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Prolactin prevents hepatocellular carcinoma by restricting innate immune activation of c-Myc in mice

Hadley J. Hartwellb, Keiko Y. Petroskyc, James G. Foxd, Nelson D. Horseman, and Arlin B. Rogers*1

*Department of Biomedical Sciences, Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA 01536; Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599; †Division of Comparative Pathology, New England Primate Research Center, Harvard Medical School, Southborough, MA 01772; ‡Division of Comparative Medicine, Massachusetts Institute of Technology, Cambridge, MA 02139; and §Department of Molecular and Cellular Physiology, University of Cincinnati, Cincinnati, OH 45267

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Results

Short-Form Prolactin Receptor Mediates Liver Signaling. The prolactin receptor (PRLR) has multiple splice variants with tissue-specific expression (8). Long-form PRLR (PRLR-L) is the primary receptor in breast and most other tissues, where it functions in part through STAT5 (9). In contrast, short-form PRLR (PRLR-S) does not meaningfully activate STAT5 or other PRLR-L pathways (10). In female reproductive tissues, the proportion of long-short-form receptor varies depending on hormonal fluctuations, whereas the liver maintains a constant preference for PRLR-S (11–13). In agreement with reports elsewhere (8), we found in mammary tissue and cells that 85–90% of total PRLR mRNA was PRLR-L, whereas in mouse and human liver tissue the vast majority was PRLR-S (Fig. S1A). Murine Hepa 1–6 and AML12 liver cells retained in vivo liver preference for PRLR-S over PRLR-L. In contrast, human liver cell lines, including HCC-derived Hep3B and HuH7, immortalized hepatocyte subclone PH5CH8, and hepatoblastoma-origin HepG2 and HuH6 exhibited variable total PRLR but a universal preference for PRLR-L over PRLR-S (Fig. S1B; all liver cell line origins are depicted in Table S1). Our findings correlated well with a published microarray comparison of PRLR expression in human liver cell lines (14). Based on the above observations, we chose the murine liver cell lines Hepa 1–6 and AML12, except where noted for the functional PRL studies below. There are at least three known splice variants of PRLR-S in mice and two in humans (15, 16). In mice, we found that variant S3 comprised

Significance

Hormonally active women are better protected from the primary liver cancer hepatocellular carcinoma (HCC) than men. In rodent models, the pituitary gland governs sexually dimorphic HCC risk. We found that the estrogen-responsive pituitary hormone prolactin (PRL) inhibits HCC by binding liver short-form prolactin receptors, resulting in accelerated degradation of a multimolecular “trafosome” involved in tumor-promoting innate immune signaling and preventing activation of the HCC-associated gene c-Myc. Mouse models confirmed sex-dependent HCC regulation upstream of c-Myc and a requirement for PRL but not estrogen in female tumor resistance. Importantly, a preclinical trial in mice showed that pharmacologic PRL mobilization using the human drug domperidone protected males from HCC. PRL-targeted therapy may help prevent liver cancer in high-risk men and women.

Author contributions: A.B.R. designed research; H.J.H. performed research; N.D.H. contributed new reagents/analytic tools; K.Y.P., J.G.F., and A.B.R. analyzed data; and K.Y.P. and A.B.R. wrote the paper.

The authors declare no conflict of interest.

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Data deposition: The data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) database, www.ncbi.nlm.nih.gov/geo (accession no. GSE55669).

1To whom correspondence should be addressed. Email: Arlin.Rogers@tufts.edu.

