Tyrosine 129 of the murine gammaherpesvirus M2 protein is critical for M2 function in vivo

Udaya S. Rangaswamy, Emory University
Brigid M. O'Flaherty, Emory University
Samuel Speck, Emory University

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Introduction

Gammaherpesviruses, members of the Herpesviridae family, are lymphotropic viruses that are characterized by their ability to establish latency in lymphocytes – particularly in B cells. The human viruses of this family, Epstein-Barr Virus (EBV) and Kaposi’s Sarcoma associated Herpesvirus (KSHV) are associated with a range of lymphoproliferative diseases and lymphomas in immunocompromised situations [reviewed in [1]]. EBV, a member of the lymphocryptovirus genus, is found in all cases of endemic Burkitt’s lymphoma, and is associated with other lymphoid cancers such as gastric carcinoma and nasopharyngeal carcinoma [reviewed in [2]]. KSHV, a member of the more common rhadinovirus genus, is the etiologic agent of AIDS-related KS, and is also associated with the development of primary effusion lymphoma (PEL) and multicentric Castleman’s disease [reviewed in [3]]. However, the strict species tropism of EBV and KSHV greatly hampers detailed studies of viral pathogenesis and host defense in vivo. Much of the in vivo studies have been accumulated from limited utilization of either small-animal models or primate models.

Murine gammaherpesvirus 68 (MHV68) infection of inbred strains of mice provides a powerful and well-characterized rodent model for analysis of gammaherpesvirus pathogenesis. Infection of mice with MHV68 via intranasal inoculation results in a productive acute replication phase in the lung, and subsequently in the spleen – the latter being cleared by 2–3 weeks post-infection [reviewed in [1]]. Latency is established primarily in splenic B cells – particularly in naive, germinal center B cells and memory B cell subsets, as well as macrophages, dendritic cells and lung epithelial cells, as is the case for EBV [4–6]. Long-term latency is established predominantly in memory B cells [7]. Recently we have shown that, similar to EBV and KSHV, plasma cells represent the major reactivation reservoir for MHV68 as well [8], strongly linking the conserved strategies utilized by this virus family. Moreover, it was shown that a MHV68 gene called M2 plays a pivotal role in driving differentiation of infected B cells to plasma cells [8].

Sequence analysis and characterization of the MHV68 genome initially identified M2 as a latency associated gene product that bears no homology to any known cellular or viral protein [9,10]. M2 is crucial for both establishment and reactivation from latency, in a route- and dose-specific manner, but dispensable for acute viral replication in lungs of mice [11,12]. M2 contains several PxxP motifs that are potential SH3 domain docking sites, as well as two closely-spaced tyrosine residues (Y120 and Y129). Notably, we have previously shown the functional importance of some of these motifs in vivo [13]. Although MHV68 M2 does not bear sequence homology to any known gene product, the organization of the
functional domains in M2 resembles domains present in the cytoplasmic N-terminal domain of EBV LMP2A. Furthermore, M2 shares with EBV LMP1 the ability to induce cellular IL-10 expression [14]. We have recently shown that M2 activates the NFAT pathway, similar to K1 of KSHV which has been shown to mimic constitutive ITAM-mediated BCR signaling to activate the NFAT pathway [15,16]. M2 induces IL10 expression in primary murine B cells [17] and we have shown that this induction occurs via a NFAT-dependent pathway involving IRF4 induction [16]. Depending on the cell type, IL10 activates the JAK-STAT pathway via activation of JAK1 (associated with the IL10 receptor alpha chain) and/or TYK2 (associated with the IL10 receptor β chain) and induces the activation of STAT1, STAT3, and, in some cases, STAT5 [11,18–21].

In vitro studies have shown that Y120 residue and a C-terminal PxxP motif of M2 are involved in the formation of a complex comprising of M2, Vav1 and Fyn [22]. Additionally, it was shown that Y120 of M2 is constitutively phosphorylated in a B cell line and a mutant virus with Y120 and Y129 mutated to phenylalanine exhibits M2 null phenotype in latency establishment [23]. It was also recently shown that M2 interacts with several cellular proteins via Y120 and/or Y129. While Y120 was predominantly associated with Vav1, p85α subunit of PI3K and NCK1, Y129 was found to interact with PLCγ2, p85α subunit of PI3K and SHP2 [24]. However, the requirement of these individual tyrosine residues in some essential functions of M2, namely establishment of latency, reactivation from latency coupled with plasma cell differentiation, and IL-10 production is unknown. In an earlier study, we have shown that both of these tyrosines are required independently for activation of the NFAT pathway and IRF4 induction [16]. In this study, we aimed to further characterize the roles of Y120 and Y129 in key functional aspects of M2, both in vitro and in vivo.

