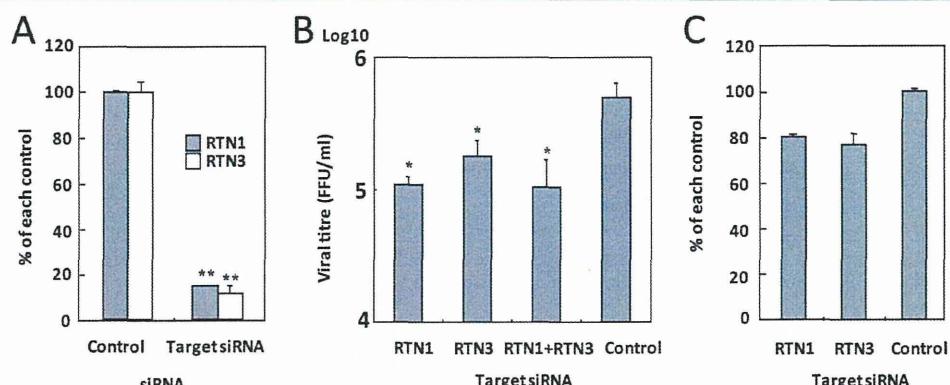


**Figure 3.** ER-localized host factors RTN1 and RTN3 were found to interact (blue edges) with NSSA in an Y2H screening of human liver cDNA library using NSSA as bait.



**Figure 4.** Effects of knockdown of RTN1 and RTN3 on HCV propagation and replication. Host factors RTN1 and RTN3 were suppressed by RNAi (A) in Huh7OK1 cells infected with HCV JFH1 strain (genotype 2a). The amounts of viral titer (B) and intracellular viral RNA (C) were estimated. Each value was represented as percentage of the cells transfected with the control siRNA. FFU: Focus-forming units; \*:  $p < 0.05$ , \*\*:  $p < 0.01$ .

#### Cellular Transport

Cellular factors associated with endocytic trafficking are key facilitators of the HCV life cycle, particularly HCV entry into the hepatic cells.<sup>91–93</sup> Endocytosis of the extracellular growth factor receptor (EGFR) in association with the cell surface glycoprotein CD81 plays a crucial role in HCV internalization and entry and is, therefore, an attractive target of anti-HCV strategies.<sup>94</sup> In the NSSA infection network, NSSA interactors ARAP1 and HSPA1A together with two bottlenecks (SRC, TGFBR1) were mapped to the enriched KEGG pathway “Endocytosis” ( $p = 2.97 \times 10^{-8}$ ; Supporting Information, Tables S7a, S8a). ARAP1, a Golgi associated protein, negatively regulates EGFR trafficking, and decreased ARAP1 expression contributes to enhanced EGFR endocytosis.<sup>95</sup> Therefore, NSSA

interaction with ARAP1 may facilitate EGFR internalization and thus viral entry in HCV infection.

#### NS5A Interacting Host Proteins RTN1 and RTN3 Function in HCV Propagation but Not Replication

Traditionally, viral and host proteins associated with the HCV lifecycle (internalization, replication, assembly and release) have been preferred targets in the anti-HCV studies. During infection, HCV localizes to the detergent-resistant membrane fraction (DRM) derived from the ER, where the viral replication and assembly take place.<sup>4</sup> Thus, of the novel interactions identified in our Y2H assay, we focused on two ER-localized host factors RTN1 and RTN3 (Figure 3). RTN1 and RTN3 belong to a group of proteins named Reticulons, which are integral to maintaining the shape and organization of the

ER and have been implicated in facilitating the replication of various positive-strand RNA viruses.<sup>96–98</sup> Furthermore, both RTN1 and RTN3 have been specifically detected in the very low density lipoprotein (VLDL) transport vesicle (VTV);<sup>99</sup> VTV is a key component of the VLDL secretory pathway, which plays an essential role in the production and the release of the infectious HCV particles.<sup>100</sup> Therefore, NSSA interactions with RTN1 and RTN3 suggested novel and potentially crucial roles of the two host proteins in the replication and/or release stages of the HCV lifecycle.

We performed cellular assays to assess the impact of RTN1 and RTN3 siRNA knockdowns on HCV replication and release. Since the HCV-production systems using the HCV JFH1 infectious strain (genotype 2a) isolates alone are capable of both efficient replication and the production of the infectious HCV particles, JFH1 was used to infect the Huh7OK1 cell line 24 h after transfection with each siRNA (see Materials and Methods). The infected cells were harvested after 72 h postinfection, and the expression of each host protein was assessed by qRT-PCR (Figure 4A). The viral titer was significantly decreased by individual and double knockdowns of RTN1 and RTN3 (Figure 4B). However, RTN1 and RTN3 knockdowns had no effect on the intracellular viral RNA levels in the HCV infected cells (Figure 4C), suggesting that RTN1 and RTN3 regulate HCV propagation but not HCV replication.

## CONCLUSIONS

We describe here our observations of PPIs between HCV NSSA and host proteins. By employing a multifold approach involving an experimental Y2H assay and literature mining, we derived a comprehensive set of experimentally determined binary interactions between NSSA and host proteins. We proceeded to map the combined NSSA–host interactions onto an overall interaction network, which comprised a repertoire of connections, which potentially enable NSSA to link up with and modulate the components of the host cellular networks. We then employed a network-based approach to understand the biological context of these connections in HCV pathogenesis with the help of the TargetMine data warehouse.

A functional analysis of the PPI networks highlighted NSSA interactions with several well connected host factors (hubs) and centrally located “bottlenecks” in the host cellular networks that function in cellular pathways associated with immune system and cell signaling, cellular adhesion and cell transport, cell growth and cell death and ER homeostasis among others. The “bottlenecks” include several proteins that were previously implicated in HCV pathogenesis, thereby suggesting that NSSA interactions with centrally connected host factors may enable the virus to influence strongly the host cellular processes in HCV infection. Notably, many bottlenecks were mapped to pathways associated with the infectious diseases induced by diverse bacterial and viral pathogens of the human host. These observations thus suggest the presence of some common themes underlying the onset of various human diseases associated with pathogenic infection in humans, a better understanding of which may be helpful in optimizing broad spectrum approaches to counteracting a wide range of pathogenic infections.

Cellular assays based on siRNA knockdowns in the HCV infected and replicon cells demonstrated RTN1 and RTN3, ER-localized NSSA interacting proteins, to be novel regulators of HCV propagation, but not replication, and thus promising novel candidates for anti-HCV therapy.

Our analysis therefore provides further insights into the role of NSSA–host interactions in HCV infection, a deeper understanding of which may aid in the identification of new clinically relevant targets for optimizing the therapeutic strategies to manipulate HCV–host interactions and thus more effectively combating HCV infection. Our analysis also emphasizes the importance of elaborate network-based computational approaches that integrate diverse biological data types in investigating host–pathogen interactions.

## ASSOCIATED CONTENT

### Supporting Information

Supporting methods, figures, and tables. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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### Notes

The authors declare no competing financial interest.

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## REFERENCES

- (1) Dubuisson, J. Hepatitis C virus proteins. *World J. Gastroenterol.* 2007, 13 (17), 2406–15.
- (2) Moriishi, K.; Matsuura, Y. Host factors involved in the replication of hepatitis C virus. *Rev. Med. Virol.* 2007, 17 (5), 343–54.
- (3) Myrmeal, H.; Ulvestad, E.; Asjo, B. The hepatitis C virus enigma. *APMIS* 2009, 117 (5–6), 427–39.
- (4) Tang, H.; Grise, H. Cellular and molecular biology of HCV infection and hepatitis. *Clin. Sci.* 2009, 117 (2), 49–65.
- (5) Pol, S.; Vallet-Pichard, A.; Corouge, M.; Mallet, V. O. Hepatitis C: epidemiology, diagnosis, natural history and therapy. *Contrib. Nephrol.* 2012, 176, 1–9.
- (6) Kuiken, C.; Simmonds, P. Nomenclature and numbering of the hepatitis C virus. *Methods Mol. Biol.* 2009, 510, 33–53.
- (7) Moradpour, D.; Penin, F.; Rice, C. M. Replication of hepatitis C virus. *Nat. Rev. Microbiol.* 2007, 5 (6), 453–63.
- (8) Love, R. A.; Brodsky, O.; Hickey, M. J.; Wells, P. A.; Cronin, C. N. Crystal structure of a novel dimeric form of NSSA domain I protein from hepatitis C virus. *J. Virol.* 2009, 83 (9), 4395–403.
- (9) Yamasaki, L. H.; Arcuri, H. A.; Jardim, A. C.; Bittar, C.; de Carvalho-Mello, I. M.; Rahal, P. New insights regarding HCV-NSSA structure/function and indication of genotypic differences. *Virol. J.* 2012, 9, 14.
- (10) Appel, N.; Zayas, M.; Miller, S.; Krijnse-Locker, J.; Schaller, T.; Friebel, P.; Kallis, S.; Engel, U.; Bartenschlager, R. Essential role of domain III of nonstructural protein 5A for hepatitis C virus infectious particle assembly. *PLoS Pathog.* 2008, 4 (3), e1000035.