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>90% of all PRLR-S (Fig. S1C). In human liver, PRLR-S1α was significantly more abundant than isoform S1b. We confirmed site-specific PRLR isoform expression at the protein level by Western blot (Fig. S1D). To determine the impact of pituitary hormones on STAT5 and MAPK signaling, we withdrew serum from Hepa 1–6 cells and subsequently reintroduced PRL or growth hormone. Phosphorylation of STAT3 and ERK1/2 was not affected by any treatment in these cells (Fig. S1E), whereas serum starvation activated the stress-associated protein kinase p38 MAPK. Intriguingly, PRL but not growth hormone decreased p38 MAPK phosphorylation to levels found in unstressed cells grown with serum. Inhibition of MAP kinases including p38 MAPK was shown elsewhere to be a feature of PRLR-S but not PRLR-L signaling (17). These data highlight PRLR-S as the primary prolactin receptor in differentiated hepatocytes, and show that PRL exposure constrains at least one cell stress-associated pathway.

PRL Inhibits IL-1β Induction of p38 MAPK, NF-κB, and AKT. IL-1β is an injury-associated innate immune cytokine implicated in tumor-promoting liver inflammation (18). To begin our search for PRL-sensitive innate immune pathways in hepatocytes, we exposed Hepa 1–6 and AML12 cells with or without PRL preconditioning to recombinant murine IL-1β. In addition to p38 MAPK, we found that PRL exposure decreased IL-1β–induced phosphorylation of AKT and NF-κB p65/RelA, but not ERK1/2 or JNK (Fig. L4). At the message level, PRL inhibited transcription of important murine acute-phase response (APR) genes in IL-1β–challenged hepatocytes, including serum amyloid A1 and A3, lipocalin-2, and orosomucoid (α-1-glycoprotein) (Fig. 1B). The Toll-like receptor (TLR)4 ligand LPS also invoked immune responses in these cells (Fig. S2A). In a time-course study, hepatocyte preconditioning with PRL for 1 h significantly reduced IL-1β– and LPS-induced target phosphorylation, although 2 h was required for maximal inhibition; this effect was durable up to 8 h (Fig. S2B). Because 1–2 h of PRL incubation was required to achieve maximal inhibition, we tested whether PRL interruption of IL-1β responses required de novo transcription. However, by microarray we identified few PRL-inducible genes and no common gene sets shared between Hepa 1–6 and AML12 cells; moreover, we observed no effect by the transcription inhibitor actinomycin D on PRL-sensitive gene expression in either cell line [National Center for Biotechnology Information Gene Expression Omnibus (GEO) SuperSeries accession no. GSE55669]. Viewed together, these data suggest that PRL inhibits IL-1β phosphorylation of p38 MAPK, NF-κB, and AKT in hepatocytes in a transcription-independent manner.

PRL Restricts TLR4 and TNF-α but Not TLR3 Signaling. To extend our investigation of innate immune pathways susceptible to PRL interruption, we challenged hepatocytes with the TLR3 ligand and dsRNA mimic poly(I:C), NFκB reporter-1 (TNFR1) ligand TNF-α, and LPS using NF-κB p65/RelA phosphorylation as a readout. PRL preconditioning reduced NF-κB activation by LPS and TNF-α but not poly(I:C) (Fig. S2C). In agreement with this, PRL-preconditioned hepatocytes showed muted APR gene expression in the face of LPS challenge, whereas there was no impact by PRL on poly(I:C)-induced APR or TLR3-specific IFN pathway–associated gene transcription (Fig. S2D). Our aggregate findings indicate that PRL dampens hepatocellular immune responses that signal through IL-1R, TLR4, and TNFR1, but not TLR3.

