). Synthetic signal peptides and Lkt preparations were pre-incubated for 1 hr on ice prior to the addition of 5 × 10⁵ cells/wells. These cells were added as a 50 µl suspension with a density of 1 × 10⁷ cells/ml in colorless RPMI. Cells were incubated with synthetic signal peptides and Lkt for 1 hr at 37°C in 5% CO₂ and subsequently centrifuged at 600 x g for 7 min at 4°C and the supernatant was removed and discarded. Cells were

resuspended in 100 μ l of colorless RPMI and 20 μ l 0.5% MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl-2H-tetrazolium bromide; Sigma-Aldrich) and incubated for 20 min at 37°C in 5% CO₂, centrifuged as before, and the supernatant was removed and discarded. The purple formazan precipitate was then dissolved in 100 μ l of acid isopropanol (0.04N HCl in isopropanol). Following a 5 min incubation, cellular debris was pelleted and the supernatant was transferred to a new 96-well plate. The optical density (OD) of the samples was measured at 570 nm and 690 nm. The background measurement at 690 nm was then subtracted from the 570 nm measurement to give the background adjusted OD. The percent cytotoxicity was calculated as follows: $(1 - (\text{OD of toxin treated cells} / \text{OD of cells without toxin})) \times 100$. The percent inhibition of cytotoxicity in the presence of synthetic CD18 peptides was calculated as follows: $((\text{percent cytotoxicity in the absence of peptide} - \text{percent cytotoxicity in the presence of peptide}) / \text{percent cytotoxicity in the absence of peptide}) \times 100$. Given normal variability in the assay, values were occasionally obtained outside the range of 0 to 100% inhibition. Negative values were replaced with 0 and values greater than 100 were replaced with 100 for graphical presentation.

Fresh bovine PBMC or PMN were used for comparison to results obtained using immortalized BL3 cells. Cells were suspended in 50 μ l colorless RPMI medium and 10 μ l Biolog Redox Dye MB, containing 500 μ M water-soluble tetrazolium (Biolog, Hayward, CA, USA). This dye was used because it was found to be more sensitive to changes in cellular respiration when assaying primary cells (data not shown). Cells were incubated for 3 hr at 37°C in 5% CO₂, centrifuged as before, and the supernatant was transferred to a clean 96 well plate prior to the OD being measured at 590 nm and 750 nm. Calculations for percent cytotoxicity and percent inhibition were calculated using background adjusted OD values as described above.

Statistical analyses of IC₅₀ values

The half maximal inhibitory concentration (IC₅₀) was estimated for each signal peptide variant to compare the concentration of peptide needed to block 50% of Lkt-induced cytotoxicity of susceptible bovine cells. Univariate nonlinear regression (NLIN procedure, SAS 9.4, SAS Institute Inc., Cary, NC, USA) was used to fit data from three replicates to the following equation: $Y_{ijk} = T + (B - T) / (1 + (C_j / \text{IC}_{50_i})^S) + e_{ijk}$, where Y_{ijk} is the measured Lkt inhibition for the k^{th} replicate of the i^{th} peptide at the j^{th} concentration (C_j) of peptide. T is the estimated maximum, B is the estimated minimum of the fitted nonlinear relationship between peptide concentration and Lkt inhibition. S_i is the slope of the relationship at IC₅₀ _{i} , the estimated concentration that the i^{th} peptide inhibits Lkt-induced cytotoxicity by 50%. e_{ijk} is random variation. Standard errors of IC₅₀ _{i} were used for comparisons of estimates.

Results

Identifying *ITGB2* polymorphisms affecting the predicted amino acid sequence of CD18

Bovine *ITGB2* consists of 16 exons spanning 29.1 kb of genomic DNA and encodes a 769 amino acid protein with

multiple functional domains (Figure 1A,B). Using software to view the aligned genome sequences from 96 diverse bulls, 13 codons with 14 missense variants were identified (Extended Data Table S2)⁴². There were no frameshifts, splice sites, or indel polymorphisms observed that would affect the predicted amino acid sequence. Two *ITGB2* regions of interest were further selected for additional Sanger sequencing in 1142 purebred cattle from 46 breeds: the signal peptide region (exon 2), and the region containing the D128G variant causing BLAD (exon 5). DNA sequence analyses revealed no additional polymorphisms that were predicted to alter the polypeptide sequence, except the previously described D128G variant in Holstein cattle (data not shown). The genotypes were independently verified with a single, multiplexed, MALDI-TOF MS assay for 14 SNPs in the 96 diverse bulls, and in 1142 of 1168 cattle from 46 breeds (Extended Data Table S3)⁴³. Thus, in total, there were 14 missense variants identified in 13 codons (Table 1).

Determining *ITGB2* haplotypes encoding different CD18 polypeptides

Identifying haplotypes that encode distinct combinations of missense variants on the CD18 polypeptide is important for evaluating their potential function. A total of 15 *ITGB2* haplotypes were identified that, when translated, were predicted to encode different CD18 proteins (Table 2). These 15 predicted polypeptide sequences were placed in the context of a maximum parsimony phylogenetic tree (Figure 1C). Haplotypes encoding CD18 protein variants “1 to 7”, “9”, “13”, and “14” were confirmed by their presence in homozygous animals. Haplotypes encoding CD18 protein variants “8”, “10”, and “15” were unambiguously confirmed in animals with only one heterozygous site. However, haplotype phase was ambiguous when the distance between two heterozygous sites exceeds the length of the DNA sequence read (150 bp in these WGS data sets). Thus, haplotypes for the remaining CD18 protein variants “11” and “12” were tentatively inferred from additional breed-level frequency information. For example, the inferred phase for variant “12” (P₁₅₅L₆₅₆) was only observed in two of 27 Braunvieh cattle that were each heterozygous for both missense variants. However, all 25 of the other Braunvieh cattle sequenced were homozygous for the variant “1” (Table 3 and Extended Data Table S3)⁴³. Thus, it was reasonable to infer that P₁₅₅ (exon 5), and L₆₅₆ (exon 14) are present on one rare haplotype in two animals, rather than on two rare haplotypes in each animal. Similarly, the inferred phase for variant “11” (C₅L₆₅₆) was only observed in six of 22 Wagyu cattle and each were heterozygous at positions 5 and 656. Since the 22 Wagyu cattle have a variant “1” frequency of 0.8 it seems likely that C₅ and L₆₅₆ variants are present on the same chromosome (i.e. diplotype “1,11”) rather than split across two chromosomes (i.e., diplotype “5,15”). In spite of the potential for ambiguous haplotype phases with rare variants, the phylogenetic tree of predicted CD18 proteins provides a solid framework for further evaluation.

Evolutionary comparison of CD18 polypeptide sequences

Determining the most likely phylogenetic root of the CD18 tree is important for establishing the likely order of mutational

