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Pattern of CD14, CD16, CD163 and CD172a expression on water buffalo (*Bubalus bubalis*) leukocytes

Mahmoud M. Elnaggar[a,b,*], Francesco Grandoni[c], Gaber S. Abdellrazeq[a,b], Lindsay M. Fry[d], Karima El-Naggar[b], Victoria Hulubei[a], Luca Buttazzoni[c], Samy A. Khaliel[b], Helmy A. Torky[b], William C. Davis[a]

[a] College of Veterinary Medicine, Washington State University, WA, USA
[b] Faculty of Veterinary Medicine, Alexandria University, Egypt
[c] Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca Zootecnia e Acquacoltura (CREA-ZA), Via Salaria 31, Monterotondo, Rome, Italy
[d] Animal Disease Research Unit, U.S. Department of Agriculture, Agricultural Research Service, Pullman, WA, 99164, USA

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ABSTRACT

Previous studies on the immune system of water buffalo (*Bubalus bubalis*) using cross-reactive monoclonal antibodies (mAbs) revealed significant similarities and differences to the bovine immune system. Herein, we extend these studies and document the pattern of expression of CD14, CD16, CD163 and CD172a on buffalo leukocytes using a set of cross-reactive mAbs that are known to recognize conserved epitopes within orthologous molecules in cattle, sheep and goats. Buffalo leukocytes were isolated and subjected to mAb labelling for flow cytometry. Single color flow cytometry confirmed mAbs recognition of buffalo orthologues of CD14, CD16, CD163 and CD172a, and revealed consistent patterns of expression similar to that reported in other ruminants. Multicolor flow cytometry revealed that buffalo $CD14^+$ monocytes uniquely co-express CD16, CD163 and CD172a, whereas buffalo granulocytes co-express CD16 and CD172a. This study expands mAbs available to define and study the buffalo monocytes, and also extends information available on the unique features of the buffalo immune system.

1. Introduction

Infectious disease control in water buffalo (*Bubalus bubalis*) is largely dependent on tools of bovine preventive medicine, including vaccines and therapeutic regimes. This strategy is employed due to the fact that both species are exposed to a similar spectrum of infectious agents, including brucellosis, tuberculosis, rinderpest and piroplasmosis (Borghese, 2005), and it is assumed that the immune systems of buffalo and cattle are not significantly different. However, recent comparative immunological studies provide evidence that the immune systems of various animal species are similar but not identical (Bailey et al., 2013; Davis and Hamilton, 1998; Elnaggar et al., 2018; Grandoni et al., 2017; Jungi et al., 2010), and thus, this approach to water buffalo preventive medical care should be re-examined.

Studies of the immune system of water buffalo are extremely limited, and scant progress has been made in the elucidation of protective immune mechanisms to infectious diseases in buffalo. This paucity of data is attributable mainly to the limited availability of monoclonal antibody (mAb) reagents needed to study the immune responses in buffalo. As part of our mission to circumvent these limitations and enhance buffalo immunology research, we conducted a previous study in which we screened a large panel of mAbs known to recognize highly conserved epitopes within orthologous CD molecules in cattle, sheep and goats for cross-reactivity with buffalo leukocytes. That study validated a large set of cross-reactive mAbs with buffalo CD molecules, and demonstrated expression patterns consistent with those observed in other ruminants (Grandoni et al., 2017).

Herein, we extend this work in a limited study to 1) Document the pattern of expression of CD14 and CD172a molecules on buffalo leukocytes using mAbs previously shown to be cross-reactive with buffalo CD14 and CD172a, 2) Determine whether mAbs to CD16 and CD163 that recognize conserved epitopes within bovine, ovine and caprine orthologues also cross-react with buffalo CD16 and CD163, and 3) Use these mAbs in multicolor flow cytometry to determine co-expression patterns of these CD molecules on buffalo leukocytes.

* Corresponding author at: Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, Pullman, WA, 99164-7040, USA.
E-mail address: mahmoud.elnaggar@wsu.edu (M.M. Elnaggar).

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2. Materials and methods

2.1. Animals and mAbs

Six healthy, adult buffalo were enrolled in the present study. Three water buffalo were used in the study conducted at Alexandria University, Egypt, where all protocols and procedures were approved and guided by Alexandria University animal care and use guidelines. The other three buffalo were Italian Mediterranean River type, and were used in the study conducted at CREA-ZA, Italy. These animals were treated in compliance with the animal testing regulations established under Italian law. All primary mAbs utilized in this study are listed in Table 1.

