







# PPRV infection hinders ovine monocyte-derived dendritic cells maturation: functionality and transcriptomics analysis

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# ABSTRACT

**Peste des Petits Ruminants** (PPR) is an economically important disease, especially in developing countries, affecting sheep and goats. Peste des Petits Ruminants virus (PPRV) is the causative agent of PPR, closely related to other Morbillivirus like measles, rinderpest virus and canine distemper virus, within the *Paramyxoviridae* family. **PPRV targets** immune cells, including dendritic cells (DC). Our goal was to assess whether PPRV infection affects the maturation process from immature DC to mature DC, an essential step for the development of adequate adaptive immunity to the infection. To do so, a number of **functional assays and RNAseg analysis** were performed. Immature monocyte-derived DC (iMoDC) were obtained by a 48-hours differentiation process of positive-selected CD14<sup>+</sup> cells (monocytes) from peripheral blood mononuclear cells (PBMCs), employing GM-CSF and IL-4 cytokines. iMoDC were then PPRV- or mock-infected and after 24 hours cultures were transfected overnight with Poly I:C for maturation. PPRV-infected mature monocyte-derived DC (mMoDC) showed an increased expression of CD14, CD11b, CD11c and CD209 cell markers, while CD80, CD86, MHC-I and MHC-II expression levels were **reduced**, compared to mock-infected mMoDCs. PPRV-infected mMoDC showed as well a decrease in antigen presentation, as detected by allogeneic MLR assays. **RNAseq** analysis was performed using RNA extracted from PPRV and mock-infected mMoDCs cultures from four different sheep. PPRV-infected mMoDCs showed 453 up-regulated and 179 down-regulated genes compared to mock-infected counterparts. KEGG analysis revealed 31 **different up-regulated pathways**, including some involving **autophagy** or mitophagy mechanisms and signalling pathways related to viral infection responses like TNF, mTOR or IL-17 pathways, among others. Taken together, these data indicate that **PPRV can target DC maturation to hinder** adaptive immunity and thus contribute to the immunosuppressive effects of PPRV infection on its natural hosts.

# **MATERIAL AND METHODS**



#### FUNCTIONAL ASSAYS <u>mMoDC cell marker changes at 48hpi</u>

Mean fluorescence intensity of cell surface markers (mean  $\pm$  SD) measured by flow cytometry in 3-4 donor sheep. Paired t test, \*p < 0.05



EXPRESSION LEVELS: 1 CD14, CD11b, CD11c & CD209 🚽 CD80, CD86, MHC-I & MHC-II

#### **FUNCTIONAL ASSAYS**

mMoDC microsphere phagocytosis assays (48hpi) Allogenic mixed lymphocyte reaction (MLR) on PPRV infected mMoDC



 No differences in microsphere phagocytosis and between PPRVand mock-infected mMoDC



T cell proliferation was assessed by <sup>3</sup>Hthymidine incorporation in 5 day co-cultures and presented as stimulation index.

 PPRV infection impairs the ability of mMoDC to activate T cells

# RNAseq ANALYSIS Differentially expressed genes (DEG)

#### Principal Coordinate Analysis (PCoA)



RNAseq analysis comparing PPRV<sup>+</sup> mMoDC vs mock-infected controls from 4 sheep:

- 453 up-regulated genes
- 179 down-regulated genes



### **RNAseq ANALYSIS**

### Selection of relevant KEGG pathway analysis

#### Number of genes



mMoDC populations infected with PPRV showed:

- 31 up-regulated pathways
- 10 down-regulated pathways

Among them, pathways with important roles in the infection process:

- Viral infection response (TLR, IL-17, TNF, NOD)
- Apoptosis / MAPK
- Virus replication and spread (Autophagy, mitophagy)



mMoDC functionality is affected by PPRV infection:

- ↓ DC cell markers
- ↓ T-cell activation / proliferation

PPRV infection induces changes in mMoDC gene expression:

- Up- (453) and down- (179) regulation of genes
- Induction of pathways associated with viral infection response, apoptosis, viral replication, among others

# ACKNOWLEDGEMENTS

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