Chloroquine enhances human CD8+ T cell responses against soluble antigens in vivo

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The presentation of exogenous protein antigens in a major histocompatibility complex class I-restricted fashion to CD8+ T cells is called cross-presentation. We demonstrate that cross-presentation of soluble viral antigens (derived from hepatitis C virus [HCV], hepatitis B virus [HBV], or human immunodeficiency virus) to specific CD8+ T cell clones is dramatically improved when antigen-presenting dendritic cells (DCs) are pulsed with the antigen in the presence of chloroquine or ammonium chloride, which reduce acidification of the endocytic system. The export of soluble antigen into the cytosol is considerably higher in chloroquine-treated than in untreated DCs, as detected by confocal microscopy of cultured cells and Western blot analysis comparing endocytic and cytosolic fractions. To pursue our findings in an in vivo setting, we boosted groups of HBV vaccine responder individuals with a further dose of hepatitis B envelope protein vaccine with or without a single dose of chloroquine. Although all individuals showed a boost in antibody titers to HBV, six of nine individuals who were administered chloroquine showed a substantial CD8+ T cell response to HBV antigen, whereas zero of eight without chloroquine lacked a CD8 response. Our results suggest that chloroquine treatment improves CD8 immunity during vaccination.
Figure 1. Cross-presentation efficiency is dependent on the inhibition of antigen degradation. (A) FC analysis of an HLA-A2–restricted NS31406–1415–specific CD8+ T cell clone producing IFN-γ in response to NS3Ag cross-presented by HLA-A2+ iDCs, in the presence or absence of the indicated compounds. Dot plots show double CD8 and IFN-γ staining. Results are expressed as percentages of cells and are indicated in each quadrant. One representative out of six different experiments is shown. (B) NS3Ag cross-presentation after 12 h of pulsing by six independent HLA-A2+ iDC populations to an NS31406–1415–specific CD8+ T cell clone (mean ± SD), in the absence (triangles), leupeptin (squares), or lactacystin (circles). *, P < 0.0001 and **, P < 0.0001 in the presence versus absence of lactacystin. (C) Chase time of 50 μg/ml NS3Ag cross-presentation after 30 min of pulsing by six independent iDC populations (mean ± SD), in the presence (squares) or absence (diamonds) of lactacystin. *, P = 0.001 and **, P < 0.0001 in the presence versus absence of lactacystin. (D) NS3Ag (closed diamonds), NS3Ag + chloroquine (triangles), or peptide (open diamonds) presentation by three independent HLA-A2+ EBV–B cells to an NS31406–1415–specific CD8+ T cell clone (mean ± SD). (E) Presentation of NS3Ag (*, P < 0.0001 in the presence versus absence of chloroquine) by four independent DC populations to an NS31241–1260–specific CD4+ T cell clone (mean ± SD), in the presence (triangles) or absence (diamonds) of chloroquine. (F and G) Presentation of the indicated peptides to the NS31406–1415–specific CD8+ T cell clone (F) or the NS31241–1260–specific CD4+ T cell clone (G) in the absence (diamonds) or presence of chloroquine (triangles) or lactacystin (circles).

Figure 2. Efficient direct presentation of endogenous NS3Ag. FC analysis of 2 × 10⁴ HLA-A2+ NS31406–1415–specific CD8+ T cell clones producing IFN-γ in response to endogenous NS3Ag directly presented by 2 × 10⁴ autologous EBV–B cells that had been infected by either 5 PFU/cell of WT VV or NS3Ag-expressing VV (VV-NS3), in the presence or absence of lactacystin (lacta.) or chloroquine (chlor.). Dot plots show IFN-γ staining. Results are expressed as percentages of cells and are indicated in each quadrant. One representative out of three different experiments is shown. SSC, side scatter.