2.2. Preparation of leukocytes, labelling of cells and flow cytometry

Blood was collected via jugular venipuncture into vacutainer tubes containing sodium heparin (BD, USA). White blood cells (WBCs) were harvested after lysis of red blood cells (RBCs) using tris-buffered ammonium chloride (0.87% w/v, pH 7.2). Leukocytes were washed in phosphate buffered saline (PBS, pH 7.2), counted, re-suspended in first wash buffer (FWB: PBS containing 0.01% w/v sodium azide, 0.02% v/v horse serum), and processed for flow cytometry (FC) labelling.

Cell labelling was conducted as previously described (Elnaggar et al., 2015; Park et al., 2016). In brief, the cells were incubated with mAbs (0.75 μg/10^6 cells of each mAb) for 15 min at 4 °C in the dark. Cells were then washed twice using FWB and re-suspended in 100 μL of goat anti-mouse isotype-specific secondary mAbs as follow; 1:1000 Alexa Fluor 647 anti-mouse IgG1, 1:400 PE-Cy5.5 anti-mouse IgG2a and 1:200 PE anti-mouse IgM. Cells were incubated for 15 min at 4 °C in the dark, and washed twice using second wash buffer (the same as FWB but without horse serum). After the final wash, cells were re-suspended in PBS-buffered 2% formaldehyde and refrigerated until examined by FC.

Cells were collected on BD FACScalibur (BD, USA) and Cytoflex (Beckman Coulter, USA) flow cytometers. Cells were visualized in forward *vs* side light scatter (FSC *vs* SSC), and color coded to distinguish the regions containing lymphocytes (red), monocytes (blue), and granulocytes (green) for analysis in SSC *vs* fluorescence (Supplementary Fig. 1). At least 2×10^5 cells were collected from each sample. Data was analyzed using FCS Express software (De Novo software, USA).

3. Results and discussion

Comparative studies have shown that major histocompatibility (MHC) and CD molecules are largely conserved in structure, function and their pattern of expression on leukocytes across animal species (Davis et al., 1995; Davis and Ellis, 1991; Davis and Hamilton, 1998; Davis et al., 1987; Naessens et al., 1993). This conservation has facilitated leukocyte characterization in less well-studied species using FC with cross-reactive mAbs (Davis et al., 2007; Davis and Hamilton, 2008; Davis et al., 2000, 2001; Grandoni et al., 2017; Rees et al., 2017). In a recent study conducted by our group, we exploited this phylogenic conservation of the structure and function of orthologous CD and MHC molecules among ruminant species to identify a panel of mAbs cross-reactive with buffalo MHC and CD molecules, and used these mAbs to characterize buffalo lymphocyte subsets in young, adult and aged buffaloes (Grandoni et al., 2017). The study revealed similarities and differences in the expression of CD molecules observed in buffalo and cattle.

Herein, we extend our work in a limited study to validate cross-reactivity of mAbs to CD16 and CD163 with buffalo and document the expression pattern of CD14, CD16, CD163 and CD172a on buffalo leukocytes using cross-reactive mAbs known to recognize conserved epitopes within bovine, ovine, and caprine orthologues. A mAb was considered cross-reactive if the observed labeling pattern on buffalo leukocytes was identical to the pattern noted in other ruminants for a given molecule.

CD172a (signal regulatory protein-α, SIRP) is a well-known marker for cells of myeloid origin, including granulocytes, monocytes, macrophages and dendritic cells. A CD172a specific mAb (DH59B), known to recognize a conserved epitope across a wide range of animals, including cattle, sheep, goats (Saalmuller et al., 2005) and buffalo (Grandoni et al., 2017) was used to determine the pattern of CD172a expression on buffalo leukocytes. Flow cytometric analysis revealed expression of CD172a on buffalo granulocytes and monocytes (Figs. 1A and 2 A), identical to that observed in cattle, sheep and goats (Corripio-Miyar et al., 2015; Elnaggar et al., 2016; Hussen et al., 2013).