Results

Tyrosines 120 and 129 of M2 are required for IL10 production and expansion of primary murine B cells in tissue culture

In vitro analyses of M2 functions have shown that Y120 of M2 is the predominant residue required for formation of a trimolecular complex of M2 with the Src kinases Fyn and Vav. It was also shown that Y120 is constitutively phosphorylated upon expression in a B cell line as well as a non-hematopoietic cell line [22]. However, in our recent studies on the signaling of M2, both Y120 and Y129 were singly required for activation of the NFAT pathway by M2. Both Y120 and Y129 were also required for induction of the plasma cell-associated transcription factor, IRF4 [16]. Since M2 induction of IRF4 leads to IL-10 induction in B cells, we wanted to further study the roles of the individual tyrosines of M2 in IL-10 production in a more physiological context, namely primary murine B cells. We generated retroviral constructs in which each of the tyrosines at positions 120 and 129 of M2 was mutated to a phenylalanine. B cells were isolated from the spleens of naïve C57Bl/6 mice and transduced with the recombinant MSCV retroviruses expressing either the M2/Y120F or the M2/Y129F mutant (recombinant MSCV expressing either wild type M2 or a null mutant of M2 (M2stop; in which a translation stop codon was introduced in place of residue 13 in the M2 open reading frame) were used as positive and negative controls, respectively). The expression of an IRES-Thy1.1 cassette downstream of the M2 open reading frame served as a surrogate marker to monitor retroviral transduction and M2 expression. To assure that the Y120F and Y129F mutant M2 proteins were expressed from the pMSCV-IRES-Thy1.1 (pMIT) vector, we assessed M2 expression by immunoblotting following transfection of the WT and M2 mutant retroviral vectors into 293T cells. Notably, both the Y120F and Y129F M2 mutants were expressed to similar levels as wild type M2 (Fig. S1).

Upon retroviral transduction, primary murine B cells expressing wild type M2 expanded in culture over time - consistent with our previous results (Fig. 1A) [17]. However, mutation of either Y120 or Y129 to phenylalanine abolished M2 mediated expansion of Thy1.1 expressing cells, with both mutants expressing levels of Thy1.1 similar to that of the negative control M2stop (Fig. 1A). Furthermore, as we have previously shown [17], supernatants from B cells transduced with the wild-type M2 retrovirus contained high levels of IL-10 compared to M2stop, while mutation of either tyrosine completely abrogated IL-10 production (Fig. 1B). We extended these analyses to assess IL-10 induction in M2 inducible cell lines, generated as previously described [16]. Consistent with the data in primary B cells, there was no IL-10 secretion upon doxycycline induction of inducible cell lines expressing either the M2/Y120F or M2/Y129F mutant (Fig. 1C). These data indicate that although Y120 is the predominant tyrosine required for interactions with Src kinases and Vav, both Y120 and Y129 are required for IL-10 production and expansion of primary B cells.

M2 induced IL-10 primarily signals through pSTAT3, but not pSTAT1 or pSTAT5

Several studies have shown that IL-10 induces positive feedback signaling by acting through the IL-10R, which signals primarily through activation of STAT3, as well as STAT1 or STAT5 in some cell types (reviewed in [25], [18,21]). To understand whether M2 induced IL-10 signals using the same pathways, we measured activation of STAT3 by determining the levels of phosphorylated STAT3 by flow cytometry. Primary murine B cells were transduced with retroviruses expressing either M2, M2stop or the tyrosine mutants and the levels of pSTAT3 were measured by phosphoflow. On days 2 and 3 post-transduction, M2 transduced cells had higher levels of pSTAT3 compared to M2stop or the tyrosine mutant transduced cells (Figure 2A and 2B). As expected, negative control B cells from IL-10 knockout mice that were transduced with either M2 or M2stop expressing retroviruses failed to up-regulate pSTAT3 (Figure 2A and 2B). Since IL-10 can signal via pSTAT1 and pSTAT5 in some cell types, we also looked at pSTAT1 and pSTAT5 levels upon M2 expression. Notably, M2 transduced B cells failed to up-regulate either pSTAT1 (Figure 2C and 2E) or pSTAT5 (Figure 2D and 2F). In contrast, positive controls in each experiment, namely, IFNy and GM-CSF induced pSTAT1 (Figure 2C and 2E) and pSTAT5 (Figure 2D and 2F), respectively, had higher levels of pSTAT1 or pSTAT5 compared to unstimulated samples. It is to be noted that pSTAT5 is predominantly activated in T cells in response to IL-2 [26] and in myeloid cells in response to GM-CSF [27]. Therefore, we observed only a modest increase in pSTAT5 levels upon GM-CSF treatment compared to unstimulated B cells. Additionally, pSTAT1 and pSTAT5 levels are moderately higher in both M2 as well as M2stop transduced samples (Figure 2E and 2F) compared to unstimulated samples indicating that LPS stimulation can activate some levels of pSTAT1 and pSTAT5 in murine B cells (note- efficiently retrovirally transduce primary murine B cells we transiently stimulated these B cell cultures overnight with LPS).