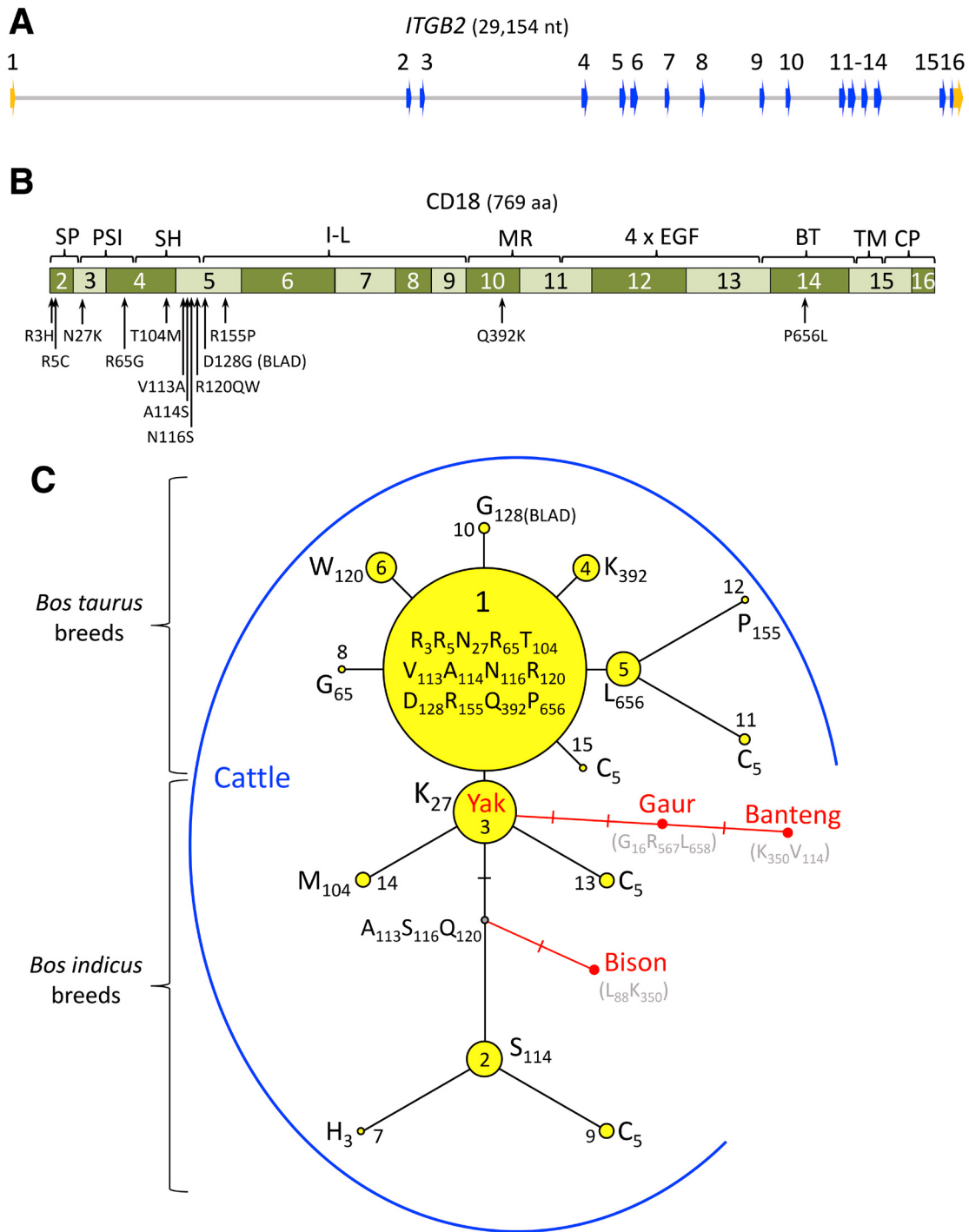


Figure 1. Physical maps of *ITGB2*, CD18, and rooted maximum parsimony phylogenetic tree of CD18 protein variants in cattle. (A) Genomic DNA map of *ITGB2*: blue arrows, coding regions of exons; orange arrows, untranslated regions of exons; grey horizontal lines, intron regions. (B) Map of CD18 domains in relationship to missense mutations found in cattle. (C) Rooted maximum parsimony phylogenetic tree of CD18 protein variants from 1142 cattle from 46 breeds with connections to closely-related species. The most frequent CD18 isoform ("variant 1") was used as the reference amino acid sequence for the trees. For "variants 1" through "14", each node in the tree represents a different isoform of CD18 that varies by one amino acid compared to adjacent nodes. The hash marks represent nodes that were inferred but not observed. The areas of the circles are proportional to the overall variant frequency in the cattle tested. Yak CD18 was identical to bovine CD18 "variant 3" and denoted as the most likely root of the phylogenetic tree based on the relationship of CD18 sequences in yak, gaur, banteng, and bison. SP, signal peptide; PSI, plexin-semaphorin-integrin domain; SH, spacer-hybrid domain; I-L, I-like domain; MR, mid-region hybrid domain; EGF, epidermal growth factor-like domain; BT, beta tail domain; TM, transmembrane domain; CP, cytoplasmic domain.

Table 1. DNA sequence information for 14 bovine *ITGB2* missense SNP variants in cattle.

Codon variant ^a	Chr 1 position (UMD3.1)	Exon	CD18 domain ^b	Consensus codon sequence ^c	Codon alleles ^d	MAF ^e		Flanking reference genomic sequence
						Ref. panel	Ext. panel	
R3H	145121452	2	SP	cRc	cGc = R cAc = H	0.010	0.0004	ctggggctctgaagctatgtcactgcccctccctcctcaggacatgctgc [R]ccagcgccccagctgctgctcctagcgggctgcttgcctccagtcog
R5C	145121447	2	SP	Ygc	Cgc = R Tgc = C	0.005	0.0123	gtctgaagctatgtcactgcccctccctcctcaggacatgctgcgccag [Y]gccccagctgctgctcctagcgggctgcttgcctccagtcoggtgag
N27K	145121043	3	PSI	aaS	aaC = N aaG = K	0.115	0.1187	ggctcaccagcccgtgtctctcccagctgtgccaggagtgaccaa [S]tacaaggtcagcacctccgggactgcatcagtgccgcccggctgctgc
R65G	145116134	4	PSI	Sga	Cga = R Gga = G	0.005	0.0004	cccagaactcaccagggcaagggagcccgactccattcgtgtgacaca [S]gagcggagctgctgctcaaggctgcccagctgatgacatcatggaaccc
T104M	145116016	4	SH	aYg	aCg = T aTg = M	0.010	0.0035	ccgggacagccagggcgggagctggaagcagctgtcccacaggaagtga [Y]gctctacctgagaccaggtaggctggctggctaggggggccgcccct
V113A	145115008	5	SH	gYt	gTt = V gCt = A	0.057	0.0299	gaccaggtggtacacctgactctcccacaaactcctggcaggtcaggcag [Y]tgcgttcaatgtgacctccggaggccaagggtaccatccatgacctgt
A114S	145115006	5	SH	Kcg	Gcg = A Tcg = S	0.057	0.0298	ccaggtggtacacctgactctcccacaaactcctggcaggtcaggcagtt [K]cgttcaatgtgacctccggaggccaagggtaccatccatgacctgtac
N116S	145114999	5	SH	aRt	aAc = N aGc = S	0.057	0.0290	gtacacctgactctcccacaaactcctggcaggtcaggcaggtgctgtca [R]tggacctccggaggccaagggtaccatccatgacctgtactacctga
R120W	145114988	5	SH	Ygg	Cgg = R Tgg = W	0.021	0.0171	ctctcccacaaactcctggcaggtcaggcaggttgcgttcaatgtgaccttc [Y]ggaggccaagggtaccatccatgacctgtactacctgatggacctctcc
R120Q	145114987	5	SH	cRg	cGg = R cAg = Q	0.057	0.0317	tctctcccacaaactcctggcaggtcaggcaggttgcgttcaatgtgaccttc [R]gaggccaagggtaccatccatgacctgtactacctgatggacctctcc
D128G ^f	145114963	5	IL	gRc	gAc = D gGc = G	^g	0.0031	ggcagttgcgttcaatgtgacctccggaggccaagggtaccatccatccg [R]cctgactacctgatggacctctcctactccatggtggatgacctgca
R155P	145114882	5	SH	cSg	cGg = R cCg = P	0.005	0.0004	catggtggatgacctcgtcaactgcaagaagctgggggggactgctctcc [S]ggccctcaatggcatcaccagctgggcccagctgggagggcagctactc
Q392K	145109830	10	MR	Mag	Cag = Q Aag = K	0.021	0.0131	ctgacacctgaaagtcacctacgactcctctcagtaaacgggaaatcg [M]aggtggaccagcccagaggggactcgcagcggctccagatcaactcccg
P656L	145107135	14	BT	cYg	cCg = P cTg = L	0.010	0.0270	cgccaagaactgcagcgcagcgtggggcagacgaagctgctgccagcc [Y]gggtcccggccgaagtgcaggagcgcgactccagggtgctggatga

^aAll sequences presented are from the sense strand bovine *ITGB2* gene. However, in the UMD3.1 reference assembly, *ITGB2* oriented in the antisense direction. ^bCD18 protein domain abbreviations: SP, signal peptide; PSI, plexin-semaphorin-integrin domain; SH, spacer-hybrid domain; IL, I-like domain; and BT, beta-tail domain. ^cIUPAC/IUBMB ambiguity codes used for nucleotides: R = a/g, Y = c/t, M = a/c, K = g/t, S = c/g, W = a/t¹⁶. ^dThe major allele is listed first. ^eMinor allele frequency in the beef cattle diversity panel MBCDPv2.9 (n = 96). ^fMinor allele frequency in the extended purebred cattle panel with 46 breeds (n = 1142). ^gAllele not detected in the indicated group of cattle. ^hMissense mutation associated with BLAD¹⁷.

events. Comparing cattle CD18 precursor protein variants to those from closely related species in the *Bos* genus indicated that variant “3” (K₂₇) was the most likely root of the phylogenetic tree (Figure 1C). Cattle are predicted to share a common ancestor with other species in the *Bos* genus approximately 5 million years ago. In addition, the K₂₇ variant was associated with indicine cattle breeds, while the N₂₇ variant was associated with taurine breeds. For example, the N₂₇ frequency in 840 cattle from 33 taurine breeds was 0.998, while the K₂₇ frequency in 70 Brahman, Indu Brazil, and Nelore cattle was 0.95. Thus, the structure of the rooted tree suggests that CD18 protein variants “1” and “3” are the ancestral polypeptide sequence of taurine and indicine breeds, respectively. The rooted tree also suggests that the distal nodes represent CD18 variants that have arisen sometime after the split between taurines and indicines, approximately 500,000 years ago.