Female Mouse Liver Constrains IL-1β Responses. In humans and in rodent models, females are more resistant to chronic progressive hepatitis and HCC than males (1, 3, 19, 20). To determine whether PRL-sensitive innate immune pathways contribute to this sex dimorphism, we challenged male and female C3H/HeN mice with IL-1β or poly(I:C). Mirroring results from PRL-preconditioned hepatocytes, females challenged with IL-1β showed reduced phosphorylation of p38 MAPK, NF-κB p65/RelA, and AKT, but not ERK1/2, JNK, or STAT3 compared with males (Fig. 1C). Also reflecting in vitro results, there were no consistent sex-dependent differences in liver gene induction in mice challenged with poly(I:C) (Fig. S2E). We found by microarray that message levels of IL-1β–inducible APR genes in vivo did not exhibit as clear a sex difference as PRL-preconditioned hepatocyte cultures (GEO accession no. GSE55669). This result was likely in part because of sex-independent IL-1β induction of IL-6 (increased >100-fold both sexes) from Kupffer cell macrophages in intact liver; significant redundancy is known to exist between IL-1β– and IL-6–inducible APR pathways (21). APR genes notwithstanding, the impact of IL-1β on transcription of many important inflammatory, cell stress, and growth-associated gene products was muted in female mouse liver, including heme oxygenase-1, early growth response-1, IL-17 receptor-α, inducible nitric oxide synthase (iNOS), TGF-α, VEGF-α, and c-Myc (Fig. 1D). In agreement with a prior study from our group (19), we also observed overrepresentation of sexually dimorphic liver genes among those altered by IL-1β, including feminine genes Cyp2b9, Cyp2b13, Cyp4a10, Cyp4a14, and Sult2a3, as well as masculine genes C6, Cyp4a12, Élovl3, Lcn13, and SpinK6 (GEO accession no. GSE55669). Thus, loss of transcriptional regulation of many sex-dependent genes (a process we previously termed “liver-gender disruption”), is an early event in the dichotomous progression of chronic liver disease (19, 22). In summary, in vivo IL-1β challenge results mirrored those observed in vitro, and confirmed that immune induction of tumour-promoting metabolic, stress, and cell proliferation pathways exhibits sexual dimorphism at an early stage.

Men Have a Proinflammatory Hepatic Microenvironment. To determine whether sex-dependent proinflammatory liver phenotypes extend to humans, we acquired tissue specimens from seven adult women and men without evidence of primary liver disease (Table S2; donor inclusion criteria in SI Materials and Methods) and performed genome-wide expression analysis (GEO accession no. GSE55669). Heat maps (Fig. 2A) and hierarchical clustering readily differentiated male from female liver. Using additional conservative filtering criteria (SI Materials and Methods), we identified 131 female-predominant and 445 male-predominant unique transcripts (Table S3). We confirmed sex specificity of selected masculine and feminine liver genes by quantitative RT-PCR (qRT-PCR) (Fig. 2B). Of interest, while
analyzing the masculine gene set we noted a large number of canonical APR and inflammation-associated genes as well as several proto-oncogenes, including c-Myc (Fig. 2C). Indeed, of the top six biological function categories distinguishing male from female liver, five were associated with cancer or inflammatory disease; the other was reproduction (Fig. 2D). Whereas our study could not control for lifestyle factors or correlate serum hormone levels, gene expression results suggest that men—even those without clinically evident liver disease—maintain more of a proinflammatory hepatic microenvironment than women. If our animal model data are indicative, then a relative inability of the human male liver to constrain minor immune stimuli may serve as a bellwether of increased sensitivity to tumor-promoting inflammation. This finding agrees with the known higher risk of men with chronic viral hepatitis to progress to cirrhosis or HCC (1, 3).

