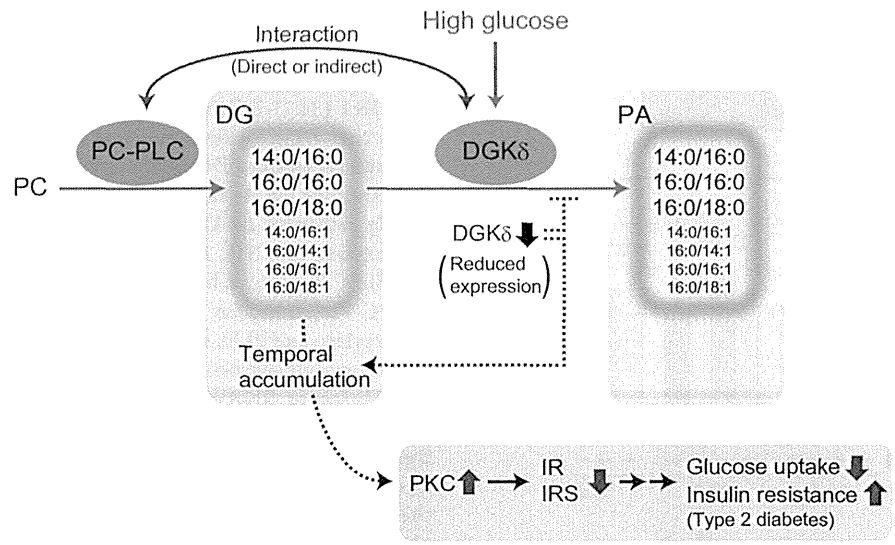

FIGURE 9. **Model for the metabolism pathway utilized by DGKδ.** *IR*, insulin receptor; *IRS*, insulin receptor substrate.

result of promoting the *de novo* synthesis of fatty acids. However, in this study, an inhibitor of acetyl-CoA carboxylase TOFA did not decrease glucose-stimulated PA production (Fig. 6*A*). Because differentiation is a long term event, the difference between acute high glucose stimulation in C2C12 myoblasts and adipocyte differentiation may be due to distinct supply pathways and/or fatty acid conversion during long term culture through the remodeling pathway (Lands' cycle) (39).

Chibalin *et al.* (15) previously reported that the transcription of DGKδ and the levels of DGKδ protein were also reduced in skeletal muscle from type II diabetes patients. Moreover, in DGKδ haploinsufficient mice (DGKδ$^{+/-}$), the accumulation of DG, which was caused by decreases in total DGK activity and DGKδ protein levels in skeletal muscle, increased phosphorylation of PKCδ and suppressed protein expression of the insulin receptor and insulin receptor substrate-1 for insulin signaling, resulting in the aggravation of type II diabetes (15). Another study reported that the accumulation of DG molecular species with palmitic acid (16:0) is involved in insulin resistance (40). It is generally accepted that saturated fatty acids including palmitic acid induce insulin resistance (41–43). In this study, MS/MS analysis demonstrated that 30:0-, 30:1-, 32:0-, 32:1-, 34:0-, and 34:1-PA commonly contained palmitic acid (16:0), and suggests that DGKδ mainly consumes 30:0-, 30:1-, 32:0-, 32:1-, 34:0-, and 34:1-DG containing palmitic acid (16:0) supplied from the PC-PLC pathway for glucose uptake in skeletal muscle in a glucose-dependent manner. Acute high glucose- and DGKδ-dependent increases in 30:0-, 30:1-, 32:0-, 32:1-, 34:0-, and 34:1-PA were relatively minor changes (20–30% increases) when compared with the total amounts of each PA species (Figs. 1 and 2). DGKδ, which was temporarily activated within 5 min (16), showed a distinct punctate localization pattern in C2C12 cells (17). Therefore, a possible explanation of these findings is that these DGKδ-dependent minor changes of DG/PA species in temporally and spatially restricted regions play a role in modulating insulin signaling. However, further studies are required to elucidate the relationship between the specific DG species accumulation in type II diabetes patients and the PC-PLC-DGKδ pathway disclosed here.

In summary, the present study strongly suggests that DGKδ preferentially consumes palmitic acid (16:0)-containing DG species such as 30:0-, 30:1-, 32:0-, 32:1-, 34:0-, and 34:1-DG, but not arachidonic acid (20:4)-containing DG species derived from the phosphatidylinositol turnover, in glucose-stimulated C2C12 myoblasts (Fig. 9). Moreover, an unexpected linkage between PC-PLC and DGKδ emerged. The route "PC → PC-PLC → DG → DGK → PA" proposed here (Fig. 9) is a novel DG metabolic pathway. This new pathway is proposed to play an important role in glucose uptake in skeletal muscle and to be involved in the pathogenesis of type 2 diabetes.

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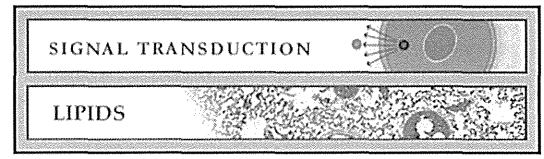
Signal Transduction:

Diacylglycerol Kinase δ Phosphorylates Phosphatidylcholine-specific Phospholipase C-dependent, Palmitic Acid-containing Diacylglycerol Species in Response to High Glucose Levels



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ORIGINAL ARTICLE

Outcomes of living donor liver transplantation for hepatitis C virus-positive recipients in Japan: results of a nationwide survey

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Keywords
hepatitis C virus, living donor liver transplantation, nationwide survey.

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The authors have declare no conflict of interest.

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Summary

A nationwide survey of living donor liver transplantation (LDLT) for hepatitis C virus (HCV)-positive recipients was performed in Japan. A total of 514 recipients are reported and included in the study. The cumulative patient survival rate at 5 and 10 years was 72% and 63%, respectively. Of the 514 recipients, 142 patients (28%) died until the end of the observation, among which the leading cause was recurrent hepatitis C (42 cases). According to Cox regression multivariate analysis, donor age (>40), non-right liver graft, acute rejection episode, and absence of a sustained virologic response were independent prognostic factors. Of the 514 recipients, 361 underwent antiviral treatment mainly with pegylated-interferon and ribavirin (preemptive treatment in 150 patients and treatment for confirmed recurrent hepatitis in 211). The dose reduction rate and discontinuation rate were 40% and 42%, respectively, with a sustained virologic response rate of 43%. In conclusion, patient survival of HCV-positive recipients after LDLT was good, with a 10-year survival of 63%. Right liver graft might be preferable for HCV-positive recipients in an LDLT setting.

Introduction

End-stage liver disease caused by chronic hepatitis C virus (HCV) infection is the leading cause of liver transplantation in Western countries [1,2] and Japan [3]. Liver transplantation, including deceased donor liver transplantation (DDLT) and living donor liver transplantation (LDLT), is an established treatment for these patients, although it unfortunately does not cure HCV-infected recipients. Reinfection by HCV occurs universally and the progression of recurrent hepatitis C in the graft is accelerated compared with chronic hepatitis C infection in the nontransplant population, resulting in the impaired outcome of HCV-positive recipients compared with those with other indications [4–6]. Recently, effective antiviral therapies with new protease inhibitors have been aggressively investigated [7]; however, post-transplant antiviral treatment with pegylated-interferon (PEG-INF) and ribavirin (RBV) has been the main strategy to improve the outcome in both DDLT and LDLT [8] in our study period. While patient survival is significantly improved by achieving a sustained virologic response (SVR) with antiviral treatment among patients with chronic hepatitis C [9], the efficacy of antiviral treatment varies among HCV-positive liver transplant recipients [10].

Here, we conducted a nationwide survey of LDLT for HCV-positive patients and investigated the outcome and prognostic factors for patient survival to further improve the LDLT outcome. We also provide an overview of the antiviral treatment for LDLT recipients in Japan.

Patients and methods

Liver transplantations performed between 1998 and 2012 were collected and reviewed, and the initial LDLT was the subject of this study. The survey was conducted by the Research Group on Hepatitis under the aegis of the Japanese Ministry of Health, Welfare, and Labor. The indication of LDLT for HCV-positive recipients in Japan is similar to that for deceased donor liver transplantation (DDLT) in Western countries [11]. As for cases with hepatocellular carcinoma (HCC), Milan criteria are basically used; however, all institutions apply center-specific extended criteria for those beyond Milan provided that they are without extrahepatic lesions and macroscopic vascular invasions [12]. Data of all consecutive HCV-positive cases were enrolled in the study during this period, completing questionnaire items on computerized database by each institution. A total of 514 HCV-positive recipients from 12 institutions were enrolled in the present retrospective analysis. We first analyzed patient outcome and investigated the factors associated with poor survival among the collected variables. Next, we administered a survey regarding antiviral treatment after LDLT in Japan.

Evaluated variables

The following variables were obtained from the nationwide survey. As for recipient factors, patient age, sex, the existence of pretransplant antiviral treatment, HCV genotype, model for end-stage liver disease (MELD) score, the coexistence of hepatocellular carcinoma, the type of calcineurin inhibitor, use of mycophenolate mofetil (MMF), existence of steroid withdrawal, existence of steroid bolus treatment, splenectomized or not, episodes of acute rejection, existence of the post-transplant antiviral treatment, and achievement of SVR were collected. The diagnosis of acute rejection was based on internationally accepted histologic criteria (Banff guidelines) based on liver biopsies, which was treated with steroid bolus injection initially in the majority of center. The second-line treatments were center dependent, such as 1500–3000 mg of MMF or basiliximab, an interleukin-2 receptor antagonist. Additionally, donor age and the type of partial liver graft were added as variables. The number of LDLT cases per year at each center was also incorporated as a variable, with a cutoff value of 20 cases per year. All these factors were completely fulfilled by each center and assessed for their association with patient outcome. Other incomplete variables which may have a possible association with patient survival, such as IL-28 gene polymorphisms, histological findings, biliary complications, and cytomegalovirus infection, were not incorporated into the analysis.

We then surveyed post-LDLT antiviral treatment. The timing of the antiviral treatment (preemptive or after confirmation of recurrent disease), the antiviral treatment regimen used, time from LDLT to starting antiviral therapy, duration of antiviral therapy, adherence to the treatment, dose reduction rate, and finally the SVR rate were summarized.

Statistical analysis

Continuous variables are reported as medians and ranges, and categorical variables are reported as numbers (proportions). Cumulative survival is presented with Kaplan–Meier curves, and differences in survival between the groups were analyzed with a log-rank test. Factors associated with survival in the log-rank test were then analyzed using a Cox regression analysis. Five patients were lost to follow up during the observation period, and they were censored in the survival analysis. The cutoff value for the continuous variables was basically set according to each mean value, except for the recipient age for which it was set at 60 (mean value of 57) based on literatures. All statistical tests were two-sided, and a *P*-value of <0.05 was considered significant. The statistical analyses were performed with SPSS statistical software (Chicago, IL, USA) 18.0 for Windows.