RESULTS
Cross-presentation of soluble antigens is up-regulated by inhibitors of intravesicular acidification in vitro
We devised a system in which human HLA–A2+ iDCs cross-presented soluble r nonstructural 3 antigen (rNS3Ag) of hepatitis C virus (HCV) to an HLA-A2–restricted NS31406–1415–specific CD8+ T cell clone (Fig. 1). Cross-presentation of soluble NS3Ag (Fig. 1, A and B), but not NS31406–1415 Peptide presentation (Fig. 1 F), was drastically blocked by lactacystin, a potent proteasome inhibitor (11–15, 28). This supports the idea that soluble NS3Ag cross-presentation requires proteasome-dependent processing. Surprisingly, cross-presentation efficiency improved when iDCs were pulsed in the presence of chloroquine (Fig. 1, A–C) or NH4Cl (not depicted), whereas the antigen presentation to CD4+ T cells was strongly inhibited (Fig. 1 E). Notably, lactacystin drastically blocked cross-presentation of soluble antigens, even in the presence of chloroquine (Fig. 1, A and B). Chloroquine did not affect the peptide presentation of DCs to either CD8+ or CD4+ T cells (Fig. 1, F and G), ruling out the possibility that it improved cross-presentation by up-regulating the costimulatory capacities of DCs. Both chloroquine and NH4Cl are lysosomotropic agents that diffuse across membranes and inhibit intravesicular acidification, which is critical to activate several acid proteases that induce proteolysis of antigens in the endocytic compart-
Furthermore, it has been reported that chloroquine causes direct lysosomal membrane permeabilization, with the subsequent release of lysosomal products (i.e., cathepsins) from the lysosomal lumen into the cytosol (43). In contrast, only a slight, or no, improvement in cross-presentation was observed with compounds that inhibit various proteases without interfering with the pH level, such as leupeptin (Fig. 1 B), pepstatin A, EDTA, or pefabloc (unpublished data). Further studies are required to verify whether this finding is caused by the protease inhibitors used not being readily membrane permeable (as opposed to chloroquine and NH₄Cl), which may thus cause them to accumulate at lower concentrations inside cells. Nonprofessional APCs, such as autologous EBV-transformed B cells (EBV–B cells; Fig. 1 D), were unable to cross-present even in the presence of chloroquine. In addition, EBV–B cells, but not iDCs, were unable to internalize 40-kD FITC-conjugated (FITC)–dextran, which is known to be efficiently captured via man-
Figure 4. Improvement of soluble antigen export from endosomes into cytosol in chloroquine-treated iDCs. (A and B) iDCs were pulsed/chased with either NS3Ag alone or NS3Ag and TRITC-Tf, in the presence or absence of chloroquine, fixed, and stained at different times with human anti-NS3 alone or with anti-NS3/H11001 rabbit anti–cathepsin D/C and D), followed by staining with the appropriate secondary antibodies. The signal of NS3 alone is green. The signals of double staining of Tf or CD and NS3 are red and green, respectively. The extent of colocalization is shown in yellow after merging. Arrows indicate NS3 enrichment or colocalization with Tf or CD. In control experiments, DCs were incubated for 1 h at 37°C in the presence of 1 mg/ml FITC-dextran with the indicated molecular masses and then fixed. One representative out of three different experiments is shown. (C) Quantitative analysis of the fluorescence intensity of cytosolic NS3Ag in iDCs pulsed/chased with NS3Ag in the presence or absence of chloroquine. (D) Quantitative analysis of the fluorescence intensity of cystolic FITC-dextran in iDCs pulsed/chased with FITC-dextran of the indicated molecular masses, in the presence or absence of chloroquine. (E) One representative out of three WB analyses on both endocytic- and

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Cross-presentation efficiency was confirmed as being substantially improved when both early and late iDCs were pulsed in the presence of chloroquine but not leupeptin (Fig. 4). This finding rules out the possibility that cross-presentation improvement was caused by either chloroquine- or NS3Ag-dependent artifacts. The specificity of cross-presentation was supported by the finding that the CD8 cell response was HLA-A2 restricted even when DCs were treated with chloroquine (Fig. S5).