PRL Interrupts IL-1β Upstream of p38 MAPK and AKT. p38 MAPK, NF-κB, and AKT have both overlapping and distinct immune signaling functions. To begin to understand how these pathways cross-talk and how PRL might impact them in the liver, we applied a variety of kinase and phosphatase inhibitors to cultured hepatocytes. However, in our hands the impact of most inhibitors on IL-1β + PRL signaling was context- and cell line-dependent (Tables S4 and S5). Because the dual-specificity phosphatase (DUSP) DUPD1 previously was implicated in PRLR-S mediated inhibition of p38 MAPK and ERK1/2 in PRLR-L-deficient mouse reproductive tissues (17), we were particularly interested in the potential role of DUPD1 in hepatocyte PRL signaling. However, none of the kinase or phosphatase inhibitors that target p38 MAPK, including the DUSP inhibitor NSC 95397, gave consistent results between mouse and human cell lines (Table S5). Moreover, neither PRL nor NSC 95397 impacted ERK1/2 phosphorylation, suggesting that a mechanism besides or in addition to DUPD1 mediates PRLR-S activity in hepatocytes. In contrast, the PI3K inhibitors wortmannin and LY294002 consistently abolished AKT phosphorylation, indicating PI3K dependence (Fig. S3A). Using specific inhibitors, we further found that IL-1β activated PI3K/AKT and p38 MAPK pathways independent of one another (Fig. S3B), suggesting that PRL intervenes at a common upstream site. In genetically engineered mice, constitutive liver activation either of PI3K/AKT or its downstream target mTORC1 results in HCC (23). To determine whether PRL interruption of PI3K/AKT also obviates mTORC1, we evaluated IL-1β–inducible phosphorylation of mTORC1 components, including mTOR, glycogen synthase kinase 3 beta (GSK-3β), 70S6-kinase (S6K), and eukaryotic translation initiation factor 4E binding protein-1 (4E-BP1). Importantly, PRL interruption of PI3K/AKT also abrogated phosphorylation of mTOR and 4E-BP1 (Fig. 3A). We were unable to detect phospho-specific GSK-3β or S6K under any of our experimental conditions. Taken together, our results demonstrate that PRL interrupts IL-1β signaling at a node upstream of p38 MAPK and PI3K, and reveal that constraint of PI3K/AKT also alleviates downstream mTORC1.

PRL Targets Are MAP3K- but Not Ras-Dependent. Ras is a well-characterized oncogene that acts in part through PI3K/AKT, whereas MAP3K enzymes (notably TAK1) may simultaneously target NF-κB and p38 MAPK (24). To clarify the role of these pathways in our system, we used the Ras inhibitor manumycin and MAP3K inhibitor 5(Z)-7-oxozeaenol. Unexpectedly, we discovered that Ras inhibition increased phosphorylation of all IL-1β targets except NF-κB (Fig. 3B). In contrast, the MAP3K inhibitor abolished endogenous and IL-1β–inducible phosphorylation of all targets (except some residual Ras-dependent NF-κB). At nanomolar concentrations, 5(Z)-7-oxozeaenol is a TAK1-specific antagonist; however, at the 10-μM concentration we used, it inhibits other MAP3K (25). We found that decreasing the concentration of 5(Z)-7-oxozeaenol below 10 μM diminished inhibition of IL-1β target activation in a dose-dependent fashion (Fig. S3C). Therefore, one or more MAP3K besides or in addition to TAK1 must transmit PRL-sensitive IL-1β signals in hepatocytes. Further work will be required to identify which of the >20 MAP3K participate in PRL-sensitive hepatocellular signaling (26). Nevertheless, our data show that innate immune pathways interrupted by PRL are MAP3K-dependent.

PRL Primes “Trafasome” for Poststimulatory Degradation. Based on the results above, we directed our search for molecular PRL targets toward MAP3K-dependent pathways shared by IL1R, TLR4, and TNFR1, but not TLR3. Of note, all of the PRL-sensitive pathways listed above, but not PRL-insensitive TLR3, involve TRAF proteins. This finding is significant because TRAF
proteins anchor modular signaling complexes ("trafasomes") (27) that may incorporate any of several MAP3K (28, 29). Trafasomes rely heavily on context-specific ubiquitination for activation and signal termination (30). To determine the impact of PRL on trafasome kinetics, we immunoprecipitated TRAF6 from hepatocytes exposed to PRL or IL-1β. As expected, IL-1β recruited interleukin-1 receptor-associated kinase 1 (IRAK1) to the trafasome, resulting in TRAF6 ubiquitination and decreased total protein consistent with proteasomal degradation or autophagy. Unexpectedly, we found that PRL alone also recruited IRAK1 to TRAF6, invoking nondegrading ubiquitination without appreciable loss of either protein (Fig. 3C). Of greatest significance, we found in PRL-preconditioned hepatocytes that virtually no IRAK1 or TRAF6 could be detected 15 min after IL-1β stimulation, indicating enhanced ubiquitination.

