**Host Genetics Predict Clinical Deterioration in HCV-Related Cirrhosis**

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Host Genetics Predict Clinical Deterioration in HCV-Related Cirrhosis

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Abstract

Single nucleotide polymorphisms (SNPs) in the epidermal growth factor (EGF, rs4444903), patatin-like phospholipase domain-containing protein 3 (PNPLA3, rs738409) genes, and near the interleukin-28B (IL28B, rs12979860) gene are linked to treatment response, fibrosis, and hepatocellular carcinoma (HCC) in chronic hepatitis C. Whether these SNPs independently or in combination predict clinical deterioration in hepatitis C virus (HCV)-related cirrhosis is unknown. We genotyped SNPs in EGF, PNPLA3, and IL28B from liver tissue from 169 patients with biopsy-proven HCV cirrhosis. We estimated risk of clinical deterioration, defined as development of ascites, encephalopathy, variceal hemorrhage, HCC, or liver-related death using Cox proportional hazards modeling. During a median follow-up of 6.6 years, 66 of 169 patients experienced clinical deterioration. EGF non-AA, PNPLA3 non-CC, and IL28B non-CC genotypes were each associated with increased risk of clinical deterioration in age, sex, and race-adjusted analysis. Only EGF non-AA genotype was independently associated with increased risk of clinical deterioration in age, sex, and race-adjusted analysis. Only EGF non-AA genotype was independently associated with increased risk of clinical deterioration (hazard ratio [HR] 2.87; 95% confidence interval [CI] 1.31–6.25) after additionally adjusting for bilirubin, albumin, and platelets. Compared to subjects who had 0–1 unfavorable genotypes, the HR for clinical deterioration was 1.79 (95%CI 0.96–3.35) for 2 unfavorable genotypes and 4.03 (95%CI 2.13–7.62) for unfavorable genotypes for all three loci (P_trend<0.0001). In conclusion, among HCV cirrhotics, EGF non-AA genotype is independently associated with increased
risk for clinical deterioration. Specific *PNPLA3* and *IL28B* genotypes also appear to be associated with clinical deterioration. These SNPs have potential to identify patients with HCV-related cirrhosis who require more intensive monitoring for decompensation or future therapies preventing disease progression.

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**Introduction**

Chronic hepatitis C (CHC) is the most common cause of liver-related death and liver transplantation in the United States [1]. The rate of progression of hepatitis C virus (HCV) infection is variable, likely due to a combination of host genetic and environmental factors. At least 20% of patients with CHC develop cirrhosis over a twenty-year period [2]. Once cirrhosis is established, patients are at risk for hepatocellular carcinoma (HCC) and decompensation, characterized by ascites, variceal hemorrhage, or hepatic encephalopathy (HE), and survival decreases from a median of 12 years to 2 years [3].

Attempts have been made to develop risk scores to predict the risk of disease progression for individual patients. Such scores have incorporated both clinical variables and genetic data [4]. The possibility of tailoring clinical management to genetic data is exciting, but the discovery of ever-increasing numbers of single nucleotide polymorphisms (SNPs) associated with liver disease mandates careful selection of polymorphisms that have independent predictive value for relevant outcomes. One of the genetic variations for which there is compelling evidence is the rs12979860 SNP near the interleukin-28B (*IL28B*) locus. The CC *IL28B* genotype is associated with spontaneous clearance of HCV and predicts interferon and ribavirin treatment response [5, 6]. However, data regarding an independent association between *IL28B* genotype and disease course are conflicting [7–9]. The epidermal growth factor (*EGF*) gene polymorphism rs4444903 has been associated with EGF levels [10], HCC [10, 11] and fibrosis [12]. Last, while the patatin-like phospholipase domain-containing protein 3 (*PNPLA3*) SNP rs738409 has mainly been studied in nonalcoholic fatty liver disease (NAFLD) [13], studies in patients with CHC have shown an association with steatosis, fibrosis [14, 15], and HCC [15, 16], although data are conflicting [17].

These data suggest that these SNPs may be useful for the prediction of the natural history of CHC. However, no study has evaluated the influence of *IL28B*, *EGF*, and *PNPLA3* genotypes on the natural history of HCV-related cirrhosis or examined these SNPs in the same population. We therefore sought to evaluate the association between these SNPs and clinical deterioration in a cohort of patients with HCV-related cirrhosis.
Materials and Methods