Table 1. Characteristics of living donor liver transplantations for HCV-positive recipients in Japan.

	Total n = 514 (%)
Age (years)	57 (19–73)
Gender: male/female	320 (62)/194 (38)
Body mass index	25 (16–41)
Pretransplant antiviral treatment: yes/no	230 (45)/284 (55)
HCV genotype: 1b/other types	404 (79)/110 (21)
Co-existence of HCC: yes/no	330 (64)/184 (36)
MELD score	15 (4–47)
Transplant at the center with LDLT cases over 20 per year: yes/no	259 (50)/255 (50)
Calcineurin inhibitor: Tac/CsA	324 (63)/198 (37)
Mycophenolate mofetil yes/no	251 (49)/ 263 (51)
Steroid withdrawal: yes/no	144 (28)/370 (72)
Splenectomy: yes/no	284 (55)/230 (45)
Episode of acute rejection: yes/no	127 (25)/387 (75)
Steroid bolus injection: yes/no	414 (81)/100 (19)
Post-transplant antiviral treatment: yes/no	361 (71)/153 (29)
Achievement of SVR: yes/no	154 (30)/360 (70)
Donor age (years)	35 (17–66)
Type of graft: right/non-right	259 (50)/255 (50)

HCV, hepatitis C virus; HCC, hepatocellular carcinoma; LDLT, living donor liver transplantation; MELD, model for end-stage liver disease; Tac, tacrolimus; CsA, cyclosporine; SVR, sustained virologic response.

Results

Patient characteristics

The characteristics of 514 HCV-positive recipients are summarized in Table 1. There were 320 men and 194 women, with a median age of 57 years (range = 19–73). The median follow-up period was 3.5 years (range = 0.4–13), with a wide spectrum of follow-up duration due to death or shorter observation period from LDLT. The median MELD score was 14.7 (range = 4–47). HCV genotype was 1b in 405 patients (79%). The median age of the living donors was 35 years (range = 17–66), and the graft type was right liver in 259 cases (50%), left liver in 239 cases (46%), and the right lateral sector in 16 cases (4%).

Patient survival

The cumulative patient survival rate at 1, 3, 5, and 10 years was 86%, 76%, 72%, and 63%, respectively (Fig. 1). The causes of patient loss are summarized in Table 2. A total of 142 patients died until the end of the observation. Patient loss due to recurrent hepatitis, which was the leading cause of recipient death in this cohort, occurred in 42 cases, corresponding to 3% of all cases and 30% of lost cases, respectively. Hepatocellular carcinoma recurrence and sepsis were second, with 22 cases each. Additionally, the number of patient death was presented among two groups stratified by the achievement of SVR.

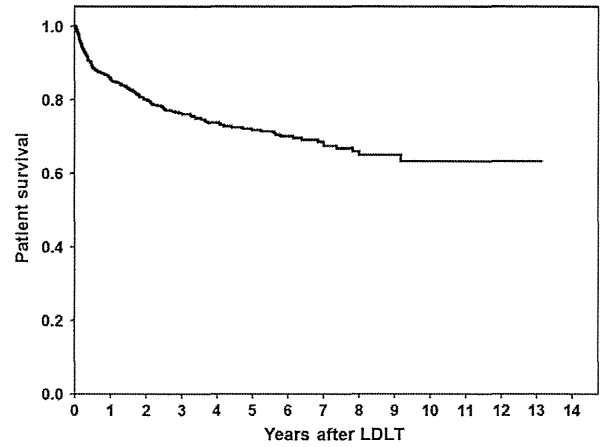

Figure 1 Kaplan–Meier survival curve of the cohort. LDLT, living donor liver transplantation.

Prognostic factors associated with patient survival after LDLT

Recipient and donor factors were analyzed for overall mortality. The results of univariate and multivariate analyses are shown in Table 3. Univariate analysis by the log-rank test revealed that donor age (>40 years; $P < 0.001$), non-right liver graft ($P = 0.036$), an episode of acute rejection ($P < 0.001$), steroid bolus injection ($P < 0.001$), and the absence of SVR ($P < 0.001$) were significant predictors of a poorer outcome of HCV-positive recipients. The Kaplan–Meier survival curves stratified by these factors are presented in Fig. 2. According to Cox regression multivariate analysis, donor age (>40), non-right liver graft, an acute rejection episode, and the absence of SVR were independent prognostic factors (Table 3).

Additionally, we did the same analysis among those achieved SVR after antiviral treatment (n = 154), in which no factor was revealed to be associated with the patient survival (Table 4).

Antiviral treatment after LDLT

Of the 514 recipients, while 153 patients have never undergone antiviral treatment including five patients achieving preoperative SVR, 361 underwent antiviral treatment. Of those, 211 patients (58%) received antiviral treatment after confirmation of recurrent hepatitis C, while the remaining 150 recipients received antiviral treatment preemptively. The summary of the antiviral treatment is shown in Table 5. Time from LDLT to beginning treatment was

Table 2. Causes of patient death.

Patient group	All patients (n = 514) n (%)	With SVR (n = 154) n (%)	Without SVR (n = 360) n (%)
Recurrent HCV	42 (30)	0	42 (37)
Recurrent HCC	22 (15)	8 (30)	14 (12)
Infection	22 (15)	4 (15)	18 (16)
Cerebrovascular diseases	12 (8)	4 (15)	8 (7)
Rejection	8 (6)	0	8 (7)
Graft thrombosis	7 (5)	0	7 (6)
Small for size syndrome	6 (4)	0	6 (5)
Other causes	23 (17)	11 (40)	12 (10)
Total	142	27	115

HCV, hepatitis C virus; HCC, hepatocellular carcinoma; SVR, sustained virologic response.

rather short (median: 3 months), whereas the treatment duration was long (median: 17 months), the rate of dose reduction (40%) and discontinuation (42%) were high, and the SVR rate was 43%.

Discussion

This is the largest series of LDLT for HCV-positive recipients reported to date. A total of 514 recipients from 12 Japanese institutions were enrolled and reviewed, with 5- and 10-year cumulative patient survival rates of 72% and 63%, respectively. A recent article from the United Network for Organ Sharing (UNOS) database in the United States of America (USA) reported patient survival rates of 76% and 71% at 5 and 10 years, respectively, among 15 147 HCV-positive DDLT recipients [1]. Similarly, the European Liver Transplant Registry reported 5- and 10-year patient survival rates of 65% and 53%, respectively, among 10 753 HCV-positive DDLT recipients [2]. Based on these reports, the present outcomes of the Japanese nationwide survey of LDLT for HCV-positive recipients are comparable with those of deceased donor whole liver transplantation (DDLT) in both the USA and Europe. However, caution should be paid in comparing the survival results of HCV-positive recipients between LDLT and DDLT. As shown in previous reports [13,14], laboratory MELD score of HCV-positive recipients was higher in DDLT recipients than that in LDLT recipients. Actually, our result, mean MELD score of 15 (median: 14.7, range: 4–47) was lower than that reported in DDLT recipients in Western countries (around 20), which might have a positive impact on patient survival in our study. Another point which should be noted is that the observation period of database of USA and Europe was longer than that of Japan, which might result in the bias of the improvement in techniques and managements in liver transplant.

Table 3. Factors associated with patient survival after living donor liver transplantation for HCV-positive recipients.

Univariate analysis	Hazard ratio (95% confidence interval)	P-value
Recipient age: ≥60 years vs. <60 years	1.322 (0.915–1.876)	0.122
Recipient gender: male versus female	1.072 (0.765–1.432)	0.682
Body mass index: ≥25 vs. <25	0.999 (0.64–1.559)	0.995
Pretransplant antiviral treatment: yes versus no	0.921 (0.721–1.387)	0.912
HCV genotype: 1b versus other types	1.211 (0.781–1.901)	0.723
Co-existence of HCC: yes versus no	0.893 (0.612–1.223)	0.754
MELD score: ≥15 vs. <15	1.125 (0.878–1.389)	0.801
LDLT cases per year: ≥20 vs. <20	1.122 (0.669–1.881)	0.663
Calcineurin inhibitor: Tac versus CyA	0.887 (0.643–1.511)	0.789
Mycophenolate mofetil: yes versus no	0.963 (0.642–1.446)	0.857
Steroid withdrawal: yes versus no	1.003 (0.761–1.621)	0.932
Splenectomy: yes versus no	0.961 (0.623–1.367)	0.889
Episode of acute rejection: yes versus no	3.101 (2.013–5.871)	<0.001
Steroid bolus injection: yes versus no	2.512 (1.541–3.512)	0.003
Achievement of SVR: yes versus no	0.167 (0.121–0.254)	<0.001
Donor age: ≥40 years vs. <40 years	2.231 (1.401–3.331)	<0.001
Type of graft: right liver versus non-right liver	0.422 (0.311–0.711)	0.029
Multivariate analysis		
Episode of acute rejection: yes versus no	3.241 (1.789–5.329)	<0.001
Achievement of SVR: yes versus no	0.181 (0.124–0.301)	<0.001
Donor age: ≥40 years vs. <40 years	2.311 (1.498–3.311)	<0.001
Type of graft: right liver versus non-right liver	0.467 (0.331–0.621)	0.001

HCV, hepatitis C virus; HCC, hepatocellular carcinoma; LDLT, living donor liver transplantation; MELD, model for end-stage liver disease; Tac, tacrolimus; CsA, cyclosporine; SVR, sustained virologic response.

The present analysis of prognostic factors for impaired patient survival revealed four variables as independent predictors: donor age over 40 years, an acute rejection episode, absence of SVR, and a non-right liver graft. In contrast to the report from USA [13], the center experience did not affect the outcome of patient outcome.

