Cell Host & Microbe, Volume 7

Supplemental Information

Protein Kinase R Contributes to Immunity against Specific Viruses by Regulating Interferon mRNA Integrity

Oliver Schulz, Andreas Pichlmair, Jan Rehwinkel, Neil C. Rogers, Donalyn Scheuner, Hiroki Kato, Osamu Takeuchi, Shizuo Akira, Randal J. Kaufman, and Caetano Reis e Sousa

Supplemental Information

Figure S1, related to Figure 1 Figure S2, related to Figure 5A-C Figure S3, related to Figure 5E

Supplemental Figure Legends



Figure S1. Failure of PKR^{-/-} **BM-DCs to produce IFN-α/β does not correlate with reduced levels of viral RNA or increased cell death**. (A) BM-DCs were infected with EMCV (MOI=10), SFV (MOI=5) or left untreated (mock) and stained with a mAb (K1) specific for dsRNA before analysis by flow cytometry. Dot plots show cells expressing the DC lineage-specific marker CD11c and dsRNA. The frequency of CD11c/dsRNA double positive cells is shown inside the rectangular gates. (B) Wild-type (left panel) and PKR^{-/-} BM-DCs (right panel) were stained with a live/dead cell discriminating dye after overnight incubation in the absence or presence of EMCV (MOI=10) and analyzed by flow cytometry. Histogram shown represent percentage of dead cells (filled section of bar) and live cells (open section of bar) for each treatment. Data in A and B are representative of two independent experiments.



Figure S2. PKR^{-/-} BM-DCs fail to up-regulate MDA5 mRNA after EMCV infection.

BM-DCs ($5x10^{5}$ /well) were infected with EMCV (MOI=10), SeV (MOI=1) or treated with IFN A/D for 12 hours. MDA5 mRNA was analyzed by quantitative PCR and levels were calculated relative to 18s rRNA. Data are the mean \pm SD of triplicate wells and are representative of three independent experiments with similar results.



Figure S3. Quantitative PCR analysis of adenylation status of various inducible and constitutive genes following viral infection. BM-DCs were infected with EMCV (MOI=10) or SeV (Moi=1) for 12 hrs and 6 hrs respectively. cDNA for GAPDH (A), IL-6 (B), TNF- α (C), and RPS-16 (D) was generated from total RNA using random hexamer (open bars) or oligo dT (filled bars) nucleotides. The relative expression of each gene in PKR^{+/+} versus PKR^{-/-} cells was calculated from the Ct values and converted into fold difference using the formula 2^(- Δ Ct). Data are representative of two independent experiments.