For CD14, the definitive marker of monocytes (Goyert et al., 1986), a caprine-specific mAb (CAM66A) known to recognize a CD14 epitope conserved across ruminant species, including buffalo (Elnaggar et al., 2016; Grandoni et al., 2017), was used. Analysis showed CD14 is expressed only on buffalo monocytes (Figs. 1B and 2 A–C). This is similar to what has been reported in cattle (Corripio-Miyar et al., 2015; Elnaggar et al., 2016; Hussen et al., 2013), but differs from sheep and goats, in which CD14 is expressed on both monocytes and granulocytes (Elnaggar et al., 2016).

CD163 (refers to CD163A, and previously known as M130 and hemoglobin scavenger receptor) is the prototypic member of CD163 family of molecules, a well-known subset of the scavenger receptor cysteine-rich (SRCR) superfamily (Graversen et al., 2002; Herzig et al., 2010; PrabhuDas et al., 2017). CD163 is a receptor for haptoglobin-hemoglobin complexes, and is expressed on monocytes, macrophages, and a subpopulation of hematopoietic progenitor cells (Graversen et al., 2002; Herzig et al., 2010; PrabhuDas et al., 2017). Three bovine-specific mAbs (LND5A, LND37A and LND68A) known to recognize epitopes conserved in bovine, ovine and caprine CD163 (Elnaggar et al., 2016) also recognized the buffalo CD163 orthologue. In buffalo peripheral blood leukocytes, CD163 was only expressed on monocytes (Figs. 1C, and 2 B and D). The pattern of CD163 expression on buffalo monocytes matches expression observed on cattle, sheep, and goat monocytes (Elnaggar et al., 2016). Of note, the nomenclature for the broad group of molecules defined as scavenger receptors has been revised with a new consensus definitive classification, including CD163 family of molecules (PrabhuDas et al., 2017).

CD16 is known as low-affinity IgG receptor III (FcγRIII), and is

Table 1
List of mAbs used in this study, their specificity, isotype, sources, primary species specificity and reactivity with Egyptian and Italian lineages of buffalo.

mAb clone	Specificity	Isotype	Source	Primary species specificity	Egyptian buffalo	Italian buffalo	Reference
CAM66A	CD14	IgM	WSUMAC, USA	Caprine	+	+	Grandoni et al. (2017)
KD1	CD16	IgG2a	Bio-Rad Antibodies	Human	+	+	This report
LND68A	CD163	IgG1	WSUMAC, USA	Bovine	+	+	This report
LND37A	CD163	IgG1	WSUMAC, USA	Bovine	NT	+	This report
LND5A	CD163	IgG1	WSUMAC, USA	Bovine	NT	+	This report
DH59B	CD172a	IgG1	WSUMAC, USA	Multiple species[a]	+	+	Grandoni et al. (2017)

NT = not tested, WSUMAC = Washington State University Monoclonal Antibody Center.
[a] Indicates the mAb is reactive to a wide arrange of animal species, all the listed antibodies are mouse mAbs.