The impact of donor age on outcome has gained increased attention in the DDLT setting due to the

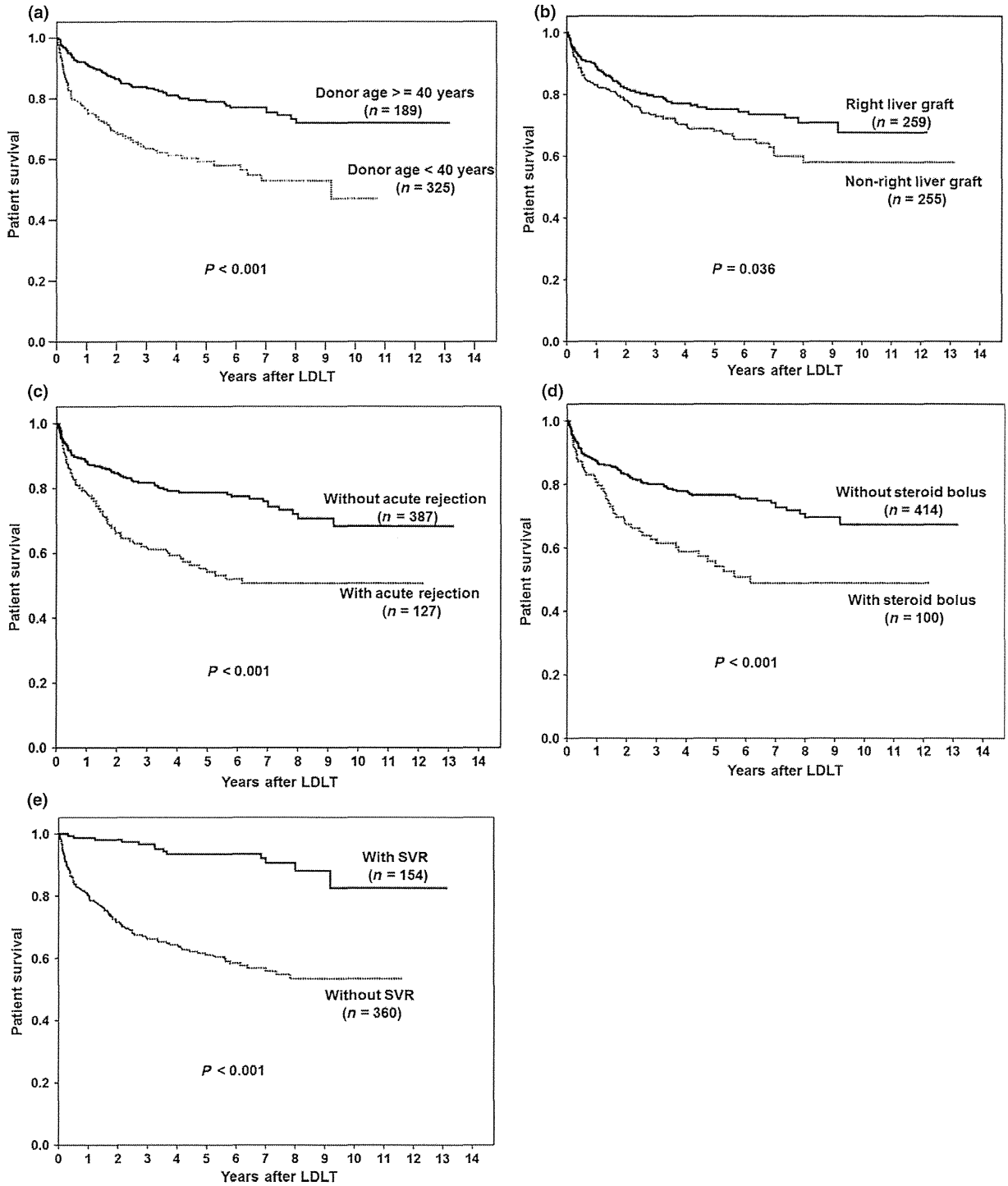

Figure 2 Kaplan–Meier curves stratified by each variable: (a) donor age, (b) graft type, (c) acute rejection, (d) steroid bolus, and (e) sustained virologic response. LDLT, living donor liver transplantation; SVR, sustained virologic response.

increased use of liver grafts from older donors. For HCV-positive recipients, two large retrospective reports from the Scientific Registry of Transplant Recipients and UNOS databases reported that donor age over 40 is an independent predictor of patient death [15,16]. Other accumulating reports [14,17,18] indicate that the grafts from older

Table 4. Factors associated with patient survival among those achieved SVR (n = 154).

Cox regression analysis	Hazard ratio (95% confidence interval)	P-value
Recipient age: ≥60 years (n = 43) vs. <60 years (n = 111)	1.424 (0.318–2.385)	0.644
Recipient gender: male (n = 100) versus female (n = 54)	4.709 (0.918–24.161)	0.063
Pretransplant antiviral treatment: yes (n = 66) versus no (n = 88)	1.666 (0.350–7.931)	0.522
HCV genotype: 1b (n = 112) versus other types (n = 42)	0.873 (0.203–3.747)	0.855
Co-existence of HCC: yes (n = 54) versus no (n = 100)	0.728 (0.179–2.694)	0.635
MELD score: ≥15 (n = 54) vs. <15 (n = 98)	1.354 (0.578–3.204)	0.785
LDLT cases per year: ≥20 (n = 82) vs. <20 (n = 72)	1.054 (0.458–1.254)	0.854
Calcineurin inhibitor: Tac (n = 94) versus CyA (n = 60)	3.580 (0.736–17.421)	0.114
Mycophenolate mofetil: yes (n = 78) versus no (n = 76)	0.932 (0.456–1.884)	0.781
Steroid withdrawal: yes (n = 40) versus no (n = 114)	0.449 (0.096–2.102)	0.31
Splenectomy: yes (n = 59) versus no (n = 95)	1.402 (0.335–5.873)	0.644
Episode of acute rejection: yes (n = 34) versus no (n = 120)	1.854 (0.216–15.914)	0.574
Steroid bolus injection: yes (n = 26) versus no (n = 128)	0.16 (0.019–1.386)	0.096
Donor age: ≥40 years (n = 43) vs. <40 years (n = 111)	1.18 (0.296–4.698)	0.815
Type of graft: right liver (n = 80) versus non-right liver (n = 74)	2.799 (0.818–9.573)	0.101

HCV, hepatitis C virus; HCC, hepatocellular carcinoma; LDLT, living donor liver transplantation; MELD, model for end-stage liver disease; Tac, tacrolimus; CsA, cyclosporine; SVR, sustained virologic response.

donors are at greater risk for disease progression and impaired graft/patient survival compared with those from younger donors. Our results are definitely consistent with these reports.

Acute rejection in conjunction with treatment with a steroid bolus is one of the most critical factors to address with respect to HCV recurrence. Historical studies [19,20] have demonstrated that steroid bolus for acute rejection in HCV-positive recipients accelerates the recurrence of hepatitis and decreases patient survival. A recent study reported that HCV-positive recipients who receive high-dose steroid treatment for acute rejection are at increased risk of severe recurrent hepatitis, in which older donor age and an episode of rejection are the two most important predictors of developing fibrosing cholestatic hepatitis [21]. Similarly, our study also revealed that both older donor age and acute rejection are independent predictors for impaired patient outcome among LDLT recipients.

Table 5. Summary of antiviral treatment.

	Total (n = 361)	Treatment for established recurrent hepatitis C (n = 211)	Preemptive treatment (n = 150)
Time since LDLT (months)	3 (0–102)	4 (0.5–102)	1 (0–68)
Treatment duration (months)	15 (0.3–99)	14 (0.3–99)	17 (0.3–55)
Regimen: PEG-INF alfa-2a/RBV	45 (12%)	33 (16%)	12 (8%)
PEG-INF alfa-2b/ RBV	223 (62%)	146 (69%)	77 (51%)
INF alfa-2b	93 (26%)	32 (15%)	61 (41%)
Dose reduction	143 (40%)	85 (40%)	58 (39%)
Discontinuation	150 (42%)	66 (31%)	84 (56%)
Sustained virologic response	154 (43%)	89 (42%)	65 (43%)

LDLT, living donor liver transplantation; PEG-INF, pegylated-interferon; RBV, ribavirin; INF, interferon.

The association between achieving SVR and graft/patient survival after liver transplantation for HCV-positive recipients is a matter of debate [10]. Many studies with standard dual treatment of PEG-INF/RBV for 12 months in a DDLT setting have implied a survival benefit of achieving SVR [8,22], but there has been no evidence to support the recommendation of antiviral treatment for recurrent graft hepatitis C due to the lack of clinical benefit with sufficient long-term observation and the existence of frequent severe adverse effects, as concluded by a recent Cochrane meta-analysis [10]. Recent retrospective cohort studies with a long follow-up duration reported improved patient/graft survival in patients who obtained an SVR after antiviral treatment [23–25]. In accordance with those reports, our retrospective analysis indicated a positive effect of achieving SVR on patient survival. Caution should be taken in interpreting our results; however, as SVR was assessed among the whole cohort, including patients who were not indicated for antiviral treatment, the follow-up period after achieving SVR was rather short, and most importantly, a large variety of antiviral treatment regimens were used in Japan, which will be described later.

A noteworthy finding in the present retrospective analysis is the impaired patient survival in recipients who received a non-right liver graft (left liver in 239 cases and right lateral sector in 16 cases). Recent studies comparing outcomes between LDLT and DDLT in HCV-positive recipients have reported equal or even improved outcomes both in patient/graft survival and in fibrosis progression in the LDLT setting, which could be attributed to the younger donor age and shorter ischemic time of LDLT grafts [13,14,26–29].

Based on these findings, LDLT for HCV-positive recipients is now widely accepted as an established alternative to DDLT, even in Western countries. On the contrary, however, the present finding may raise an alarm for reduced size grafts, as a left or posterior graft is clearly smaller than a right liver graft. Another point to be emphasized here is that all LDLTs investigated in the aforementioned studies comparing LDLT and DDLT were universally performed with right liver grafts. One possible explanation for the inferior outcome of the smaller graft is that the intense hepatocyte proliferation that occurs in smaller partial liver grafts may lead to increased viral translation and replication, as advocated by previous authors [30–32]. However, there are several limitations among these speculations. First, the data of the viral load, which is reported to reach a maximum level between the first and third post-transplant months [33], were not available in this study to demonstrate the higher viral replication in the smaller grafts during this period. Another is that the graft type selection is based on the ratio of the volume of the graft to recipient body weight or standard liver volume in our society, which will lead to the bias in the comparison of the right liver versus non-right liver graft. Despite these limitations, considering that comparable outcomes between left liver graft and right liver graft have been reported by us [34] and others [35] in LDLT recipients as a whole, caution should be taken in selecting the type of graft (left versus right) for HCV-positive recipients. Thus, future LDLT studies are required to investigate whether a smaller partial liver graft (left liver) is potentially inferior compared with a larger graft (right liver) in terms of graft/patient survival and recurrent hepatitis severity among HCV-positive recipients.

The antiviral treatment for recurrent hepatitis C after LDLT in Japan was also reviewed in the present study. As described elsewhere in detail [11], the antiviral treatment regimen in Japan differs widely from center to center; preemptive treatment versus treatment after confirmation of recurrent disease, starting dose and method of escalation, and the duration of treatment (usually longer than 12 months). Consequently, our data only present an overview of antiviral treatment in Japan, and no definite conclusion can be drawn regarding the actual efficacy of antiviral treatment after LDLT. Moreover, based on the recent prospective, multicenter, randomized study by Bzowej *et al.* [36], European and USA transplant societies do not support the routine use of preemptive antiviral therapy. A review of Western literature regarding the standard 12-month PEG-INF/RBV treatment for established recurrent hepatitis C after DDLT reveals that the median SVR rate is 33% (0–56%) with a dose reduction rate of 70% and a discontinuation rate of 30% [37]. The present result of an SVR rate of 43% with a dose reduction rate of 40% and a discontinuation rate of 42% seems not so different from those of previous literatures; however, as discussed above, the diversity in the methods, the doses, and the duration of treatment in Japan preclude the direct comparison with Western findings.