- (11) Gale, M. J., Jr.; Korth, M. J.; Tang, N. M.; Tan, S. L.; Hopkins, D. A.; Dever, T. E.; Polyak, S. J.; Gretch, D. R.; Katze, M. G. Evidence that hepatitis C virus resistance to interferon is mediated through repression of the PKR protein kinase by the nonstructural 5A protein. *Virology* 1997, 230 (2), 217–27.
- (12) Ghosh, S.; Ahrens, W. A.; Phatak, S. U.; Hwang, S.; Schrum, L. W.; Bonkovsky, H. L. Association of filamin A and vimentin with hepatitis C virus proteins in infected human hepatocytes. *J. Viral Hepatitis* 2011, 18 (10), e568–77.
- (13) Gao, M.; Nettles, R. E.; Belema, M.; Snyder, L. B.; Nguyen, V. N.; Fridell, R. A.; Serrano-Wu, M. H.; Langley, D. R.; Sun, J. H.; O'Boyle, D. R., 2nd; Lemm, J. A.; Wang, C.; Knipe, J. O.; Chien, C.; Colonna, R. J.; Grasela, D. M.; Meanwell, N. A.; Hamann, L. G. Chemical genetics strategy identifies an HCV NSSA inhibitor with a potent clinical effect. *Nature* 2010, 465 (7294), 96–100.
- (14) Lee, C. Discovery of hepatitis C virus NSSA inhibitors as a new class of anti-HCV therapy. *Arch. Pharmacal Res.* 2011, 34 (9), 1403–7.
- (15) Lemm, J. A.; O'Boyle, D., 2nd; Liu, M.; Nower, P. T.; Colonna, R.; Deshpande, M. S.; Snyder, L. B.; Martin, S. W.; St Laurent, D. R.; Serrano-Wu, M. H.; Romine, J. L.; Meanwell, N. A.; Gao, M. Identification of hepatitis C virus NSSA inhibitors. *J. Virol.* 2010, 84 (1), 482–91.
- (16) Lemon, S. M.; McKeating, J. A.; Pietschmann, T.; Frick, D. N.; Glenn, J. S.; Tellinghuisen, T. L.; Symons, J.; Furman, P. A. Development of novel therapies for hepatitis C. *Antiviral Res.* 2010, 86 (1), 79–92.
- (17) Fusco, D. N.; Chung, R. T. Novel therapies for hepatitis C: insights from the structure of the virus. *Annu. Rev. Med.* 2012, 63, 373–87.
- (18) Buhler, S.; Bartenschlager, R. New targets for antiviral therapy of chronic hepatitis C. *Liver Int.* 2012, 32 (Suppl 1), 9–16.
- (19) Sarrazin, C.; Hezode, C.; Zeuzem, S.; Pawlotsky, J. M. Antiviral strategies in hepatitis C virus infection. *J. Hepatol.* 2012, 56 (Suppl), S88–S100.
- (20) Wang, S.; Wu, X.; Pan, T.; Song, W.; Wang, Y.; Zhang, F.; Yuan, Z. Viperin inhibits hepatitis C virus replication by interfering with binding of NSSA to host protein hVAP-33. *J. Gen. Virol.* 2012, 93 (Pt 1), 83–92.
- (21) Durmus Tekir, S.; Cakir, T.; Ulgen, K. O. Infection strategies of bacterial and viral pathogens through pathogen-human protein-protein interactions. *Front. Microbiol.* 2012, 3, 46.
- (22) de Chassey, B.; Navratil, V.; Tafforeau, L.; Hiet, M. S.; Aublin-Gex, A.; Agaue, S.; Meiffren, G.; Pradezynski, F.; Faria, B. F.; Chantier, T.; Le Breton, M.; Pellet, J.; Davoust, N.; Mangeot, P. E.; Chaboud, A.; Penin, F.; Jacob, Y.; Vidalain, P. O.; Vidal, M.; Andre, P.; Rabourdin-Combe, C.; Lotteau, V. Hepatitis C virus infection protein network. *Mol. Syst. Biol.* 2008, 4, 230.
- (23) Tan, S. L.; Ganji, G.; Paeper, B.; Proll, S.; Katze, M. G. Systems biology and the host response to viral infection. *Nat. Biotechnol.* 2007, 25 (12), 1383–9.
- (24) Tripathi, L. P.; Kataoka, C.; Taguwa, S.; Moriishi, K.; Mori, Y.; Matsuura, Y.; Mizuguchi, K. Network based analysis of hepatitis C virus Core and NS4B protein interactions. *Mol. BioSyst.* 2010, 6 (12), 2539–53.
- (25) Friedel, C. C.; Haas, J. Virus-host interactomes and global models of virus-infected cells. *Trends Microbiol.* 2011, 19 (10), 501–8.
- (26) Tafforeau, L.; Rabourdin-Combe, C.; Lotteau, V. Virus-human cell interactomes. *Methods Mol. Biol.* 2012, 812, 103–20.
- (27) Aizaki, H.; Aoki, Y.; Harada, T.; Ishii, K.; Suzuki, T.; Nagamori, S.; Toda, G.; Matsuura, Y.; Miyamura, T. Full-length complementary DNA of hepatitis C virus genome from an infectious blood sample. *Hepatology* 1998, 27 (2), 621–7.
- (28) Hamamoto, I.; Nishimura, Y.; Okamoto, T.; Aizaki, H.; Liu, M.; Mori, Y.; Abe, T.; Suzuki, T.; Lai, M. M.; Miyamura, T.; Moriishi, K.; Matsuura, Y. Human VAP-B is involved in hepatitis C virus replication through interaction with NSSA and NSSB. *J. Virol.* 2005, 79 (21), 13473–82.
- (29) Rebholz-Schuhmann, D.; Kirsch, H.; Arregui, M.; Gaudan, S.; Riethoven, M.; Stoehr, P. EBIMed—text crunching to gather facts for proteins from Medline. *Bioinformatics* 2007, 23 (2), e237–44.
- (30) Rebholz-Schuhmann, D.; Arregui, M.; Gaudan, S.; Kirsch, H.; Jimeno, A. Text processing through Web services: calling Whatizit. *Bioinformatics* 2008, 24 (2), 296–8.
- (31) Stark, C.; Breitkreutz, B. J.; Reguly, T.; Boucher, L.; Breitkreutz, A.; Tyers, M. BioGRID: a general repository for interaction datasets. *Nucleic Acids Res.* 2006, 34 (Database issue), D535–9.
- (32) Turner, B.; Razick, S.; Turinsky, A. L.; Vlasblom, J.; Crowdy, E. K.; Cho, E.; Morrison, K.; Donaldson, I. M.; Wodak, S. J. iRefWeb: interactive analysis of consolidated protein interaction data and their supporting evidence. *Database* 2010, 2010, baq023.
- (33) Chen, Y. A.; Tripathi, L. P.; Mizuguchi, K. TargetMine, an integrated data warehouse for candidate gene prioritisation and target discovery. *PLoS One* 2011, 6 (3), e17844.
- (34) Cline, M. S.; Smoot, M.; Cerami, E.; Kuchinsky, A.; Landys, N.; Workman, C.; Christmas, R.; Avila-Campilo, I.; Creech, M.; Gross, B.; Hanspers, K.; Isserlin, R.; Kelley, R.; Killcoyne, S.; Lotia, S.; Maere, S.; Morris, J.; Ono, K.; Pavlovic, V.; Pico, A. R.; Vailaya, A.; Wang, P. L.; Adler, A.; Conklin, B. R.; Hood, L.; Kuiper, M.; Sander, C.; Schmulevich, I.; Schwikowski, B.; Warner, G. J.; Ideker, T.; Bader, G. D. Integration of biological networks and gene expression data using Cytoscape. *Nat. Protoc.* 2007, 2 (10), 2366–82.
- (35) Smoot, M. E.; Ono, K.; Ruscheinski, J.; Wang, P. L.; Ideker, T. Cytoscape 2.8: new features for data integration and network visualization. *Bioinformatics* 2011, 27 (3), 431–2.
- (36) Assenov, Y.; Ramirez, F.; Schelhorn, S. E.; Lengauer, T.; Albrecht, M. Computing topological parameters of biological networks. *Bioinformatics* 2008, 24 (2), 282–4.
- (37) Lees, J.; Yeats, C.; Perkins, J.; Sillitoe, I.; Rentzsch, R.; Dessailly, B. H.; Orengo, C. Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. *Nucleic Acids Res.* 2012, 40 (Database issue), D465–71.
- (38) Ashburner, M.; Ball, C. A.; Blake, J. A.; Botstein, D.; Butler, H.; Cherry, J. M.; Davis, A. P.; Dolinski, K.; Dwight, S. S.; Eppig, J. T.; Harris, M. A.; Hill, D. P.; Issel-Tarver, L.; Kasarskis, A.; Lewis, S.; Matese, J. C.; Richardson, J. E.; Ringwald, M.; Rubin, G. M.; Sherlock, G. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat. Genet.* 2000, 25 (1), 25–9.
- (39) Aoki-Kinoshita, K. F.; Kanehisa, M. Gene annotation and pathway mapping in KEGG. *Methods Mol. Biol.* 2007, 396, 71–91.
- (40) Benjamini, Y.; Hochberg, Y. Controlling the false discovery rate—A practical and powerful approach to multiple testing. *J. R. Stat. Soc. B* 1995, 57 (1), 289–300.
- (41) Noble, W. S. How does multiple testing correction work? *Nat. Biotechnol.* 2009, 27 (12), 1135–7.
- (42) Okamoto, K.; Mori, Y.; Komoda, Y.; Okamoto, T.; Okochi, M.; Takeda, M.; Suzuki, T.; Moriishi, K.; Matsuura, Y. Intramembrane processing by signal peptide peptidase regulates the membrane localization of hepatitis C virus core protein and viral propagation. *J. Virol.* 2008, 82 (17), 8349–61.
- (43) Okamoto, T.; Omori, H.; Kaname, Y.; Abe, T.; Nishimura, Y.; Suzuki, T.; Miyamura, T.; Yoshimori, T.; Moriishi, K.; Matsuura, Y. A single-amino-acid mutation in hepatitis C virus NSSA disrupting FKBP8 interaction impairs viral replication. *J. Virol.* 2008, 82 (7), 3480–9.
- (44) Wakita, T.; Pietschmann, T.; Kato, T.; Date, T.; Miyamoto, M.; Zhao, Z.; Murthy, K.; Habermann, A.; Krausslich, H. G.; Mizokami, M.; Bartenschlager, R.; Liang, T. J. Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. *Nat. Med.* 2005, 11 (7), 791–6.
- (45) Taguwa, S.; Kambara, H.; Omori, H.; Tani, H.; Abe, T.; Mori, Y.; Suzuki, T.; Yoshimori, T.; Moriishi, K.; Matsuura, Y. Co-chaperone activity of human butyrate-induced transcript 1 facilitates hepatitis C virus replication through an Hsp90-dependent pathway. *J. Virol.* 2009, 83 (20), 10427–36.
- (46) Kukihara, H.; Moriishi, K.; Taguwa, S.; Tani, H.; Abe, T.; Mori, Y.; Suzuki, T.; Fukuhara, T.; Taketomi, A.; Maehara, Y.; Matsuura, Y.

