Lipid raft-dependent endocytosis: a new route for hepcidin-mediated regulation of ferroportin in macrophages

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Online Supplementary Figure S1. Confocal analysis of ferroportin and caveolin 1 staining in iron treated BMDM. After overnight incubation with Fe-NTA, BMDM were fixed in methanol, processed for Fpn and Caveolin 1 immunofluorescence staining and analyzed by confocal microscopy. Single confocal images of isolated BMDM cells (A). In merged images and insets, arrows indicate partial co-localization of Fpn with caveolin 1. White bar in upper left coin of each panel represents 5 μ m. (B) Partial colocalization of Fpn with caveolin 1 in some vesicular compartments was controlled by calculations of the red and green pixel areas in a single section as described previously.¹ Single image overlays were opened in the software Image J. Pixel areas on yellow/orange dots (white arrow) which were then measured using the plot profile function and exported to Excel (Microsoft). In this example, the partial colocalization of the two proteins was observed on 4.5 pixel = 270 nm (1 pixel = 60nm), a distance longer than the microscope resolution (150 nm).

Online Supplementary Figure S2. Sequential separation of detergent resistant membranes containing Fpn in J774 treated with iron. After a first iodixanol gradient (A) the lightest fraction 1 &2 containing Fpn were processed on a second density gradient (B). The density fractions obtained were analyzed by Western blot for the presence of Fpn and flotillin 1. In such an experiment, the raft markers flotilin was still enriched in the lightest density fractions (N. 1) whereas Fpn was distributed in other more dense fractions (until N. 6), suggesting some heterogeneity of the detergent resistant membranes containing Fpn.







Online Supplementary Figure S5. Filipin affects both hepcidin-mediated endocytosis and degradation of ferroportin. Fe-NTA treated J774a1 were incubated or not with filipin prior treatment with Hepc (300 nM; 1 h). After biotinylation labeling, cell surface (biotinylated proteins) and intracellular (flow-through) extracts were then analyzed by Western blotting using anti-Fpn or anti-TfR1 (control) antibodies. The position and size in kilodaltons (kDa) of molecular mass markers are indicated on the left. Protein species were revealed either using ECL (A) or using specific fluorescent secondary antibodies and the Odyssey infrared imaging system (LI-COR Biosciences; B) . For both detection, quantification of specific signals in each sample was represented in A' (densitometry analysis of the autoradiogramms) and B' (fluorescence quantification), respectively. In B', the values obtained after Hepc treatment are expressed as a percentage of the basal Fpn expression (untreated with Hepc). After 1 h of hepc treatment, up to four times more Fpn were present at the plasma membrane in cells pretreated with filipin when compared to untreated cells.



Online Supplementary Figure S4. In-cell-Western detection and quantification of Fpn expression after Hepc treatment on cells pre-treated with increasing concentration of filipin. (***P<0.001, Student's t-test).



Online Supplementary Figure S6. Immunofluorescence staining of Fpn in iron treated BMDM incubated with or without M β CD prior Hepc treatment. Arrows and arrowheads indicate cell surface staining and intracellular detection of the iron transporter, respectively. As observed with filipin, pre-treatment of the cells with M β CD prevent degradation of Fpn by Hepc.



Online Supplementary Figure S7. Schematic representation of Fpn in cell membrane with positions of putative CRAC domains along the backbone of the iron transporter. CRAC is a common cholesterol recognition and interaction amino acid consensus pattern. It is defined as a sequence pattern -L/V-(X) (1-5)-Y-(X) (1-5)-R/K- where (X) (1-5)- is a sequence of one to five random amino acids. In the sequence of Fpn, there are four putative CRAC motifs (red boxes). According to the recent topology model of Fpn proposed by Rice A. et al.,² two are present in two predictive transmembrane domains (I and XII; aas 17-25 and 535-539) and two (aas 218-225; 223-229) are near the membrane interface of transmembrane domain VI of the transporter. These CRAC motifs could play a role in sequestering Fpn into a cholesterol-rich membrane domain.

References

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