Conclusion

This retrospective analysis of the largest series of LDLT for HCV-positive recipients in Japan revealed 5- and 10-year survival rates of 72% and 63%, respectively, and that donor age (>40), non-right liver graft, an acute rejection episode, and the absence of SVR are independent predictors of patient survival. Based on the present result, caution should be made in the selection of the left liver graft for HCV-positive recipients; however, the development of more effective antiviral treatment in the near future may facilitate the application of the left liver graft.

Authorship

YM: designed the study. TI: collected data. NA, YS, NK, SE, TF, HO, HN, AT, YK, MS, YK, KY, KS, MM and MT: performed the study. NA and YS: analyzed and wrote the paper.

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Heat shock factor 1 accelerates hepatocellular carcinoma development by activating nuclear factor-κB/mitogen-activated protein kinase

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Heat shock factor 1 (HSF1), a major transactivator of stress responses, has been implicated in carcinogenesis in various organs. However, little is known about the biological functions of HSF1 in the development of hepatocellular carcinoma (HCC). To clarify the functional role of HSF1 in HCC, we established HSF1-knockdown (HSF1 KD) KYN2 HCC cells by stably expressing either small hairpin RNA (shRNA) against HSF1 (i.e. HSF1 KD) or control shRNA (HSF1 control). Tumorigenicity was significantly reduced in orthotopic mice with HSF1 KD cells compared with those with HSF1 control cells. Reduced tumorigenesis in HSF1 KD cells appeared attributable to increased apoptosis and decreased proliferation. Tumor necrosis factor-α-induced apoptosis was increased in HSF1 KD cells and HSF1$^{-/-}$ mouse hepatocytes compared with controls. Decreased expression of IκB kinase γ, a positive regulator of nuclear factor-κB, was also observed in HSF1 KD cells and HSF1$^{-/-}$ mouse hepatocytes. Furthermore, expression of bcl-2-associated athanogene domain 3 (BAG3) was dramatically reduced in HSF1 KD cells and HSF1$^{-/-}$ mouse hepatocytes. We also found that epidermal growth factor-stimulated mitogen-activated protein kinase signaling was impaired in HSF1 KD cells. Clinicopathological analysis demonstrated frequent overexpression of HSF1 in human HCCs. Significant correlations between HSF1 and BAG3 protein levels and prognosis were also observed. In summary, these results identify a mechanistic link between HSF1 and liver tumorigenesis and may provide as a potential molecular target for the development of anti-HCC therapies.

Introduction

Hepatocellular carcinoma (HCC) is one of the most common malignant tumors and the third leading cause of cancer death worldwide (1). Despite marked advances in diagnostic and therapeutic techniques, prognosis remains unsatisfactory for HCC patients (2,3). An understanding of HCC carcinogenesis at the molecular level is thus urgently needed in order to identify novel molecular targets for the development of more effective therapies.

Heat shock factor 1 (HSF1) is the main regulator of the heat shock response, which is involved in protecting cells and organisms from heat, ischemia, inflammation, oxidative stress and other noxious conditions (4,5). Under various forms of physiological stress, HSF1 drives the production of heat shock proteins (HSPs), such as HSP27, HSP70 and HSP90, which act as protein chaperones (5,6). The functions of HSF1 are not limited to increasing the expression of chaperones; HSF1 also modulates the expression of hundreds of genes other than chaperones that are critical for survival under an array of potentially lethal stressors (6–8). As a result, HSF1 influences fundamental cellular processes such as cell cycle control, protein translation, glucose metabolism and proliferation (7–12). In human tumors, constitutive expression of Hsp27, Hsp70 and Hsp90 at high levels predicts poor prognosis and resistance to therapy (13–15). These effects are often attributable to HSF1-dependent mechanisms (16). Thus, as a master regulator of cellular processes, the roles of HSF1 in carcinogenesis and tumor progression are now emerging. Several recent investigations using mouse models have suggested that HSF1 is involved in carcinogenesis (9,17). In clinical samples, HSF1 is often constitutively expressed at high levels in a variety of tumors, including breast cancer (7,18), pancreatic cancer (19), prostate carcinoma (20) and oral squamous cell carcinoma (21).

Hepatocarcinogenesis is a multistep process, in the majority of cases slowly developing within a well-defined etiology of viral infection and chronic alcohol abuse, leading to the chronic hepatitis and cirrhosis that are regarded as preneoplastic stages (22). A great number of factors, receptors and downstream elements of signaling cascades regulate proliferation and apoptosis. Dysregulation of the balance between cell proliferation and apoptosis thus plays a critical role in hepatocarcinogenesis (23,24). Two of the major pathways of cell proliferation and apoptosis are nuclear factor kappa B (NF-κB) signaling and mitogen-activated protein kinase (MAPK) signaling. NF-κB transcription factors are critical regulators of genes involved in inflammation and the suppression of apoptosis. NF-κB has been shown to be instrumental for tumor promotion in colitis-associated cancer and inflammation-associated liver cancer (25,26). Activation of the extracellular signal-regulated kinase (ERK)/MAPK pathway regulates many important cellular processes, such as proliferation, differentiation, angiogenesis, survival and cell adhesion (27). Importantly, the ERK/MAPK pathway is constitutively activated in HCC (28).

The present study investigated the biological influences of HSF1 in HCC cell proliferation and apoptosis involving the NF-κB and MAPK signal pathways. We found that HSF1 deficiency significantly diminished NF-κB and MAPK activation in primary hepatocytes and HCC cells, so HSF1 deficiency inhibited the development of HCC. Furthermore, clinicopathological analysis demonstrated a significant correlation between HSF1 protein level and prognosis. Our results suggest HSF1 as a promising molecular target for the development of anti-HCC therapeutics.

Abbreviations: BAG3, bcl-2-associated athanogene domain 3; EGFR, epidermal growth factor receptor; ERK, extracellular signal-regulated kinase; FACS, fluorescence-activated cell sorting; HCC, hepatocellular carcinoma; HSF1, heat shock factor 1; HSF1 KD, HSF1 knockdown; HSP, heat shock protein; IKKγ, IκB kinase gamma; LPS, lipopolysaccharide; MAPK, mitogen-activated protein kinase; MEK, mitogen-activated protein kinase kinase; mRNA, messenger RNA; NF-κB, nuclear factor kappa B; PCNA, proliferating cell nuclear antigen; SCID, severe combined immune-deficient mice; shRNA, small hairpin RNA; TNF-α, tumor necrosis factor alpha; TUNEL, terminal deoxynucleotidyl transferase-mediated deoxyuridine triphosphate nick-end labeling; WT, wild type.

Materials and methods

Cell cultures and reagents

Human HCC cell lines HepG2, PLC/PRF/5, HLE and HLF were obtained from the American Type Culture Collection. Huh7 was obtained from the Japanese Collection of Research Bioresources Cell Bank (Ibaraki, Japan). KIM-1 and KYN2 were kindly provided by Dr Hirohisa Yano (Department of Pathology, Kurume University, Kurume, Japan). Li7 was kindly provided by Dr Yae Kanai (Division of Molecular Pathology, National Cancer Center Research Institute,

Tokyo, Japan). HepG2, PLC/PRF/5, Huh7, HLE and HLF cells were maintained in Dulbecco's modified Eagle's medium containing 10% fetal bovine serum. KIM-1 and KYN2 was maintained in RPMI medium containing 10% fetal bovine serum.

Antibodies and chemicals

The antibodies used included: anti-HSF1, ERK1/2, phosphor-ERK1/2, MAPK kinase (MEK), phospho-MEK, phosphor- efficiently activated epidermal growth factor receptor (EGFR), cyclin D1, cdc2, CDK4, phospho-IκBα, IκB kinase gamma (IKKγ), IKKβ, caspase-3 and Bcl-X_L (Cell Signaling Biotechnology, Danvers, MA); anti-HSP90, HSP72, β-actin and proliferating cell nuclear antigen (PCNA) (Santa Cruz Biotechnology, Santa Cruz, CA); anti-EGFR (Millipore, Billerica, MA); anti-HSP70/HSP72 (Enzo Life science, NY); and anti-BAG3 (Abcam, Cambridge, UK).

Biochemical and immunohistochemical analyses

Protein lysates were prepared from tissues and cultured cells, separated by sodium dodecyl sulfate–polyacrylamide gel electrophoresis, transferred onto Immobilon membranes (Millipore) and analyzed by immunoblotting. Total cellular RNA was extracted using Trizol reagent (Invitrogen, Carlsbad, CA), then cDNA was synthesized using SuperScript II (Invitrogen), and expression of specific messenger RNAs (mRNAs) was quantified using real-time PCR and normalized against glyceraldehyde-3-phosphate dehydrogenase mRNA expression. Details of real-time PCR conditions and primer sequences are available in Supplementary Materials and methods, available at *Carcinogenesis* Online. Immunohistochemical staining was performed on formalin-fixed, paraffin-embedded tissue sections using immunoperoxidase methods, as described previously (15). For array analysis, we used the Human WG-6 BeadChip-kit (Illumina, San Diego, CA) in accordance with the instructions from the manufacturer (details are given in Supplementary Materials and methods, available at *Carcinogenesis* Online).

Establishment of HSF1-knockdown cells

A HSF1 small hairpin RNA (shRNA) plasmid and negative control plasmid were purchased from SABiosciences (QIAGEN, Valencia, CA). The shRNA sequences targeting HSF1 were from position 5′-CAGGTTGTTCATAGTCAGAAT-3′ as in the nucleotide sequence of HSF1. As a negative control, a shRNA was designed with the sequence 5′-GGAATCTCATTCGATGCATAC-3′. Transfection was achieved using Oligofectamine reagent (Invitrogen) according to the instructions from the manufacturer. To establish stable knockdown cell lines, shRNA plasmids were transfected into KYN2 cells and cultured in the presence of puromycin (Sigma–Aldrich, St Louis, MO).

Cell proliferation and bromodeoxyuridine assay

Cell proliferation in response to HSF1 silencing was determined by trypan blue exclusion assay. DNA synthesis was determined by bromodeoxyuridine assay according to the instructions from the manufacturer (Roche Diagnostics, Basel, Switzerland). The result was expressed as a percentage of the maximum absorbance at 450 nm, based on three independent experiments. Cells were counted using a Coulter Counter (Beckman Coulter, Pasadena, CA).