Confocal microscopy evaluation of soluble antigen trafficking in DCs
To support the hypothesis that chloroquine increases the export of soluble antigens from endosomes to cytosol, NS3Ag trafficking was evaluated using a confocal laser scan microscope (CLSM) in whole DCs or EBV–B cells. After the initial 5–15 min of pulsing with NS3Ag, both untreated iDCs and the chloroquine-treated iDCs revealed colocalization of NS3Ag with transferrin (Tf) R (a marker of early endosomes; Fig. 4, A and B). After 40 min of chase, the majority of NS3Ag migrated from TfR+ into cathepsin D+ (a marker of late endosomes) compartments, and only a tiny part was exported into the cytosol in untreated DCs (Fig. 4 B). Conversely, chloroquine treatment considerably increased NS3Ag export into cytosol in the late phases, and only a small amount of antigen was colocalized with cathepsin D in late endosomes (Fig. 4 B). The magnitude of fluorescence intensity in cytosolic NS3Ag was much greater in chloroquine-treated than untreated DCs, after both 40 and 120 min of chase (Fig. 4 C). In control experiments, DCs were pulsed with different molecular masses of FITC-dextran. Dextrans are nondegradable molecules that are internalized via mannose receptors and transported into cytosol in a size-dependent fashion (49). Only the 40-kD FITC-dextran, not the 500 kD, was visualized in the cytosol by confocal microscopy, irrespective of the presence or absence of chloroquine (Fig. 4, A and D). This finding rules out the possibility that the improvement in cytosolic NS3Ag export was caused by a trivial endosomal membrane rupture by chloroquine. Consistent with their incapacity to cross-present, both chloroquine-treated and untreated EBV–B cells showed only a low NS3Ag export from the endocytic compartments into the cytosol (Fig. S6, available at http://www.jem.org/cgi/content/full/jem.20051106/DC1).

Biochemical analyses of soluble antigen trafficking in DCs
To confirm the evidence that chloroquine favors the export of soluble antigens from endosomes into cytosol, we performed Western blot (WB) analyses of both cytosol- and endocytic-enriched preparations from DCs that had been pre-

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previously pulsed/chased with NS3Ag, in the presence or absence of chloroquine. After 60–120 min of chase, chloroquine increased antigen accumulation in both the endocytic and cytosolic fractions (Fig. 4 E). The chloroquine effect at the level of the cytosolic fractions was particularly evident at the lowest antigen concentrations (5 μg/ml) used, which were visible only in the chloroquine-treated DCs (Fig. 4 E). In control experiments, the cytosolic and endocytic fractions derived from DCs incubated with 40- or 500-kD FITC-dextran, in the presence or absence of chloroquine, were analyzed by a fluorometer. After 1 h of incubation, the 40-kD FITC-dextran was found in both endocytic and (more importantly) cytosolic fractions in considerably higher amounts than the 500-kD FITC-dextran, in the presence or absence of chloroquine (Fig. 4 F). This finding further corroborates the interpretation that the greater antigen accumulation in cytosolic fractions of chloroquine-treated DCs (as detected by WB analysis; Fig. 4 E) was not determined by an endosomal membrane rupture by chloroquine. In addition, flow cytometry (FC) analysis was performed on phagosomes isolated from iDCs (50, 51), which had been previously pulsed and chased with a combination of soluble NS3Ag and latex beads (LBs) in the presence or absence of chloroquine. In the early phases, the expression of NS3Ag was substantially higher in phagosomes from chloroquine-treated DCs, confirming that chloroquine also increases antigen accumulation in early phagosomes (Fig. 4 G). In contrast, chloroquine treatment did not affect the kinetics of expression of either phagosomal TAP-2 (as a marker of early phagosomes) (33–36) or LAMP-2 (as a marker of late phago/endosomes), suggesting that it does not interfere with the phago/endosome maturation process (Fig. 4 G).

