

**IL-1 receptor antagonist ameliorates inflammasome-dependent alcoholic steatohepatitis
in mice**

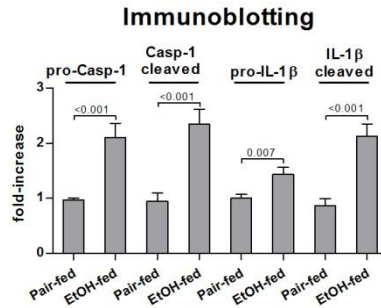
Jan Petrasek, Shashi Bala, Timea Csak, Dora Lippai, Karen Kodys, Victoria Menashy, Matthew
Barrieau, So-Yun Min, Evelyn A. Kurt-Jones, Gyongyi Szabo

Department of Medicine, University of Massachusetts Medical School, Worcester, MA, USA

Supplementary material

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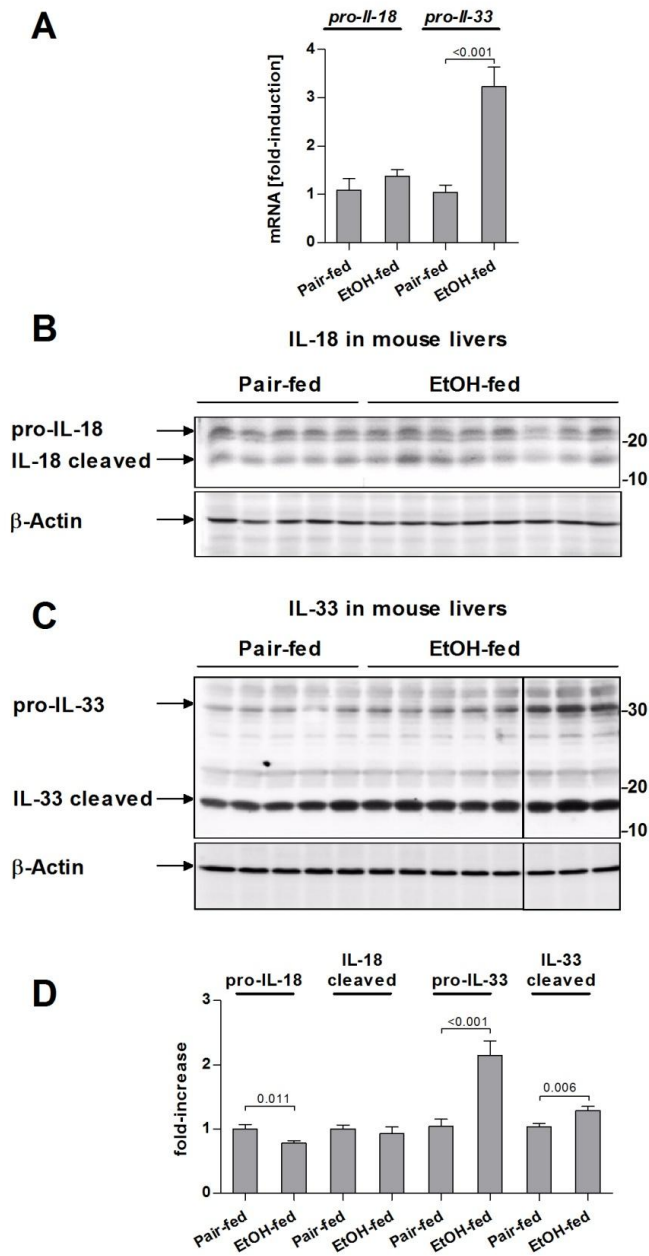
A. Supplementary figures



Supplementary Fig. 1 - *Activation of the inflammasome and IL-1 β in alcohol-induced liver injury*

