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# **Development and characterization of two porcine monocytederived macrophage cell lines**

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### **How to cite this manuscript**

If you make reference to this version of the manuscript, use the following information:

Chitko-McKown, C. G., Chapes, S. K., Miller, L. C., Riggs, P. K., Ortega, M. T., Green, B. T., & McKown, R. D. (2013). Development and characterization of two porcine monocyte-derived macrophage cell lines. Retrieved from http://krex.ksu.edu

### **Published Version Information**

**Citation**: Chitko-McKown, C. G., Chapes, S. K., Miller, L. C., Riggs, P. K., Ortega, M. T., Green, B. T., & McKown, R. D. (2013). Development and characterization of two porcine monocyte-derived macrophage cell lines. Results in Immunology, 3, 26-32.

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**Digital Object Identifier (DOI)**: doi:10.1016/j.rinim.2013.03.001

**Publisher's Link**: http://www.sciencedirect.com/science/article/pii/S2211283913000051

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### **Abstract**

 Cell lines CΔ2+ and CΔ2- were developed from monocytes obtained from a 10-month-old, crossbred, female pig. These cells morphologically resembled macrophages, stained positively 36 for  $\alpha$ -naphthyl esterase and negatively for peroxidase. The cell lines were bactericidal and highly phagocytic. Both cell lines expressed the porcine cell-surface molecules MHCI, CD11b, CD14, CD16, CD172, and small amounts of CD2; however, only minimal amounts of CD163 39 were measured. The lines were negative for the mouse marker  $H2K<sup>k</sup>$ , bovine CD2 control, and secondary antibody control. Additionally, cells tested negative for Bovine Viral Diarrhea Virus 41 and Porcine Circovirus Type 2. Therefore, these cells resembled porcine macrophages based on morphology, cell-surface marker phenotype, and function and will be useful tools for studying porcine macrophage biology. 

 *Keywords:* Monocyte, Macrophage, Cytokine, Phagocytosis, Morphology, Cell surface molecule

**1. Introduction**

 Macrophages are an important component of the innate immune response against pathogens. These cells are of myeloid origin and after circulating in the blood as monocytes, differentiate into tissue macrophages. In addition to protecting the host, macrophages also contribute to the infectious process by maintaining intracellular pathogens such as Porcine Reproductive and Respiratory Disease Syndrome Virus (PRRSV; Van Reeth and Adair, 1997), *Brucella* (Maria-Pilar et al., 2005), and *Salmonella* (Donné et al., 2005). Monocytes make up only a small percentage of mononuclear cells in peripheral whole blood. In pigs, this value ranges from 0-10% (The Merck Veterinary Manual, 1991). Isolating sufficient numbers of these cells to perform *in vitro* experiments is time consuming and variation among animals in cell numbers and activity level is high. Although numerous human and murine monocytic/macrophage cell lines are publicly available, the same is not true for pigs. There are only three pig monocytic/macrophage cell lines (CRL-2843, -2844, and -2845), (ATCC "Cell Lines and Hybridomas" catalogue; [https://www.atcc.org/ATCCAdvancedCatalogSearch/tabid/112/Default.aspx\)](https://www.atcc.org/ATCCAdvancedCatalogSearch/tabid/112/Default.aspx). All of these are virus transformed which can affect the function of the cells (Beharka et al., 1998). Other porcine cell lines of monocyte lineage have been described; however, these are not available in a public repository (Wardley et al., 1980; Kadoi et al., 2001; Weingartl et al., 2002; Lee et al., 2010). Therefore, there is a strong need for available, non-transformed, porcine monocyte-derived cell lines for agricultural research. These cells would allow for the completion of "proof of concept studies" and drug development work requiring macrophages without the time and expense (i.e., Institutional Animal Care and Use Committee [IACUC] approval and monitoring) of obtaining whole blood from experimental animals. We describe the development of porcine monocyte-

 derived cell lines with the characteristics of macrophages that will be deposited in a cell repository for public access.