**Chloroquine elicits antigen-specific CD8+ T cells ex vivo**

To verify whether chloroquine might expand memory CD8+ T cell responses ex vivo, PBMCs isolated from three HCV- (52) and three HIV-infected patients were cultured in the presence or absence of chloroquine with rNS3Ag or rNef, respectively, in IL-2–conditioned medium for 15 d. Under conditions in which PBMCs were first elicited with NS3Ag in the presence (Fig. 5 A), but not in the absence, of chloroquine (Fig. 5 B), a noteworthy expansion of CD8+ T cells was observed. More important, CD8+ T cells, which were primarily elicited with NS3Ag in
the presence of chloroquine (Fig. 5 A), produced large amounts of IFN-γ in response to a secondary stimulation with the relevant NS3Ag peptide plus autologous APCs. Under these conditions, the generation of antigen-specific CD4+ T cells was completely abrogated. It is noteworthy that CD8+ T cells efficiently responded to a secondary stimulation with the entire NS3Ag only when the latter was cross-presented by chloroquine-treated DCs (Fig. 5 A). Meanwhile, stimulation of the NS3Ag-specific CD8+ T cell clone, used in the cross-presentation assays shown in Figs. 1 and 3 and Figs. S1, S2, and S5 above, was already obtained in steady state cross-presentation conditions and was considerably augmented by adding chloroquine. Furthermore, the short-term NS3Ag-specific CD8+ T cell line, shown in Fig. 5, responded to the same peptide concentration several folds less than the clone used in the cross-presentation assays (see Fig. 1 F and Fig. S2). This means that the efficiency of CD8+ T cell stimulation by cross-presentation is not only dependent on the capacity of APCs to cross-present but also on the affinity/avidity of CD8+ T cells. In contrast, PBMCs, which were first antigen stimulated in the absence of chloroquine (Fig. 5 B), only generated CD4+ T cells capable of recognizing (on a secondary stimulation) both the entire NS3Ag and the MHC class II–restricted promiscuous NS31241–1260 epitope. The response of the same antigen-specific CD4+ T cells to a secondary stimulation with the entire NS3Ag in the presence of chloroquine was strongly inhibited. Comparable results were obtained by Nef stimulation of PBMCs from HIV-infected patients (Fig. 5, C and D).