The conservation of amino acid residues throughout vertebrate species is a measure of their potential impact on protein function. Highly conserved residues are more likely to be indispensable for function and thus, variation at these positions is assumed to be deleterious. The 769 amino acid sequence of cattle CD18 is highly similar to those from yak, sheep, whale, and humans (99, 95, 90, and 83% identity, respectively). The cattle CD18 sequence is also remarkably similar to chicken, frog, fish, lamprey, and fruit fly (63, 57, 49, 42, and 19% identity, respectively), and has some polypeptide regions that are invariant throughout the Bilateria (Extended Data Table S4)⁴⁴. The 13 variant amino acid positions in the bovine CD18 precursor protein were compared to those in 35 representative Bilateria species. The aspartate residue at position 128 (D₁₂₈) is invariant throughout the Bilateria, except in cattle wherein G₁₂₈ causes the complete loss of CD18 function and results in BLAD in homozygous individuals

Table 2. Frequencies of predicted full-length CD18 protein variants in U.S. cattle.

Protein variant code ^a	Variant amino acids ^b													Protein variant frequency ^c	
	R3	R5	N27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	Beef cattle diversity panel (n = 96)	Extended purebred cattle panel (n = 1142)
1	R3	R5	N27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	0.828	0.820
2	R3	R5	K27	R65	T104	A113	S114	S116	Q120	D128	R155	Q392	P656	0.042	0.025
3	R3	R5	K27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	0.047	0.081
4	R3	R5	N27	R65	T104	V113	A114	N116	R120	D128	R155	K392	P656	0.021	0.013
5	R3	R5	N27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	L656	0.005	0.024
6	R3	R5	N27	R65	T104	V113	A114	N116	W120	D128	R155	Q392	P656	0.021	0.017
7	H3	R5	K27	R65	T104	A113	S114	S116	Q120	D128	R155	Q392	P656	0.010	- ^d
8	R3	R5	N27	G65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	0.005	-
9	R3	C5	K27	R65	T104	A113	S114	S116	Q120	D128	R155	Q392	P656	0.005	0.004
10	R3	R5	N27	R65	T104	V113	A114	N116	R120	G128	R155	Q392	P656	-	0.003
11	R3	C5	N27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	L656	-	0.003
12	R3	R5	N27	R65	T104	V113	A114	N116	R120	D128	P155	Q392	L656	0.005	-
13	R3	C5	K27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	-	0.005
14	R3	R5	K27	R65	M104	V113	A114	N116	R120	D128	R155	Q392	P656	0.010	0.004
15	R3	C5	N27	R65	T104	V113	A114	N116	R120	D128	R155	Q392	P656	-	0.001

^aCD18 protein variant allele definitions are shown in Figure 1C. ^bThe red bold residues are those differing from "variant 1". ^cThe coefficient of determination for these frequencies (r^2) was 99.7. ^dAllele not detected in the indicated group of cattle.

Table 3. Frequencies of predicted CD18 protein variants in 46 U.S. breeds.

Breed group	Animals typed (n=1142)	C5 ^b	CD18 protein variant allele frequency ^a														
			1	2	3	4	5	6	7	8	9 ^b	10 ^c	11 ^b	12	13 ^b	14	15 ^b
Angus	24	-	0.96	-	-	0.04	-	-	-	-	-	-	-	-	-	-	-
Ankole-Watusi	20	-	0.25	-	0.75	-	-	-	-	-	-	-	-	-	-	-	-
Ayrshire	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Beefmaster	24	-	0.88	0.08	0.02	-	-	-	-	-	-	-	-	-	-	0.02	-
Belgian Blue	24	-	0.90	-	-	0.04	0.06	-	-	-	-	-	-	-	-	-	-
Blonde d'Aquitaine	24	-	0.77	-	-	0.04	0.08	0.10	-	-	-	-	-	-	-	-	-
Brahman	23	-	0.11	0.27	0.58	-	0.02	-	0.02	-	-	-	-	-	-	-	-
Brahmousin	24	0.10	0.71	0.06	0.13	-	-	-	-	-	0.10	-	-	-	-	-	-
Brangus	24	-	0.55	0.09	0.21	0.15	-	-	-	-	-	-	-	-	-	-	-
Braunvieh	24	-	0.98	-	-	-	-	-	-	-	-	-	-	0.02	-	-	-
Brown Swiss	26	-	0.98	-	-	-	0.02	-	-	-	-	-	-	-	-	-	-
Charolais	24	0.02	0.79	-	0.06	-	-	0.13	-	-	-	-	-	-	0.02	-	-
Chianina	24	-	0.98	-	-	0.02	-	-	-	-	-	-	-	-	-	-	-
Corriente	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Devon	23	-	0.87	-	-	0.04	0.09	-	-	-	-	-	-	-	-	-	-
Dexter	22	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Gelbvieh	23	-	0.70	-	-	-	0.07	0.24	-	-	-	-	-	-	-	-	-
Guernsey	23	-	0.96	-	-	0.02	0.02	-	-	-	-	-	-	-	-	-	-

Breed group	Animals typed (n=1142)	C5 ^b	CD18 protein variant allele frequency ^a														
			1	2	3	4	5	6	7	8	9 ^b	10 ^c	11 ^b	12	13 ^b	14	15 ^b
Hereford	24	-	0.98	-	-	-	-	0.02	-	-	-	-	-	-	-	-	-
Highland	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Holstein	81	-	0.93	-	-	0.02	0.01	-	-	-	-	0.04	-	-	-	-	-
Indu-Brazil	25	0.09	-	0.32	0.55	-	0.02	-	-	-	0.06	-	-	-	0.02	0.02	-
Jersey	29	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Limousin	24	-	0.90	-	-	0.10	-	-	-	-	-	-	-	-	-	-	-
Maine-Anjou	24	-	0.96	-	-	-	-	0.04	-	-	-	-	-	-	-	-	-
Marchigiana	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mini Hereford	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mini Zebu	24	-	0.33	0.15	0.48	-	-	-	-	-	-	-	-	-	-	0.04	-
Montbeliard	24	-	0.94	-	-	-	0.06	-	-	-	-	-	-	-	-	-	-
Murray Gray	20	-	0.78	-	-	-	0.23	-	-	-	-	-	-	-	-	-	-
Nelore	24	-	-	0.16	0.82	-	-	-	-	-	-	-	-	-	-	0.02	-
Piedmontese	25	-	0.92	-	-	-	0.08	-	-	-	-	-	-	-	-	-	-
Pinzgauer	23	-	0.89	-	-	-	0.11	-	-	-	-	-	-	-	-	-	-
Red Angus	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Red Poll	23	-	0.98	-	-	-	-	0.02	-	-	-	-	-	-	-	-	-
Romagnola	24	-	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Salers	24	-	0.77	-	-	-	-	0.21	-	0.02	-	-	-	-	-	-	-
Santa Gertrudis	24	0.02	0.63	0.02	0.25	-	0.02	-	-	-	0.02	-	-	-	-	0.06	-
Senepol	23	-	0.89	0.04	-	-	0.07	-	-	-	-	-	-	-	-	-	-
Shorthorn	23	-	0.96	-	-	-	0.04	-	-	-	-	-	-	-	-	-	-
Simmental	23	-	0.87	-	-	-	0.09	0.04	-	-	-	-	-	-	-	-	-
Tarentaise	24	-	0.94	-	-	0.02	0.02	0.02	-	-	-	-	-	-	-	-	-
Texas Longhorn	23	-	0.74	0.07	0.15	0.04	-	-	-	-	-	-	-	-	-	-	-
T. Longhorn, CTLR ^e	19	-	0.95	-	0.05	-	-	-	-	-	-	-	-	-	-	-	-
Tuli	23	0.04	0.91	-	0.04	-	-	-	-	-	-	-	-	-	-	-	0.04
Wagyu	22	0.14	0.80	-	-	-	0.07	-	-	-	-	-	0.14	-	-	-	-

^aCD18 protein variant allele definitions are shown in Table 2. ^bThe CD18 C5 missense variant appears in protein variants 9, 11, 13, and 15. ^cThe CD18 G128 missense variant causes BLAD in Holstein cattle. ^dAllele not detected in the indicated group of cattle. ^eTexas Longhorn, Cattlemen's Texas Longhorn Registry.

of the Holstein breed (Figure 2). CD18 positions 65, 104, and 155 are also conserved and the variant allele in cattle is rare. Based only on the degree of residue conservation across species, the proposed predicted order of negative impact on CD18 function in cattle was: $G_{128} > G_{65} = M_{104} > P_{155}$. The CD18 K₂₇ indicine variant was conserved throughout the jawed vertebrates and thus, the major N₂₇ taurine variant was not observed in any other species. However, based on its high frequency in most taurines, the N₂₇ variant does not appear to be deleterious.