Our combined results outline a model whereby PRL recruits IRAK1 to TRAF, resulting in sensitizing ubiquitination and accelerated degradation of the trafasome following immune stimulation; this in turn terminates downstream MAP3K-dependent signaling through p38 MAPK, NF-κB, and PI3K/AKT/mTORC1.

**In Vivo Sex-Dependent HCC Is Regulated Above c-Myc.** In addition to immunity, p38 MAPK, NF-κB, and PI3K/AKT/mTORC1 have known associations with cancer in part through induction of c-Myc (31). Of importance, c-Myc is up-regulated in males in a sex-dependent fashion at an early stage in rodent hepatocarcinogenesis (32). If the present hypothesis is correct and PRL impedes liver tumorigenesis at the level of the trafasome, then release of c-Myc from immunoregulatory control should abolish sex-dependent HCC phenotypes. To test this theory, we monitored spontaneous tumor development in mice with constitutive hepatic c-Myc expression under control of the sex-independent albumin promoter/enhancer (33). To obviate any potential confounding by proinflammatory gut microbes, mice were housed in a *Helicobacter*-free barrier facility (22). Under these conditions, we found no sex difference in the incidence or multiplicity of preneoplastic foci of cellular alteration (FCA) at 3 mo or frank neoplasms at 9 and 15 mo (Fig. 4A). Functional transgene expression was confirmed by immunohistochemistry in 3-mo-old male and female mice (Fig. 4B). Results of this experiment are consistent with universal liver tumor promotion through—but sex-dependent regulation above—the level of c-Myc.

**PRL Deficiency Accelerates Liver Tumorigenesis.** If PRL constrains liver tumorigenesis, then PRL deficiency should increase HCC vulnerability. To test this hypothesis, we inoculated infant C57BL/6 and strain-matched Prl−/− mice with the liver carcinogen diethylnitrosamine (DEN) or vehicle. Compared with WT controls, DEN-initiated Prl−/− females developed a significantly higher incidence and multiplicity of liver tumors (Fig. 4C). Moreover, neoplasms from Prl−/− females exhibited increased malignancy, as indicated by invasion of adjacent nonneoplastic tissue and vessels (Fig. 4D). Because factors in addition to PRL contribute to male HCC vulnerability (i.e., disturbances arising from growth hormone-mediated liver masculinization) (19), Prl−/− males still developed a greater tumor burden than females. Nevertheless, PRL deficiency also increased the multiplicity and malignancy of HCC in Prl−/− males. Importantly, it has been shown that Prl−/− female mice maintain circulating E2, albeit at lower levels than WT mice (34), indicating a requirement for PRL in hormone-based tumor inhibition. Viewed together, results from Prl−/− mice indicate that PRL deficiency accelerates hepatocarcinogenesis in both sexes, but is especially pronounced in females.