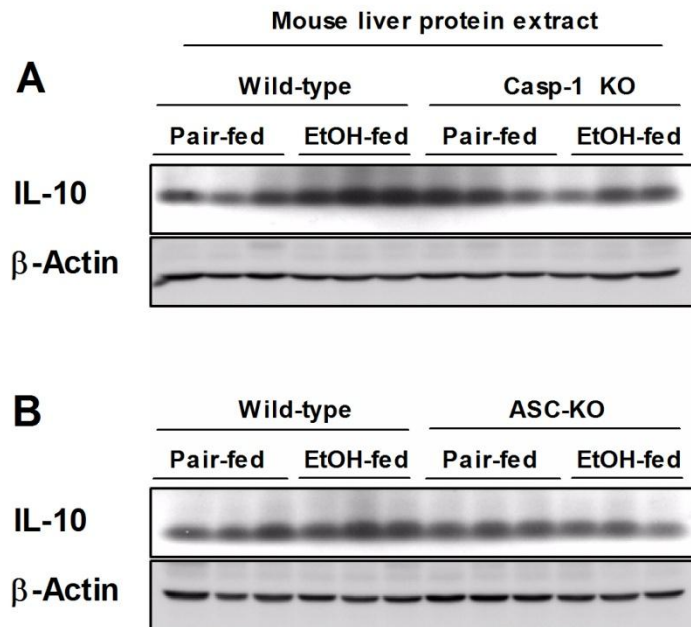
Wild-type mice were fed with control (pair-fed) or alcohol (EtOH-fed) diet and sacrificed 4 weeks later. Cleaved forms of caspase-1 and IL-1 β in the livers were analyzed using antibodies that identify both full-length pro-form and cleaved forms, normalized to beta-actin and subjected to densitometry. Total number of mice used for statistical analysis were n=14 (pair-fed); n=19 (EtOH-fed). Means and SEM values are shown. Numbers in the graph denote *P* values.

Representative Western blots are shown in Fig. 1 G, H.



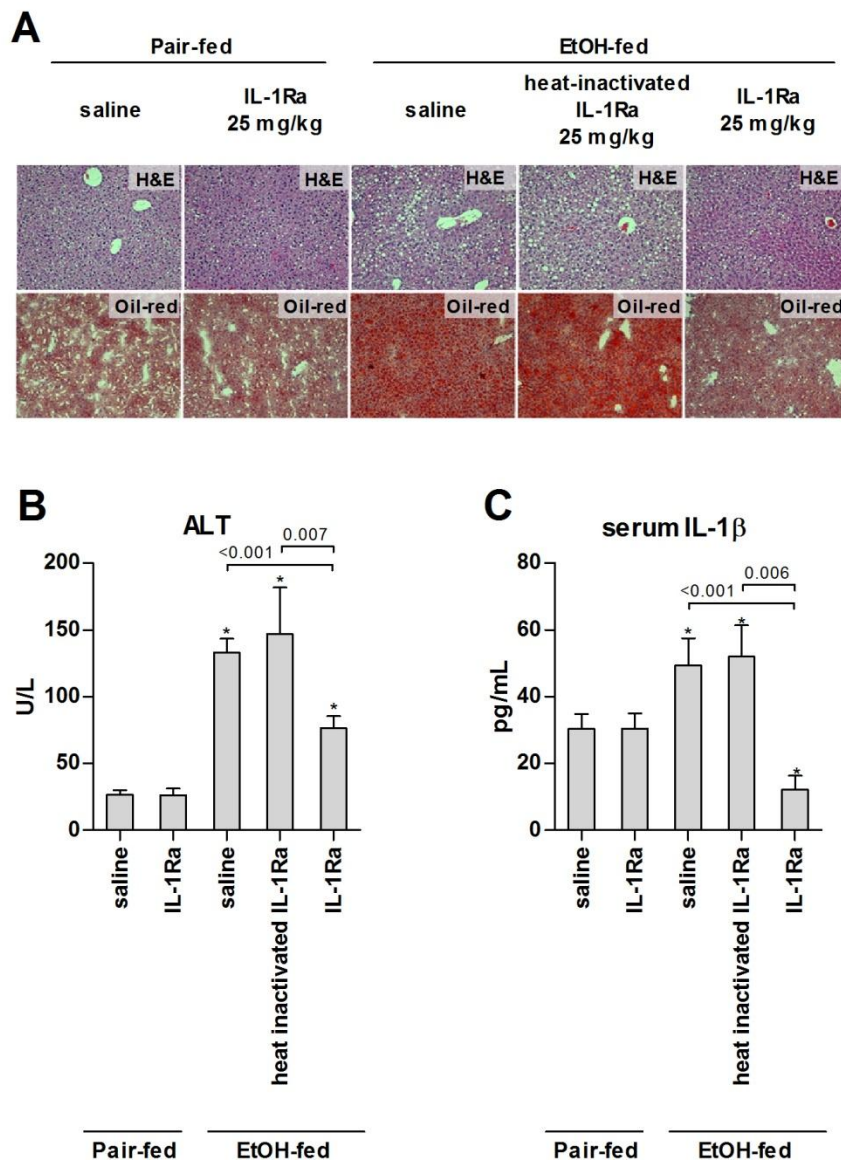
Supplementary Fig. 2- Alcoholic liver disease is associated with increased IL-33, but not IL-18, in the liver

Wild-type mice were fed with control (pair-fed) or alcohol (EtOH-fed) diet and sacrificed 4 weeks later. IL-18 and IL-33 (encoded by *pro-Il-18* and *pro-Il-33*, respectively) in the livers were analyzed by qPCR (A). IL-18 and IL-33 proteins in the liver were analysed in the livers using antibodies that identify both full-length and cleaved forms (B,C), normalized to beta-actin, and measured using densitometric analysis (D). Total number of mice used were n=5 (pair-fed); n=8 (EtOH-fed). Vertical line in (C) is used to divide two non-contiguous parts of the same blot. Numbers in graphs denote *P* values.