Based on the requirement of both Y120 and Y129 for induction of IL-10 expression, we extended these analyses to assess STAT3 phosphorylation with the M2/Y120F and M2/Y129F mutants. As shown in Figure 3A and Figure 3B, both the M2/Y120F and M2/Y129F mutants failed to induce phosphorylation of STAT3. This
is consistent with our hypothesis that the pSTAT3 levels we observe upon M2 expression are a result of M2-mediated IL-10 induction feeding back upon the IL-10R to activate pSTAT3, rather than M2 itself activating STAT3 to increase pSTAT3 levels. Furthermore, when we blocked IL-10 signaling with an antibody against the IL-10R, we failed to see an increase in the level of pSTAT3 (data not shown). Together, these results indicate that M2 induced IL-10 signals predominantly through pSTAT3 in primary murine B cells, and that M2 requires both Y120 and Y129 for induction of IL-10 expression in primary murine B cells.

Y129, but not Y120, of M2 is required for an efficient reactivation from latency in vivo

Given the requirement of both Y120 and Y129 in M2-mediated functions in vitro in primary murine B cells, we sought to further determine the requirement of each of these tyrosines in vivo in the pathogenesis of MHV68—focusing on establishment of latency and reactivation. Notably, Pires de Miranda et al have shown that a mutant virus with both tyrosines Y120 and Y129 mutated to phenylalanine exhibits a severe defect in latency similar to that of an M2 null virus, indicating that at least one or both of these tyrosines are required for M2 mediated functions in vivo [23]. To identify the requirement of each of the tyrosines, we generated mutant viruses in which either Y120 or Y129 was mutated to phenylalanine (designated Y120F.HY and Y129.HY, respectively). We used the ζRed recombineering system utilizing the galK selection method described by Warming et al [28] to generate the mutant viruses. To this end, we utilized as the starting platform, the MHV68-H2bYFP-BAC which harbors an EYFP cassette fused to the histone H2B open reading frame, which allows infected B cells to be monitored by flow cytometry and immunofluorescence. This recombinant MHV68 has been extensively characterized and behaves like wild-type MHV68 [29]. The introduction of these mutations into the viral genome was confirmed by PCR of the M2 region derived from BAC-purified DNA, as well as from DNA obtained from latently infected splenocytes to rule the presence of any revertants that had restored wild-type M2 sequence. To further confirm the absence of unwanted mutations or insertions within the region of homologous recombination, we performed Southern blotting analyses combined with RFLP analyses (Figure S2). We have previously described a M2null virus, and a marker rescue virus termed M2stop.HY and M2MR.HY, respectively. These viruses were also created using the MHV68-H2bYFP background and behave similarly to their non-transgenic counterparts [16].

Previous studies have shown that the requirements for M2 in both the establishment of latency and reactivation from latency are dependent on the dose and route of infection [12]. Low dose intranasal (IN) inoculation with 100 PFU of M2stop virus resulted in a severe latency defect which was overcome by a higher dose of inoculation at 4×10^5 PFU, or by intraperitoneal (IP) inoculation at a dose of 100 PFU [11,12]. Because the transgenic H2BYFP viruses have been characterized primarily with a 1000 PFU dose administered either IN or IP, we chose to look at the requirement for Y120 and Y129 at 1000 PFU. Since the kinetics of IP infection are faster than that observed following IN infection, we analyzed days 14–15 post-infection compared to days 16–18 post infection for IN infections. We initially examined virus reactivation from latency following intranasal inoculation. Consistent with our previous characterization of M2 null mutants, we observed a severe defect in M2 null virus (M2stop.HY) reactivation compared to marker rescue virus (M2MR.HY) (estimated to be ~24-fold lower) (Figure 4A). Surprisingly, reactivation of the Y120F mutant was very similar to the marker rescue virus, while reactivation of