- Human VAP-C negatively regulates hepatitis C virus propagation. *J. Virol.* **2009**, *83* (16), 7959–69.
- (47) Nanda, S. K.; Herion, D.; Liang, T. J. The SH3 binding motif of HCV [corrected] NSSA protein interacts with Bin1 and is important for apoptosis and infectivity. *Gastroenterology* **2006**, *130* (3), 794–809.
- (48) Liu, A. W.; Cai, J.; Zhao, X. L.; Jiang, T. H.; He, T. F.; Fu, H. Q.; Zhu, M. H.; Zhang, S. H. ShRNA-targeted MAP4K4 inhibits hepatocellular carcinoma growth. *Clin. Cancer Res.* **2011**, *17* (4), 710–20.
- (49) Woodhouse, S. D.; Narayan, R.; Latham, S.; Lee, S.; Antrobus, R.; Gangadharan, B.; Luo, S.; Schroth, G. P.; Klenerman, P.; Zitzmann, N. Transcriptome sequencing, microarray, and proteomic analyses reveal cellular and metabolic impact of hepatitis C virus infection in vitro. *Hepatology* **2010**, *52* (2), 443–53.
- (50) MacPherson, J. I.; Sidders, B.; Wieland, S.; Zhong, J.; Targett-Adams, P.; Lohmann, V.; Backes, P.; Delpuech-Adams, O.; Chisari, F.; Lewis, M.; Parkinson, T.; Robertson, D. L. An integrated transcriptomic and meta-analysis of hepatoma cells reveals factors that influence susceptibility to HCV infection. *PLoS One* **2011**, *6* (10), e25584.
- (51) Yamashita, T.; Honda, M.; Kaneko, S. Molecular mechanisms of hepatocarcinogenesis in chronic hepatitis C virus infection. *J. Gastroenterol. Hepatol.* **2011**, *26* (6), 960–4.
- (52) Yu, H.; Kim, P. M.; Sprecher, E.; Trifonov, V.; Gerstein, M. The importance of bottlenecks in protein networks: correlation with gene essentiality and expression dynamics. *PLoS Comput. Biol.* **2007**, *3* (4), e59.
- (53) Rasmussen, A. L.; Diamond, D. L.; McDermott, J. E.; Gao, X.; Metz, T. O.; Matzke, M. M.; Carter, V. S.; Belisle, S. E.; Korth, M. J.; Waters, K. M.; Smith, R. D.; Katze, M. G. Systems virology identifies a mitochondrial fatty acid oxidation enzyme, dodecenoyl coenzyme A delta isomerase, required for hepatitis C virus replication and likely pathogenesis. *J. Virol.* **2011**, *85* (22), 11646–54.
- (54) Diamond, D. L.; Krasnoselsky, A. L.; Burnum, K. E.; Monroe, M. E.; Webb-Robertson, B. J.; McDermott, J. E.; Yeh, M. M.; Dzib, J. F.; Susnow, N.; Strom, S.; Proll, S. C.; Belisle, S. E.; Purdy, D. E.; Rasmussen, A. L.; Walters, K. A.; Jacobs, J. M.; Gritsenko, M. A.; Camp, D. G.; Bhattacharya, R.; Perkins, J. D.; Carithers, R. L., Jr.; Liou, I. W.; Larson, A. M.; Benecke, A.; Waters, K. M.; Smith, R. D.; Katze, M. G. Proteome and computational analyses reveal new insights into the mechanisms of hepatitis C virus-mediated liver disease posttransplantation. *Hepatology* **2012**, *56* (1), 28–38.
- (55) He, Y.; Nakao, H.; Tan, S. L.; Polyak, S. J.; Neddermann, P.; Vijaysri, S.; Jacobs, B. L.; Katze, M. G. Subversion of cell signaling pathways by hepatitis C virus nonstructural 5A protein via interaction with Grb2 and P85 phosphatidylinositol 3-kinase. *J. Virol.* **2002**, *76* (18), 9207–17.
- (56) Jiang, Y. F.; He, B.; Li, N. P.; Ma, J.; Gong, G. Z.; Zhang, M. The oncogenic role of NSSA of hepatitis C virus is mediated by up-regulation of survivin gene expression in the hepatocellular cell through p53 and NF-kappaB pathways. *Cell Biol. Int.* **2011**, *35* (12), 1225–32.
- (57) Pfannkuche, A.; Buther, K.; Karthe, J.; Poenisch, M.; Bartenschlager, R.; Trilling, M.; Hengel, H.; Willbold, D.; Haussinger, D.; Bode, J. G. c-Src is required for complex formation between the hepatitis C virus-encoded proteins NSSA and NSSB: a prerequisite for replication. *Hepatology* **2011**, *53* (4), 1127–36.
- (58) Calderwood, M. A.; Venkatesan, K.; Xing, L.; Chase, M. R.; Vazquez, A.; Holthaus, A. M.; Ewence, A. E.; Li, N.; Hirozane-Kishikawa, T.; Hill, D. E.; Vidal, M.; Kieff, E.; Johannsen, E. Epstein-Barr virus and virus human protein interaction maps. *Proc. Natl. Acad. Sci. U. S. A.* **2007**, *104* (18), 7606–11.
- (59) Pichlmair, A.; Kandasamy, K.; Alvisi, G.; Mulhern, O.; Sacco, R.; Habjan, M.; Binder, M.; Stefanovic, A.; Eberle, C. A.; Goncalves, A.; Burckstummer, T.; Muller, A. C.; Fauster, A.; Holze, C.; Lindsten, K.; Goodbourn, S.; Kochs, G.; Weber, F.; Bartenschlager, R.; Bowie, A. G.; Bennett, K. L.; Colinge, J.; Superti-Furga, G. Viral immune modulators perturb the human molecular network by common and unique strategies. *Nature* **2012**, *487* (7408), 486–90.
- (60) Huang, H.; Jedynak, B. M.; Bader, J. S. Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. *PLoS Comput. Biol.* **2007**, *3* (11), e214.
- (61) Nordle Gilliver, A.; Griffin, S.; Harris, M. Identification of a novel phosphorylation site in hepatitis C virus NSSA. *J. Gen. Virol.* **2010**, *91* (Pt 10), 2428–32.
- (62) Qiu, D.; Lemm, J. A.; O'Boyle, D. R., 2nd; Sun, J. H.; Nowell, P. T.; Nguyen, V.; Hamann, L. G.; Snyder, L. B.; Deon, D. H.; Ruediger, E.; Meanwell, N. A.; Belema, M.; Gao, M.; Fridell, R. A. The effects of NSSA inhibitors on NSSA phosphorylation, polyprotein processing and localization. *J. Gen. Virol.* **2011**, *92* (Pt 11), 2502–11.
- (63) Tellinghuisen, T. L.; Foss, K. L.; Treadaway, J. Regulation of hepatitis C virion production via phosphorylation of the NSSA protein. *PLoS Pathog.* **2008**, *4* (3), e1000032.
- (64) Chen, K. C.; Wang, T. Y.; Chan, C. H. Associations between HIV and human pathways revealed by protein-protein interactions and correlated gene expression profiles. *PLoS One* **2012**, *7* (3), e34240.
- (65) Rozenblatt-Rosen, O.; Deo, R. C.; Padi, M.; Adelman, G.; Calderwood, M. A.; Rolland, T.; Grace, M.; Dricot, A.; Askenazi, M.; Tavares, M.; Pevzner, S. J.; Abderazzaq, F.; Byrdsong, D.; Carvunis, A. R.; Chen, A. A.; Cheng, J.; Correll, M.; Duarte, M.; Fan, C.; Felkamp, M. C.; Ficarro, S. B.; Franchi, R.; Garg, B. K.; Gulbahce, N.; Hao, T.; Holthaus, A. M.; James, R.; Korkhin, A.; Litovchick, L.; Mar, J. C.; Pak, T. R.; Rabello, S.; Rubio, R.; Shen, Y.; Singh, S.; Spangle, J. M.; Tasan, M.; Wanamaker, S.; Webber, J. T.; Roecklein-Canfield, J.; Johannsen, E.; Barabasi, A. L.; Beroukhim, R.; Kieff, E.; Cusick, M. E.; Hill, D. E.; Munger, K.; Marto, J. A.; Quackenbush, J.; Roth, F. P.; DeCaprio, J. A.; Vidal, M. Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. *Nature* **2012**, *487* (7408), 491–5.
- (66) Barnaba, V. Hepatitis C virus infection: a “liaison à trois” amongst the virus, the host, and chronic low-level inflammation for human survival. *J. Hepatol.* **2010**, *53* (4), 752–61.
- (67) Hiroishi, K.; Ito, T.; Imawari, M. Immune responses in hepatitis C virus infection and mechanisms of hepatitis C virus persistence. *J. Gastroenterol. Hepatol.* **2008**, *23* (10), 1473–82.
- (68) Kawai, T.; Akira, S. Toll-like receptor and RIG-I-like receptor signaling. *Ann. N. Y. Acad. Sci.* **2008**, *1143*, 1–20.
- (69) Sklan, E. H.; Charuworn, P.; Pang, P. S.; Glenn, J. S. Mechanisms of HCV survival in the host. *Nat. Rev. Gastroenterol. Hepatol.* **2009**, *6* (4), 217–27.
- (70) Kang, S. M.; Won, S. J.; Lee, G. H.; Lim, Y. S.; Hwang, S. B. Modulation of interferon signaling by hepatitis C virus non-structural 5A protein: implication of genotypic difference in interferon treatment. *FEBS Lett.* **2010**, *584* (18), 4069–76.
- (71) Li, K.; Li, N. L.; Wei, D.; Pfeffer, S. R.; Fan, M.; Pfeffer, L. M. Activation of chemokine and inflammatory cytokine response in hepatitis C virus-infected hepatocytes depends on Toll-like receptor 3 sensing of hepatitis C virus double-stranded RNA intermediates. *Hepatology* **2012**, *55* (3), 666–75.
- (72) Tanaka, S.; Arii, S. Molecularly targeted therapy for hepatocellular carcinoma. *Cancer Sci.* **2009**, *100* (1), 1–8.
- (73) Tanaka, S.; Arii, S. Current status of molecularly targeted therapy for hepatocellular carcinoma: basic science. *Int. J. Clin. Oncol.* **2010**, *15* (3), 235–41.
- (74) Villanueva, A.; Chiang, D. Y.; Newell, P.; Peix, J.; Thung, S.; Alsina, C.; Tovar, V.; Roayaie, S.; Minguez, B.; Sole, M.; Battiston, C.; Van Laarhoven, S.; Fiel, M. I.; Di Feo, A.; Hoshida, Y.; Yea, S.; Toffanin, S.; Ramos, A.; Martignetti, J. A.; Mazzaferro, V.; Bruix, J.; Waxman, S.; Schwartz, M.; Meyerson, M.; Friedman, S. L.; Llovet, J. M. Pivotal role of mTOR signaling in hepatocellular carcinoma. *Gastroenterology* **2008**, *135* (6), 1972–83.
- (75) Cheng, D.; Zhao, L.; Zhang, L.; Jiang, Y.; Tian, Y.; Xiao, X.; Gong, G. p53 controls hepatitis C virus non-structural protein 5A-mediated downregulation of GADD45alpha expression via the NF-kappaB and PI3K-Akt pathways. *J. Gen. Virol.* **2013**, *94* (Pt 2), 326–35.
- (76) Tripathi, L. P.; Kambara, H.; Moriishi, K.; Morita, E.; Abe, T.; Mori, Y.; Chen, Y. A.; Matsuura, Y.; Mizuguchi, K. Proteomic analysis