The conservation of arginine at positions 3 (R₃) and 5 (R₅) in CD18 signal peptides was of particular interest because this region binds bacterial Lkt in ruminant species, which includes the Bovids, Cervids, Giraffids, musk deer, chevrotains, and pronghorns. The R₃ residue was conserved throughout the Bovinae, but not in sheep and goat, which have proline at that position (Figure 2). The histidine residue at position 3 (H₃) was rare in cattle, not observed in other ruminants, and on a distal node of

the phylogenetic tree (CD18 polypeptide variant “7”, Figure 1C). Two animals from the Brahman breed group were identified with the H₃ and one was homozygous, indicating that H₃ is not a lethal recessive variant (H₃,H₃, Extended Data Table S2⁴⁵, and R₃,H₃, Extended Data Table S3⁴³). Unlike R₃, the R₅ variant was not conserved in Bovinae, since eland have cysteine at this site (C₅). In addition, the C₅ variant was present on four distinct putative CD18 polypeptide variants: “9”, “11”, “13”, and “15” (Figure 1C), including both taurine- and indicine-influenced breeds. The presence of the C₅ variant on multiple but infrequent haplotypes indicates recombination has occurred between this and other CD18 missense variants.

Comparison of batch production methods of biologically-active Lkt with two reference strains of *M. haemolytica*

The discovery of missense variants in the CD18 signal peptide provided the opportunity to test these variants using *in vitro* cell assays with bacterial Lkt. However, producing sufficient and

Taxonomic group	Species common name	TMRCA (Ma)	Overall identity (%)	Position in CD18															
				Exon 2			Exon 3			Exon 4			Exon 5			Exon 10		Exon 14	
				3	5	27	65	104	113	114	116	120	128	155	392	656			
Bovinae	Cattle variant 1	0	100.0	R	R	N	R	T	V	A	N	R	D	R	Q	P			
	Cattle variant 2	0	99.3	.	.	K	.	.	A	S	S	Q			
	Cattle variant 3	0	99.9	.	.	K			
	Cattle variant 4	0	99.9	K	.			
	Cattle variant 5	0	99.9	L			
	Cattle variant 6	0	99.9	W			
	Cattle variant 7	0	99.2	H	.	K	.	.	A	S	S	Q			
	Cattle variant 8	0	99.9	.	.	.	G			
	Cattle variant 9	0	99.2	.	C	K	.	.	A	S	S	Q			
	Cattle variant 10	0	99.9	G	.	.	.			
	Cattle variant 11	0	99.7	.	C	L			
	Cattle variant 12	0	99.7	P	.	L			
	Cattle variant 13	0	99.6	.	C	K			
	Cattle variant 14	0	99.7	.	.	K	.	M			
	Cattle variant 15	0	99.9	.	C			
Bovidae	Yak	5	99.9	.	.	K			
	Bison	5	99.2	.	.	K	.	.	A	.	S	Q			
	Gaur	5	99.5	.	.	K			
	Banteng	5	99.2	.	.	K	.	.	.	V			
	Water buffalo	15	98.2	.	.	K	.	.	A			
	Eland	17	95.8	.	C	K	.	.	A	V	.	Q			
	Sheep	26	95.4	P	.	K	.	.	A	.	.	Q	.	.	.	V			
	Goat	26	96.0	P	.	K	.	.	A	.	.	Q	.	.	.	V			
	Elk	27	95.1	.	.	K	.	.	A	.	.	Q	.	.	K	.			
	Artiodactyla	Dolphin	56	89.7	.	.	K	.	.	A	V	.	Q	.	.	K	.		
Orca		56	89.9	.	.	K	.	.	A	V	.	Q	.	.	K	.			
Swine		62	88.0	C	C	K	.	.	A	-	M			
Laurasiatheria	Alpaca	64	88.0	-	.	K	.	.	A	.	T			
	Camel	64	88.0	P	.	K	.	.	A	.	T			
	Horse	78	81.4	-	.	G	.	.	A	-	.	Q	.	Q	N	.			
	Panda	78	81.9	.	A	K	.	.	A	-			
Boreoeutheria	Pangolin	78	80.5	W	S	K	.	.	A	T	R	.			
	Human	97	83.1	G	.	K	H	.			
	Chimp	97	83.5	G	.	K	H	.			
	Gorilla	97	83.0	G	.	K	.	.	A	H	.			
	Baboon	97	82.1	G	.	K	.	.	-	.	T	.	.	Q	L	.			
	Hampster	97	83.1	G	H	K	.	.	-	-	S	.			
	Rat	97	81.3	G	H	K	.	.	-	-	.	.	.	Q	S	.			
	Mouse	97	81.4	G	.	K	.	.	-	-	.	.	.	Q	S	.			
	Opossum	164	73.0	Y	S	K	S	Q	A	.	.	K	.	.	S	.			
	Amniota	Eagle	310	64.4	.	C	K	M	H	A	V	E	.	.	.	I	L		
Chicken		310	63.5	.	C	K	I	H	-	.	D	.	.	.	A	R			
Alligator		310	63.5	.	C	K	I	N	-	-	.	H	.	E	S	L			
Tetrapoda	Frog	350	56.6	W	Y	K	D	S	-	.	D	.	.	E	K	E			
Sarcopteryii	Coelacanth	400	54.5	L	Q	K	A	A	G	P	S	K	.	Q	K	V			
Euteleostomi	Fish	450	49.2	Q	V	K	V	Q	-	P	Q	K	.	E	K	K			
Gnathostomata	Shark	483	48.8	M	M	K	L	R	K	I	K	K	.	D	V	T			
Vertebrata	Lamprey	631	41.7	L	I	A	V	R	E	Q	R	L			
Bilateria	Fruit fly	847	18.7	S	G	C	L	Y	Q	R	K	.	.	Q	P	D			

Figure 2. Evolutionary comparison of CD18 residues at their variant sites in U.S. cattle. Aligned and gapped protein sequences from a representative set of 56 bilateria species were compared (Extended Data Table S4). At variant sites in cattle, the residues were summarized for a representative subset of 35 species. TMRCA, estimated time to most recent common ancestor in millions of years⁴⁷; letters, IUPAC/IUBMB codes for amino acids; dot, amino acid residues identical to those in cattle "variant 1"; dash, not enough sequence similarity for comparison or missing residue in that peptide region.

consistent batches of biologically-active Lkt from reference bacterial strains was a challenge with traditional cell culture medium (RPMI). In an effort to overcome this barrier, Lkt production in RPMI was compared with that in a semi-defined bacterial culture medium (SDM2, Methods) with two wild-type *M. haemolytica* strains. The total biological activity of Lkt excreted into SDM2 culture was up to 80-fold greater at its peak than that in RPMI for a given reference strain of *M. haemolytica* (e.g. Strain 183, **Figure 3A**). In both media, Lkt activity was induced in late log phase as batch cultures made the transition to stationary phase. Although the biological activity quickly diminished as the culture progressed to stationary phase, the total Lkt protein measured by SDS PAGE continued to increase and the level was stable for hours in the culture supernatant (**Figure 3B**). The Lkt of clarified SDM2 culture supernatants with the highest cytolytic activity (Strain 183, fraction C, **Figure 3B**) was estimated to be 90% pure based on gel densitometry imaging of coomassie-stained SDS-PAGE gels. Preparations of similar quality were used for *in vitro* assays. The cytolytic activity of these toxin preparations was stable at -80°C for more than 2 years.

CD18 signal peptide variant C₅ has enhanced binding to bacterial Lkt

Analysis of cattle *ITGB2* haplotypes showed that three distinct polypeptide sequences are encoded in the 22-amino acid signal peptide region: the common variant with arginine at positions 3 and 5 (R₃R₅), a rare variant with histidine at position three (H₃R₅), and second rare variant with cysteine at position 5 (R₃C₅). Synthetic 22-mer peptides representing these three, full-length, signal peptides were tested for their ability to bind Lkt. The synthetic peptides were pre-incubated with *M. haemolytica* Lkt preparations to allow binding, and applied to Lkt-sensitive BL3 cell cultures *in vitro* (**Figure 4A**). The common R₃R₅ signal peptide was used as a reference since it has a frequency of approximately 0.98 in U.S. cattle, and is predicted to be present on 10 of the full-length CD18 sequences. The synthetic R₃R₅ signal peptide had a IC50 of 17.9 μM, which represents the concentration of peptide needed to block 50% of Lkt-induced cytotoxicity of BL3 cells. The rare H₃R₅ signal peptide variant, which is only found on one full-length CD18 variant (**Figure 1C**, variant 7), was similar to the reference, with an IC50 of 21.6 μM. In contrast, the rare R₃C₅ signal peptide found on full-length CD18 variants 9, 11, 13, and 15 had an IC50 of 5.9 μM, which was 3-fold lower than the reference, indicating an increased affinity for Lkt (**Figure 4A**).