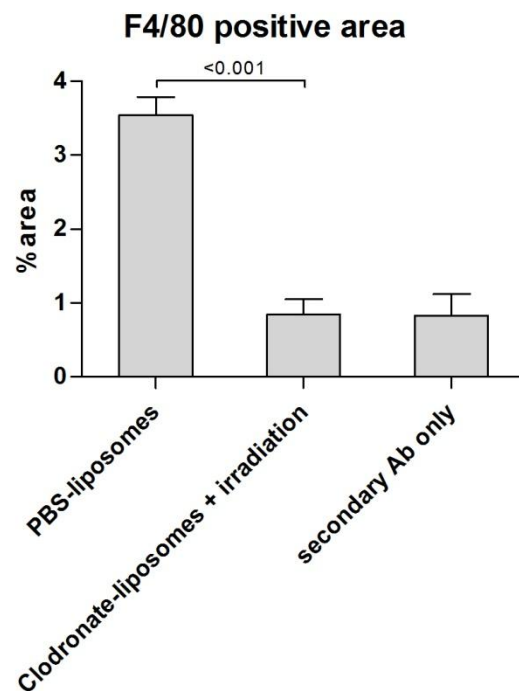
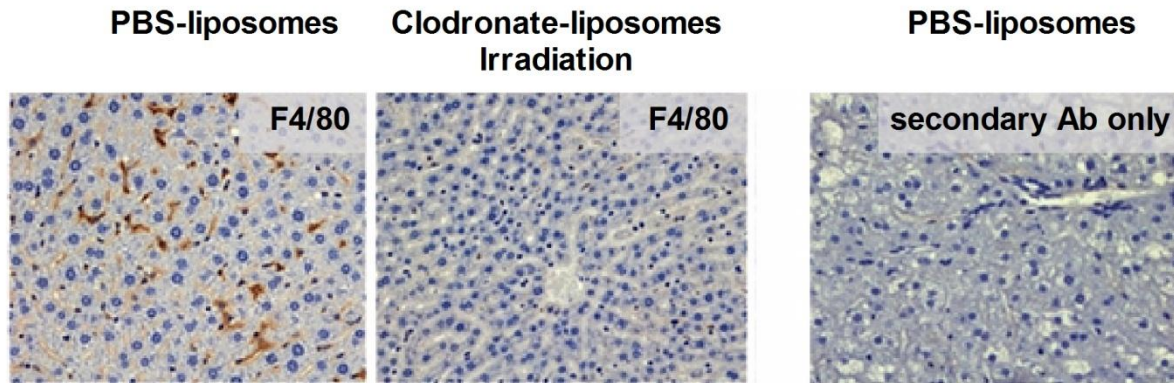
Supplementary Fig. 3 - *Deficiency of caspase-1 or ASC prevents upregulation of IL-10 in the livers of alcohol-fed mice*

Wild-type, caspase-1- or ASC-deficient mice were fed with control (pair-fed) or alcohol (EtOH-fed) diet and sacrificed 4 weeks later. IL-10 in the livers was analyzed using immunoblotting, and normalized to beta-actin. Densitometric analysis of these blots is presented in Fig. 2 I (for A) or Fig. 4 G (for B).



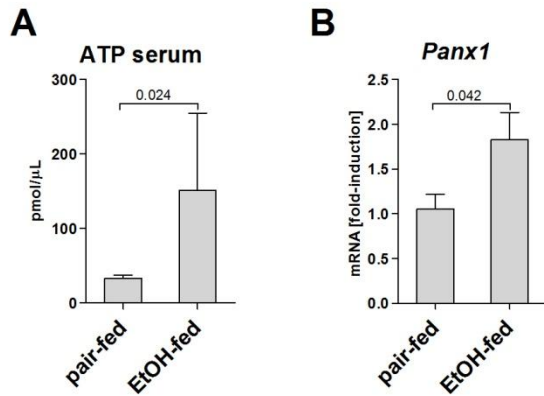
Supplementary Fig. 4- Active form of human recombinant IL-1Ra is required for protection from alcoholic liver disease