**Pharmacologic PRL Mobilization Protects Males from HCC.** Estrogen-based HRT protects postmenopausal women from liver cancer (3), likely in part through PRL induction. However, HRT is not a viable strategy for liver cancer prevention in men. To prove in principle that E2-independent PRL agonism can protect males from HCC, we initiated tumor-prone C3H/HeN mice with DEN or vehicle, and administered the PRL-mobilizing dopamine D2 receptor antagonist (α-DRD2) domperidone to a cohort of males. Domperidone was withheld until mice had developed preneoplastic FCA to recapitulate tumor risk profiles characteristic of humans with chronic progressive hepatitis or cirrhosis. As expected, domperidone increased serum PRL in males to near-female levels (Fig. 5A). All DEN-initiated untreated males developed HCC, whereas females presented with FCA and dysplastic nodules only. The multiplicity of grossly evident dysplastic nodules in domperidone-treated mice was intermediate between females and untreated males (Fig. 5B). However, with regard to HCC, DEN-initiated males that received α-DRD2 therapy showed significant protection (22% incidence vs. 100% in untreated males; *P < 0.01) (Fig. 5C). Moreover, message levels of inflammation-associated gene products, including SAA3, iNOS, and IL-23α were decreased in domperidone-treated males to feminine levels, along with tumor-associated biomarkers c-Myc, Ki-67, and pyruvate kinase M2 (Fig. 5D) (35). Lesions from domperidone-treated males also more closely resembled female preneoplastic foci with regard to morphology and oxidative stress biomarkers (e.g., 8-oxoguanine) than the frank malignancies from untreated males (Fig. 5E).

Combined with studies elsewhere involving the PRL-mobilizing agents perphenazine and cimetidine (36, 37), our results establish E2-independent PRL induction as a rational strategy to prevent HCC.
We found that no.

Discussion

Hormonally active women are better protected from HCC than men and postmenopausal women who do not take HRT (3). Our study implicates a crucial role for prolactin in female HCC resistance. PRL interrupted innate immune pathways in hepatocytes mediated by TRAF-dependent IL-1β, LPS/TLR4, and TNF-α, but not TIR-domain-containing adapter-inducing interferon-β (TRIF)-dependent poly(I:C)/TLR3. We found that PRL alone invoked sensitizing ubiquitination of a trafosome comprised of IRAK1, TRAF6, and MAP3K proteins, leading to accelerated complex degradation following immune stimulation. This process prevented activation of c-Myc via multiple MAP3K-dependent pathways, including p38 MAPK, NF-κB, and PI3K/AKT/mTORC1 (Fig. 6). We hypothesize that PRL function in liver is mediated predominantly by PRLR-S. Our finding of weak transcriptional induction by PRL in murine hepatocytes is consistent with the limited impact of PRL on STAT5 signaling in mouse liver (38). In vivo, circadian/ultradian hormone secretory patterns regulate gene transcription kinetics (39, 40). It is possible that ultradian secretion of PRL (7) also influences extra-nuclear functions of PRLR-S. Delayed onset but persistent activity of PRL in our model (Fig. S2B) is consistent with the slow subcellular trafficking and diminished turnover of ligand-bound PRLR-S compared with PRLR-L (41). Additional work will be required to parse the role of different hormones and receptors in the complex process of human liver carcinogenesis. Nonetheless, our model reconciles previously disconnected rodent studies, and introduces a mechanism by which an E2-responsive pituitary hormone may help prevent HCC.

Our results confirm and extend reports from other groups showing reduced HCC in mice and rats with PRL mobilization via pituitary allograft or pharmacologic induction (36, 37). However, another study reported no impact of PRL receptor deficiency on DEN-initiated liver carcinogenesis in Prlr−/− mice (42). There are several potential explanations for this apparent discrepancy. First, Prlr−/− and Prdr−/− mice show numerous biological differences, including energy metabolism, reproductive viability, and behavior (43–45). Therefore, PRL ligand and receptor knockout mice have different phenotypes. Second, Prlr−/− mice acquire extremely high levels of circulating PRL because of an absence of negative feedback inhibition (46), which could result in off-target effects. Finally, the Prdr−/− study limited analysis to grossly visible liver masses, whereas histopathology allowed us to distinguish preneoplastic nodules from bona fide malignancies, which proved to be an important differentiator (Fig. 4D). Our findings also contrast with a paper that correlated JAK2 with human HCC, and implied a role for PRL signaling in tumor progression (47). However, the association between serum PRL and HCC in patients was correlational only and did not take into account circulating E2. Additionally, the in vitro experiments relied on HepG2 cells, a cell line derived from hepatoblastoma and not HCC (48), and which preferentially express PRLR-L over PRLR-S (Fig. S1B). Finally, the only STAT sensitive to chemical (AG490) or siRNA JAK2 knockdown in their system was STAT3, not PRLR-associated STAT5. Because JAK2 is an upstream kinase for STAT3 as well as STAT5 (49), it is possible that the role of JAK2 in human HCC involves non-PRLR pathways. Further work will be needed to reconcile our findings with both studies above.