Apoptosis assay

Assessment of apoptosis was performed by measuring the intensity of the sub-G_1 peak. For the sub-G_1 peak, HSF1 control KYN2 cells or HSF1-knockdown (HSF1 KD) KYN2 cells were tumor necrosis factor alpha (TNF-α) treatment for 24 h. Cells were treated with propidium iodide and then the sub-G_1 peak was analyzed with a fluorescence-activated cell sorting (FACS) flow cytometer (FACSCalibur; Becton Dickinson, San Jose, CA). Terminal deoxynucleotidyl transferase-mediated deoxyuridine triphosphate nick-end labeling (TUNEL) assay was performed in accordance with the manufacturer's instructions (ApopTag kit; Intergen, Burlington, MA).

Animals

HSF1-deficient ($HSF^{-/-}$) mice have been described previously (29). C57BL/6 wild-type (WT) mice were purchased from CLEA Japan (Tokyo, Japan) for use in the experiments, with primary hepatocytes isolated using a collagenase perfusion method as described in a previous report (26). For orthotopic implantation, C.B-17/Icr-scid/scidJcl [severe combined immune-deficient mice (SCID)] mice were obtained from CLEA Japan. All mice were maintained in filter-topped cages on autoclaved food and water at the University of Hokkaido and the Institute for Adult Diseases, Asahi Life Foundation, according to National Institutes of Health (NIH) guidelines. All experimental protocols were approved by the ethics committee for animal experimentation at Hokkaido University and Asahi Life Foundation. Orthotopic implantation of KYN2 cells and KYN2 transfectants were performed as described previously (30). Briefly, mice were inoculated orthotopically with 5×10^6 HSF1 control ($n = 12$) and HSF1 KD ($n = 12$) cells in 100 μl of phosphate-buffered saline, injected into the liver. Mice were killed 6 weeks after inoculation and autopsies were performed immediately. In the lipopolysaccharide (LPS)/D-galactosamine (GalN)-induced liver injury model, mice were injected intraperitoneally with LPS (20 lg/kg; Sigma) and GalN (1000 mg/kg; Wako, Osaka, Japan) (24).

Patients and tissue samples

For immunohistochemical analysis, a total of 226 adult patients with HCC who underwent curative resection between 1997 and 2006 at Hokkaido University Hospital were enrolled in this study. A preoperative clinical diagnosis of HCC was required to meet the diagnostic criteria of the American Association for the Study of Liver Diseases. Briefly, inclusion criteria were as follows: (i) distinctive pathological diagnosis, (ii) no preoperative anticancer treatment or distant metastases, (iii) curative liver resection (exclusion of extrahepatic tumor spread/metastasis) and (iv) complete clinicopathological and follow-up data. The study protocols were approved by the institutional review board and performed in compliance with the Helsinki of Declaration. Written informed consent was obtained from as many of the patients who were alive as possible (deceased cases were approved for use without written informed consent). Histological diagnosis was made according to World Health Organization criteria. The main clinicopathological features are presented in Table I. During follow-up, clinical evaluations and biochemical tests were performed every 1–3 months. Patients underwent triphasic computed tomography of the liver every 2–3 months.

Statistical analysis

Data are expressed as mean ± standard error of the mean (SEM). Significant differences were detected using non-parametric testing. Correlations between protein expression and clinicopathological features of the specimens were assessed, and the resulting data were analyzed using the χ^2 test and Fisher's exact test. Cumulative survival rate was calculated from the first date of treatment using the Kaplan–Meier life-table method. Differences were evaluated by log-rank testing. Independent factors for survival were assessed with the Cox proportional hazard regression model. Differences between the two groups were analyzed using the log-rank test. Statistical analyses were performed using Stat View software (version 5.0; SAS Institute, Cary, NC). Values of $P < 0.05$ were considered significant.

Results

Effect of HSF1 on tumor growth

We first investigated expression of HSF1 in cultured HCC cell lines. HSF1 expression was detected in all eight HCC cell lines analyzed. KYN2 cells showed significantly higher expression of HSF1 than other cell lines (Figure 1A). To further elucidate the functional role of HSF1 in HCC, we established HSF1 KD KYN2 cells by expressing the shRNA against HSF1 or control shRNA. To evaluate the effects of HSF1 on cell growth, we measured cell numbers at several time points and found that the growth of HSF1 KD cells was significantly inhibited compared with control cells (HSF1 control) (Figure 1B). Cell cycle regulators including PCNA, cyclin D1, cdc2 and CDK4 were suppressed in HSF1 KD cells compared with HSF1 control cells (Figure 1C). These results indicate that HSF1 enhances HCC cell growth. Concordantly, HSF1 KD reduced DNA synthesis as measured by bromodeoxyuridine incorporation (Figure 1D).

To evaluate the effects of HSF1 on HCC *in vivo*, orthotopic xenografts were established by HSF1 control and HSF1 KD KYN2 cells in nude mice. Maximum primary tumor diameters and tumor volumes were significantly decreased in HSF1 KD xenografts compared with HSF1 control ones (Figure 1E), suggesting that HSF1 accelerated HCC tumor growth *in vivo*. We confirmed that the tumor of HSF1 KD cells showed significantly lower expression of HSF1 and PCNA than the tumor of HSF1 control cells (Figure 1E).

We performed gain-of-function experiments for HSF1 *in vitro*. No apparent changes in cell growth were seen with overexpression of HSF1 in HCC cell lines with low HSF1 expression (Supplementary Figure 1, available at *Carcinogenesis* Online), whereas cell growth was reduced in HSF1 KD experiments, as above. Based on these

Table I. HSF1, BAG3 expression and clinicopathological variables in HCC

Parameter	Total	HSF1		*P*	BAG3		*P*
		High	Low		High	Low	
		n = 115	*n* = 111		*n* = 112	*n* = 114	
		≥30	<30		≥25	<25	
Age (years)							
≥60	126	66	60	0.69	59	67	0.42
<60	100	49	51		53	47	
Sex							
Male	185	95	90	0.86	94	91	0.49
Female	41	20	21		18	23	
Etiology							
HBsAg(+)/HCV(−)	85	45	40	0.70	39	46	0.67
HBsAg(−)/HCV(+)	84	43	41		44	40	
HBsAg(+)/HCV(+)	6	4	2		2	4	
HBsAg(−)/HCV(−)	51	23	28		27	24	
Cirrhosis							
Presence	121	64	57	0.59	62	59	0.59
Absence	105	51	54		50	55	
Tumor size (cm)							
<5	149	67	82	0.017*	66	83	0.035*
≥5	77	48	29		46	31	
No. of tumor nodules							
Solitary	168	78	90	0.032*	79	89	0.22
Multiple (≥2)	58	37	21		33	25	
TNM stage							
I and II	139	62	77	0.017*	63	76	0.11
III and IV	87	53	34		49	38	
BCLC stage							
A	81	27	54	<0.001*	32	49	0.065
B	108	64	44		58	50	
C	37	24	13		22	15	
Differentiation							
Well	36	11	25	0.010*	10	26	0.014*
Moderate	143	74	69		75	68	
Poor	47	30	17		27	20	
Capsular formation							
Presence	184	95	89	0.73	91	93	1.0
Absence	42	20	22		21	21	
Vascular invasion							
Present	37	24	13	0.073	22	15	0.21
Absent	189	91	98		90	99	
Serum AFP level							
<20	117	53	64	0.086	52	65	0.14
≥20	109	62	47		60	49	

AFP, alpha-fetoprotein; BCLC, Barcelona Clinic Liver Cancer; HCV, hepatitis C virus; TNM, tumor node metastasis.
*Significant *P* value.

findings, we concluded that HSF1 expression is a necessary condition for cell growth, but it is not a sufficient condition. We, therefore, did not further investigate gain of function of HSF1.

Impaired EGF-mediated MEK/ERK activation in HSF1 KD cells and HSF1$^{-/-}$ hepatocytes

Activation of the MEK/ERK pathway regulates many important cellular processes in carcinogenesis. To further elucidate the function of HSF1 on tumor growth, we investigated the cascade of MAPK. In WT hepatocytes and HSF1 control cells, EGF, a potent activator of MAPK, efficiently activated EGFR, MEK1/2 and ERK1/2 (Figure 2A). In contrast, activation of EGFR, MEK1/2 or ERK1/2 was significantly decreased in HSF-knockout mice (HSF$^{-/-}$) hepatocytes and HSF1 KD cells (Figure 2A and B). Regarding protein levels of EGFR, MEK1/2 and ERK1/2, EGFR protein levels were significantly decreased in HSF1$^{-/-}$ hepatocytes and HSF1 KD compared with controls, whereas other proteins were unchanged (Figure 2A and B). This result was consistent with the previous report (31). Immunohistochemical staining revealed that HSF1 control tumor showed strong phosphorylated ERK1/2 levels, whereas almost no ERK1/2 activation was observed in HSF1 KD tumors (Figure 2C).

Role of HSF1 in TNF-α-induced apoptosis

Since tumor growth inhibition is caused mainly by increased cell death and decreased cellular proliferation, we compared numbers of apoptotic cell deaths in HSF1 control and HSF KD xenografts using the TUNEL assay. Significantly more apoptotic tumor cells were found in HSF1 KD tumors than in HSF1 control tumors (Figure 3A). Next, we examined whether HSF1 was involved in apoptosis *in vitro*. FACS analysis showed very few apoptotic cells in HSF KD or HSF control in the absence of any stimuli. In contrast, treatment with TNF-α, a potent inducer of apoptosis, caused more extensive apoptotic cell death in HSF1 KD cells (23.9%) than in HSF control cells (8.7%) (Figure 3B). Furthermore, we also confirmed increased TNF-α-induced apoptosis in HSF KD cells as determined by TUNEL assay and caspase-3 activation (Figure 3C and D). To examine whether HSF1 is required for TNF-α-induced liver apoptosis *in vivo*, we used an LPS/GalN liver injury model that depends on TNF-α-mediated apoptosis (32). At 7 h LPS/GalN