**Chloroquine elicits antigen-specific CD8+ T cells in vivo**

Finally, we wondered whether chloroquine might elicit memory CD8+ T cell responses in vivo. PBMCs of healthy individuals vaccinated with the hepatitis B envelope protein have been previously shown to contain HBenvAg-specific CD8+ T cells (10, 53, 54). This finding is one of the first to evidence that exogenous viral proteins can enter the class I processing pathway (55–58) and that the “class I/II discrimination” paradigm is not necessarily a rule (59). These data served as a basis for the experiments reported here, which were designed to elucidate the role of chloroquine in improving the generation and expansion of HBenvAg-specific CD8+ T cell responses in vivo. Thus, we selected 17 healthy individuals who had efficiently responded to an anti-HBV vaccine program. Figure 6. Chloroquine-boosted cross-presentation elicits antigen-specific CD8+ T cells in vivo. ELISPOT assays on fresh CD8+ T cells isolated from PBMCs of high responders to HBV vaccine, performed before (A) and after (B) chloroquine treatment and anti-HBV vaccine boost, or before (C) and after (D) only the anti-HBV vaccine boost. Fresh CD8+ T cells were tested for their capacity to form IFN-γ spots within 6 h of contact with autologous irradiated APCs, which had been previously pulsed or not with entire HBenvAg plus chloroquine or HLA-A2–binding HBenvAg213–221 peptide, in the presence or absence of blocking anti-HLA–A,B,C mAb or the corresponding isotype antibody, as indicated in A. Results are expressed as spot-forming cells (SFC) in 2 × 10^5 CD8+ T cells. The SFC values were subtracted by background, which was below 10 SFC in 2 × 10^5 cells in each test. SFC values obtained in response to the entire HBenvAg were significantly higher in chloroquine-treated than in untreated high responders (P < 0.001), as well as those obtained in response to the HLA-A2–binder HBenvAg peptide (P < 0.05) calculated among the HLA-A2+ high responders. The numbers with asterisks represent HLA-A2+ individuals. Histograms, attached to the right of each panel, report serum anti-HBenvAg (anti-HBs) antibody levels determined before and after the anti-HBV vaccination boost in all individuals studied (either chloroquine-treated or untreated).
vaccination protocol 8–10 yr ago, in terms of both specific antibody and T cell responses (high responders). In particular, nine of them received a brief chloroquine treatment per os, followed by a booster dose of anti-HBV vaccine, whereas eight underwent the same vaccine boost without the chloroquine treatment (controls). The majority of individuals studied (13/17) were HLA-A2+ in order to minimize the possible diversity of antigen presentation caused by the HLA polymorphism (Fig. 6). A noteworthy expansion of HBenvAg-specific effector CD8+ T cells was detected by ELISPOT assay in six of the nine high responders who received both chloroquine treatment and the booster dose of anti-HBV vaccine (Fig. 6, A and B), but was not observed in the controls (Fig. 6, C and D). The generation of antigen-specific CD8+ T cell responses after the anti-HBV vaccination boost plus the chloroquine treatment was corroborated by an efficient CD8+ response to the immunodominant HLA-A2+-related HBenvAg213–221 epitope in the HLA-A2+ individuals (Fig. 6, A and B). These data suggest that chloroquine can enhance the antigen-specific CD8+ T cell response to a soluble antigen in vivo. In addition, serum anti-HBenvAg antibody levels were not affected by chloroquine treatment (Fig. 6), suggesting that although chloroquine is not detrimental to the generation of strong antibody responses, it nonetheless exerts a specific effect on cross-presentation rather than a general adjuvant effect.

**DISCUSSION**

The most important finding of this paper is that we demonstrate for the first time that human CD8+ T cell responses can be efficiently enhanced in vivo with a short course of treatment with chloroquine followed by a booster dose of a soluble antigen immunization. Furthermore, we provide evidence that lysosomotropic agents (i.e., chloroquine or NH4Cl) increase the cross-presentation efficiency in our model in vitro. The most probable explanation of this finding is that, in the presence of the lysosomotropic agents, internalized antigens are less efficiently degraded, accumulate to a higher level in the endosomes, and are ultimately more efficiently exported into cytosol, as indicated by CLSM and WB analyses. The finding that cross-presentation was not enhanced by bafilomycin A1 or various protease inhibitors supports the hypothesis that the exclusive capacity of the lysosomotropic agents to induce membrane permeabilization (43), in concert with the capacity to inhibit the endosomal acidification and, thus, antigen degradation, allows an increased and rapid export of nondegraded antigens from the endosomes into cytosol. Recent evidences demonstrated that cross-presentation of soluble antigens that are captured by DCs via macrophagocytosis requires direct delivery into the perinuclear ER, where they can access the ER-dependent class I processing machinery, precluding their destruction by endo/lysosomal proteolysis (41). Whether the improved cross-presentation by chloroquine is determined by increased delivery into perinuclear ER (41) remains an interesting and relevant issue that requires further study. Nonetheless, our data highlight that the efficiency of cross-presentation seems directly related to the level of antigen escape from endocytic processing (60–62). Recently, it has been suggested that DCs accumulate and process antigens for presentation to T cells more efficiently than macrophages because DCs contain considerably lower levels of lysosomal proteases, which rapidly destroy internalized antigens (63).

However, even if limited, the lysosomal degradation capacity of DCs may be sufficient to restrain cross-presentation of soluble antigens. This hypothesis is supported by our finding that chloroquine improves cross-presentation of soluble antigens by DCs and by the well-known evidence that internalization of soluble antigens only results in cross-presentation at very high concentrations of antigen (11, 12, 14, 15, 28, 38). In contrast, the efficient cross-presentation of particulate antigens (11, 12, 14, 15, 28, 37) may be explained by the phagocytosis uptake of particulate antigens being more efficient than fluid-phase uptake of soluble antigens (12, 38, 64).