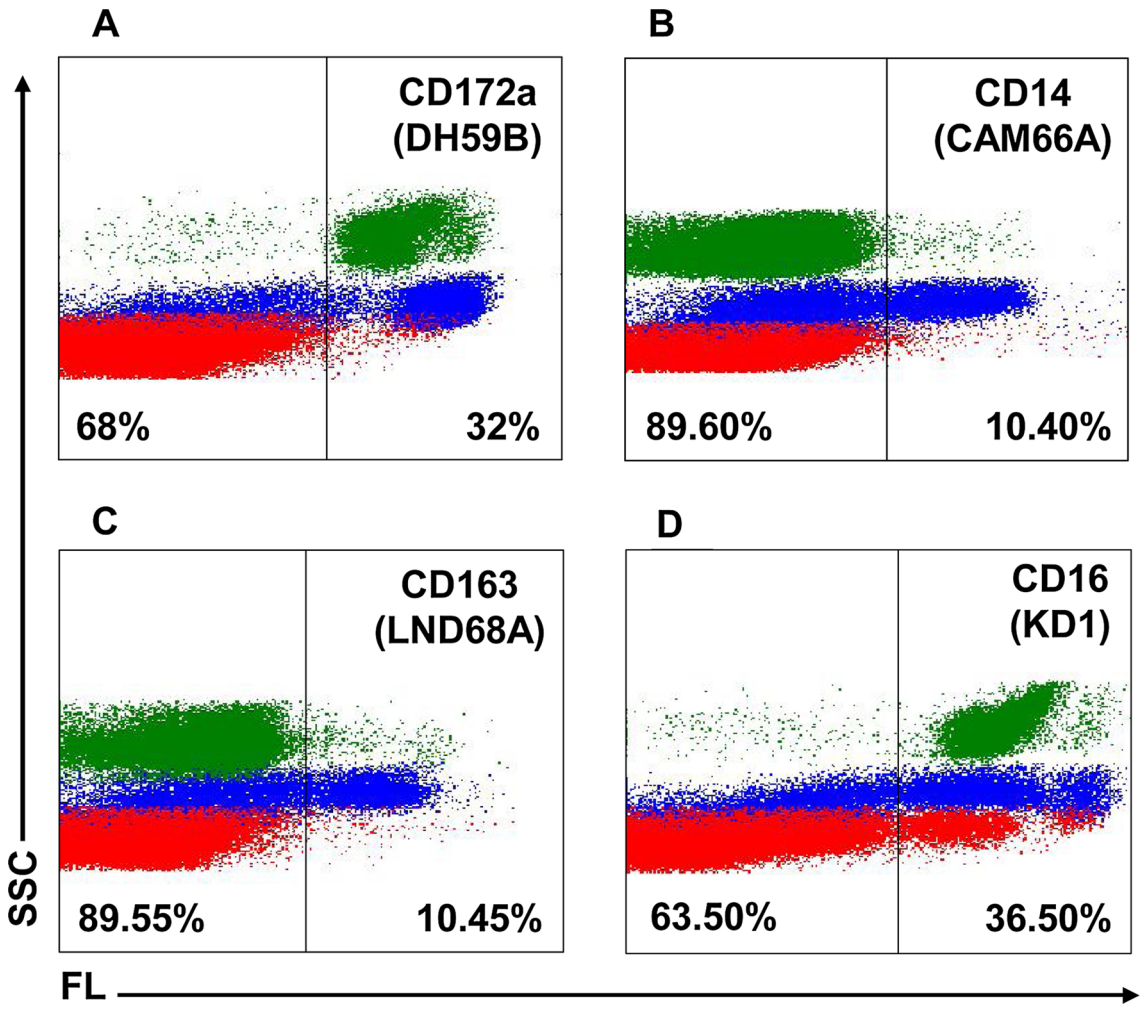

Fig. 1. Representative dot plot profiles of Egyptian buffalo leukocytes labeled with the mAbs indicated and CD molecule. The leukocytes were gated according to FSC *vs* SSC and color coded; lymphocytes as red, monocytes as blue and granulocytes as green. The FC profiles show the indicated mAbs recognize orthologues of CD172a (A), CD14 (B), CD163 (C), and CD16 (D).

expressed in two distinct forms: CD16A and CD16B. CD16A (FcγRIIIA) is expressed on the surface of NK cells, a subset of T-cells, monocytes and macrophages, whereas CD16B (FcγRIIIB) is expressed on granulocytes (Ravetch and Kinet, 1991). One human specific mAb to CD16 (KD1), known to recognize both CD16A and CD16B, was utilized in this study based on findings that it identifies CD16 in a range of species, including cattle (Boysen et al., 2008), sheep (Elhmouzi-Younes et al., 2010) and goats (Elnaggar et al., 2016). Analysis revealed CD16 is expressed on buffalo granulocytes, monocytes (Figs. 1D and 2 C–D), NK cells (Supplementary Fig. 2) and a subset of $CD14^{-}$ (Fig. 2C) and $CD335^{-}$ cells (Supplementary Fig. 2). Further characterization of the latter subset was not possible. This expression pattern differs from that observed in cattle, sheep and goats. In cattle, CD16 is only expressed on a subset of monocytes (Corripio-Miyar et al., 2015; Elnaggar et al., 2016; Hussen et al., 2013) and on NK cells (Boysen et al., 2008), in sheep, CD16 is expressed on granulocytes (like goats, and buffalo as reported here), a subset of monocytes (Elnaggar et al., 2016), and NK cells (Connelley et al., 2011; Elhmouzi-Younes et al., 2010), in goats, CD16 is expressed on granulocytes, monocytes (Elnaggar et al., 2016), and on NK cells (personal observation).