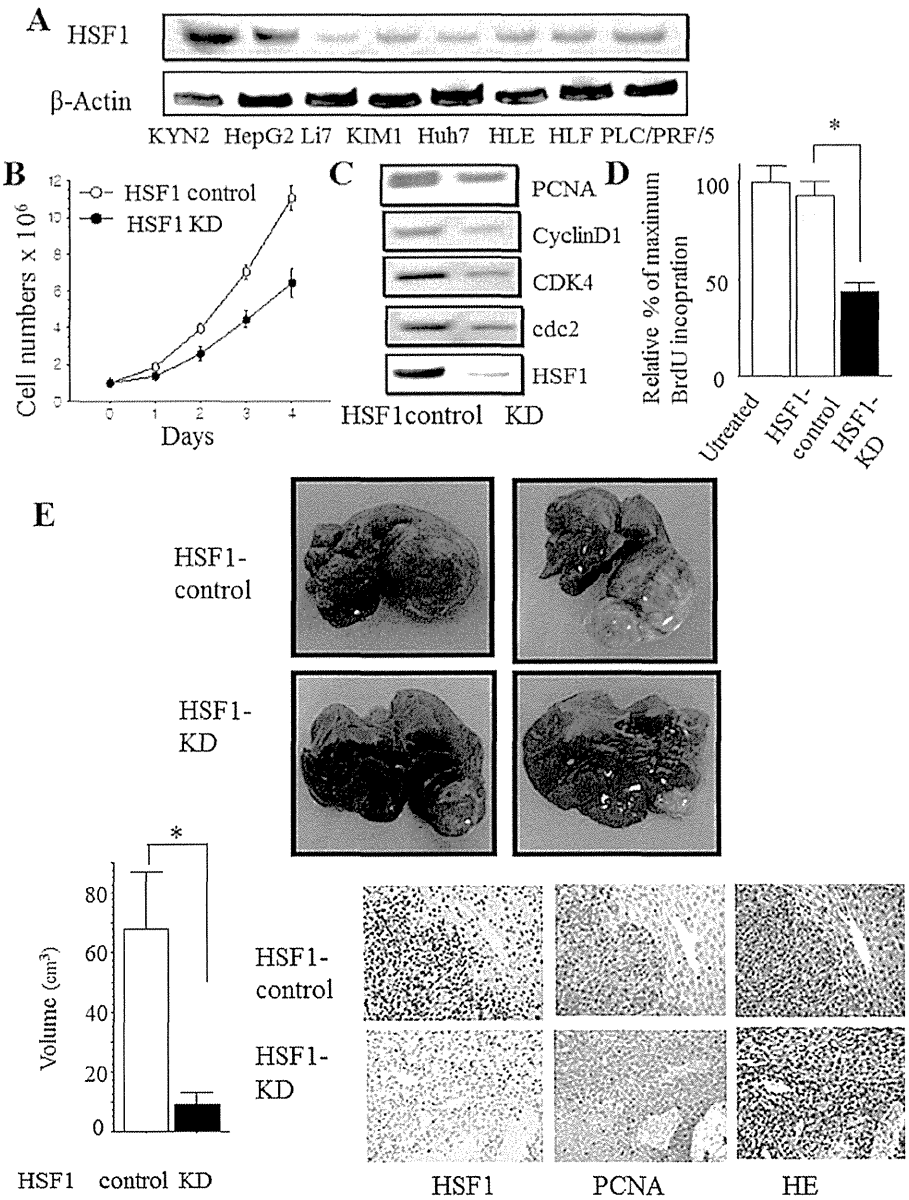

Fig. 1. Role of HSF1 in HCC growth. (**A**) Expression of HSF1 in the eight indicated HCC cell lines was determined by western blot analysis, using β-actin as a control. (**B**) Cell growth of HSF1 control KYN2 cells and HSF1 KD KYN2 cells was measured by counting the number of cells. One representative experiment from three experiments is shown. Data are plotted as mean ± SEM. (**C**) Expression of cell-cycle-related protein in HSF1 control KYN2 cells and HSF1 KD KYN2 cells, as determined by western blot analysis. (**D**) Cells were pulsed with BrdU (10 mmol/l) for 4 h. Optical density values are expressed as a percentage relative to the group expressing control. $^*P < 0.05$. Bars: SEM. (**E**) Growth appearance of HSF1 KD and HSF1 control cells in SCID mice after orthotopic implantation (upper panel). Orthotopic tumor volume was measured. Data are expressed as mean ± SEM (HSF1 control, $n = 12$; HSF1 KD, $n = 12$). $^*P < 0.05$. Bars: SEM (lower left panel). HE and immunohistochemical staining for HSF1 and PCNA (original magnification: ×40): lower right panel. BrdU, bromodeoxyuridine; HE, hematoxylin and eosin.

administration, $HSF^{-/-}$ exhibited marked alanine aminotransferase elevation (Figure 3E), severe histological liver damage and hepatocyte apoptosis compared with WT mice (Figure 3E). This was also in accordance with the notable depression of HSF1 inducing apoptosis *in vitro*.

HSF1 is involved in TNF-α-mediated NF-κB activation

Regarding the association between HSF1 and antiapoptosis, expression of bcl-2-associated athanogene domain 3 (BAG3) was reportedly reduced in HSF1 KD cells compared with control cells (7,11). In addition, microarray array analysis showed that BAG3 was dramatically downregulated in HSF1 KD cells compared with HSF1 control cells (Supplementary Table I, available at *Carcinogenesis* Online). Immunoblot analysis showed that BAG3 protein expression was reduced in $HSF1^{-/-}$ hepatocytes and HSF1 KD cells relative to the respective controls (Figure 4A and B). Meanwhile, activation of IKK and NF-κB pathway represents one of the most important antiapoptotic signals. In addition, BAG3 is also reported to control proteasomal degradation of IKKγ, the regulatory subunit (also called NF-κB essential modulator) of the IKK complex, and

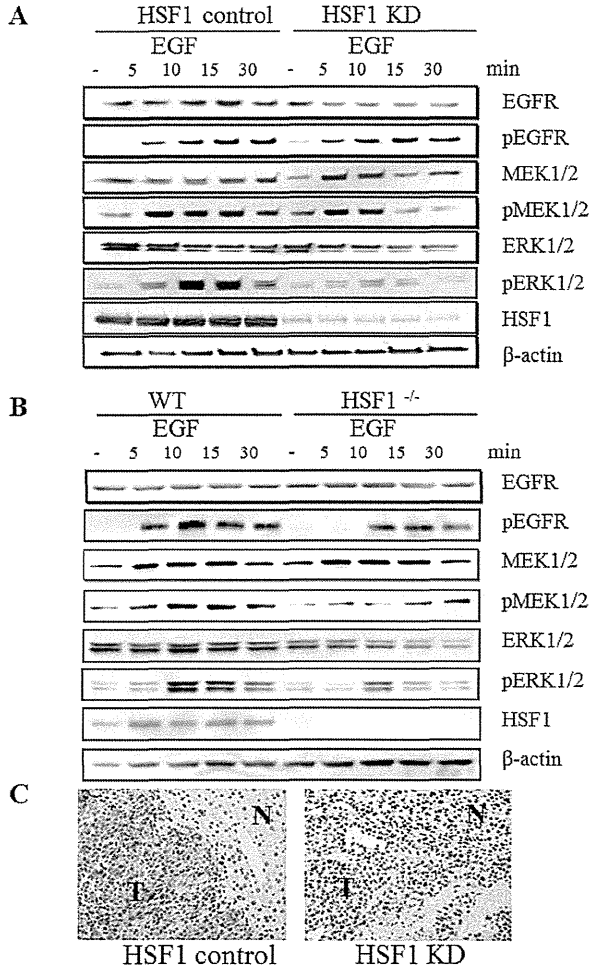

Fig. 2. EGF-mediated MEK/ERK activation is impaired in HSF1 KD cells and HSF1$^{-/-}$ hepatocytes. (**A**) HSF1 control and KD cells were treated with EGF (10 ng/ml), lysed at the indicated times, gel separated and immunoblotted with antibodies against indicated proteins. (**B**) HSF1 WT and HSF$^{-/-}$ hepatocytes were treated with TNF-α (30 ng/ml), lysed in indicated times, gel separated and immunoblotted with antibodies against indicated proteins. (**C**) Representative phosphorylated ERK (p-ERK) staining of orthotopic tumors of HSF1 control and KD cells (original magnification: ×40). N, non-cancerous liver; T, tumor.

NF-κB activity (33). Regarding the NF-κB pathway, NF-κB activation by TNF-α was decreased in HSF1 KD cells compared with the control cells (Figure 4A). In contrast, without any treatment, basal NF-κB activity was very weak and no differences were apparent between HSF1 control cells and HSF1 KD cells (Figure 4A). Consistent with this, microarray analysis showed no apparent differences in the expression of typical NF-κB-regulated genes. We also performed NF-κB pathway analysis and found that the pathway was not overrepresented by the microarray results (Supplementary Figure 2, available at *Carcinogenesis* Online). Next, we investigated whether HSF1 is involved in TNF-α-mediated NF-κB activation and found that phosphorylated Iκk-B (p-IκB), a marker of NF-κB activation, was significantly decreased in HSF$^{-/-}$ hepatocytes and HSF1 KD cells compared with their controls. As expected, IKKγ protein levels were dramatically reduced in HSF1$^{-/-}$ hepatocytes and HSF1 KD cells compared with their controls (Figure 4A and B). To investigate whether decreased IKKγ protein was degraded via proteasome, we used the proteasomal inhibitor, MG-132, and found that protein levels of IKKγ in HSF1 KD cells recovered with the inhibitor, whereas protein expression of BAG3 was unchanged (Figure 4C). Although mRNA levels of BAG3 were significantly downregulated in HSF1 KD cells compared with HSF1 control cells, mRNA levels of IKKγ were not changed (Figure 4D). HSP70 mRNA and protein levels were similar between HSF1 control and HSF1 KD cells (Figure 4A–D). These results suggest that HSF1 positively regulated BAG3 expression, which stabilized the IKKγ protein necessary for NF-κB activation. Immunohistochemical staining revealed that downregulation of HSF1 dramatically reduced BAG3 levels in HSF1 KD xenografts compared with the HSF1 control xenografts.

We performed real-time PCR analysis of the putative NF-κB-regulated antiapoptotic genes. The levels of A20, cellular inhibitor of apoptosis 2 (c-IAP2) RNA expression were decreased in HSF1 KD cells by TNF-α-mediated compared with HSF1 control cells, whereas cylindromatosis, cIAP1 were unchanged (Figure 4E). These results suggest that HSF1 plays an important role in tumor growth via MAPK-mediated cellular proliferation and NF-κB-mediated antiapoptosis.