- of hepatitis C virus (HCV) core protein transfection and host regulator PA28gamma knockout in HCV pathogenesis: a network-based study. *J. Proteome Res.* **2012**, *11* (7), 3664–79.
- (77) Zhao, L. J.; Zhao, P.; Chen, Q. L.; Ren, H.; Pan, W.; Qi, Z. T. Mitogen-activated protein kinase signalling pathways triggered by the hepatitis C virus envelope protein E2: implications for the prevention of infection. *Cell Proliferation* **2007**, *40* (4), 508–21.
- (78) Basaranoglu, M.; Basaranoglu, G. Pathophysiology of insulin resistance and steatosis in patients with chronic viral hepatitis. *World J. Gastroenterol.* **2011**, *17* (36), 4055–62.
- (79) Del Campo, J. A.; Romero-Gomez, M. Steatosis and insulin resistance in hepatitis C: a way out for the virus? *World J. Gastroenterol.* **2009**, *15* (40), S014–9.
- (80) Douglas, M. W.; George, J. Molecular mechanisms of insulin resistance in chronic hepatitis C. *World J. Gastroenterol.* **2009**, *15* (35), 4356–64.
- (81) Das, G. C.; Hollinger, F. B. Molecular pathways for glucose homeostasis, insulin signaling and autophagy in hepatitis C virus induced insulin resistance in a cellular model. *Virology* **2012**, *434* (1), S–17.
- (82) Miyamoto, H.; Moriishi, K.; Moriya, K.; Murata, S.; Tanaka, K.; Suzuki, T.; Miyamura, T.; Koike, K.; Matsuuwa, Y. Involvement of the PA28gamma-dependent pathway in insulin resistance induced by hepatitis C virus core protein. *J. Virol.* **2007**, *81* (4), 1727–35.
- (83) Kaneko, K.; Ueki, K.; Takahashi, N.; Hashimoto, S.; Okamoto, M.; Awazawa, M.; Okazaki, Y.; Ohsugi, M.; Inabe, K.; Umehara, T.; Yoshida, M.; Kakei, M.; Kitamura, T.; Luo, J.; Kulkarni, R. N.; Kahn, C. R.; Kasai, H.; Cantley, L. C.; Kadowaki, T. Class IA phosphatidylinositol 3-kinase in pancreatic beta cells controls insulin secretion by multiple mechanisms. *Cell Metab.* **2010**, *12* (6), 619–32.
- (84) Milward, A.; Mankouri, J.; Harris, M. Hepatitis C virus NSSA protein interacts with beta-catenin and stimulates its transcriptional activity in a phosphoinositide-3 kinase-dependent fashion. *J. Gen. Virol.* **2010**, *91* (Pt 2), 373–81.
- (85) Alberstein, M.; Zornitzki, T.; Zick, Y.; Knobler, H. Hepatitis C core protein impairs insulin downstream signalling and regulatory role of IGFBP-1 expression. *J. Viral Hepatitis* **2012**, *19* (1), 65–71.
- (86) Benedicto, I.; Molina-Jimenez, F.; Bartosch, B.; Cosset, F. L.; Laville, D.; Prieto, J.; Moreno-Otero, R.; Valenzuela-Fernandez, A.; Aldabe, R.; Lopez-Cabrera, M.; Majano, P. L. The tight junction-associated protein occludin is required for a postbinding step in hepatitis C virus entry and infection. *J. Virol.* **2009**, *83* (16), 8012–20.
- (87) Carloni, G.; Crema, A.; Valli, M. B.; Ponzetto, A.; Clementi, M. HCV infection by cell-to-cell transmission: choice or necessity? *Curr. Mol. Med.* **2012**, *12* (1), 83–95.
- (88) Wilson, G. K.; Brimacombe, C. L.; Rowe, I. A.; Reynolds, G. M.; Fletcher, N. F.; Stamatakis, Z.; Bhogal, R. H.; Simoes, M. L.; Ashcroft, M.; Afford, S. C.; Mitry, R. R.; Dhawan, A.; Mee, C. J.; Hubscher, S. G.; Balfe, P.; McKeating, J. A. A dual role for hypoxia inducible factor-1alpha in the hepatitis C virus lifecycle and hepatoma migration. *J. Hepatol.* **2012**, *56* (4), 803–9.
- (89) Daugherty, R. L.; Gottardi, C. J. Phospho-regulation of beta-catenin adhesion and signaling functions. *Physiology* **2007**, *22*, 303–9.
- (90) Presser, L. D.; Haskett, A.; Waris, G. Hepatitis C virus-induced furin and thrombospondin-1 activate TGF-beta1: role of TGF-beta1 in HCV replication. *Virology* **2011**, *412* (2), 284–96.
- (91) Berger, K. L.; Cooper, J. D.; Heaton, N. S.; Yoon, R.; Oakland, T. E.; Jordan, T. X.; Mateu, G.; Grakoui, A.; Randall, G. Roles for endocytic trafficking and phosphatidylinositol 4-kinase III alpha in hepatitis C virus replication. *Proc. Natl. Acad. Sci. U. S. A.* **2009**, *106* (18), 7577–82.
- (92) Katsarou, K.; Lavdas, A. A.; Tsitoura, P.; Serti, E.; Markoulatos, P.; Mavromara, P.; Georgopoulou, U. Endocytosis of hepatitis C virus non-enveloped capsid-like particles induces MAPK-ERK1/2 signaling events. *Cell. Mol. Life Sci.* **2010**, *67*, 2491–506.
- (93) Mankouri, J.; Griffin, S.; Harris, M. The hepatitis C virus non-structural protein NSSA alters the trafficking profile of the epidermal growth factor receptor. *Traffic* **2008**, *9* (9), 1497–509.
- (94) Diao, J.; Pantua, H.; Ngu, H.; Komuves, L.; Diehl, L.; Schaefer, G.; Kapadia, S. B. Hepatitis C virus (HCV) induces epidermal growth factor receptor (EGFR) activation via CD81 binding for viral internalization and entry. *J. Virol.* **2012**, *86* (20), 10935–49.
- (95) Yoon, H. Y.; Kales, S. C.; Luo, R.; Lipkowitz, S.; Randazzo, P. A. ARAP1 association with CIN85 affects epidermal growth factor receptor endocytic trafficking. *Biol. Cell* **2011**, *103* (4), 171–84.
- (96) Katsarou, K.; Lavdas, A. A.; Tsitoura, P.; Serti, E.; Markoulatos, P.; Mavromara, P.; Georgopoulou, U. Endocytosis of hepatitis C virus non-enveloped capsid-like particles induces MAPK-ERK1/2 signaling events. *Cell. Mol. Life Sci.* **2010**, *67* (14), 2491–506.
- (97) Diaz, A.; Ahlquist, P. Role of host reticulon proteins in rearranging membranes for positive-strand RNA virus replication. *Curr. Opin. Microbiol.* **2012**, *15* (4), 519–24.
- (98) Diaz, A.; Wang, X.; Ahlquist, P. Membrane-shaping host reticulon proteins play crucial roles in viral RNA replication compartment formation and function. *Proc. Natl. Acad. Sci. U. S. A.* **2010**, *107* (37), 16291–6.
- (99) Rahim, A.; Nafivalecia, E.; Siddiqi, S.; Basha, R.; Runyon, C. C.; Siddiqi, S. A. Proteomic analysis of the very low density lipoprotein (VLDL) transport vesicles. *J. Proteomics* **2012**, *75* (7), 2225–35.
- (100) Coller, K. E.; Heaton, N. S.; Berger, K. L.; Cooper, J. D.; Saunders, J. L.; Randall, G. Molecular determinants and dynamics of hepatitis C virus secretion. *PLoS Pathog.* **2012**, *8* (1), e1002466.
- (101) Lai, C. K.; Jeng, K. S.; Machida, K.; Lai, M. M. Association of hepatitis C virus replication complexes with microtubules and actin filaments is dependent on the interaction of NS3 and NSSA. *J. Virol.* **2008**, *82* (17), 8838–48.
- (102) Randall, G.; Panis, M.; Cooper, J. D.; Tellinghuisen, T. L.; Sukhodolets, K. E.; Pfeffer, S.; Landthaler, M.; Landgraf, P.; Kan, S.; Lindenbach, B. D.; Chien, M.; Weir, D. B.; Russo, J. J.; Ju, J.; Brownstein, M. J.; Sheridan, R.; Sander, C.; Zavolan, M.; Tuschl, T.; Rice, C. M. Cellular cofactors affecting hepatitis C virus infection and replication. *Proc. Natl. Acad. Sci. U. S. A.* **2007**, *104* (31), 12884–9.
- (103) Saxena, V.; Lai, C. K.; Chao, T. C.; Jeng, K. S.; Lai, M. M. Annexin A2 is involved in the formation of hepatitis C virus replication complex on the lipid raft. *J. Virol.* **2012**, *86* (8), 4139–50.
- (104) Quintavalle, M.; Sambucini, S.; Summa, V.; Orsatti, L.; Talamo, F.; De Francesco, R.; Neddermann, P. Hepatitis C virus NSSA is a direct substrate of casein kinase I-alpha, a cellular kinase identified by inhibitor affinity chromatography using specific NSSA hyperphosphorylation inhibitors. *J. Biol. Chem.* **2007**, *282* (8), 5536–44.
- (105) Ivanov, A. V.; Tunitskaya, V. L.; Ivanova, O. N.; Mitkevich, V. A.; Prassolov, V. S.; Makarov, A. A.; Kukhanova, M. K.; Kochetkov, S. N. Hepatitis C virus NSSA protein modulates template selection by the RNA polymerase in in vitro system. *FEBS Lett.* **2009**, *583* (2), 277–80.
- (106) Park, C. Y.; Choi, S. H.; Kang, S. M.; Kang, J. I.; Ahn, B. Y.; Kim, H.; Jung, G.; Choi, K. Y.; Hwang, S. B. Nonstructural 5A protein activates beta-catenin signaling cascades: implication of hepatitis C virus-induced liver pathogenesis. *J. Hepatol.* **2009**, *51* (5), 853–64.
- (107) Zhang, Z.; Harris, D.; Pandey, V. N. The FUSE binding protein is a cellular factor required for efficient replication of hepatitis C virus. *J. Virol.* **2008**, *82* (12), 5761–73.
- (108) Chen, Y. J.; Chen, Y. H.; Chow, L. P.; Tsai, Y. H.; Chen, P. H.; Huang, C. Y.; Chen, W. T.; Hwang, L. H. Heat shock protein 72 is associated with the hepatitis C virus replicase complex and enhances viral RNA replication. *J. Biol. Chem.* **2010**, *285* (36), 28183–90.
- (109) Choi, Y. W.; Tan, Y. J.; Lim, S. G.; Hong, W.; Goh, P. Y. Proteomic approach identifies HSP27 as an interacting partner of the hepatitis C virus NSSA protein. *Biochem. Biophys. Res. Commun.* **2004**, *318* (2), 514–9.
- (110) Ahn, J.; Chung, K. S.; Kim, D. U.; Won, M.; Kim, L.; Kim, K. S.; Nam, M.; Choi, S. J.; Kim, H. C.; Yoon, M.; Chae, S. K.; Hoe, K. L. Systematic identification of hepatocellular proteins interacting with NSSA of the hepatitis C virus. *J. Biochem. Mol. Biol.* **2004**, *37* (6), 741–8.