Alternatively, the evidence that phagosomes export proteins into the cytosol more efficiently than endosomes may explain the efficient cross-presentation of particulate antigens (33–36, 65, 66), which possibly require minimal degradation (by the partial protease repertoire of DCs [63]) to be cross-presented (49). This may account for previous observations reporting that chloroquine did not affect or even inhibit cross-presentation of particulate antigens (49, 67). The contradictory results between our study demonstrating that chloroquine improves CD8+ T cell responses against soluble antigens both in vitro and in vivo in humans and findings obtained in various mouse models (66, 68) may be partially explained by differences between human and mouse models (69) and/or by the different DC populations used. It is difficult to establish whether chloroquine enhanced antigen-specific CD8+ T cell responses in HBV-vaccinated individuals in vivo via its capacity to improve cross-presentation, as our in vitro studies indicated. However, putting together the latter with the indication that chloroquine reduces protein degradation in human beings in vivo (70), we are tempted to hypothesize that the mechanism of chloroquine in our vaccination trials might be that of improving cross-presentation via the inhibition of antigen degradation.

On the basis of data obtained with three different soluble proteins (NS3Ag, Nef, and HBenvAg), we can, on the other hand, deduce that the endosomal processing machinery plays a critical role in limiting cross-presentation of soluble antigens. The endosomal processing machinery may thus represent a valid checkpoint that contains excessive autoimmune CD8+ T cell responses against soluble self-antigens. In contrast, the high cross-presentation efficiency of DCs reported for particulate antigens will provide either control of infections or an efficient tolerance toward inert apoptotic cells in physiological conditions.

Finally, our observations may represent a major breakthrough in “vaccinology.” In general, conventional vaccines (constituted by soluble proteins) used in humans are unable to prime efficient CD8+ T cell responses. The evidence that...
chloroquine favors strong CD8+ T cell responses in vivo suggests that it could be exploited for the design of innovative strategies eliciting protective CD8 immunity.

MATERIALS AND METHODS

Antigens. The rNS3Ag1187–1465 expressed in Escherichia coli and affinity purified was purchased from Biodesign International. The rHBenvAg (ad subtype), containing the preS1, preS2, and the entire S sequences, was obtained from GlaxoSmithKline Biologicals. The full-length nRF56 or the protein of HIV-1 was expressed in E. coli and purified as previously described (71).

Cell preparation and surface phenotype. PBMCs were isolated, and antigen-specific T cell clones were generated as previously described (10). CD8+ cells were purified from PBMCs by positive selection with anti-CD8 mAb coupled to magnetic beads (Miltenyi Biotec). FACs analysis demonstrated >99% CD8+ cells in the positively purified population and <5% in the CD8-depleted population. iDCs were derived from peripheral monocytes, which had been purified by positive selection with anti-CD14 mAb coupled to magnetic beads. CD14+ cells were then cultured for 5 or 10–11 d in RPMI 1640 with 5% FCS medium containing 2 mM glutamine, 1% nonessential amino acids, 1% sodium pyruvate, 50 μg/ml kanamycin (GIBCO BRL), 50 ng/ml GM-CFS (Novartis Pharma), and 1,000 U/ml rIL-4 (provided by A. Lanzavecchia, Institute for Research in Biomedicine, Bellinzona, Switzerland). Mature DCs were obtained by a 40-h stimulation of iDCs with CD40L-transfected J558L cells (DC/J558L ratio = 1:1) provided by P. Lane (University of Birmingham Medical School, Birmingham, UK), as previously described (13, 46). Both iDCs and mDCs were stained with anti-CD14, anti-CD86 (Caltag Laboratories), anti-CD32, and anti-CD83 (Becton Dickinson), or anti–MHC class I molecule (Serotec, Ltd.) mAbs, followed by staining with the appropriate secondary labeled antibodies (BD Biosciences), and were analyzed by a flow cytometer (FACSCalibur; Becton Dickinson) using CellQuest software (Becton Dickinson).