Wild-type mice were fed with control (pair-fed, n=5) or alcohol diet (EtOH-fed, n=10 per treatment group), treated daily with saline, recombinant human IL-1Ra (Anakinra) or heat-inactivated IL-1Ra i.p., as described in Methods. Mice were sacrificed 4 weeks later. Liver injury and steatosis was quantified by H&E and Oil-red-O staining (A) and by serum ALT (B). Serum levels of the inflammatory cytokine IL-1 β (C) were measured using specific ELISA. Total number of mice used was n=5 (pair-fed), n=10 (EtOH-fed, per treatment). Means and SEM values are shown. Numbers in graphs denote *P* values. Original magnification 200x. **P* < 0.05 vs. pair-fed, saline-treated mice.



Supplementary Fig. 5 - *Depletion of Kupffer cells in the liver following treatment with clodronate and whole-body irradiation*

Wild-type mice were injected with clodronate-liposomes or control PBS-liposomes i.v. (n=3 per group) and subjected to whole body irradiation, as described in Methods. Depletion of Kupffer cells was assessed 48 hours after clodronate or PBS-liposome injection using the F4/80 staining. Means and SEM values are shown. Number in the graph denotes *P* value. Original magnification 200x.



Supplementary Fig. 6 - Alcoholic liver disease is associated with increased levels of ATP in the serum and upregulation of pannexin-1 in the liver

Wild-type mice were fed with control (pair-fed, n=5) or alcohol (EtOH-fed, n=10) diet and sacrificed 4 weeks later. Levels of ATP were measured in the serum (A) and expression of pannexin-1, encoded by *Panx1* (B) was measured in the liver by qPCR, as described in Methods. Means and SEM values are shown. Numbers in graphs denote *P* values.

B. Supplementary table

qPCR primers

Target gene	Forward primer (5'→ 3')	Reverse primer (5'→ 3')
<i>18S</i>	gta acc cgt tga acc cca tt	cca tcc aat cgg tag tag cg
<i>Asc</i>	gaa gct gct gac agt gca ac	gcc aca gct cca gac tct tc
<i>Nlrp3</i>	agc ctt cca gga tcc tct tc	ctt ggg cag cag ttt ctt tc
<i>Panx1</i>	tgt ggc tgc aca agt tct tc	aca gac tct gcc cca cat tc
<i>pro-Casp-1</i>	aga tgg cac att tcc agg ac	gat cct cca gca gca act tc
<i>pro-Coll1a1</i>	gct cct ctt agg ggc cac t	cca cgt ctc acc att ggg g
<i>pro-Il-1a</i>	ggc acg ggg act gcc ctc tat	tgt cgg ggt ggc tcc act
<i>pro-Il-1b</i>	tct ttg aag ttg acg gac cc	tga gtg ata ctg cct gcc tg
<i>pro-Il-18</i>	cag gcc tga cat ctt ctg caa	tct gac atg gca gcc att gt
<i>pro-Il-33</i>	agc tct cca ccg ggg ctc ac	gcc tgc ggt gct gct gaa ct
<i>Tgfb1</i>	att cct ggc gtt acc ttg	ctg tat tcc gtc tcc ttg gtt

Quantitative polymerase chain reaction (qPCR) was performed using the iCycler (Bio-Rad Laboratories, Hercules, CA). The PCR conditions were: 95°C for 15 minutes followed by 40 cycles at 95°C for 15 seconds, 60°C for 10 seconds, and 72°C for 30 seconds. The reaction mixture for the SYBR Green assay contained 12.5 µL SYBR Green PCR Master Mix (Bio-Rad laboratories, Hercules, CA, USA), 0.5 µM of forward and reverse primer and 1 µL of complementary DNA (corresponding to 100 ng RNA) for a total volume of 25 µL. All amplifications and detections were carried out in a MicroAmp optical 96-well reaction plate with optical tape. At each cycle, accumulation of PCR products was detected by monitoring the increase in fluorescence by double-stranded DNA-binding SYBR Green. After PCR, a dissociation melting curve was constructed in the range of 55°C to 95°C. All data were analyzed using Bio-Rad iCycler software. The 18S was used for normalization of all experiments. Data was analyzed using the comparative Ct method ($\Delta\Delta Ct$ method) using the following formula: $\Delta Ct = Ct(\text{target}) - Ct(\text{normalizer})$. The comparative $\Delta\Delta Ct$ calculation involved finding the difference between the sample ΔCt and the baseline ΔCt . Fold increase in the expression of specific mRNA compared with 18S was calculated as $2^{-(\Delta\Delta Ct)}$.

C. Supplementary references

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