Cohort assembly
The patient cohort was identified from pathology reports at Massachusetts General Hospital. A natural language search for biopsies performed between 1990 and 2007 was previously performed for the keywords: HCV, HBV, NAFLD, NASH, and hepatitis. Pathology reports were reviewed to identify patients whose biopsies were consistent with HCV-related cirrhosis. Inclusion criteria were age ≥18 years at time of biopsy, positive HCV antibody or HCV RNA, and presence of cirrhosis (Ishak stage 5 or 6/6 or Metavir stage 4/4). Exclusion criteria included co-infection with human immunodeficiency virus or hepatitis B virus (HBV), liver transplantation, ascites, variceal hemorrhage, HE, or HCC prior to or within one month of the biopsy, and lack of follow-up data following the biopsy. The electronic medical records of patients identified by the pathology database search as having biopsies consistent with HCV-related cirrhosis were manually reviewed by two independent reviewers. The keyword search of the pathology database yielded 370 patients whose reports were consistent with a diagnosis of HCV-related cirrhosis. After review of the medical record, 220 patients were eligible. Formalin-fixed, paraffin-embedded (FFPE) blocks were not available for 38 patients, and genotyping could not be performed on 13 patients. Thus, the final cohort included 169 patients (Fig. 1). Nine patients overlapped with the cohort in which we previously identified the association between EGF genotype and HCC [10]. This study was approved by the Partners Human Research Committee. The Committee waived the need for written, informed consent for this retrospective study. All data was analyzed anonymously.

Ascertainment of Outcomes
The follow-up period for each patient was defined as the date of the index biopsy until the occurrence of the first episode of clinical deterioration, death, loss to follow-up, or December 31, 2012, whichever came first. Clinical deterioration was defined as the development of ascites, HE, variceal hemorrhage, HCC, or liver-related death. Outcomes were identified by manual chart review performed by two independent reviewers. The primary outcome was the time to the first episode of clinical deterioration after the index biopsy.

Other covariates
We collected the following baseline variables from the electronic medical record: age, gender, race, medical history, body mass index, alanine aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin, albumin, platelet count, creatinine, international normalized ratio (INR), prothrombin time, HCV genotype and HCV RNA, alcohol use, and smoking history. For all baseline laboratory values, we used the value determined at the time of the index biopsy. If no value was available at that time, we used the value collected closest to the biopsy within the year prior to the biopsy. Heavy alcohol use was defined as
documentation of alcohol abuse or dependence, a history of substance abuse counseling, or consumption >14 drinks per week by males or >7 drinks per week by females. Diabetes was defined as a history of diabetes mellitus in the medical record or the use of diabetic medications. The number of subjects with incomplete data was 48 for HCV RNA; 39 for creatinine; 22 for HCV genotype; 16 for either prothrombin time or INR; 13 for smoking status; 13 for ALT, AST, albumin, total bilirubin; 9 for platelets; and 8 for alcohol use.

Fig. 1. Flow chart for identification of the cohort. The following keywords were used in the pathology database search: HCV, HBV, NAFLD, NASH, and hepatitis. HCV: hepatitis C virus; HBV: hepatitis B virus; HIV: human immunodeficiency virus; HCC: hepatocellular carcinoma; FFPE: formalin-fixed, paraffin-embedded;

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Genotyping
DNA was extracted from FFPE liver tissue (Five 10 μm sections from each patient) using the QiaAMP FFPE Tissue Kit (Qiagen Inc, Valencia, CA). Genotyping was performed on 5 ng of DNA using the 7900HT Fast Real-Time PCR System with commercial TaqMan SNP Genotyping Assays for IL28B rs12979860, EGF rs4444903, and PNPLA3 rs738409 (Life Technologies, Grand Island, NY) according to the manufacturer’s instructions. Genotypes were assigned using Sequence Detection System (SDS 2.4) software with manual review by two independent investigators, blinded to subject phenotype.

Statistical analysis
We calculated the person-years of follow-up for each individual from the date of the biopsy to the development of the first episode of clinical deterioration, date of death, or end of follow-up, whichever came first. Kaplan-Meier method was used to analyze the time to clinical deterioration. The log rank test was used for comparison between genotypes. The crude and adjusted hazard ratios (HRs) and 95% confidence intervals (CIs) for the effect of the SNPs on the rate of clinical deterioration were estimated with Cox proportional hazards regression models. The proportional hazard assumption was checked via the statistical significance of the interaction between log (follow-up time) and genotype. For our primary analysis, we examined each SNP in an age, sex, and race-adjusted model. In a secondary analysis, we also examined the association of each SNP in a multivariable model additionally adjusting for established predictors of clinical deterioration including baseline albumin, platelets, and total bilirubin [3, 19]. Lastly, we included all 3 SNPs in a combined genotype model in which we compared subjects who had an unfavorable genotype for all 3 SNPs to subjects who had two, one or zero unfavorable genotypes.