Multicolor FC analysis of buffalo leukocytes revealed that buffalo monocytes identified based on expression of CD14 co-express CD16, CD163 and CD172a (Fig. 2A–C), which is similar to the monocyte phenotype reported in goats (Elnaggar et al., 2016) and dolphins (Elnaggar et al., 2017), but different from cattle and sheep (Corripio-Miyar et al., 2015; Elnaggar et al., 2016; Hussen et al., 2013). Studies have shown that bovine monocytes are a complex population that co-expresses CD14, CD163 and CD172a, with three subsets distinguished based on the differential expression of CD14 and CD16. These monocyte subsets are referred to as classical (cM) $CD14^{++}$ $CD16^{-}$, intermediate (intM) $CD14^{++}$ $CD16^{+}$, and non-classical (ncM) $CD14^{+}$ $CD16^{++}$ (Corripio-Miyar et al., 2015; Elnaggar et al., 2016; Hussen et al., 2013). Studies conducted to define functions of these monocyte subsets revealed they share many functional homologies with human monocyte subsets (Hussen et al., 2013). The bovine cM subset exhibits the highest phagocytic capacity, while the intM subset produces abundant inflammatory cytokines and reactive oxygen species (Hussen et al., 2013). The function of ncM is not fully described. Studies conducted in sheep showed their monocytes co-express CD14, CD163 and CD172a with two subsets distinguished based on the differential expression of CD14 and CD16, $CD14^{++}$ $CD16^{-}$ and $CD14^{++}$ $CD16^{++}$ (Elnaggar et al., 2016).

In this study, we also found that buffalo granulocytes co-express CD172a and CD16 (Fig. 2 A, C and D), which is different from the expression pattern reported in cattle, sheep and goats. In cattle, granulocytes express CD172a (Elnaggar et al., 2016), whereas sheep and goat granulocytes co-express CD14, CD16 and CD172a (Elnaggar et al., 2016).

It is clear from this study and others that the immune systems of different ruminant species are similar, but not identical (Bailey et al., 2013; Davis and Hamilton, 1998; Elnaggar et al., 2018; Grandoni et al.,