The optimum blocking of Ltk-induced cytotoxicity has been previously reported to occur with the 13-mer peptide corresponding to CD18 signal peptide residues 5 to 17¹⁰. Thus, we tested the effect of cysteine at position 5 (C₅) in this shorter peptide. The synthetic 13-mer C₅ peptide was 3.6-fold more effective at blocking Lkt toxicity compared to the 22-mer R₃C₅ peptide (IC50 of 1.6 and 5.9 μM, respectively). When compared to the 13-mer reference peptide with arginine at position five (R₅), the 13-mer C₅ peptide was 8-fold better at blocking Lkt-induced cytotoxicity (IC50 13.0 and 1.6 μM, respectively; **Figure 4B**). A negative control 13-mer peptide containing randomly assorted amino acids from the reference peptide sequence failed to inhibit Lkt-induced cytotoxicity, even at the highest concentration

tested (50 μM), indicating that inhibition of cytotoxicity was sequence specific (**Extended Data File S2**)⁴⁸. Together, these results suggest that peptide sequence and length affect Lkt binding.

Synthetic C₅ variant CD18 signal peptide blocks Lkt-induced cytotoxicity of primary bovine cells

The 13-mer C₅ synthetic signal peptide containing CD18 residues 5 to 17 were also tested for their ability to inhibit Lkt-induced cytotoxicity of primary cells isolated from cattle. The purpose was to demonstrate that the reduction in cytotoxicity observed with C₅ signal peptides was comparable between the immortalized cell line and freshly isolated leukocytes from cattle. Like the BL3 cell line, the animals used as donor were homozygous for CD18 variant “1”, and thus have the reference (R₃R₅) signal peptide. With primary PBMC (**Figure 5A**) or PMN (**Figure 5B**), the 13-mer C₅ synthetic signal peptide was significantly better at blocking Lkt-induced cytotoxicity compared to the R₅ signal peptide (7- and 14-fold respectively) and was similar to that for BL3 cells (8-fold).

Arginine at position 4 (R₄) in the eland CD18 signal peptide disrupts the enhanced Lkt binding attributed by C₅

Some bovid species have CD18 signal peptide sequences that are slightly different from those in cattle (**Figure 6A** and **Table S3**). In water buffalo, the 13-mer peptide sequence corresponding to CD18 signal peptide amino acids 5 to 17 differs at position 16 (S₁₆), while the same region in sheep differs at positions 10 and 12 (F₁₀S₁₂). However, synthetic peptides corresponding to the water buffalo and sheep sequences were similar to the R₅ reference cattle signal peptide when tested for their ability to bind Lkt and inhibit cytotoxicity of BL3 cells *in vitro*. In contrast, the eland signal peptide was variant at three positions in this region compared to cattle (C₅V₈G₁₆), and its 13-mer synthetic signal peptide had a 24-fold decrease in IC50 compared to the reference cattle R₅ signal peptide and a similar IC50 compared to the reference cattle C₅ signal peptide (**Figure 6A**). However, if the synthetic peptide is expanded to include the eland residue at position 4, the results were different. Eland have an arginine residue at position 4 (R₄) where other ruminants have a glutamine (Q₄). A synthetic 14-mer signal peptide with R₄ (i.e., Eland R₄C₅V₈G₁₆) caused a 66-fold reduction in the ability of the eland signal peptide to bind Lkt compared to the 13-mer (C₅V₈G₁₆) as measured by IC50 (**Figure 6B**). When R₄ was replaced with the Q₄ normally found in cattle and other ruminants (i.e. Eland Q₄C₅V₈G₁₆ versus R₄C₅V₈G₁₆), Lkt binding was restored. Similarly, when Q₄ in the cattle signal peptide (Q₄C₅) was replaced with R₄ (R₄C₅) there was a significant reduction in the ability of this peptide to bind Lkt (5.6-fold increase in IC50). These results suggest that the amino acid position 4 in the signal peptide can affect Lkt binding and that R₄ amino acid sequence in eland may disrupt the enhanced Lkt binding conferred by the C₅ variant residue.

A truncated CD18 C₅ signal peptide has high affinity for Lkt

Toxin inhibitors represent a potentially potent class of therapeutics that could protect animals during acute lung infection. Since truncated synthetic C₅ signal peptides showed increase

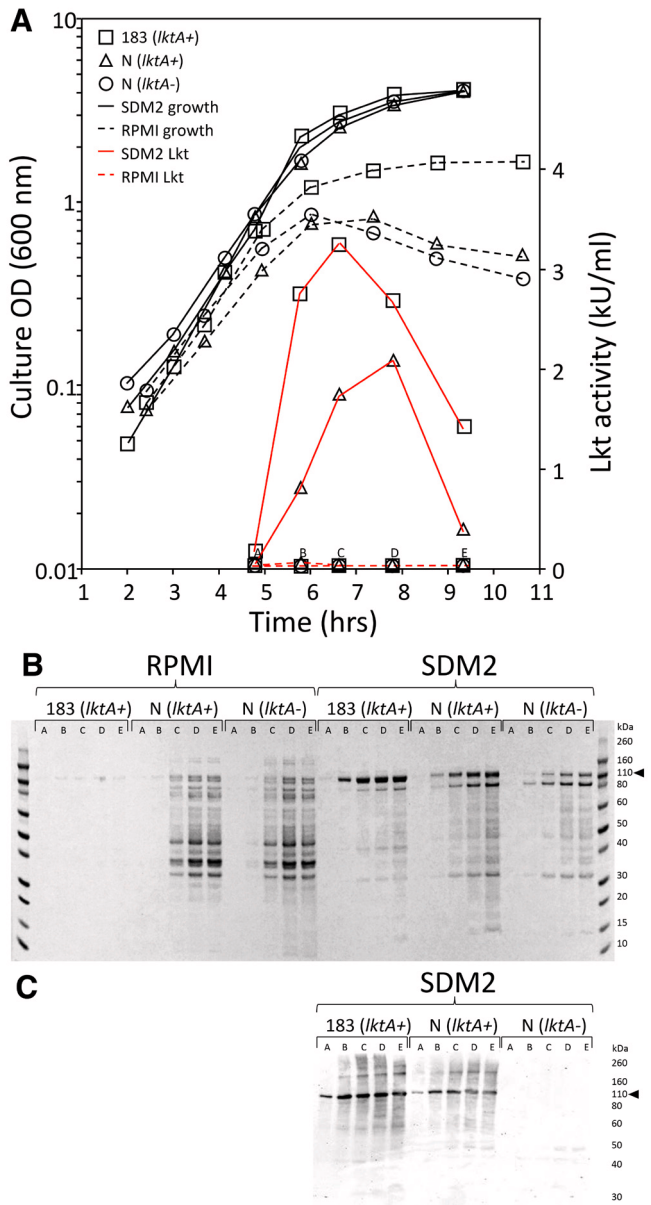


Figure 3. Comparison of *M. haemolytica* leukotoxin (Lkt) production in cell culture medium and a semi-defined bacterial culture broth. (A) Growth curves of *M. haemolytica* strains (black lines) and the cytolytic activity of their secreted Lkt (red lines). The strain abbreviations: 183 (*lktA+*), USDA-ARS-USMARC-183 (*lktA+*); N (*lktA+*), 89010807N (*lktA+*); and N (*lktA-*), 89010807N (*lktA-*). Clarified culture supernatants were collected at time points indicated on the x-axis as A through E. **(B)** Coomassie-stained SDS-PAGE of proteins from 50 μ l each of clarified culture supernatants. **(C)** Western blot of SDS-PAGE from the same clarified SDM2 culture supernatants that were used in panel **(B)**. The black arrow indicates the expected position of Lkt on SDS-PAGE.

affinity for Lkt, various peptide lengths were tested to identify those with maximum Lkt binding. Removing the first four N-terminal amino acids (MLRQ) resulted in no significant difference in Lkt binding for the C₅ or reference R₅ signal peptides