HSF1 and BAG3 were frequently overexpressed in human HCCs

To analyze the involvement of HSF1 in HCCs, we examined expression levels of HSF1 in human primary HCCs. Immunoblot analysis showed that levels of HSF1 in HCC tissues were significantly higher than in non-cancerous liver tissues in 5 of 10 samples (50%) (Figure 5A). We tested 226 samples from tumor tissues of patients with HCCs by immunohistochemistry. The median percentage of positive cells was 30% (range: 0–90.0%) and we divided patients into two groups of high expressers and low expressers based on the percentage of HSF1-positive cells using a cutoff level of 30%, representing the median value of HSF1. We found that 50.9% (115/226) of tumor samples showed high HSF1 expression. Typical examples of high HSF1 expression samples are shown in Figure 5B. The characteristics of patients in this analysis are shown in Table I. Significant differences were apparent between high and low HSF1 expression groups in terms of tumor size ($P = 0.017$), tumor node metastasis stage ($P = 0.017$), Barcelona Clinic Liver Cancer stage ($P < 0.001$), number of tumor nodules ($P = 0.032$) and histological grade ($P = 0.010$) (Table I), but no significant correlations were observed between HSF1 expression and other clinicopathological variables such as etiology or cirrhosis (Table I). Furthermore, patients with tumors showing HSF1 overexpression displayed significantly shorter overall survival (median: 75.2 months) compared with patients whose tumors showed HSF1 low expression (median: 136.0 months; $P = 0.004$, log-rank test) (Figure 5C). These findings suggest that overexpression of HSF1 was frequently observed in human HCCs, particularly in tumors exhibiting aggressive features.

To explore the pathological relationship between HSF1 and BAG3 in HCC samples, we performed immunohistochemical analysis for BAG3 in 226 HCC samples, which were also analyzed for HSF1 immunohistochemistry. The median percentage of positive cells was 25% (range: 0–85.0%) and we divided them into two groups—high expressers and low expressers—based on the percentage of BAG3-positive cells using a cutoff level of 25%, representing the median value of BAG3. Representative examples of immunohistochemical reactivity for BAG3 are shown in Figure 5B. Expressions of BAG3 protein were significantly increased in HCC specimens, whereas no or only low BAG3 expression was seen in adjacent non-cancerous tissue. BAG3 expression correlated significantly with histological grade ($P = 0.014$), and tumor size ($P = 0.035$), but no significant correlations were observed between BAG3 expression and other clinicopathological variables (Table I). Furthermore, a positive correlation between expressions of HSF1 and BAG3 was found in HCC ($P < 0.05$; Figure 5D) and patients with tumors showing BAG3 overexpression displayed significantly shorter overall survival (median: 84.0 months) compared with those patients whose tumors showed BAG3 low expression (median: 134.2 months; $P = 0.015$, log-rank test) (Figure 5E). Multivariate Cox regression

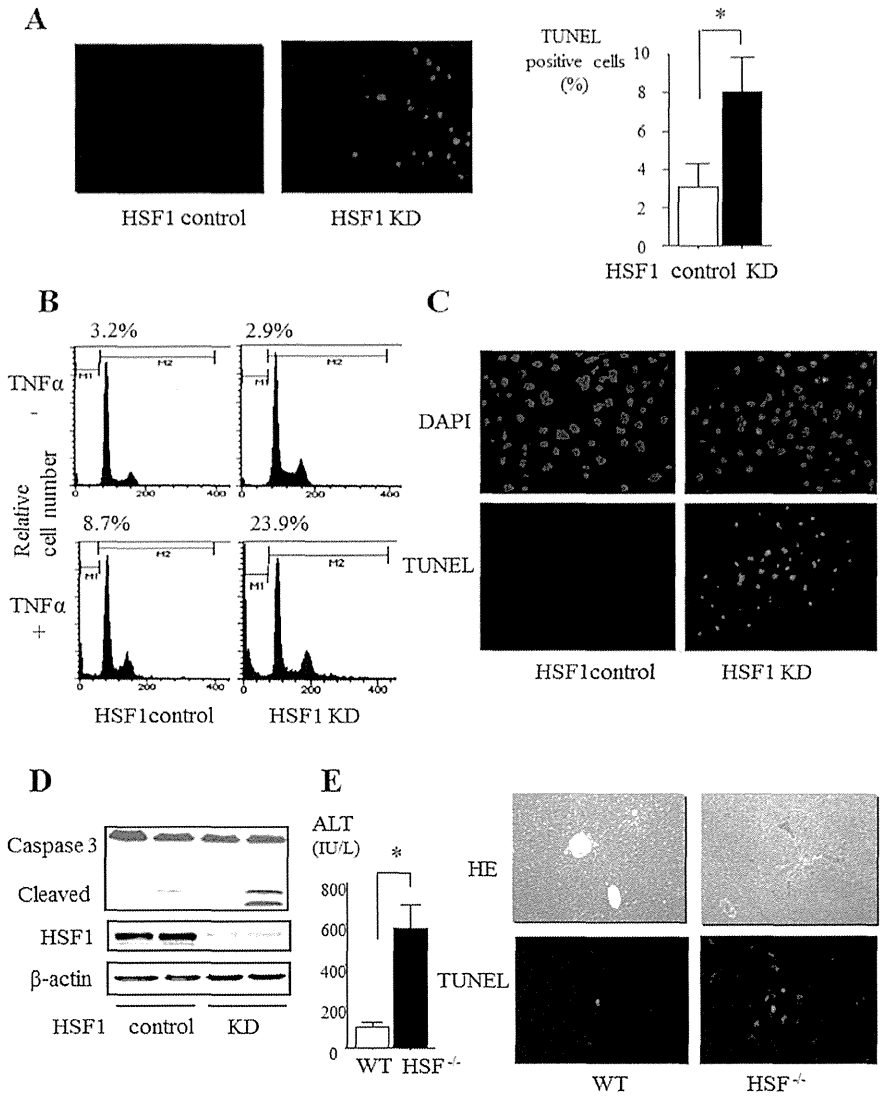

Fig. 3. Antiapoptotic effect of HSF1 in HCC cells and hepatocytes. (**A**) TUNEL staining was performed in tumors of HSF1 control and HSF1 KD cells from orthotopic implanted mice (left panel). TUNEL-positive cells were counted in tumors of HSF1 control and HSF1 KD cells. $*P < 0.05$. Bars: SEM (right panel). (**B**) Apoptotic cells were evaluated by FACS at 24 h after incubation with TNF-α (30 ng/ml). Values indicate percentages of cells with sub-G_1 DNA content. Representative data are shown from three independent experiments. (**C**) TUNEL staining was performed in HSF1 control and KD cells after incubation with TNF-α. (**D**) Protein expressions of caspase 3, HSF1 and β-actin in TNF-α-treated HSF1 control and KD cells were determined by western blot analysis. (**E**) Serum ALT levels 7 h after injection of WT and HSF1$^{-/-}$ mice with LPS (5 μg/kg) and GalN (500 mg/kg). $*P < 0.05$, compared with WT mice (left panel). HE and TUNEL stainings were performed in sections of livers obtained 7 h after injecting LPS (5 μg/kg) and GalN (500 mg/kg) into WT and HSF1$^{-/-}$ mice (right panel). ALT, alanine aminotransferase; DAPI, 4′,6-diamidino-2-phenylindole; HE, hematoxylin and eosin.

analysis identified high HSF1 expression (hazard ratio: 2.07; $P = 0.04$) as an independent prognostic factor for overall survival (Table II).

Discussion

As a master regulator of the heat shock response, HSF1 enhances organism survival and longevity in the face of environmental challenges. However, HSF1 can also act to the detriment of organisms by supporting malignant transformation (34). As reported previously, loss of HSF1 negatively impacts tumorigenesis driven by p53 or Ras mutations (8,16). Since HSF1 does not act as a classic oncogene, the increased resistance to proteotoxic stress induced by HSF1 was suggested to support tumor initiation and growth by enabling cells to accommodate the genetic alterations that accumulate during malignancy (35). However, the specific mechanisms by which HSF1 may support the growth of tumors are not well understood. Here, we have demonstrated that HSF1 has detrimental effects on liver tumor growth. We also proposed that the antiapoptotic effect of HSF1 may play a role in HCC tumor growth.

To clarify the mechanisms underlying this effect, we investigated associations between HSF1 and the NF-κB signaling pathway. Although, in a previous study, heat shock blocked the degradation of IκB (36) and nuclear translocation of NF-κB, the recent literature has reported that the presence of constitutively active HSF1 does not block TNF-α-induced activation of the NF-κB pathway or expression of a set of NF-κB-dependent genes (37). The current study established HSF1 KD cells and showed that HSF1 was necessary for TNF-α-induced NF-κB activation. We analyzed the function of BAG3 as a candidate for the molecule connecting HSF1 with NF-κB activation. BAG3 has reportedly been characterized by the