**2. Materials and methods**

*2.1. Culture of LM-929 cells for supernatant*

 LM-929 cells (ATCC CCL 1.2) were used as the source of macrophage colony- stimulating factor (M-CSF; Beharka et al., 1998). LM-929 cells were grown to confluency in tissue culture flasks in Roswell Park Memorial Institute (RPMI) medium (Invitrogen, Carlsbad, CA) supplemented with 5% fetal bovine serum (FBS; HyClone), Antibiotic/Antimycotic (A/A; Invitrogen), and L-glutamine (L-glut; Invitrogen). Supernatants were stored at -80°C, and then 80 filter sterilized prior to use.

*2.2. Isolation of porcine monocytes and generation of cell lines*

82 Whole blood was obtained with IACUC approval in accordance with USDA animal care 83 guidelines from a 10-week-old, mixed-breed, female pig housed at the U.S. Meat Animal 84 Research Center (USMARC) swine facility. Approximately, 70 ml whole blood was obtained via jugular venapuncture, into 35-ml syringes containing 0.1 M EDTA. Peripheral blood 86 mononuclear cells (PBMC) were isolated by density gradient centrifugation over Ficoll-Paque Plus (Amersham Pharmacia Biotech AB, Uppsala, Sweden), as previously described (Chitko- McKown et al., 2004). Purified PBMC were counted, cytocentrifuged, and stained to 89 differentiate between monocytes and lymphocytes. Cells were resuspended at  $1 \times 10^6$ 90 monocytes/ml RPMI without serum and 11 ml were placed into -cm<sup>2</sup> tissue culture flasks and 91 allowed to adhere for 1 h at  $37^{\circ}$ C in a humidified atmosphere containing 5% CO<sub>2</sub>. Medium was then replaced with RPMI containing 5% FBS, A/A, and L-glut (complete RPMI**)** to remove the lymphocyte population**.** After culturing under these conditions for 17 days, cells were cultured

in medium containing 10% LM-929 supernatant as indicated by "+" in the cell line

nomenclature. After 5 months in culture, a subculture of these cells was reintroduced to medium

without LM-929 supernatant (CΔ2-). Culture medium was changed once per week until the cells

formed a confluent monolayer stage. Cells were then passaged and replated or frozen.

*2.3. Cell dispersal and freezing*

 Adherent cell monolayers were dispersed by treatment with Trypsin-EDTA (TE; Invitrogen; Helgason, 2005). Cell preparations used for cell-surface phenotyping were dispersed 101 using 0.2% EDTA without trypsin.  $1 - 5 \times 10^6$  cells/vial/ml were prepared for storage in liquid nitrogen. They were suspended in freezing medium consisting of 10% dimethyl sulfoxide in

FBS (Yokoyama, 1997).

*2.4. Karyotype analysis*

 Cell lines were subcultured 1:2 for karyotyping at passages 20 to 24. Briefly, cells were 106 grown to confluence in 75-cm<sup>2</sup> flasks, trypsinized and transferred to new flasks in culture 107 medium containing 5-bromo-2'-deoxyuridine (BrdU) to a final concentration of 25  $\mu$ g/ml (Sigma; Riggs, et al., 1997). After 20 h, medium was replaced with fresh culture medium 109 lacking BrdU. Cultures were incubated for an additional 4 h, then medium was replaced with 110 0.075 M KCl. Mitotic cells were shaken from the flask into the hypotonic solution and incubated for 20 min, then fixed with multiple changes of a solution of 3:1 methanol: glacial acetic acid. Chromosomes were stained in 4% Giemsa (Life Technologies) or banded as described by Rønne (1985), and karyotyped according to international convention (Committee for the Standardized Karyotype of the Domestic Pig, 1988). Fluorescence in situ hybridization (FISH) to identify the sex chromosomes was conducted with bacterial artificial chromosome probes for *KAL1* and *CSF2RA* genes as previously described (Raudsepp et al., 2008).