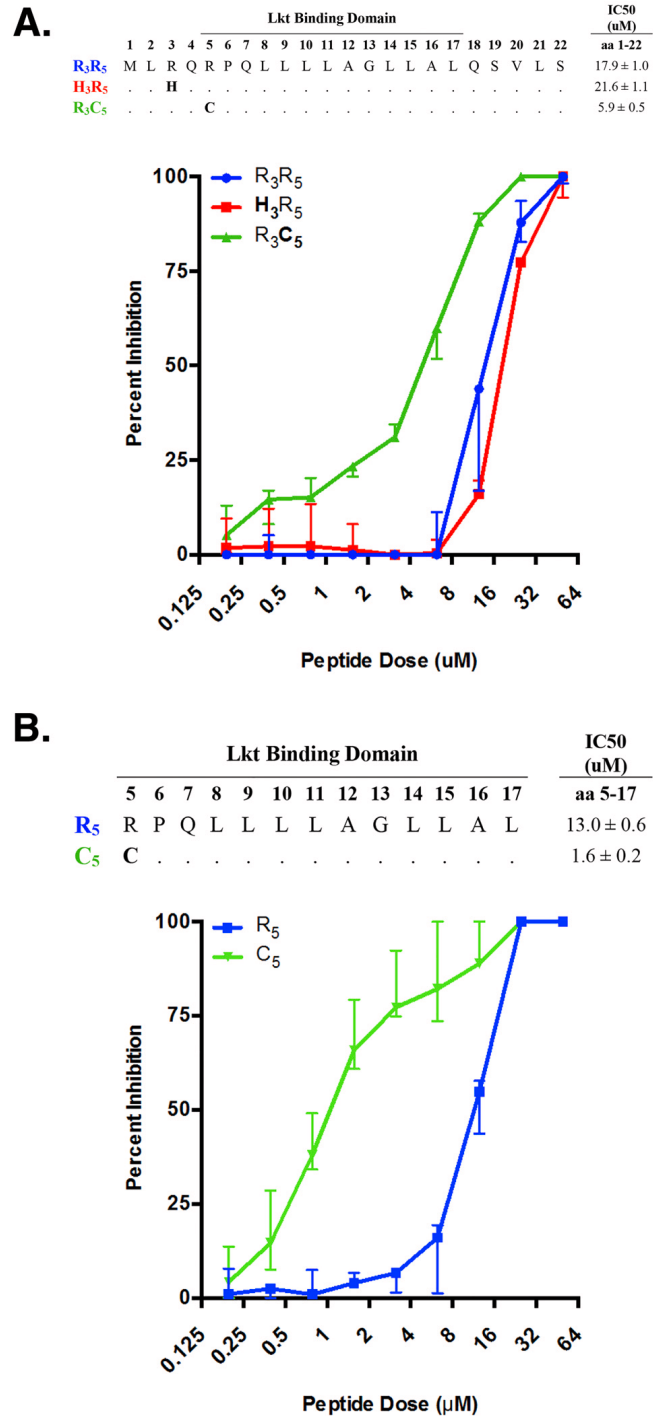


Figure 4. Cattle CD18 signal peptide variants differentially inhibit leukotoxin (Lkt)-induced cytolysis of bovine BL3 cells. CD18 signal peptide variants were tested for their ability to bind Lkt and inhibit Lkt-induced cytolysis of immortalized bovine BL3 cells using a MTT dye reduction assay. CD18 peptide variants representing amino acids 1 to 22 **(A)** or 5 to 17 **(B)** were tested using 2-fold serial dilutions at concentrations ranging from 50 μ M to 0.195 μ M. Half-maximal inhibitory concentration (IC50) for each peptide was determined using non-linear regression analyses. Data are expressed as the mean with standard deviation (n=3).

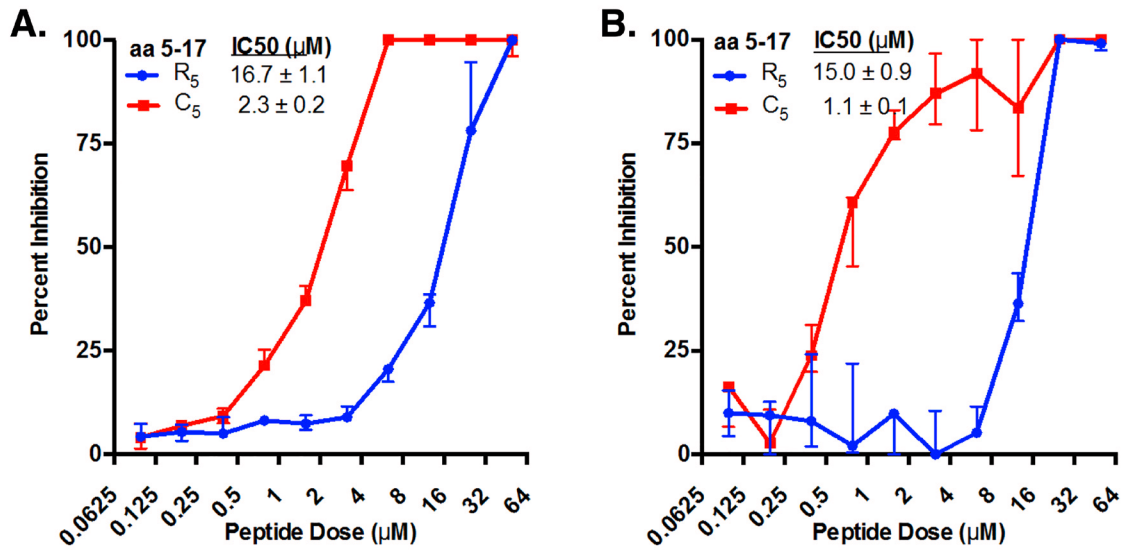


Figure 5. Cattle CD18 signal peptides inhibit leukotoxin (Lkt)-induced cytolysis of primary bovine cells. The 13-mer synthetic signal peptides (from Figure 1B) containing cattle CD18 residues 5 to 17 were tested for their ability to inhibit Lkt-induced cytolysis of primary bovine peripheral blood mononuclear cells (PBMC) (A) and polymorphonuclear leukocytes (PMN) (B). Donor animals were genotyped at the CD18 locus and were homozygous for CD18 variant “1”. Peptides were tested using 2-fold dilutions at concentrations ranging from 50 µM to 0.098 µM. The half-maximal inhibitory concentration (IC50) for each peptide was determined using non-linear regression analyses. Data are expressed as the mean with standard deviation (n = 3).

(Extended Data Figure S2)⁴². In contrast, stepwise deletions of C-terminal residues of the C₅ signal peptide had a significant impact on Lkt binding with the highest affinity being a 12-mer C₅ signal peptide with amino acids 5 to 16. The IC₅₀ of this 12-mer C₅ peptide (CPQLLLLAGLLA) was 23-fold lower than the 13-mer reference R₅ signal peptide (residues 5 to 17) and 30-fold lower than the 12-mer R₅ signal peptide. Thus, the 12-mer C₅ peptide (CPQLLLLAGLLA) represents the minimal naturally-occurring peptide sequence with maximal inhibition of Lkt-induced BL3 cell lysis (Figure 7).

Discussion

The present report describes bovine CD18 amino acid sequence differences encoded by *ITGB2* in 46 breeds of beef and dairy cattle. All of the protein coding variants discovered were missense mutations and their haplotypes were predicted to encode 15 distinct polypeptide sequences. A C₅ variant in the CD18 signal peptide region was shown to cause increased binding to *M. haemolytica* Lkt, a secreted toxin that causes cell lysis and acute inflammation leading to lung injury characteristic of bovine respiratory disease. The C₅ signal peptide variant increased the affinity for Lkt, and this effect was influenced by variation at adjacent residues. The increased Lkt binding and protection from cytotoxic effects were observed in the immortalized BL3 cell line, and freshly isolated PBMC and PMN from beef cattle.

The identification of naturally-occurring CD18 variants with increased binding to Lkt has important potential implications for animal health. For example, cattle with the CD18 C₅ signal peptide variant may be at increased risk for toxin-related

respiratory disease. However, despite the fact that the C₅ variant was found in four predicted protein variants in taurine and indicine cattle, its overall frequency in the U.S. cattle population is still very low (0.01). Thus, identifying available homozygous cattle for testing their leukocytes *ex vivo* for altered Lkt sensitivity will be challenging. Determining whether this altered binding phenotype contributes to differences in lung lesion severity or disease outcome following *M. haemolytica* infection will also be difficult. Together, these factors suggest that identifying and removing animals with the CD18 C₅ signal peptide would be premature and unwarranted for most cattle operations at this time.