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Figure 1. Y120 and Y129 of M2 are required for expansion of primary murine B cells and for IL-10 production. (A and B) Primary murine B cells were transduced with retroviral vectors encoding Y120F or Y129F mutations of M2, wild type M2 or M2stop as a negative control. On days 2–5 post transduction, the cells were analyzed by (A) flow cytometry to monitor Thy1.1 expression, and (B) the supernatants from cells in (A) were analyzed for IL-10 secretion by ELISA. (C) 1–2×10^6 cells each of the Y120F or Y129F inducible cell lines described in materials and methods were induced with doxycycline for 48 hours and supernatants were harvested for measurement of IL-10 secretion by ELISA. Data shown is a representative of one experiment with three replicates per condition. Each experiment was performed at least twice with at least three independent replicates per experiment. doi:10.1371/journal.pone.0105197.g001
Figure 2. M2 induced IL-10 signals through positive feedback involving STAT3, but not STAT1 or STAT5. (A–F) Primary B cells from either wild type C57BL6 (B6) mice or IL10−/− mice (as indicated) were transduced with retroviral vectors encoding either M2 or M2stop. On days 2 and 3 post transduction, the cells were analyzed by phosphoflow as described in materials and methods. (A) B cells from B6 or IL10−/− mice transduced as mentioned above were analyzed for pSTAT3 levels after gating on live cells by forward and side scatter characteristics. Representative histograms of pSTAT3 levels, one each on day 2 and day 3 are shown. (B) Mean Fluorescent Intensities (MFIs) of pSTAT3 fluorescence from three independent replicates are shown for each condition shown in A. (C–D) B cells from B6 mice transduced as mentioned above were analyzed for pSTAT1 or pSTAT5 levels, respectively. Positive control for pSTAT1 induction is IFNc treatment of cells at 100 ng/mL for 15 minutes and positive control for pSTAT5 induction is treatment of cells with GM-CSF at 100 ng/mL for 15 minutes. Representative histogram from day 2 post-transduction for each condition is shown. (E–F) Mean Fluorescent Intensities (MFIs) of pSTAT1 or pSTAT5 fluorescence from average of three independent replicates are shown for each condition shown in C and D. The experiments were done at least three times with three replicates in each experiment. doi:10.1371/journal.pone.0105197.g002
the Y129F mutant was similar to the M2 null mutant (Figure 4A). Analysis of virus reactivation following intraperitoneal inoculation, as expected, showed a more modest phenotype of the M2 null mutant (Figure 4B). Notably, the Y120F mutant again was very similar to the marker rescue virus (1 in 6729 cells reactivating virus from M2MR.HY infected mice vs 1 in 11614 cells from Y120F.HY infected mice), while the Y129F mutant behaved like the M2 null mutant (a 3–5 fold defect in reactivation compared to M2MR) (Figure 4B). Of note, we did not observe significant levels of preformed infectious virus in any of the assays described (data not shown) – thus indicating that the cytopathic effect observed in the reactivation analyses was due to reactivation of latently infected cells. To assess whether the absence of a strong phenotype with the Y120F mutant could be due to reversion of the Y120F mutation back to the wild type sequence, we PCR amplified and sequenced the M2 gene from latently infected splenocytes. These analyses confirmed detected only the presence of Y120F mutation (data not shown) – thus indicating that the cytopathic effect observed in the reactivation analyses was due to reactivation of latently infected cells. To assess whether the absence of a strong phenotype with the Y120F mutant could be due to reversion of the Y120F mutation back to the wild type sequence, we PCR amplified and sequenced the M2 gene from latently infected splenocytes. These analyses confirmed detected only the presence of Y120F mutation (data not shown). Taken together, these analyses show that despite an absolute requirement for both Y120 and Y129 in M2-mediated functions in vitro, only Y129 appears to play a critical role for M2-mediated functions in vivo.