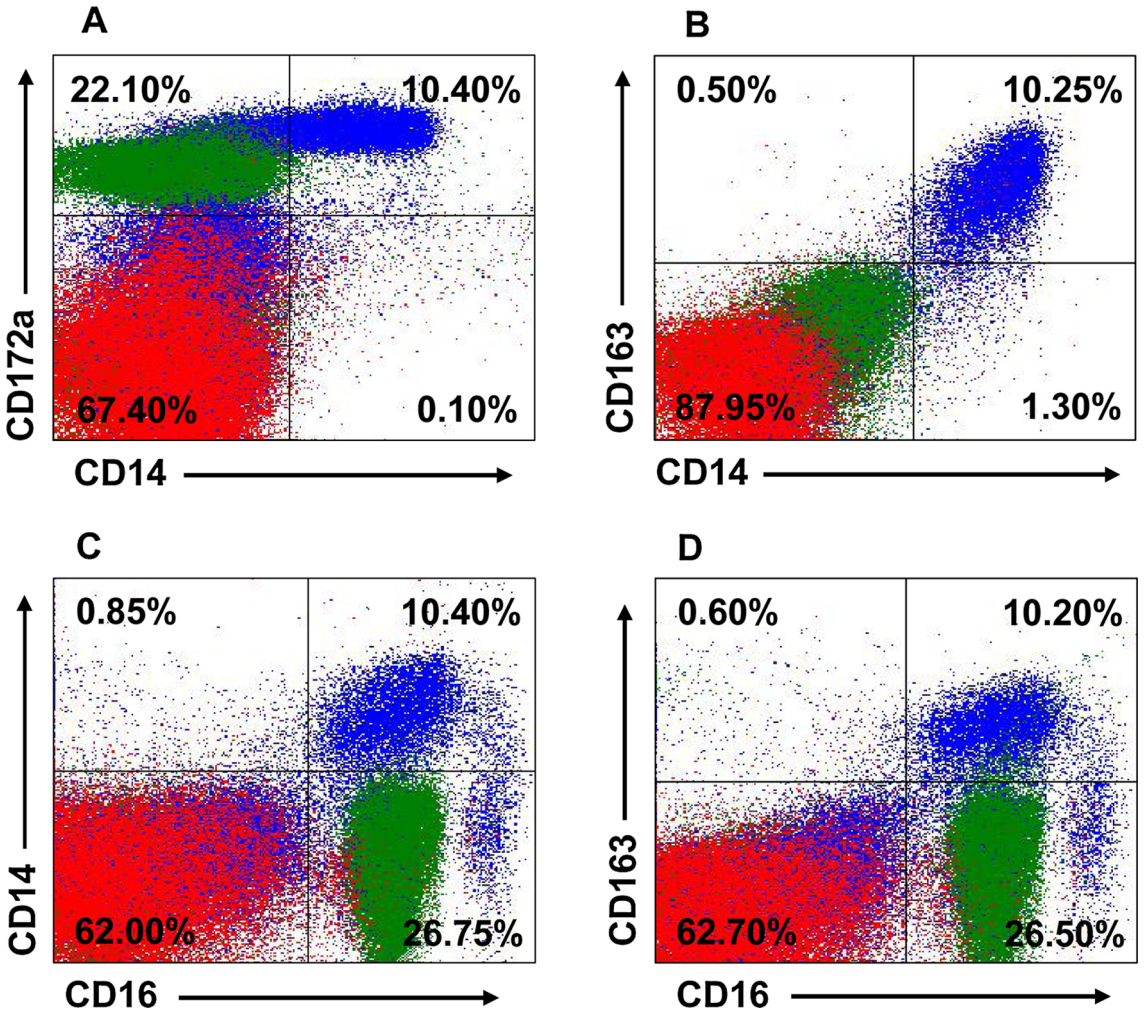

Fig. 2. Multicolor FC on Egyptian buffalo leukocytes. The leukocytes were gated according to FSC *vs* SSC and color coded; lymphocytes as red, monocytes as blue and granulocytes as green. The FC profiles show buffalo $CD14^+$ monocytes co-express CD16, CD163 (using LND68A mAb), and CD172a (A–C), whereas granulocytes co-express CD16 and CD172a (A, C and D).

2017; Jungi et al., 2010). The similarities and differences in the expression of different CD molecules and cytokines likely accounts for the differential function of each cell population and subsets, and consequently, the development and regulation of immune responses to pathogens. One unique feature of buffalo immune system that has emerged from our previous study, is the co-expression of CD8 on $WC1^+$ $\gamma\delta$ T cells when compared to expression in cattle (Grandoni et al., 2017). Herein, we are extending these unique features, unlike cattle monocytes, all buffalo monocytes co-express CD16. The CD16 as low affinity FcγRIII is an activating receptor with an essential role in innate immunity, where it facilitates phagocytosis and acts as a lysis receptor, mediating direct NK cell cytotoxicity, and NK cell and monocyte-mediated antibody-dependent cellular cytotoxicity (ADCC) (Mandelboim et al., 1999). A recent study showed that CD16 is indispensable for ADCC mediated by human monocytes (Yeap et al., 2016). In this study, $CD16^+$, but not $CD16^-$, monocytes exerted ADCC against antibody-coated target tumor cell lines and virus-infected cells (Yeap et al., 2016). The study also revealed that ADCC mediated by $CD16^+$ monocytes requires TNF-α secretion (Yeap et al., 2016). Given the CD16 expression pattern on buffalo leukocytes, future studies to determine the role of these $CD16^+$ cells in the buffalo immune response are warranted, and are now possible due to the discovery of new reagents.

In conclusion, we have validated mAbs cross-reactive to buffalo CD16 and CD163, and documented the pattern of expression of CD14, CD16, CD163 and CD172a on buffalo leukocytes showing the unique features of buffalo monocytes. This set of mAbs will prove useful to study buffalo monocytes, and opens the way for future studies on the innate immune system of buffalo.

Disclosures

The authors declare no conflict of interest.

Author contributions

ME, FG, WD, LB, SK and HT conceived and designed the experiments. ME, FG and KE performed the experiments. ME, FG and GA analyzed the data. VH contributed to reagents/materials/analysis tools. ME, FG, LF, GA and WD wrote the manuscript. All authors approved the manuscript for publication.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.vetimm.2019.03.010.

References

Bailey, M., Christoforidou, Z., Lewis, M.C., 2013. The evolutionary basis for differences between the immune systems of man, mouse, pig and ruminants. Vet. Immunol. Immunopathol. 152, 13–19.

Borghese, A., 2005. Buffalo Production and Research. REU 67. FAO.

Boysen, P., Gunnes, G., Pende, D., Valheim, M., Storset, A.K., 2008. Natural killer cells in lymph nodes of healthy calves express CD16 and show both cytotoxic and cytokine-producing properties. Dev. Comp. Immunol. 32, 773–783.