Recent examples of gene editing in animals have shown that this can be a successful strategy for creating novel host genetic resistance. Groundbreaking work with porcine reproductive and respiratory syndrome virus (PRRSV) has shown that gene editing of a critical entry factor (CD163) confers complete resistance to infection in pigs^{49,50}. Similarly, genetic resistance to *M. haemolytica* Lkt has been demonstrated in leukocytes isolated from a homozygous, gene-edited, bovine fetus expressing a cleavable CD18 signal peptide¹⁵. However, the uncleaved CD18 signal peptide is universally conserved in ruminants and thus, its removal may have deleterious effects on the animal. CD18 forms heterodimers with distinct, but structurally homologous alpha integrin subunits (e.g., CD11a/CD18, CD11b/CD18, and CD11c/CD18), and thus the effect of a cleaved signal peptide may have unknown, but far-reaching effects on biological functions. To date there are no reports of a healthy, live calf expressing a cleavable CD18 signal peptide. Thus, modifying the

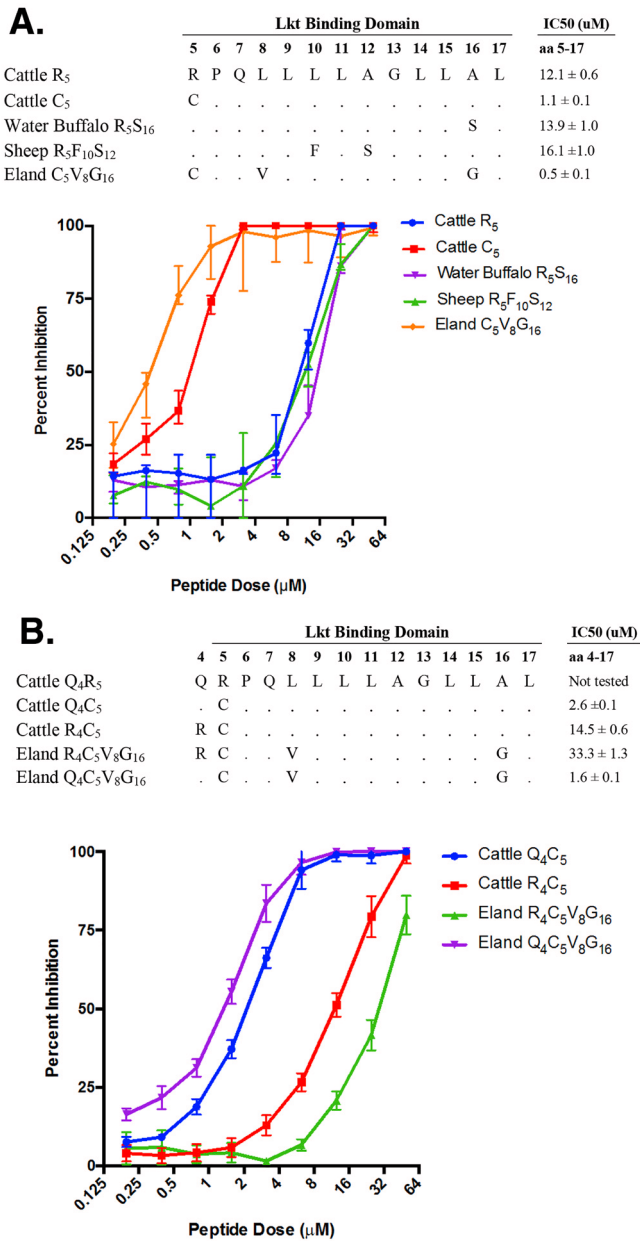


Figure 6. CD18 signal peptides from related mammalian species differentially inhibit leukotoxin (Lkt)-induced cytolysis of bovine BL3 cells. (A) Synthetic 13-mer signal peptides representing amino acids 5 to 17 of sheep, water buffalo, and eland were compared to cattle variants R₅ and C₅ for their ability to inhibit Lkt-induced cytolysis of bovine BL3 cells. Peptides were tested using 2-fold dilutions at concentrations ranging from 50 μM to 0.195 μM. **(B)** Synthetic 14-mer signal peptides representing CD18 amino acids 4 to 17 from eland and cattle variant C₅ were tested for their ability to bind Lkt. In addition, eland CD18 signal peptides were synthesized where the amino acid at position 4 in eland (arginine, R) was replaced with the amino acid normally found in cattle at this position (glutamine, Q; Eland Q₄C₅V₈G₁₆). Similarly, cattle variant C₅ peptides were synthesized where the amino acid at position 4 in cattle was replaced with the amino acid naturally encoded in eland (Cattle R₄C₅). The half-maximal inhibitory concentration (IC50) for each peptide was determined using non-linear regression analyses. Data are expressed as the mean with standard deviation (n=3 or 4).

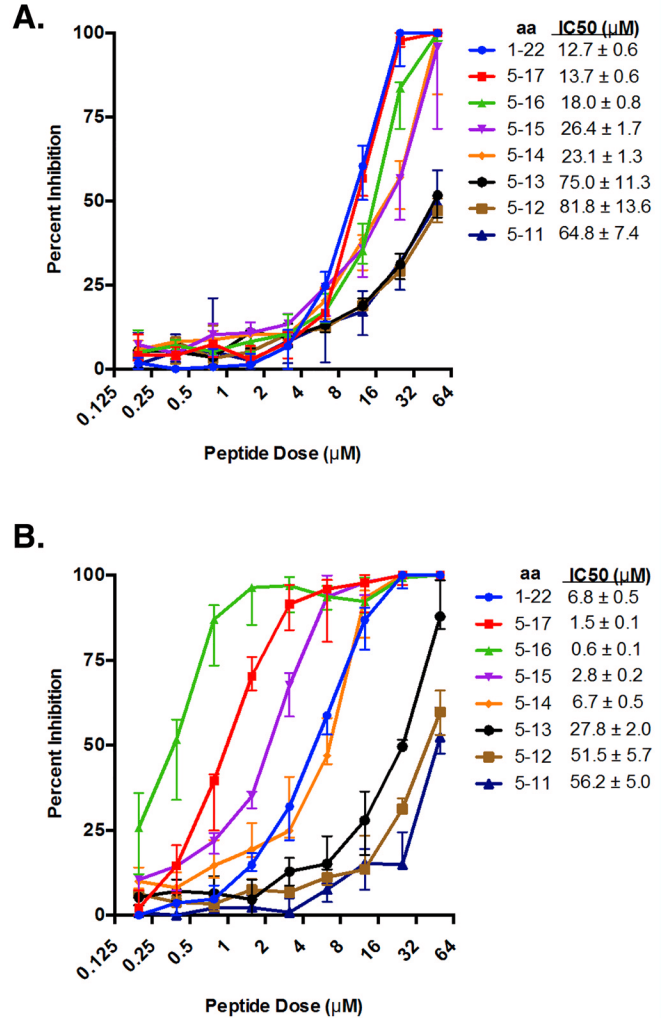


Figure 7. C-terminal truncations reveal the minimal peptide sequence for inhibition of leukotoxin (Lkt)-induced cytolysis. Synthetic CD18 signal peptides were synthesized with single amino acid C-terminal deletions. These peptides were tested for their ability to inhibit Lkt-induced cytolysis of bovine BL3 cells. Peptides were tested at concentrations ranging from 50 μM to 0.195 μM. The half-maximal inhibitory concentration (IC50) for each peptide was determined using non-linear regression analyses. Data are expressed as the mean with standard deviation (n=3).

amino acid sequence of an uncleaved ruminant CD18 signal peptide may be useful as an alternative strategy to reduce Lkt binding, while preserving its normal evolutionarily conserved cellular function.

Identifying the naturally-occurring CD18 signal peptide residues that influence Lkt binding provides a guide for more extensive analyses that may inform gene edits. Previously, synthetic signal peptides containing the R₅ residue were used to identify a 13-amino acid minimum CD18 binding site for Lkt (spanning residues 5 through 17,¹⁰). Using synthetic peptides representing cattle Q₄C₅ and eland R₄C₅, we showed that residues in position 4 can drastically affect Lkt binding and that the net charge

of the signal peptide is important. The positively charged side chain of R₄ apparently disrupts the enhanced binding of C₅ signal peptides compared to the neutral side chain of Q₄. In addition, the most common CD18 22-mer signal peptide (R₃R₅) and the rare H₃R₅ signal peptide have a net charge of +2 and reduced Lkt binding compared the R₃C₅ peptide (net charge of +1). It would be of interest to determine whether increasing the signal peptide net charge to +3 by introducing another positively charged residue could further reduce Lkt binding. However, there are numerous combinatorial peptide possibilities that could lead to a significantly reduced affinity of CD18 for Lkt, while only a few may preserve the basic biological functions of the signal peptide. Although large-scale screening of candidate peptides *in vitro* and testing them *in vivo* is beyond the scope of this study, our results suggest this as a possible future avenue of research.