Y129, but not Y120, of M2 is required for efficient access of infected B cells to the plasma cell reservoir

Previously, we have shown that M2 is required for plasma cell differentiation of infected cells and that plasma cells are the major reactivation reservoir in infected spleens [8]. Using a transgenic virus that can mark infected cells (M2stop.YFP), it was shown that upon infection with a M2 null virus, there was a significant decrease in the frequency of infected cells with a plasma cell phenotype. Since the viruses used in this study express an H2bYFP cassette, we can identify the frequencies of infected cells by monitoring YFP expression by flow cytometry of splenocytes recovered from infected mice. On days 16–18 post infection via IN route, M2MR.HY, M2stop.HY and Y120F.HY had similar frequencies of YFP\(^+\) B cells (doublet-discriminated/CD3\(^-\)CD4\(^-\)CD8\(^-\)/B220\(^+\)), whereas Y129F.HY infected mice had a lower frequency of infected B cells (Figure 5A). It was surprising that the Y129F.HY infection appears to have a significant defect in the frequency of infected cells compared to M2stop.HY. This may indicate that expression of this mutant M2 is more deleterious to establishment of MHV68 infection than the absence of any M2 expression (i.e., the M2 Y129F mutant may function as a dominant negative that interferes with viral latency). Notably, the Y129F.HY mutant did not have any defect in growth - growing to similar titers as that of M2MR.HY and M2stop.HY (data not shown). Importantly, taken together these analyses demonstrate that both the M2stop.HY and Y129F.HY mutants have a pronounced reactivation defect and a mild to moderate impact on establishment of latency. In contrast, mutation of Y120 has little impact on MHV68 latency and reactivation.

While the frequency of M2stop.HY and M2MR.HY infected cells was very similar following IN infection, we did observe a significant decrease in the YFP\(^+\) B cell fraction upon infection with the M2stop.HY compared to M2MR.HY following IP inoculation (0.05% in M2stop.HY compared to 0.24% in M2MR.HY) (Figure 5B). We believe that this disparity may be due to the high mouse-to-mouse variability we observe with the YFP marking of infected cells (as observed here in Figures 5A and 5B and also in
of total GC cells upon M2stop.YFP infection at a dose of 100PFU. In our earlier analyses of infections with M2stop.YFP virus, we noticed a decreased number of marker rescue infected B cells following IP inoculation were more reflective of the frequency observed with wild type MHV68, while the frequency of YFP+ cells with a GC phenotype was similar between the different groups – with the majority of the virus infected cells exhibiting a GC phenotype in all the cases (Figure 6A and 6B). In contrast, there was a striking difference in the frequency of YFP+ cells with a plasma cell phenotype in M2stop.HY virus infected cells compared to the M2MR.HY infected cells upon either IN or IP inoculation (Figure 6C and 6D). ~7% of M2MR.HY infected cells vs 1.4% in M2stop.HY infected cells via IN route and ~10% of M2MR.HY infected cells vs 2.8% in M2stop.HY infected cells via IP route. In addition, the Y120F.HY mutant exhibited a ~2-fold decrease in the fraction of infected cells with plasma cell phenotype, indicating that the Y120 residue may be partially required for infected cells to differentiate into plasma cells. Consistent with our above results, the Y129F.HY virus was similar to that of the M2stop.HY virus exhibiting a significant defect in infection of plasma cells (Figure 6C and 6D). Taken together, the data strongly indicates that the majority of M2 mediated functions in vivo require Y129.

Discussion

From prior studies on the functions of M2, it is hypothesized that M2 primarily functions as a molecular scaffold - acting to relay signals that mimic those involved in BCR signaling [16,22–24,31–33]. M2 contains nine PxxP motifs capable of binding cellular proteins with SH3 domains, as well as two tyrosine residues that upon phosphorylation are capable of binding SH2 domain containing proteins. Several candidate interacting partners for M2 have been identified, but the importance of these interactions in vivo remains unclear. Identifying specific domains in M2 that are involved in these interactions, and the role of these domains in M2 function in vivo, is crucial to gaining insights into how MHV68 utilizes M2 to hijack the host cell signaling machinery to its own benefit. As a first step towards this, we sought to identify the requirement of each of these tyrosines in functions mediated by M2.