DC phagocytosis. The phagocytic capacity of DCs was evaluated according to methods described previously (72). In brief, activated T cells (derived from a CD8 clone) were dyed red with PKH26 (Sigma-Aldrich), induced to undergo Fas-mediated apoptosis as previously described (13), and co-cultured with iDCs or mDCs, which were dyed green with PKH27 (Sigma-Aldrich) at a 1:1 ratio. After 12 h at 37°C, phagocytosis was detected as double-positive cells by FC.

Cross-presentation and antigen stimulation assays. DCs or EBV–B cells, as APCs, were pulsed with increasing concentrations of soluble anti–MHC class I molecule (Serotec, Ltd.) mAbs, and tested in an ELISPOT assay, as previously described (52), for the IFN-γ spot formation. They were then ho-}

In vivo experiments. Of the 17 high HBV vaccine responders selected for the in vivo experiments, 9 (7 HLA-A2+) assumed 500 mg per os of Chloroquine Bayer (Bayer AG), corresponding to a 300-mg base chloroquine, followed by a booster dose of anti-HBV vaccine (Engerix-B; GlaxoSmithKline) on day 2. As a control, the remaining eight high responders (six HLA-A2+) only underwent the booster dose of their regular procedure of anti-HBV vaccination. The study was performed according to the ethical guidelines of the 1975 Declaration of Helsinki and a priori approval by our Institutional Review Board. PBMCs were collected in both groups before and 10 d after the vaccination booster and tested for the HLA-A2 expression by FC analysis. CD8+ T cells were positively selected from PBMCs and tested in an ELISPOT assay, as previously described (52), for the IFN-γ spot formation in response to a 6-h stimulation with irradiated autologous CD8-depleted PBMCs as APCs, previously pulsed or not with rHBenvAg or peptide, in the presence of chloroquine, blocking anti–HLA–Ab, IgC mAb (W6/32, IgG2a; Serotec, Ltd.), or the corresponding isotype. Spots were quantified using an ELISPOT reader (cod. 99022004; AID GmbH).

Confocal microscopy. APCs were pulsed and chased with 50 μg/ml rNS3Ag alone or together with 50 μg/ml tetrarhodamine isothiocyanate–labeled transferrin (TRITC–Tf; Molecular Probes) in the presence or absence of 10 μg/ml chloroquine for 15 min, washed, and chased for 40 or 120 min at 37°C. They were then fixed with 4% paraformaldehyde, permeabilized with 0.1% Triton X-100 in PBS, and stained with different combinations of the following primary antibodies: human anti–HCV–NS3161–1614 mAb (1:100 in PBS; CM3.B6, IgG1) (73) and rabbit anti–cathepsin D polyclonal antibodies recognizing the active form (46 kD) of human cathepsin D (1:50 in PBS; UBI). The primary antibodies were visualized using a FITC–conjugated goat anti–human IgG (1:800 in PBS; Sigma-Aldrich); (b) Texas red–conjugated goat anti–rabbit IgG (1:50 in PBS; Jackson Immunoresearch Laboratories); and (c) Texas red–conjugated rabbit anti–goat IgG (1:20 in PBS; Sigma-Aldrich). Nonspecific fluorescence was assessed in control samples by omitting the secondary antibodies from the staining procedure. In some experiments, DCs were incubated with 1 mg/ml 40- or 500-kD FITC–dextran (Sigma-Aldrich) in the presence or absence of chloroquine at 37°C and fixed. Fluorescence signals were analyzed by recording staining images using a cooled CCD color digital camera (SPOT-2; Diagnostic Instruments Inc.) and IAS 2000/H1 software (Delta Sistemi). Colorization of fluorescence signals was evaluated using a CLSM (LSM 5 PASCAL; Carl Zeiss MicroImaging, Inc.). The multitrack function was used to prevent cross talk between the two signals. Quantitative analysis of the fluorescence intensity was performed by evaluating three different cytoplasmic areas (1 mm2 each) per cell in 200 cells for each condition and randomly taken from three different experiments. The results represent the mean values ± SD. The fluorescence intensity of the control samples was subtracted from that of the positive-stained samples for each time point.