- (111) Amako, Y.; Sarkeshik, A.; Hotta, H.; Yates, J., 3rd; Siddiqui, A. Role of oxysterol binding protein in hepatitis C virus infection. *J. Virol.* **2009**, *83* (18), 9237–46.
- (112) Lim, Y. S.; Tran, H. T.; Park, S. J.; Yim, S. A.; Hwang, S. B. Peptidyl-prolyl isomerase Pin1 is a cellular factor required for hepatitis C virus propagation. *J. Virol.* **2011**, *85* (17), 8777–88.
- (113) Chen, Y. C.; Su, W. C.; Huang, J. Y.; Chao, T. C.; Jeng, K. S.; Machida, K.; Lai, M. M. Polo-like kinase 1 is involved in hepatitis C virus replication by hyperphosphorylating NSSA. *J. Virol.* **2010**, *84* (16), 7983–93.
- (114) Waller, H.; Chatterji, U.; Gallay, P.; Parkinson, T.; Targett-Adams, P. The use of AlphaLISA technology to detect interaction between hepatitis C virus-encoded NSSA and cyclophilin A. *J. Virol. Methods* **2010**, *165* (2), 202–10.
- (115) Chatterji, U.; Lim, P.; Bobardt, M. D.; Wieland, S.; Cordek, D. G.; Vuagniaux, G.; Chisari, F.; Cameron, C. E.; Targett-Adams, P.; Parkinson, T.; Gallay, P. A. HCV resistance to cyclosporin A does not correlate with a resistance of the NSSA-cyclophilin A interaction to cyclophilin inhibitors. *J. Hepatol.* **2010**, *53* (1), 50–6.
- (116) Georgopoulou, U.; Tsitoura, P.; Kalamvoki, M.; Mavromara, P. The protein phosphatase 2A represents a novel cellular target for hepatitis C virus NSSA protein. *Biochimie* **2006**, *88* (6), 651–62.
- (117) Helbig, K. J.; Eyre, N. S.; Yip, E.; Narayana, S.; Li, K.; Fiches, G.; McCartney, E. M.; Jangra, R. K.; Lemon, S. M.; Beard, M. R. The antiviral protein viperin inhibits hepatitis C virus replication via interaction with nonstructural protein SA. *Hepatology* **2011**, *54* (5), 1506–17.
- (118) Kumthip, K.; Chusri, P.; Jilg, N.; Zhao, L.; Fusco, D. N.; Zhao, H.; Goto, K.; Cheng, D.; Schaefer, E. A.; Zhang, L.; Pantip, C.; Thongsawat, S.; O'Brien, A.; Peng, L. F.; Maneekarn, N.; Chung, R. T.; Lin, W. Hepatitis C virus NSSA disrupts STAT1 phosphorylation and suppresses type I interferon signaling. *J. Virol.* **2012**, *86* (16), 8581–91.
- (119) Inubushi, S.; Nagano-Fujii, M.; Kitayama, K.; Tanaka, M.; An, C.; Yokozaki, H.; Yamamura, H.; Nuriya, H.; Kohara, M.; Sada, K.; Hotta, H. Hepatitis C virus NSSA protein interacts with and negatively regulates the non-receptor protein tyrosine kinase Syk. *J. Gen. Virol.* **2008**, *89* (Pt 5), 1231–42.