An alternative strategy for reducing the impact of Lkt would be to block its activity *in vivo* with synthetic CD18 “decoy” peptides such as the 12-mer C₅ signal peptide identified here. A similar strategy has been used to neutralize anthrax toxin from *Bacillus anthracis* (reviewed in 51). A synthetic 12-mer peptide antitoxin, attached to liposome scaffolds in multiple copies, protected host cells from cytotoxicity *in vitro* and protected rats from becoming moribund *in vivo*⁵². Although the feasibility of delivering decoy peptides is unknown in cattle, it could be used to neutralize Lkt, and thus protect calves from the major virulence factor associated with lung pathology in bovine respiratory disease complex. One can further imagine combining decoy peptide technology with gene editing to have alveolar leukocytes secrete decoy peptide inhibitors of Lkt at the sites of *M. haemolytica* infection. Although the theoretical possibilities of using antitoxin and gene editing strategies may be vast, the feasibility of these technologies are still relatively unknown. A better understanding of the underlying molecular mechanisms involved, together with significant improvements in livestock gene editing and decoy peptide technologies, are needed to move the field forward.

Conclusion

There are more than a dozen missense variants in the CD18 polypeptide, including a C₅ variant in the signal peptide that affects Lkt binding. Results *in vitro* suggest that animals carrying the C₅ allele may be more susceptible to the effects of Lkt. These results also identify a potentially potent class of non-antibiotic Lkt inhibitors that could protect cattle from cytotoxic effects during acute lung infections.

Data availability

Underlying data

Whole genome sequence files (FASTQ) for the BL3 cell line are available in the NCBI SRA under accession number [SRX4645762](https://www.ncbi.nlm.nih.gov/sra/SRX4645762).

The BL3 sequence data have also been deposited with links to BioProject accession number [PRJNA325058](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA325058) (BioSample SAMN05217649) in the NCBI BioProject database.

In addition, access to the aligned sequences is available via the USDA internet site: <https://www.ars.usda.gov/plains-area/clay-center-ne/marc/wgs/celllines/> as described in the Methods.

Extended data

Table S1. MALDI-TOF MS assay design for 14 *ITGB2* missense SNPs. DOI: <https://doi.org/10.6084/m9.figshare.7449374.v1>⁵³.

Table S2. *ITGB2* genotypes recorded manually from WGS reads mapped to UMDv3.1 assembly for the USMARC Beef Cattle Diversity Panel v2.9. DOI: <https://doi.org/10.6084/m9.figshare.7449989.v1>⁴⁵.

Table S3. Haplotype-phased genotypes (diplotypes) for *ITGB2* from MALDI-TOF MS assays for 1142 cattle. DOI: <https://doi.org/10.6084/m9.figshare.7450673.v1>⁴³.

Table S4. Alignment of CD18 sequences from Bilateria species. DOI: <https://doi.org/10.6084/m9.figshare.7450796.v1>⁴⁴.

Figure S1. Screen image of Integrated Genome Viewer software displaying *ITGB2* N27KI genotype data for eight bulls. DOI: <https://doi.org/10.6084/m9.figshare.7450814.v1>³⁵.

Figure S2. Effect of N-terminal truncations of synthetic CD18 signal peptides on Lkt binding. Synthetic CD18 signal peptides were synthesized with four amino acids removed from N-terminus (MLRQ). The common R₃R₅ (A) or the rare R₃C₅ variant (B) signal peptides were tested for their ability to inhibit leukotoxin-induced cytolysis of bovine BL3 cells using a MTT cytotoxicity assay. Peptides were tested at concentrations ranging from 50 μM to 0.195 μM. Data are expressed as the mean with standard deviation (n=3). DOI: <https://doi.org/10.6084/m9.figshare.7450823.v1>⁴².

File S1. VCF file with SNPs from BL3 WGS aligned to the bovine UMD3.1 reference assembly. <https://doi.org/10.6084/m9.figshare.7450826.v1>³².

File S2. MTT dye-reduction cytotoxicity assay results. Percent inhibition of cytotoxicity was calculated as described in the Methods. Shown are the results used for statistical analyses of data and for generating Figure 1–Figure 3, Figure 7. DOI: <https://doi.org/10.6084/m9.figshare.7451039>⁴⁸.

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Jonathan E. Beever

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This is an excellent manuscript. The work is very well done and the conclusions drawn are well thought out. This manuscript will be well-sited from a scientific standpoint and the results are very translatable.

Comments:

In the Abstract -- 'Background' perhaps add bovine as in " ...binds to the CD18 receptor on bovine leukocytes, ..." followed by "Binding of Lkt to bovine CD18 results from an intact 22-amino acid signal peptide which remains uncleaved in all ruminant species." Although these are minor changes, they reflect the knowledge that this binding phenomenon is described specifically in cattle and is now inferred in other susceptible ruminant species based on the Lkt/SD18 signal peptide binding studies in cattle.

A similar argument could also be applied to the beginning of the second paragraph of the Introduction. However, this paragraph is better in its logical progression.

It is completely unclear as to why the whole-genome sequencing of the BL3 cell line was performed. Suggest removing that section from the M&M.

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

Yes

If applicable, is the statistical analysis and its interpretation appropriate?

Yes

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular genetics of livestock species.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 06 March 2019

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Holly L. Neibergs 

Department of Animal Sciences, Washington State University, Pullman, WA, USA

The authors have presented a well written article describing a nicely designed and thorough set of experiments to determine if variants in the CD18 signal peptide gene (*ITGB2*) effect Lkt binding in leukocytes. Lkt is a protein secreted by *M. haemolytica* that activates an inflammatory response leading to fibrinous bronchopneumonia in cattle. *M. haemolytica* is an important bacterial pathogen associated with bovine respiratory disease that causes the death of over one million cattle annually in the U.S. alone. This article provides a better understanding of the molecular mechanisms involved in *M. haemolytica* infection that may lead to more effective means to prevent and treat this common disease in cattle.

Suggested minor edits were very few:

- Page 3, line 1 of paragraph 1; insert "one of" after "Manheimia haemolytica is"
- Page 6, line 10 of paragraph 2; replace "at run" with "and run at" after (Thermo Fisher Scientific)
- Page 6, line 17 of paragraph 3; remove "in" after "times"
- Page 9, line 9 of paragraph 2; I am not sure I would agree that a conserved sequence with less than 20% identity is remarkable

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

Yes

If applicable, is the statistical analysis and its interpretation appropriate?

Yes

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genetic susceptibility to disease

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 08 January 2019

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Alan L. Archibald

The Roslin Institute, Royal (Dick) School of Veterinary Studies (R(D)SVS), University of Edinburgh, Midlothian, UK

The authors have provided a clear and thorough description of their analysis of sequence variation in the bovine ITGB2 gene that encodes CD18. They have not only identified and characterised sequence variants, particularly in two exons of interest, but also tested the effect of these variants in a functional assay in respect of binding to Mannheimia hemolytica leukotoxin. The methods used are described in exemplary detail.

There would be value in noting that some of the missense variants that are a key focus of the analyses have been reported by others previously and citing the relevant rs-identifiers:

R5C rs517776076

N27K rs521222417

R120W rs109222573

R120Q rs522421330

D128G rs445709131

Q392K rs469652717

P656L rs379267066

The authors should be encouraged to submit their new variants to the European Variation Archive that now hosts sequence variation data for non-human species now that dbSNP has ceased this service. The authors should not only submit the sequence variants but also the genotype data and frequencies. Two of the variants listed above do not appear to have survived the migration from dbSNP to EVA and may need to be resubmitted (i.e. R120W / rs109222573; Q392K / rs469652717).

There a few (very few) minor typographical errors:

5 uM rather than 5 μ M on page 4, column 2 line 11

a missing gap after the comma on page 6, column 2, line 1

50 ul rather than 50 μ l on page 6, column 2, 5 line from the bottom

It may be appropriate to mention the contribution of *Mannheimia hemolytica* to "shipping fever" and note the cost of this disease and pathogen to the US cattle industry.

The authors discuss their results in the context of a report of gene editing the bovine ITGB2 gene. The paper by Shanthalingam et al. 2016 (cited as reference 15 in this manuscript) report that gene editing a single codon in the ITGB2 gene and generation of a fetus carrying the edited yielded cells that were resistant to *Mannheimia hemolytica* in an in vitro assay. The current authors correctly note that there are no reports of live born calves carrying this edit in homozygous form and thus the viability of this gene edit for resistance to *Mannheimia hemolytica* remains unproven. However, none of the natural ITGB2 variants characterised by the authors delivers resistance. As the authors search for variation was thorough and should have identified almost all variants of useful frequency, then designing variant signal peptide sequences that are not cleaved but do not bind the leukotoxin may be the way forward. The authors' discussion of these points could be more explicit.

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

Yes

If applicable, is the statistical analysis and its interpretation appropriate?

Yes

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Yes

Competing Interests: I have undertaken collaborative research with Dr Smith on topics unrelated to this manuscript and we published an article together in 2009 and conference abstracts more recently.

Reviewer Expertise: molecular genetics, gene editing

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

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