In this study, we have identified Y129 as the critical tyrosine residue important for the function of the MHV68 gene M2 in vivo. Surprisingly, mutation of Y120 to phenylalanine had very little effect on the functions of M2 in vivo – only a moderate defect in the differentiation of infected B cells to plasma cells (Figure 6C). This strongly indicates that Y120 is mostly dispensable for M2 mediated functions in vivo. However, in vitro Y120 was required for M2 induction of the NFAT pathway, IRF4 [16] and IL-10 levels (Figure 1B). Notably, Y120 has been shown to be constitutively phosphorylated in a B cell line and to be the key residue important for the function of the MHV68 gene M2 in vivo. Consequently, mutation of Y120 to phosphorus had very little effect on the functions of M2 in vivo. However, in vitro Y120 was required for M2 induction of the NFAT pathway, IRF4 [16] and IL-10 levels (Figure 1B). Notably, Y120 has been shown to be constitutively phosphorylated in a B cell line and to be the key residue important for the function of the MHV68 gene M2 in vivo.
formation of the appropriate signaling complex; (ii) constitutive phosphorylation of Y120 is required for “tonic” signaling in B cells expressing M2, and that this tonic signaling is required for M2 function (e.g., B cell survival and expansion) in vitro but plays a less dominant role in vivo; and/or (iii) expression of IL-10 from an uninfected cell type (e.g., macrophages or T cells) largely substitutes for the critical function of Y120.

In contrast, Y129 phosphorylation is possibly tightly regulated and active only upon antigen-dependent signaling and therefore plays a vital role in functions of M2 in vivo in the context of infection. If the latter is the case, the discrepancy with the requirement of Y120 in vitro may be due to the absence of potential overlapping effector signaling molecules required by both the tyrosines in the in vitro settings, but substituted for or compensated by other factors in the in vivo setting. Indeed, Pires de Miranda have shown that in a latently infected B cell line, S11, Y129 is required for the interaction of M2 with PLCγ2 [24], an activator of calcium signaling required for activation of the NFAT pathway. Consistent with this, we have shown that the NFAT pathway is partially required for induction of IRF4, a key player in plasma cell differentiation [16]. It is therefore worthwhile to speculate that the phosphorylation status of M2 strongly dictates the outcome of M2-mediated functions.

Additionally, we also made mutations of Y120 and Y129 to aspartic acids in an effort to mimic constitutive phosphorylation. However, in the primary B cell assays, we found similar results as...
those observed with the Y→F mutations (data not shown). This might mean that either constitutive phosphorylation is deleterious to the function of the protein, rendering it unstable or that the mutations fail to mimic phosphorylation effectively. We did not pursue the Y→D mutations further since the focus of the study was aimed at understanding the requirement of Y120 and Y129 in M2-mediated function (s), rather than the effect of phosphorylation of M2 itself. It is also formally possible that the disconnect we observe with Y120 in vitro vs in vivo is due to the fact that most of the in vitro studies are done in B cell lines which are transformed, or in primary B cells that are stimulated with LPS. Under these conditions the status of the signal transduction pathways is likely dysregulated compared to B cell infection in vivo. This highlights the importance of extending tissue culture based findings to in vivo infection models.

Exploitation of the IL-10 pathway is a shared strategy among various virus families (reviewed in [34]). Several viruses are known to encode viral IL-10 homologues or induce cellular IL-10 as a means to simultaneously evade host immune response and enhance survival of infected cells. In particular, the human gammaherpesvirus EBV encodes a viral homolog, vIL-10 which is highly homologous (92.3% sequence identity) to cellular IL-10 and incapable of enhancing transformation of human B cells [35–37]. In addition, the latent membrane protein-1 (LMP-1) of EBV induces cellular IL-10 via activation of the PI3K, Akt, NFkB pathway as well as activation of STAT3 [38–40]. Furthermore, serum IL-10 levels are increased in renal transplant patients undergoing EBV reactivation [41]. Although the role of IL-10 in KSHV pathogenesis remains unclear, KSHV encodes a viral IL-6 homolog which possesses overlapping functions with cellular IL-10 and IL-6. In macrophages and monocytes, KSHV microRNAs can increase cellular IL-10 and IL-6 secretion. Consistent with M2 phosphorylation of STAT3 (Figure 2), KSHV infection results in STAT3 activation in endothelial cells and dendritic cells (DCs) [42,43]. In DCs, phosphorylation of STAT3 was also accompanied by an increase in the levels of IL-10, IL-6 and IL-23 [42]. Human betaherpesvirus CMV also encodes an IL-10 homolog, cmvIL-10 [44] known to possess immunosuppressive roles [45]. cmvIL-10 also results in activation of STAT3 similar to that of EBV vIL-10 and cellular IL-10, as well as M2-mediated IL-10 as
described in Figure 2. Thus, IL-10 likely plays a dual role - an
immunostimulatory role, as well as act as an immunosuppressive
role depending on the cell type that it acts on. Taken together, the
results from our study describe the residues on M2 that are
required for IL-10 secretion and plasma cell differentiation and
reactivation, thus aiding in better understanding the molecular
basis of M2 mediated functions.