## *2.5. Phenotypic and immunophenotypic analysis*



 Colorimetric bactericidal assays using *Escherichia. coli* O157 and *Staphylococcus aureus* as targets were performed essentially as described by Stevens, et al. (1991). Bacteria were

140 opsonized by incubation at 37<sup>o</sup>C with heat-inactivated bovine serum previously determined to

have high antibody titers against *E. coli* O157. Non-opsonized bacteria were incubated in

**142** medium without serum. Cells  $(3 \times 10^4)$  were placed into 96-well tissue culture plates with

either opsonized on non-opsonized bacteria at an effecter to target ratio (E:T) of 1:100 for *E. coli*

O157 and 1:10 for *S. aureus.* MTT (Sigma-Aldrich)

*2.9. Phagocytosis assay*

 Phagocytosis was measured by the uptake of fluorescent microspheres as previously described, with some modifications (Potts and Chapes, 2008). Flow cytometric analysis to 148 calculate microsphere uptake was performed on a Becton Dickinson FACSCalibur flow cytometer.

*2.10. RNA isolation and cytokine expression*

 Total RNA was extracted from LPS-treated cells by acid guanidine phenol extraction (Chomczynski and Sacchi, 1987). First strand cDNA synthesis was performed on 1 μg total 153 RNA using the SuperScript<sup>TM</sup> III Platinum<sup>®</sup> Two Step qRT-PCR Kit (Invitrogen) as per the manufacturer's instructions. Cytokine PCR was performed using a quantitative simultaneous multiplex real-time assay (Duvigneau et al., 2005). Three multiplexed reactions were run: Primer/Probe Set 1 assayed for the lymphokines IL-2, IL-4, and IFN-γ; Primer/Probe Set 2 assayed for the proinflammatory cytokines IL-1α, IL-6, and IL-10; and Primer/Probe Set 3 assayed for the housekeeping genes β-actin, GAPDH, and cyclophilin. Resulting values for cytokine Cts were normalized against the numerical average of the three housekeeping gene Cts. *2.11. Virus infection* Cells were tested by PCR for bovine viral diarrhea virus (BVDV) infection using the

primer set F5'-CATGCCCATAGTAGGAC-3' and R5'-CCATGTGCCATGTACAG-3' for first

 round PCR amplification and cycle sequencing. This primer set amplifies sequences from the genomic 5' untranslated region of type 1 and type 2 BVDV, but does not appear to amplify sequences from BVDV (Bolin et al., 1994; Ridpath and Bolin., 1998). Additionally, aliquots of CΔ2+ and CΔ2- lysates were mixed 1:1 with Minimum Essential Medium (MEM, Invitrogen) and inoculated onto bovine turbinate (BT) cells that had been seeded into a 24-well plate. After 168 14 days of incubation at 37°C, the BT cell lysates were tested by PCR for propagation of BVDV. Cell lines were tested for PCV2 by real-time PCR as described by Opriessnig et al. (2003).

### **3. Results and discussion**

 We isolated monocytes from the peripheral blood of a crossbred pig in order to develop porcine monocyte-derived macrophage cell lines. The peripheral blood mononuclear cell 173 population was isolated over a density gradient, and monocytes were obtained by removal of 174 non-adherent cells from cultures. After two weeks in culture, the monocytes were adhered to the culture flasks and were considered monocyte-derived macrophages. At this time, LM929 176 supernatant was added to the cultures to provide a source of M-CSF to stimulate cell proliferation. Monolayers soon formed and cells morphologically resembled cultured 178 macrophages (Figure 1A). The addition of LPS to the medium caused the cells to develop the 179 "fried egg" appearance of activated macrophages (Figure 1B). This cell line was named  $C\Delta 2+$ , 180 the "+" denoting the inclusion of LM929 supernatant in the culture medium. After several months in culture, the LM929 supernatant was removed from the medium of a subculture of the CΔ2+ cell line, and these cells continued to proliferate and this subculture was named CΔ2- to designate the absence of supernatant in the medium (Figure 1A). The CΔ2- line responded to the 184 addition of LPS to the medium similarly to the C $\Delta$ 2+ cells (Figure 1B). The cell lines were characterized both earlier and later than ten passages, and were found to be stable.