Connelley, T., Storset, A.K., Pemberton, A., MacHugh, N., Brown, J., Lund, H., Morrison, I.W., 2011. NKp46 defines ovine cells that have characteristics corresponding to NK cells. Vet. Res. 42, 37.

Corripio-Miyar, Y., Hope, J., McInnes, C.J., Wattegedera, S.R., Jensen, K., Pang, Y., Entrican, G., Glass, E.J., 2015. Phenotypic and functional analysis of monocyte populations in cattle peripheral blood identifies a subset with high endocytic and allogeneic T-cell stimulatory capacity. Vet. Res. 46, 112.

Davis, W.C., Ellis, J.A., 1991. Individual antigens of goats. Vet. Immunol. Immunopathol. 27, 121–131.

Davis, W.C., Hamilton, M.J., 1998. Comparison of the unique characteristics of the immune system in different species of mammals. Vet. Immunol. Immunopathol. 63, 7–13.

Davis, W.C., Hamilton, M.J., 2008. Use of flow cytometry to develop and characterize a set of monoclonal antibodies specific for rabbit leukocyte differentiation molecules. J. Vet. Sci. 9, 51–66.

Davis, W.C., Marusic, S., Lewin, H.A., Splitter, G.A., Perryman, L.E., McGuire, T.C., Gorham, J.R., 1987. The development and analysis of species specific and cross reactive monoclonal antibodies to leukocyte differentiation antigens and antigens of the major histocompatibility complex for use in the study of the immune system in cattle and other species. Vet. Immunol. Immunopathol. 15, 337–376.

Davis, W.C., Davis, J.E., Hamilton, M.J., 1995. Use of monoclonal antibodies and flow cytometry to cluster and analyze leukocyte differentiation molecules. Methods Mol. Biol. 45, 149–167.

Davis, W.C., Heirman, L.R., Hamilton, M.J., Parish, S.M., Barrington, G.M., Loftis, A., Rogers, M., 2000. Flow cytometric analysis of an immunodeficiency disorder affecting juvenile llamas. Vet. Immunol. Immunopathol. 74, 103–120.

Davis, W.C., Khalid, A.M., Hamilton, M.J., Ahn, J.S., Park, Y.H., Cantor, G.H., 2001. The use of crossreactive monoclonal antibodies to characterize the immune system of the water buffalo (Bubalus bubalis). J. Vet. Sci. 2, 103–109.

Davis, W.C., Drbal, K., Mosaad, A.E., Elbagory, A.R., Tibary, A., Barrington, G.M., Park, Y.H., Hamilton, M.J., 2007. Use of flow cytometry to identify monoclonal antibodies that recognize conserved epitopes on orthologous leukocyte differentiation antigens in goats, llamas, and rabbits. Vet. Immunol. Immunopathol. 119, 123–130.

Elhmouzi-Younes, J., Boysen, P., Pende, D., Storset, A.K., Le Vern, Y., Laurent, F., Drouet, F., 2010. Ovine CD16+/CD14- blood lymphocytes present all the major characteristics of natural killer cells. Vet. Res. 41, 4.

Elnaggar, M.M., Abdellrazeq, G.S., Sester, M., Khaliel, S.A., Singh, M., Torky, H.A., Davis, W.C., 2015. Development of an improved ESAT-6 and CFP-10 peptide-based cytokine flow cytometric assay for bovine tuberculosis. Comp. Immunol. Microbiol. Infect. Dis. 42, 1–7.

Elnaggar, M.M., Abdellrazeq, G.S., Mack, V., Fry, L.M., Davis, W.C., Park, K.T., 2016. Characterization and use of new monoclonal antibodies to CD11c, CD14, and CD163 to analyze the phenotypic complexity of ruminant monocyte subsets. Vet. Immunol. Immunopathol. 178, 57–63.

Elnaggar, M.M., Abdellrazeq, G.S., Venn-Watson, S.K., Jensen, E.D., Hulubei, V., Fry, L.M., Sacco, R.E., Davis, W.C., 2017. Identification of monoclonal antibodies cross-reactive with bottlenose dolphin orthologues of the major histocompatibility complex and leukocyte differentiation molecules. Vet. Immunol. Immunopathol. 192, 54–59.