Purification and FC of phagosomes. DCs were previously pulsed/chased with a combination of 0.8 μm LbS (Sigma-Aldrich) and 50 μg/ml rNS3Ag in the presence or absence of chloroquine. They were then homogenized, and phagosomes were purified as described previously (28, 34, 50). LB-containing phagosomes were isolated at the 25–10% interface of a discontinuous sucrose gradient and analyzed by FC as previously described (51). In brief, LB+ phagosomes were fixed and permeabilized using Cytofix/Cytoperm solution (BD Biosciences) at 4°C for 20 min and rewashed with Perm Wash Buffer (BD Biosciences). They were then stained with human anti–NS3 mAb (73), followed by secondary PE–labeled anti–human IgG (BD Biosciences) and goat anti–TAP-2 polyclonal antibody (Santa Cruz Biotechnology, Inc.), followed by PE–labeled anti–goat IgG antibod-
ies (Caltag) or mouse FITC-labeled anti–LAMP-2 mAb (Santa Cruz Biotechnology, Inc.), and analyzed by FC.

**Analyses of cytosolic- and endocytic-enriched fractions.** To detect NS3Ag in both cytosolic and endocytic enriched fractions, 10–15 × 10^6 DCs were pulsed with different concentrations of rNS3Ag in the presence or absence of 10 μg/ml chloroquine for 20 min, washed, and chased for 90 min at 37°C. In some experiments, they were pulsed with 1 mg/ml of 40- or 500-kD FITC-dextran for 1 h at 37°C. DCs were then homogenized (49, 50), and the cytosolic and vesicular fractions were isolated as described previously (49, 50) and analyzed by WB or fluorometer as described below. The β-hexosaminidase activity (specific to endo/lysosomes), as detected with the fluorochrome substrate 4-methylumbelliferyl-N-acetyl-D-glucosamine and lactate dehydrogenase by measuring the decrease in the absorbance of nicotinamide adenine dinucleotide (49, 50, 74, 75), was 10% below that of the whole cell lysate in the cytosolic fraction (unpublished data). The cytosolic- and endocytic-enriched fractions, obtained as described above, were separated by SDS-PAGE and immunoblotted for NS3Ag with the relevant human mAb and the secondary peroxidase-conjugated goat anti-human IgG antibody (Nordic Immunology). Optical density was calculated by the Imman mAb and the secondary peroxidase-conjugated goat anti–human IgG

Cytosol- and endocytic fractions were analyzed using a fluorometer (Wallac 1420 Victor; PerkinElmer Life and Analytical Sciences, Inc.), and values were computed using the software provided (Victor Manager; PerkinElmer Life and Analytical Sciences, Inc.). The contents of FITC-dextran were determined from a standard curve of the values of different FITC-dextran concentrations. All values were converted into microgram per milliliter (μg/ml).

**Statistical analysis.** Differences in the cross-presentation assays in the presence or absence of chloroquine or other drugs (both in vitro and in vivo) were analyzed by the Mann-Whitney U test.

**Online supplemental material.** Fig. S1 shows that chloroquine enhances cross-presentation of NS3Ag by DCs in a dose-dependent fashion. Fig. S2 shows the inability of bafilomycin A1 to improve cross-presentation. Fig. S3 shows the improvement of soluble HBeAg cross-presentation by chloroquine. Fig. S4 shows that rNS3Ag does not affect the surface phenotype of iDCs. Fig. S5 shows the HLA restriction of NS3Ag cross-presentation. Fig. S6 shows the inability of EBV–B cells to export soluble NS3Ag from endosomes into the cytosol, as detected by CLSM. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20051106/DC1.

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