## Comparative Analysis of T-Cell Depletion Method for Clinical Immunotherapy—Anti-Hepatitis C Effects of Natural Killer Cells Via Interferon- $\gamma$ Production

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### ABSTRACT

Liver transplantation (LT) is a life-saving treatment for liver cirrhosis patients with hepatocellular carcinoma (HCC). However, 10%–20% HCC recurrence rate after LT is due to the immunosuppression inducing tumor growth. We recently reported a novel immunotherapy with donor liver natural killer (NK) cells to prevent HCC and hepatitis C virus (HCV) recurrence after LT. In this cell processing procedure, Muromonab-CD3 (Orthoclone OKT3, an anti-CD3 antibody) was added to the culture medium to deplete CD3 $^{+}$  T cells to prevent graft-versus-host disease. However, the manufacture of OKT3 was discontinued in 2010, when other treatments with similar efficacy and fewer side effects became available. In this study, we examined alternative reagents for T-cell depletion-MACS GMP CD3 pure (GMP CD3), antithymocyte globulin, and alemtuzumab-for NK cell immunotherapy in the allogeneic setting. We observed that GMP CD3 showed exactly the same effects on liver mononuclear cells as OKT3, including activation of NK cells and depletion of T cells. Interestingly, binding of T-cell depletion antibodies to NK cells led to an anti-HCV effect via interferon- $\gamma$  production. These results with the use of in vitro culture systems suggested that antibodies which produce T-cell depletion affected NK cell function.

Liver failure and hepatocellular carcinoma (HCC) caused by chronic hepatitis C virus (HCV) infection are the most common indications for liver transplantation (LT). The incidences of both conditions have been projected to increase further. On the one hand, the rate of HCC recurrence after LT is 10%–20%.<sup>1,2</sup> On the other hand, recurrent HCV infection in the allograft, which is universal, occurs immediately after LT and is associated with accelerated progression to liver cirrhosis, graft loss, and death.<sup>3,4</sup> These recurrences remain the most serious issue with LT. The use of postoperative immunosuppressants poses an additional risk for recurrences and hinders the use of chemotherapeutic or interferon (IFN) agents.<sup>5,6</sup> However, no definitive treatment or prevention for HCC recurrence after LT is known.

Natural killer (NK) cells are innate immune lymphocytes that are identified by their expression of the CD56 surface antigen and the absence of CD3 markers.<sup>7,8</sup> NK cells can directly kill targets through the release of granzymes, which are granules containing perforin and serine proteases, and/or by surface-expressed ligands that engage and activate death receptors expressed on target cells. Unlike T

cells, NK cells do not require the presence of a specific antigen to kill cancer cells, modified cells, or invading infectious microbes. NK cells are abundant in the liver, in

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contrast to their relatively small distribution in peripheral lymph and lymphatic organs in rodents<sup>9–11</sup> and humans.<sup>12,13</sup> In addition, hepatic NK cells in humans have been shown to mediate cytotoxic activity against HCC<sup>12</sup> and to display anti-HCV effects<sup>14</sup> compared with their peripheral blood counterparts. We have successfully applied adoptive immunotherapy with liver NK cells to LT recipients with HCC in Japan and the United States.<sup>14–16</sup> In this regimen, LT recipients are injected intravenously with interleukin (IL) 2-activated NK cells derived from the donor liver allograft. After treatment with IL-2 and OKT3 (Orthoclone OKT3, an anti-CD3 monoclonal antibody [mAb]; Ortho Biotech, Raritan, NJ), liver NK cells expressed significantly elevated levels of the tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), a crucial molecule for killing of tumor cells. Furthermore, these cells showed great cytotoxicity against HCC without any effect on normal cells.<sup>12</sup>

OKT3, a potent immunosuppressant, has been shown to reverse renal allograft rejection episodes.<sup>17,18</sup> It has also been widely used for immunotherapy, as well as to expand cytotoxic T cells<sup>19</sup> and enhance the activity of lymphokine-activated killer (LAK) cells,<sup>20–25</sup> and prevent graft-versus-host disease (GVHD).<sup>26–29</sup> In the latter setting, administration of OKT3-coated T cells *in vivo* opsonizes for the reticuloendothelial system to subsequently trap or lyses cells.<sup>30–32</sup> This method has been used for clinical NK therapy in Japan, achieving protection against GVHD.<sup>14</sup> However, because of its numerous side effects, the availability of better-tolerated alternatives, and its declining use, OKT3 has been recently removed from the market. Therefore, alternative reagents need to be evaluated for this immunotherapy. In the present study, we evaluated the effect of alternative reagents-GMP CD3 (MACS GMP CD3 pure; Miltenyi Biotec, Bergisch Gladbach, Germany), anti-thymocyte globulin (Thymoglobulin; Genzyme, Cambridge, MA), and alemtuzumab (Campath; Genzyme) using culture systems with NK and T cells for subsequent application in clinical trials.

## MATERIALS AND METHODS

### Isolation of Liver Mononuclear Cells

Liver mononuclear cells (LMNCs) from liver perfusates were isolated by gradient centrifugation with Ficoll-Hypaque (GE Healthcare, Pittsburgh, PA) before suspension in X-Vivo 15 medium (Lonza, Walkersville, MD) supplemented with 100 µg/mL gentamicin (APP Pharmaceuticals, Schaumburg, IL), 10% human AB serum (Valley Biomedical, Winchester, VA), and 10 U/mL sodium heparin (APP Pharmaceuticals), as previously described.<sup>16</sup> Our Institutional Review Board (IRB) approved this study.