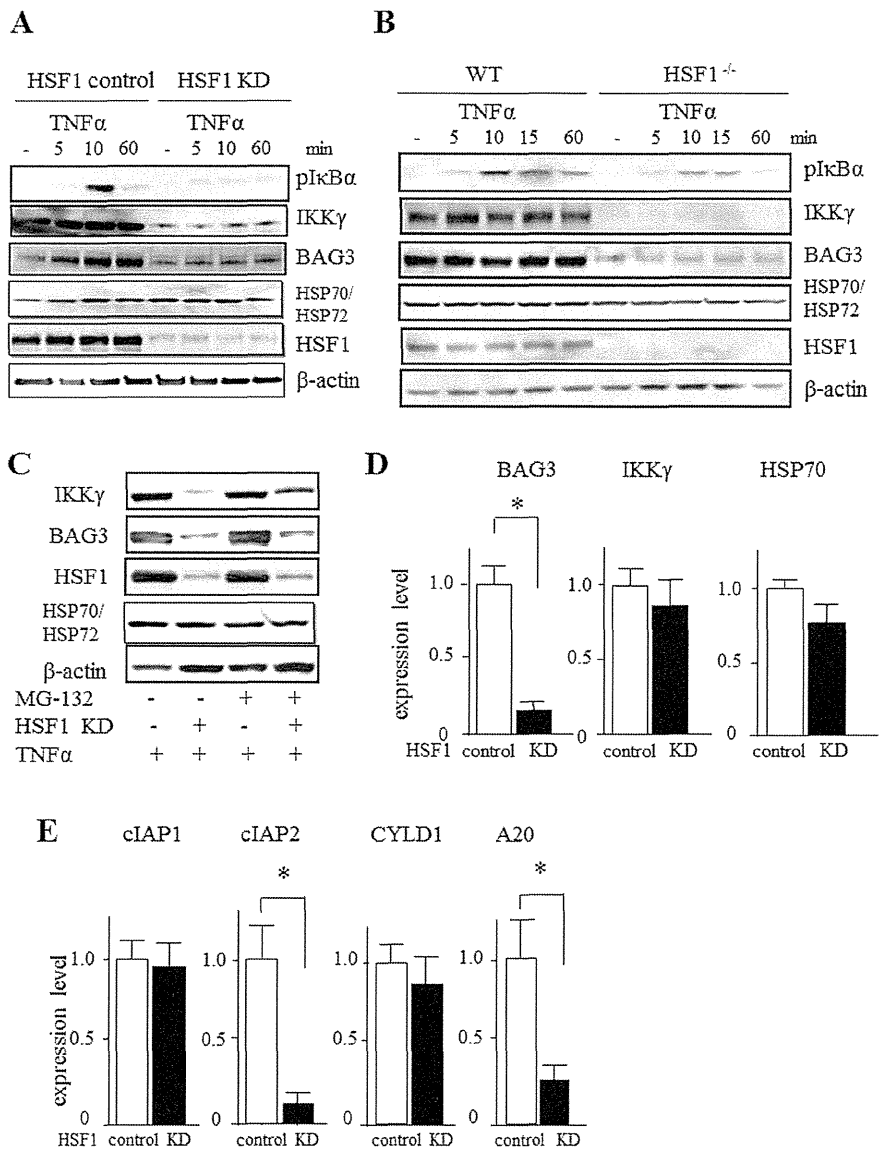

Fig. 4. HSF1 is involved in TNF-α-mediated NF-κB activation. (**A**) HSF1 control and KD cells were treated with TNF-α (30 ng/ml), lysed at the indicated times, gel separated and immunoblotted with antibodies against the indicated proteins. (**B**) HSF1 WT and HSF$^{-/-}$ hepatocytes treated with TNF-α (30 ng/ml), lysed at the indicated times, gel separated and immunoblotted with antibodies against the indicated proteins. (**C**) HSF1 control and KD cells were treated with TNF-α (30 ng/ml) with or without MG-132, lysed at 24 h, gel separated and immunoblotted with antibodies against indicated proteins. (**D**) Relative mRNA levels for BAG3, IKKγ and HSP70 in HSF1 control and KD cells determined by real-time PCR. Data are expressed as mean ± SEM ($n = 4$ per group). *$P < 0.05$. Bars: SEM. (**E**) Relative mRNA levels for antiapoptosis-related gene in HSF1 control and KD cells as determined by real-time PCR. Data are expressed as mean ± SEM ($n = 4$ per group). *$P < 0.05$. Bars: SEM. CYLD, cylindromatosis.

interaction with a variety of partners (Raf-1, steroid hormone receptors and HSP70) and is involved in regulating a number of cellular processes, particularly those associated with antiapoptosis (38). This molecule was expressed in response to stressful stimuli in a number of normal cell types and appears constitutively in a variety of tumors (33,39), and gene expression is regulated by HSF1 (40). In addition, knockdown of BAG3 protein decreased IKKγ levels, increasing tumor cell apoptosis and inhibiting tumor growth (33). Based on these considerations, we investigated whether attenuating HSF1 would enhance IKKγ protein expression, and data with MG-132 show that proteasomal degradation of IKKγ is enhanced in HSF1 KD cells. In addition, knowledge of the role BAG3 plays in preventing the proteasomal turnover of certain proteins suggests that the loss of BAG3 in HSF1 KD cells may be responsible for the enhanced turnover of IKKγ in this setting.

NF-κB activation is a master regulatory step in antiapoptosis. Several mechanisms have been reported regarding this antiapoptotic effect of NF-κB activation (41). NF-κB exerts its prosurvival activity primarily through the induction of target genes, the products of which inhibit components of the apoptotic machinery. These include Bcl-X_L and c-IAP (41), which binds directly to and inhibits the effect of caspases. This study showed that inactivation of NF-κB promoted apoptotic effects against TNF-α in HSF1$^{-/-}$ hepatocytes and HSF1 KD HCC cells. Real-time PCR analyses indicated that expression levels of apoptosis-related genes such as A20 and c-IAP2 were decreased by inhibition of NF-κB activation, whereas apoptosis-related genes such

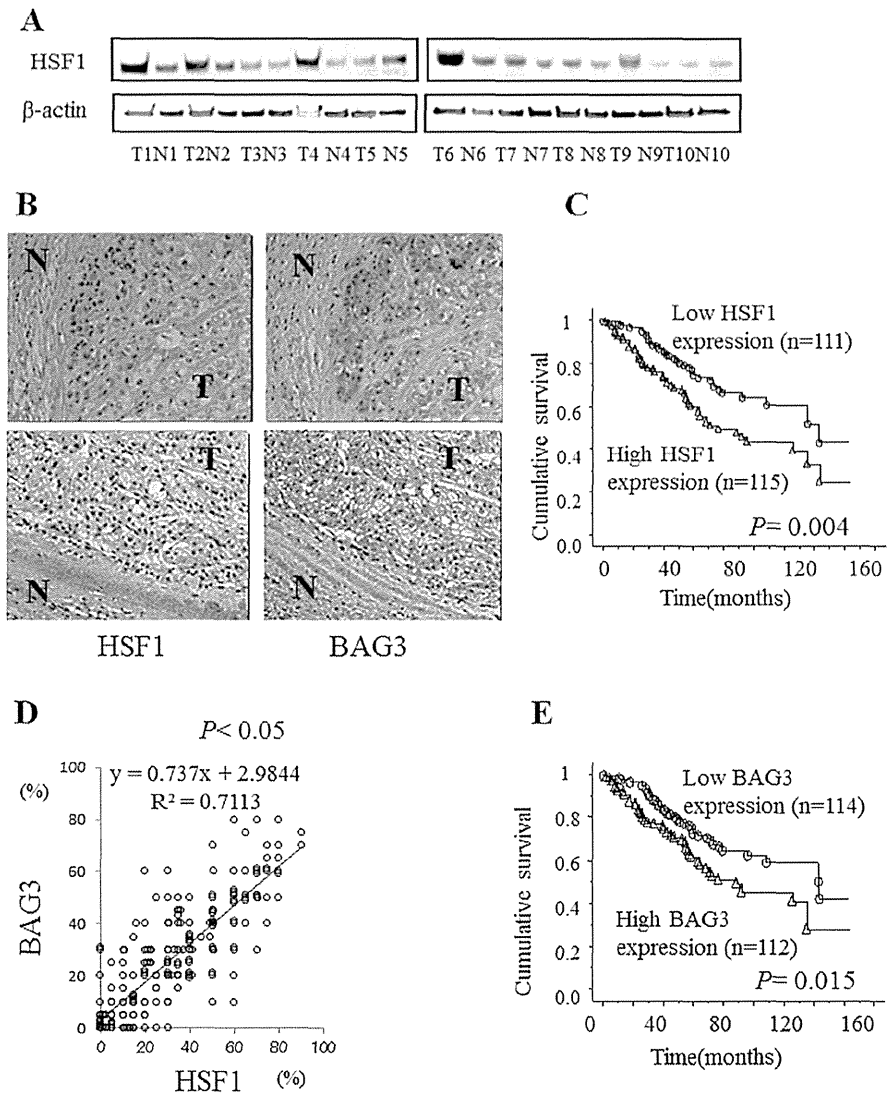

Fig. 5. Overexpression of HSF1 protein in human HCCs and pathological relationship between HSF1 and BAG3 in HCC samples. (**A**) HSF1 protein expression was determined in paired samples of human non-neoplastic liver and HCC by western blot, using β-actin as a control. N, non-cancerous liver; T, tumor. (**B**) Representative HSF1 and BAG3 staining of HCC and surrounding tissue. (**C**) Correlation of HSF1 overexpression with overall survival rates of patients. (**D**) Relationship between BAG3 and HSF1 expression in HCC. Scatterplot of BAG3 versus HSF1 with regression line displaying a correlation according to Spearman's correlation coefficient ($P < 0.01$). (**E**) Correlation of BAG3 overexpression with overall survival rates of patients.

as cIAP1 and cylindromatosis, which are known to be regulated by NF-κB activation, were apparently unaffected. Whether gene expression regulated by NF-κB activity differs between inducible and basal activation remains to be determined.

Regarding the relationship between HSF1 and HCC development, HSF1-deficient mice recently revealed dramatically reduced numbers and sizes of tumors compared with WT controls when tumors were induced by the chemical carcinogen, diethylnitrosamine. The same study suggested that the presence of extensive pathology associated with severe steatosis by diethylnitrosamine was prevented by HSF1 deletion and may be associated with reduced HCC development (42). On the other hand, ablation of IKKγ in liver parenchymal cells caused spontaneous development of HCC in mice, with tumor development preceded by steatohepatitis (43). Based on these observations, we assume that reductions in diethylnitrosamine-induced HCC development among HSF1-deficient mice may be associated with reduced expression of IKKγ, the reduction of which caused the steatosis.

BAG3 is a critical regulator of apoptosis in HSF1-deficient hepatocytes and HSF1 KD HCC cells. Moreover, the relationship between HSF1 and BAG3 has been shown not only in cell cultures and mouse models, but also in human HCC tissue samples; a correlation between HSF1 expression and BAG3 expression was found in HCC. Clinicopathological features and biological results provide a mechanistic link between HSF1 and HCC development via BAG3.

As for the ERK signal, a previous study demonstrated that impairment of JNK and ERK signaling in HSF1$^{-/-}$ MEF cells was caused in part by the reduced expression of EGFR (33). We showed a slight decrease in expression of EGFR among HSF1-deficient hepatocytes and HSF1 KD cells. On the other hand, the level of reduced activation of ERK, as a downstream molecule of EGFR, was larger than expected. However, the detailed mechanisms by which HSF1 regulates MAPK need further investigation.

In conclusion, we found that HSF1 deficiency significantly diminished NF-κB and MAPK activation in HCC hepatocytes and

Table II. Multivariate analysis with a Cox proportional hazards regression model

Characteristic	Univariate analysis	Multivariate analysis	Hazard ratio (95% CI)
Age (≥60 years)	0.22	0.15	
Gender (male)	0.92	0.53	
HCV status (positive)	0.28	0.82	
Cirrhosis (positive)	0.15	0.066	
Tumor size (≥50 mm)	<0.01*	0.011*	2.21 (1.18–4.12)
No. of tumor nodule (multiple)	<0.01*	<0.01*	2.67 (1.38–5.62)
Tumor differentiation (poor)	<0.01*	0.031*	2.34 (1.33–4.11)
Capsular formation (absence)	0.18	0.36	
Vascular invasion (presence)	0.062	0.10	
TNM stage (III + IV versus I + II)	<0.01*	0.020*	2.35 (1.14–4.82)
AFP (≥20 ng/ml)	0.18	0.36	
HSF1 expression (high)	0.018*	0.040*	2.07 (1.22–3.50)
BAG3 expression (high)	0.043*	0.056	

AFP, alpha-fetoprotein; CI, confidence interval; HCV, hepatitis C virus; TNM, tumor node metastasis.
*Significant *P* value.

HCC cells; accordingly, HSF1 deficiency inhibited the development of HCC. Furthermore, clinicopathological analysis demonstrated a significant correlation between HSF1 or BAG3 protein levels and prognosis. Our results demonstrate the importance of HSF1 in human HCCs and suggest inhibition of HSF1 as a novel strategy to target that subset of HCC patients in whom this protein is overexpressed.

Supplementary material

Supplementary Materials and methods, Table I and Figures 1 and 2 can be found at http://carcin.oxfordjournals.org/

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