Elnaggar, M.M., Abdellrazeq, G.S., Dassanayake, R.P., Fry, L.M., Hulubei, V., Davis, W.C., 2018. Characterization of αβ and γδ T cell subsets expressing IL-17A in ruminants and swine. Dev. Comp. Immunol. 85, 115–124.

Goyert, S.M., Ferrero, E.M., Seremetis, S.V., Winchester, R.J., Silver, J., Mattison, A.C., 1986. Biochemistry and expression of myelomonocytic antigens. J. Immunol. 137, 3909–3914.

Grandoni, F., Elnaggar, M.M., Abdellrazeq, G.S., Signorelli, F., Fry, L.M., Marchitelli, C., Hulubei, V., Khaliel, S.A., Torky, H.A., Davis, W.C., 2017. Characterization of leukocyte subsets in buffalo (Bubalus bubalis) with cross-reactive monoclonal antibodies specific for bovine MHC class I and class II molecules and leukocyte differentiation molecules. Dev. Comp. Immunol. 74, 101–109.

Graversen, J.H., Madsen, M., Moestrup, S.K., 2002. CD163: a signal receptor scavenging haptoglobin-hemoglobin complexes from plasma. Int. J. Biochem. Cell Biol. 34, 309–314.

Herzig, C.T., Waters, R.W., Baldwin, C.L., Telfer, J.C., 2010. Evolution of the CD163 family and its relationship to the bovine gamma delta T cell co-receptor WC1. BMC Evol. Biol. 10, 181.

Hussen, J., Düvel, A., Sandra, O., Smith, D., Sheldon, I.M., Zieger, P., Schuberth, H.-J., 2013. Phenotypic and functional heterogeneity of bovine blood monocytes. PLoS One 8, e71502.

Jungi, T.W., Farhat, K., Burgener, I., Werling, D., 2010. Toll-like receptors in domestic animals. Cell Tissue Res. 343, 107–120.

Mandelboim, O., Malik, P., Davis, D.M., Jo, C.H., Boyson, J.E., Strominger, J.L., 1999. Human CD16 as a lysis receptor mediating direct natural killer cell cytotoxicity. Proc. Natl. Acad. Sci. U. S. A. 96, 5640–5644.

Naessens, J., Olubayo, R.O., Davis, W.C., Hopkins, J., 1993. Cross-reactivity of workshop antibodies with cells from domestic and wild ruminants. Vet. Immunol. Immunopathol. 39, 283–290.

Park, K.T., ElNaggar, M.M., Abdellrazeq, G.S., Bannantine, J.P., Mack, V., Fry, L.M., Davis, W.C., 2016. Phenotype and function of CD209+ bovine blood dendritic cells, monocyte-derived-Dendritic cells and monocyte-derived macrophages. PLoS One 11, e0165247.

PrabhuDas, M.R., Baldwin, C.L., Bollyky, P.L., Bowdish, D.M.E., Drickamer, K., Febbraio, M., Herz, J., Kobzik, L., Krieger, M., Loike, J., McVicker, B., Means, T.K., Moestrup, S.K., Post, S.R., Sawamura, T., Silverstein, S., Speth, R.C., Telfer, J.C., Thiele, G.M., Wang, X.Y., Wright, S.D., El Khoury, J., 2017. A consensus definitive classification of scavenger receptors and their roles in health and disease. J. Immunol. 198, 3775–3789.

Ravetch, J.V., Kinet, J.P., 1991. Fc receptors. Annu. Rev. Immunol. 9, 457–492.

Rees, J., Haig, D., Mack, V., Davis, W.C., 2017. Characterisation of monoclonal antibodies specific for hamster leukocyte differentiation molecules. Vet. Immunol. Immunopathol. 183, 40–44.

Saalmuller, A., Lunney, J.K., Daubenberger, C., Davis, W., Fischer, U., Gobel, T.W., Griebel, P., Hollemweguer, E., Lasco, T., Meister, R., Schuberth, H.J., Sestak, K., Sopp, P., Steinbach, F., Xiao-Wei, W., Aasted, B., 2005. Summary of the animal homologue section of HLDA8. Cell. Immunol. 236, 51–58.

Yeap, W.H., Wong, K.L., Shimasaki, N., Teo, E.C., Quek, J.K., Yong, H.X., Diong, C.P., Bertoletti, A., Linn, Y.C., Wong, S.C., 2016. CD16 is indispensable for antibody-dependent cellular cytotoxicity by human monocytes. Sci. Rep. 6, 34310.