### Cell Culture

LMNCs were cultured with 1,000 U/mL human recombinant IL-2 (Proleukin; Novartis, Emeryville, CA) in culture medium at 37°C in an atmosphere supplemented with 5% CO<sub>2</sub>. LMNCs were exposed to a OKT3 (1 µg/mL), GMP CD3 (1 µg/mL), antithymocyte globulin (100 µg/mL), or alemtuzumab (100 µg/mL) at 1 day

before cell harvest. After 4 days of culture, cells were subjected to further analyses.

### Flow Cytometry

All flow cytometry (FCM) analyses were performed on an LSR II Flow Cytometer (BD Biosciences, San Jose, CA). The following mAbs were used for surface staining of the lymphocytes: fluorescein isothiocyanate-conjugated anti-CD3 (HIT3a; BD Pharmingen, San Diego, CA) or anti-CD56 (B159; BD Pharmingen); phycoerythrin (PE)-conjugated anti-TRAIL (RIK-2; BD Pharmingen), anti-NKp44 (P44-8.1; BD Pharmingen), or anti-CD158b (CH-L; BD Pharmingen); allophycocyanin (APC)-conjugated anti-CD56 (B159; BD Pharmingen), anti-CD25 (M-A251; BD Pharmingen), or anti-NKG2A (Z199; Beckman Coulter, Fullerton, CA); APC-eFluor780-conjugated anti-CD3 (UCHT1; eBioscience, San Diego, CA); PE-Cy7-conjugated anti-CD69 (FN50; Biolegend, San Diego, CA), or anti-NKG2D (1D11; Biolegend); eFluor 605NC-conjugated anti-CD16 (eBioCB16; eBioscience); Alexa Fluor 647-conjugated anti-NKp30 (P30-15; Biolegend); peridinin chlorophyll protein complex (PerCP)-Cy5.5-conjugated anti-CD158a (HP-MA4; eBioscience); and biotin-conjugated anti-CD122 (Mik-b3; BD Pharmingen), anti-NKp46 (9E2; Biolegend), or CD132 (TuGh4; BD Pharmingen). The biotinylated mAbs were visualized with the use of PerCP-Cy5.5-streptavidin (eBioscience) or PE-Cy7-streptavidin (Biolegend). Dead cells were excluded by light scatter and 4',6-diamidino-2-phenylindole staining (DAPI; Invitrogen, Carlsbad, CA). FCM analyses were performed with Flowjo software (Tree Star, Ashland, OR).

### Cytotoxic Assay

The cytotoxicity assay was performed by FCM as previously described.<sup>16</sup> Briefly, target cells labeled with 0.1 µmol/L carboxyfluorescein diacetate succinimidyl ester Cell Tracer Kit (Invitrogen) for 5 minutes at 37°C in 5% CO<sub>2</sub> were washed twice in phosphate-buffered saline solution, resuspended in complete medium, and counted with the use of trypan blue staining. The effector and target cells were coincubated at various ratios for 1 hour at 37°C in 5% CO<sub>2</sub>. As a control, target cells or effector cells were incubated alone in complete medium to measure spontaneous cell death after DAPI was added to each tube. The data were analyzed with the use of Flowjo software. Cytotoxic activity was calculated as a percentage with the following formula: % cytotoxicity = [(% experimental DAPI<sup>+</sup> dead targets) – (% spontaneous DAPI<sup>+</sup> dead targets)]/[100 – (% spontaneous DAPI<sup>+</sup> dead targets)] × 100.

### ELISA

IFN-γ production of LMNCs during the culture was measured by enzyme-linked immunosorbent assay (ELISA) (Biolegend). Supernates collected after the incubation were stored at -80°C until further use. IFN-γ ELISA was performed according to the manufacturer's instructions.

### Coculture with HCV Replicon Cells

The HuH7/Rep-Feo cell line (HCV replicon cells) was kindly provided by Dr N Sakamoto (Department of Gastroenterology and Hepatology, Tokyo Medical and Dental University, Tokyo, Japan). The HCV subgenomic replicon plasmid, pRep-Feo, was derived from pRep-Neo (originally pHCV1bneo-delS).<sup>33</sup> pRep-Feo carries a fusion gene comprising firefly luciferase and neomycin phosphotransferase, as described elsewhere.<sup>34,35</sup> After culture in the pres-

ence of G418 (Invitrogen), Huh7/Rep-Feo cell lines showed stable expression of the replicons. We used transwell tissue culture plates (pore size 1  $\mu\text{m}$ ; Costar, Cambridge, MA) for coculture experiments. HCV replicon cells ( $10^5$  cells) were incubated in the lower compartment with various numbers of lymphocytes in the upper compartment. The HCV replicon cells in the lower compartments were collected at 48 hours after the coculture for luciferase assays in duplicate with the use of a luminometer (TriStar LB 941; Berthold Technologies, Oak Ridge, TN) with the Bright-Glo Luciferase Assay System (Promega, Madison, WI).

#### Statistical Analysis

Data are presented as mean  $\pm$  SEM. The statistical difference between results were analyzed by Student *t* test (2 tailed), using the Statistical Package for the Social Sciences (SPSS) software version 19 for Windows (IBM Corp, Armonk, NY). *P* values of  $\leq 0.05$  were considered to be statistically significant.

## RESULTS

### Effect on the Surface Phenotype of LMNCs

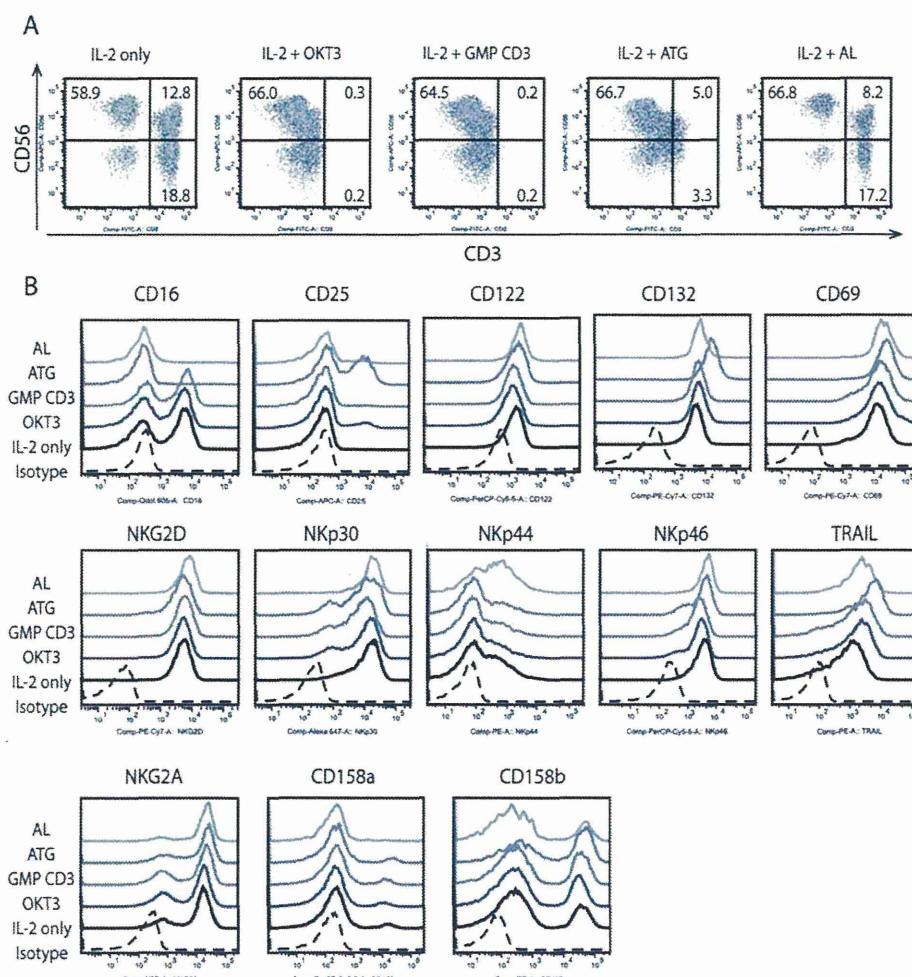
In 5 LMNC preparations, the addition of OKT3 GMP CD3 to IL-2-stimulated LMNCs decreased CD3 $^+$ CD56 $^-$  T cells to

0.2%  $\pm$  0.1% and 0.2%  $\pm$  0.1%, respectively, from the IL-2-only control value of 28.1%  $\pm$  12.3%. In contrast, CD3 $^+$ CD56 $^-$  T cells were retained among LMNCs with the addition of antithymocyte globulin or alemtuzumab: 3.3%  $\pm$  2.0% and 17.2%  $\pm$  7.3%, respectively. The proportion of CD3 $^-$ CD56 $^+$  NK cells increased by  $\sim 10\%$  in all groups (Fig 1A).