186 Monocytes stain weakly for the enzyme myeloperoxidase found only in their lysozomal vacuoles, and staine diffusely for α-naphthyl-esterase (Van Furth, 1988). Resident and resident- exudate macrophages have peroxidase-positive nuclear envelopes (Van Furth, 1988). In the mouse, 95% of blood monocytes are positive for esterase activity as are 99% of resident peritoneal macrophages (Van Furth, 1988). In contrast, only 60% of blood monocytes and 0% of resident peritoneal macrophages stain positively for peroxidase (Van Furth, 1988). The CΔ2+ cell line stained strongly positively for α-naphthyl-esterase and diffusely for myeloperoxidase (Figure 1C), in comparison, the CΔ2- cells stained diffusely for peroxidase, and not as strong as 194 the C $\Delta$ 2+ cell line for α-naphthyl-esterase (Figure 1C). These results suggest that these cell lines are in the macrophage lineage beyond the monocyte stage since they had properties that were consistent with those described between monocyte and resident macrophage stages (Van Furth, 1988).

 Cytogenetic analysis indicated that both cell lines are consistent with a diploid female pig karyotype of 38,XX. The CΔ2+ cell line contains a large metacentric chromosome derived 200 from a reciprocal translocation of pig chromosomes SSC 8 and SSC 16 (Figure 2A). The large derivative chromosome was observed in all metaphase nuclei examined and is stably maintained. In contrast, the translocated chromosome is not found in the CΔ2- cell line. This cell line appears to be near normal in the majority of cells, but some cells were observed to be aneuploidy, with chromosome numbers from 36 to 38. Sex chromosome identification was verified by FISH of probes for *KAL1* and *CSF2RA,* both typically located in the pseudoautosomal region at the distal p-arm of the X chromosome (SSC X). Interestingly, a small rearrangement was observed in the CΔ2- cell line. In these cells, *CSF2RA* is translocated to



231 level since they can provide a suitable porcine macrophage environment necessary for virus growth.

233 Although both cell lines have undergone chromosomal rearrangements, they appear to be fairly stable cytogenetically. Each cell line is karyotypically distinct with two derivative 235 chromosomes maintained in C $\Delta$ 2+ cell line, and a rearrangement involving the X chromosome in 236 the  $C\Delta 2$ - cells.

 The expression of iNOS and production of nitrite/nitrate by porcine monocytes/macrophages are under debate (Zelnickova et al., 2008). We used the Griess reagent 239 to measure nitrite production by the cell lines after exposure to LPS. In our hands, this assay reliably measures nitrite production by murine (Fleming et al., 1991) and bovine monocytes/macrophages (Chitko-McKown et al., 1992). However, no nitrite production was measurable from either control or LPS-treated cell line supernatants (data not shown). The absence of a nitric oxide response could be because of the relative immature stages of both the C $\Delta$ 2+ and C $\Delta$ 2- cells. Alternatively, this may reflect the fact that porcine macrophages have poor *nos2* expression and nitric oxide responses and the cell lines parallel primary porcine monocyte/macrophages (Pampusch et al., 1998; Kapetanovic et al., 2012). 247 When we measured the bactericidal activity of the  $C\Delta 2$ + and  $C\Delta 2$ - cells, we found that 248 both cell lines were bactericidal against Gram<sup>-</sup> (*E. coli*) and Gram<sup>+</sup> (*S. aureus*) organisms (Table 2). Differences were observed in the levels of killing between opsonized and non-opsonized bacteria were no statistically significant. This may be a result of the efficiency of direct bactericidal killing of bacteria, which didn't leave room for significant enhancement with

opsonization. Alternatively, the serum used for opsonization may have included some factors

which interfered with the bactericidal activity of the cell lines.





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### **Table 1. Cell surface staining/flow cytometry.**

Cells were stained for flow cytomeric analysis essentially as described in Materials and Methods. % positive are the percent positive cells after the isotype control background fluorescence was removed (Figure 3). All markers are porcine-specific unless noted.



## **Table 2. Bactivity of CD2**+ and CD2+ an  $\overline{E}$ , coli and  $\overline{S}$ .

Values are expressed as % killed mean  $\pm$  std of 2 experiments. \*Effector to target cell ratio.











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**ECA2-LPS ECA2-+LPS DCA2+-LPS DCA2++LPS** 



- **Supplemental figure**. Fluorescence in situ hybridization to CΔ2- cell line of KAL1 (green) and
- 2 CSF2RA (red). The two red and green signals are together on the normal X chromosome, while
- the CSF2RA region (red) has been translocated from the second X chromosome SSC X to the
- smaller submetacentric chromosome.
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