Materials and Methods

Ethics statement

This study was carried out in strict accordance with the
recommendations in the Guide for the Care and Use of Laboratory
Animals of the National Institutes of Health. The protocol
was approved by the Emory University Institutional Animal Care and Use Committee and in accordance with
established guidelines and policies at Emory University School of Medicine (Protocol Number: YER-2002245-031416:GN).

Mice and infections

Female C57BL6/J mice aged 6–8 weeks were purchased from
Jackson labs (Bar Harbor, ME) and infections were done at 9–12
weeks of age. Mice were housed and maintained at the Whitehead
vivarium according to Emory University and IACUC (International
Animal Care and Use Committee) guidelines. Mice were
anesthetized using isoflurane before infecting with 1000 PFU of
the respective viruses via either intranasal or intraperitoneal
infection. Splenocytes were harvested from mice that were
sacrificed at the indicated time points by CO2 inhalation per
AVMA guidelines. For flow cytometry analyses, individual mice
were analyzed and for the latency and reactivation analyses,
splenocytes from 3–5 mice per group were pooled.

Plasmids

The Y120F and Y129F mutations were created by overlapping
PCR using the following primers: Y120F–(5’GAGAAAA-
CATCTTTCGAAGACTCTACG 3’) and (5’GT TAG-
GATTTTTCGAAGATGGTTCCTTC 3’); Y129F–(5’ AGT-
GAACTGCTTGCTGCAACAAGCTCAG 3’) and
(5’GATTGCTGATTGAAAGCTGCTTGACTCTACT). The
overlapping PCR products were then cloned into pCR-BLUNT
(Invitrogen), sequenced and positive clones were then cloned into
pMSCV-IREs-Thyl.1 vector as described in [17], using Bgl II
restriction sites. The expression of M2/Y120F and M2/Y129F in
pMSCV-IREs-Thyl.1 was verified by transfection of 293 T cells.
Briefly, 60–80% confluent monolayers in 6 well plates were
transfected with 5 ug of the plasmid using Mirus TransIT293
transfection reagent. Cell lysates were harvested at 48 hours and
western blotting was performed as described in [16].

Construction of mutant viruses

M2stop.HY and M2MR.HY viruses are described previously
[16]. The Y120F.HY and Y129F.HY viruses were created in a
similar manner. Briefly, the MHV68-H2bYFP BAC described in
[29] was used as a backbone to create a M2/galK intermediate
BAC where the M2 ORF was replaced with a galK cassette. The
M2/galK intermediate was made by amplifying the galK gene
from pGalK using the following primers – gK-M2-FP (5’-
tcgaggtgcgggtcaaatcagcactagctgtagggttcttgctgcaatggAGC
ACT-GTCCTGCTCCTT-3’) and gK-M2-RP (5’-tcaggggtttaccgaa-
agaaacagttgtctcgtaggtgccctggttcgtaATGAGCAATCCGGCA-3’)
and M2-RP (5’- tccaggggtcttaaa-
gaaaaagttatgttctgcgttagcaccttcactgCCTGTTGACAATTAATAGC
ATCCCTCCCTG-3’). After confirming the presence of required
mutation by sequencing, the PCR products were electroporated
into the M2/galK intermediate and recombinants were selected on
minimal plates containing glycerol and 2-deoxy-D-galactose.
Potential colonies were screened by colony PCR and confirmed
by sequencing using primers spanning M2 ORF. RFLP analyses
was also performed with SpeI and HindIII restriction endonuclease
prior to final confirmation by Southern blotting using probes
specific for the M2 ORF and its surrounding region.

Flow cytometry

Flow cytometry on primary murine B cells were performed as
described previously [17]. Briefly, cells were resuspended in about
100 ul of FACS buffer (PBS with 2% FCS+1 mM EDTA). Fc
block was done prior to staining with fluorophores to block
FcγIII/II receptors by adding Rat monoclonal anti CD16/32
e(Bioscience) for 10 minutes. The cells were washed once with
FACS buffer prior to staining with an antibody cocktail.
Antibodies used for surface staining of primary B cells include
Thy.1.1-APC (eBioscience) and CD19-FTTC. For staining spleno-
cytes from infected mice, a similar protocol was used. Antibodies
in the cocktail for infected cells include GL7-Ax660/APC
e(Bioscience), CD95-PECy7, CD138-PE, CD3, CD4, CD8-PerCP
(BD Pharmingen), B220-Pacific Blue (Southern Biotech) described
in [29]. CD3, CD4 and CD8 were used in the same fluorophore to
eliminate T-cells. This mix is referred to in the text as dump gate.