Addition of OKT3 or GMP CD3 to IL-2-stimulated LMNCs maintained both activation and inhibitory markers on NK cells. Interestingly, the expressions of TRAIL, CD25 (IL-2 $\alpha$ R), and CD132 (IL-2 $\gamma$ R) were increased in the antithymocyte globulin group. Furthermore, both antithymocyte globulin and alemtuzumab completely blocked the expression of CD16 on NK cells (Fig 1B).

### Cytotoxic Capacity

Cytotoxicity assays were performed with the use of freshly isolated cultured LMNCs as effectors and K562 cells as targets. Fig 2 shows freshly isolated LMNCs barely mediated cell death, whereas IL-2-stimulated LMNCs produced significant cytotoxicity. Although the ratios of CD3 $^-$ CD56 $^+$  to CD3 $^+$ CD56 $^+$  cells varied after treatment with various



**Fig 1.** Effect of the T-cell depletion antibodies on the phenotypic characteristics of liver mononuclear cells (LMNCs). LMNCs obtained from cadaveric donors were stimulated with IL-2 (1000 U/mL) for 4 days. Anti-CD3 mAb (OKT3; 1  $\mu\text{g}/\text{mL}$ ), MACS GMP CD3 pure (GMP CD3; 1  $\mu\text{g}/\text{mL}$ ), antithymocyte globulin (ATG; 100  $\mu\text{g}/\text{mL}$ ), or alemtuzumab (AL; 100  $\mu\text{g}/\text{mL}$ ) was added to the culture medium 1 day before cell harvesting. (A) The LMNCs were stained with monoclonal antibodies against CD3 and CD56. The numbers indicate the mean percentages of the population. (B) Histograms show the logarithmic fluorescence intensities obtained on staining for each surface marker after gating on the CD3 $^-$ CD56 $^+$  NK cells. Dotted lines indicate negative control samples with isotype-matched mAbs. The flow cytometry dot plot and histogram profiles represent 5 independent experiments. TRAIL, tumor necrosis factor-related apoptosis-inducing ligand.

**Fig 2.** Antitumor effect of the T-cell depletion antibodies on IL-2-stimulated liver mononuclear cells (LMNCs). The NK cell cytotoxic activities of untreated cells and IL-2-stimulated LMNCs treated with various reagents were analyzed by a flow cytometry (FCM)-based cytotoxic assay. (A) Gate is set on cells to discriminate CFSE<sup>+</sup> targets from LMNCs. Gate is set on target to obtain the number of live and dead K562 cells. The FCM dot plot profiles represent 5 independent experiments. (B) The data represent the mean  $\pm$  SEM of the percentage of target lysis at effector-to-target (E:T) ratios of 10:1 (5 LMNCs;  $^{\#}P < .01$ ;  $^{*}P < .05$  vs untreated group, *t* test).

T-cell depletion reagents for 4 days in culture, all cultured LMNCs exhibited vigorous cytotoxicity against K562. LMNCs treated with antithymocyte globulin showed slightly decreased cytotoxicity compared with the other groups, but the difference was not significant. This tendency was similar to that reported in an earlier study.<sup>36</sup> The cultured LMNCs did not show cytotoxicity against self-lymphoblasts (data not shown).

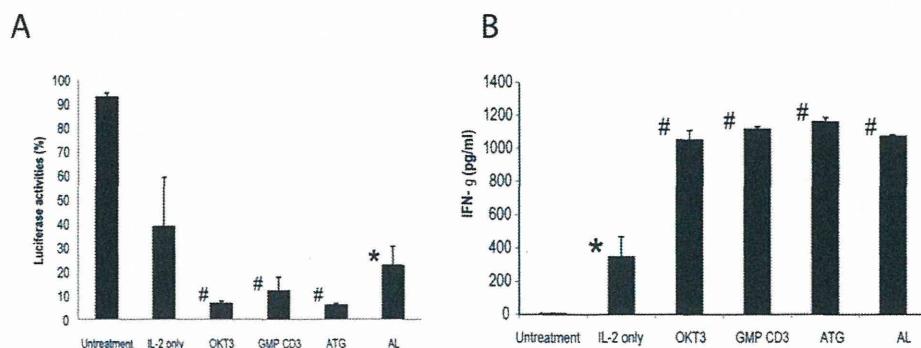
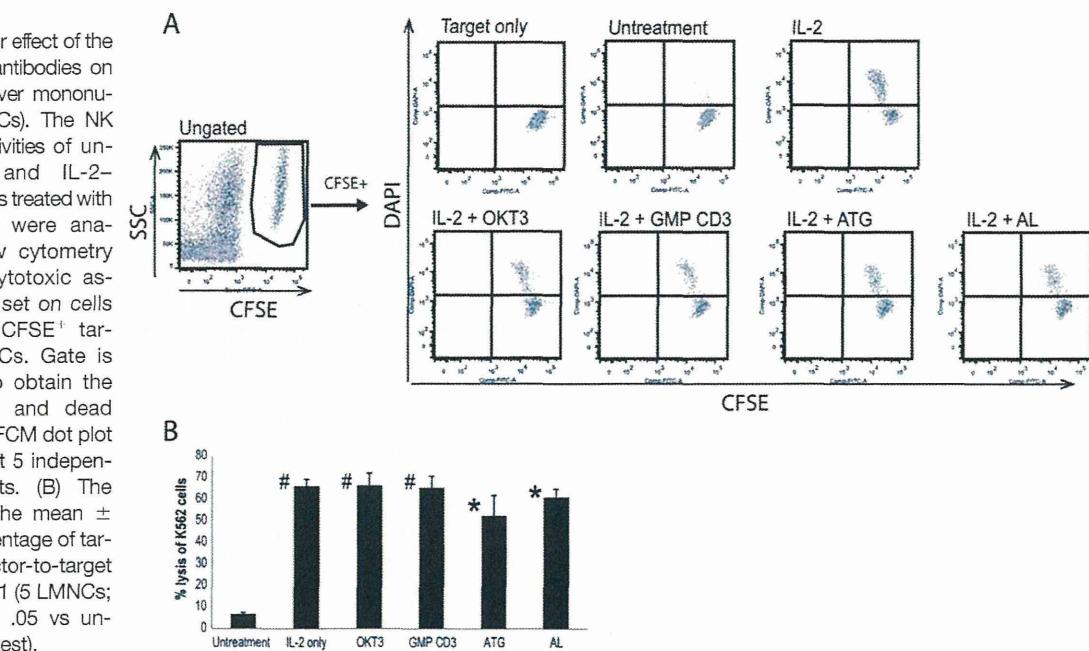
#### Anti-HCV Activity

IL-2-cultured LMNCs inhibited 40% luciferase reporter activity compared with freshly isolated LMNCs (Fig 3A). As we have reported before, the anti-HCV effect of IL-2-activated LMNCs

was strongly enhanced by OKT3 treatment.<sup>14</sup> GMP CD3 treatment showed ~80% decreased HCV replication, which was almost the same effect as that caused by OKT3. Surprisingly, antithymocyte globulin and alemtuzumab treatment also elicited robust anti-HCV effects on LMNCs. We previously reported that IFN- $\gamma$  secreted from LMNCs activated by IL-2 and OKT3 was responsible for the anti-HCV activity of these cells.<sup>14</sup> Cultured LMNCs also actively produced large amounts of IFN- $\gamma$  (Fig 3B), which probably played a pivotal role in their anti-HCV activity.

#### DISCUSSION

In this study, we discovered GMP CD3 to be an alternative reagent to OKT3 for immunotherapy using liver NK cells.



**Fig 3.** Anti-hepatitis C virus (HCV) effect of the T-cell depletion antibodies on IL-2-stimulated liver mononuclear cells (LMNCs). The LMNCs cultured for 4 days in the presence of IL-2 and various reagents were incubated with HCV replicon-containing cells for 48 hours in transwell tissue culture plates (effector-to-target ratio, 10:1). (A) Luciferase activity of HCV replicon-containing cells in the presence of effectors, normalized to luciferase activity in the absence of effectors. The difference in anti-HCV effect between the reagent-treated LMNCs and the freshly isolated LMNCs was statistically significant (5 LMNCs;  $^{\#}P < .01$ ;  $^{*}P < .05$  vs untreated group, *t* test). (B) IFN- $\gamma$  production during the culture, as measured by ELISA [mean  $\pm$  SEM (5 samples;  $^{\#}P < .01$ ;  $^{*}P < .05$  vs untreated group, *t* test)].