In summary, we have shown that PRL impedes liver carcinogenesis by restricting tumor-promoting innate immune responses within hepatocytes. Important questions remain, including whether hepatic PRL signaling is strictly PRLR-S-dependent, how ligand-bound PRLR recruits IRAK1 to the trafosome, whether TRAF molecules other than TRAF6 are targeted, and how ligand-bound PRLR mobilizes DRD2 antagonist domperidone prevents male HCC. (a) α-DRD2 domperidone increases circulating male PRL to near female levels. (b) Domperidone in male mice reduces multiplicity of dysplastic nodules to intermediate levels between untreated males and females. (c) Domperidone markedly reduces male HCC incidence (22% vs. 100% in untreated males); (d) PRLR mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization. (e) PRL mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization. (f) PRL mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization. (g) PRL mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization.

Fig. 5. PRL-mobilizing DRD2 antagonist domperidone prevents male HCC. (A) α-DRD2 domperidone increases circulating male PRL to near female levels. (B) Domperidone in male mice reduces multiplicity of dysplastic nodules to intermediate levels between untreated males and females. (C) Domperidone markedly reduces male HCC incidence (22% vs. 100% in untreated males); (D) PRLR mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization. (E) PRL mobilization increases DNA damage and reduces HCC in mice and rats with PRL mobilization.

Fig. 6. Working model of PRL interruption of TRAF/MAP3K-dependent innate immune activation of the proto-oncogene c-Myc via TRAF6/mTORC1, p38 MAPK, and/or NF-κB in hepatocytes. Inhibitory pathways shown in red, inflammatory in blue and proliferative in green. Abbreviations: DAMP, damage-associated molecular pattern; PAMP, pathogen-associated molecular pattern; PRR, pattern-recognition receptor.
inhibition through alternative mechanisms (4, 5). Nevertheless, our preclinical data show that E2-independent PRL mobilization, using a generic drug already in human use, is sufficient to protect males from liver cancer. PRL-targeted therapy may help prevent HCC in high-risk men and women.

Materials and Methods
C3H/HeN mice were purchased from the National Cancer Institute Frederick National Laboratory Production Program (Frederick, MD) and C57BL/6 mice from the Jackson Laboratory. Generation of Albumin-Myc-transgenic [ Alb-Myctg] and Prl-/- mice has been previously described (33, 45). Liver collections, tumor evaluation, histopathology, and molecular evaluations were performed as described in SI Materials and Methods and according to previously published techniques (50). Protein and nucleic acid isolation, immunoprecipitation, Western blot, and PCR were performed according to the manufacturers’ protocols. Cell lines except where indicated were obtained from the University of North Carolina at Chapel Hill (UNC) Lineberger Tissue Culture Facility and maintained according to ATCC guidelines. Deidentified human liver biopsies according a protocol approved by the UNC Institutional Review Board were obtained through the UNC Tissue Procurement Facility. In vivo sample sizes were projected to yield a study power ≥ 0.9 using GraphPad software (GraphPad). Statistical evaluations were performed by one-way ANOVA with Tukey posttest, or Student t test using Prism software (GraphPad). Animal euthanasia was performed in accordance with the American Veterinary Medical Association Panel on Euthanasia, and protocols were approved by the Institutional Animal Care and Use Committees of the University of Massachusetts Institute of Technology. Complete details are presented in SI Materials and Methods. See Table S6 for all qRT-PCR primer sequences.

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