B cell isolation

Murine primary B cells were isolated by immunomagnetic
effective negative selection using the EasySep Mouse B Cell Enrichment
Kit (Stem Cell Technologies) as per manufacturer’s instructions.
The purity of B cell isolation was routinely analyzed and found to be ≥95% as determined by staining for CD19 by flow cytometry.
The cells were plated at 1×10^6 cells/mL of a 24 well plate
overnight with cRPMI containing 20–25 µg/mL LPS (Sigma)
prior to retroviral transduction.

Retroviral transduction

Retroviruses were prepared as described in [17]. Briefly,
BOSC23 (ATCC) producer cells were plated at a density of
1.5×10^6 cells per 60 mM or 3×10^6 cells per 100 mM collagen
coated dish (BD biosciences) overnight. After 18–24 hours of
plating, the cells were transfected with 5 µg (for 60 mM) or 10 ug
(for 100 mM dish) of either pMIT-M2, pMIT-M2stop, pMIT-
Y120F or pMIT-Y129F plasmids. Supernatants were harvested at
72 hours and used immediately or frozen at −80°C until ready for
use. On the day of transduction, the retroviruses were centrifuged
to 2000 rpm for 10 minutes to remove any cellular debris and
supplemented with 5 µg/mL of polybrene. 750 µL of the media
was removed from the B cells and replaced with 1 mL of the
retrovirus containing polybrene. The cells were spin infected for
2500 rpm for one hour at 30°C. Post-transduction, 750 µL of the
 supernatant was removed from each well and 1 mL of fresh media
was added back. Triplicate wells per condition were analyzed by
flow cytometry at days 2–5 post-transduction.
Limiting Dilution analysis for latency and ex-vivo reactivation

Determination of frequency of latently infected splenocytes was done by performing a limiting dilution, single-copy sensitive nested PCR assay, as previously described [5,46]. Briefly, frozen splenocytes were thawed, counted and washed in isotonie buffer prior to plating in serial three-fold dilutions onto a background of 10^4 uninfected 3T12 cells in 96-well plates. Following a proteinase K mediated digestion step to lyse the cells, the samples were subject to two rounds of nested PCR. Twelve PCRs were performed for each dilution for a total of six dilutions starting with 10^6 cells. Each PCR plate contained control reactions that contained 0, 0.1, 1, or 10 copies of plasmid DNA in a background of uninfected cells. Products were analyzed on a 2% agarose gel. Determination of frequency of splenocytes capable of reactivating virus from latency was done by using a limiting dilution ex-vivo reactivation assay, as previously described [5,46]. Briefly, single cell suspensions of splenocytes from infected mice were plated in a two-fold serial dilution (starting with 10^6 splenocytes per well) on to MEF monolayers in 96-well tissue culture plates. Twenty-four wells were plated per dilution and 12 dilutions were plated per sample. Wells were scored microscopically for cytopathic effect (CPE) at 14–21 days post-explant. Preformed infectious virus was detected by plating parallel samples of mechanically disrupted cells onto MEF monolayers alongside intact cells. We did not observe a significant amount of preformed infectious virus in any of the assays described (data not shown).

Supporting Information

Figure S1 Expression of M2 mutants. Expression of Y120F and Y129F cloned into the pMUCV-IRESE-Thy1.1 (pMIT) vector was tested by western blotting. Mutant retroviruses were prepared as described in materials and methods and transduced into 293T cells. Cell lysates were harvested at 48 h post transfection and western blotting was performed using chicken anti-M2 antibody described in [17].

(TIF)

Figure S2 Southern blot analyses of mutant viruses. M2MR.HY, M2stop.HY, Y120F.HY and Y129F.HY viruses were made as described in materials and methods. (A) Purified baculovirus preparations were digested with the restriction endonucleases SpeI or HindIII. Restriction fragments are shown. (B) The blot in (A) was subjected to southern blotting using probes spanning the region encompassing M2.

(TIF)

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Author Contributions

Conceived and designed the experiments: USR SHS. Performed the experiments: USR BMO. Analyzed the data: USR BMO SHS. Contributed reagents/materials/analysis tools: USR BMO SHS. Contributed to the writing of the manuscript: USR SHS.

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