We performed several sensitivity analyses. First, we performed an analysis excluding HCC and HCC-related death as a first outcome. For this analysis, we calculated the person-years of follow-up for each individual from the date of biopsy to the development of the first episode of ascites, variceal hemorrhage, HE, date of death, or end of follow-up, whichever came first. Second, we performed an analysis incorporating sustained virologic response (SVR) at any point prior to the censor date into the model given the known association between IL28B genotype and SVR. Third, we performed an analysis excluding the one subject who had an outcome within 6 months of the index biopsy. Finally, we performed an analysis excluding subjects who were Child-Pugh Class B or missing a Child-Pugh score because of missing laboratory data. A 2-tailed P-value <0.05 was considered statistically significant. SAS (Cary, NC) version 9.3 was used for statistical analyses.
Results

Among the 169 patients with biopsy-proven HCV-related cirrhosis, the baseline demographic and clinical data according to EGF, IL28B, and PNPLA3 genotypes are shown in Table 1. The mean age of the cohort was 50±9 years. The cohort was predominantly Caucasian (84%), male (74%) and had Child-Pugh Class A (93%) or Class B (7%) cirrhosis. After a median follow-up of 6.6 years (IQR: 4.7–9.2 years), 66 (39%) patients developed at least one episode of clinical deterioration. Outcomes included death related to portopulmonary hypertension, n=1; ascites, n=18; variceal hemorrhage, n=13; HE n=7; HCC, n=18; ascites and HE, n=7; variceal hemorrhage and HE, n=1; and ascites and variceal hemorrhage, n=1.

To evaluate the association of genotype independent of other clinical factors, we used multivariable models adjusted for age, sex, and race (Table 2; Fig. 2). Compared with AA genotype, EGF non-AA genotype was associated with an age, sex, and race-adjusted HR of 3.20 (95% CI 1.57–6.52; p=0.001) for clinical deterioration. Compared with CC genotype, IL28B non-CC genotype was associated with an age, sex, and race-adjusted HR of 1.78 (95%CI 1.03–3.06; p=0.04) for clinical deterioration. Compared with CC genotype, PNPLA3 non-CC genotype was associated with an age, sex, race-adjusted HR of 1.79 (95%CI 1.10–2.90; p=0.02) for clinical deterioration.

In multivariable models with age, race, sex and established predictors of disease progression including albumin, platelets, and total bilirubin, EGF non-AA genotype remained an independent predictor of increased risk of clinical deterioration, multivariable-adjusted HR=2.87 (95% CI 1.31–6.25; p=0.008) (Table 2). In contrast, there was no longer a significant association between IL28B genotype (multivariable-adjusted HR 1.38; 95%CI 0.71–2.68; p=0.34 for non-CC compared with CC) and PNPLA3 genotype (multivariable HR 1.45; 95%CI 0.85–2.47, p=0.17 for non-CC compared with CC) and clinical deterioration.

When all three SNPs were analyzed together, the presence of 3 unfavorable genotypes (EGF non-AA, IL28B non-CC, and PNPLA3 non-CC, HR 4.03; 95%CI 2.13–7.62) and 2 unfavorable genotypes (HR 1.79; 95%CI 0.96–3.35) were associated with a significantly increased risk of clinical deterioration compared to the presence of one or zero unfavorable genotypes (Plinear trend<0.0001) (Table 3).

When we excluded a single subject who developed an outcome within 6 months of the index biopsy, the HRs for the association of the SNPs with risk of clinical deterioration were not materially altered. We performed a sensitivity analysis limiting the outcome to the time to development of ascites, variceal hemorrhage, or HE. EGF non-AA genotype remained a significant predictor of increased risk of clinical deterioration (age, sex, race-adjusted HR=2.93; 95%CI 1.30–6.60; p=0.01). The association between PNPLA3 genotype and clinical deterioration also persisted (age, sex, race-adjusted HR=1.93; 95%CI 1.10–3.37; p=0.02 for non-CC compared to CC). However, the association between IL28B genotype and clinical deterioration was no longer significant (age, sex, race-adjusted HR=1.52; 95%CI 0.83–2.79; p=0.18 for non-CC compared to CC). We also conducted
Table 1. Baseline Characteristics of all patients and stratified by genotype.

<table>
<thead>
<tr>
<th></th>
<th>Entire cohort</th>
<th>EGF AA</th>
<th>EGF AG/GG</th>
<th>IL28B CC</th>
<th>IL28B CT/TT</th>
<th>PNPLA3 CC</th>
<th>PNPLA3 CG/GG</th>
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<td>Number</td>
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<td>45</td>
<td>82/42</td>
<td>66</td>
<td>75/28</td>
<td>102</td>
<td>51/16</td>
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<td>Age, years</td>
<td>50.1(9.3)</td>
<td>51.6(7.6)</td>
<td>49.6(9.8)</td>
<td>51.2(9.8)</td>
<td>49.4(8.6)</td>
<td>50.4(8.8)</td>
<td>49.6(10.1)</td>
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<td>Male, %</td>
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<td>69</td>
<td>76</td>
<td>68</td>
<td>78</td>
<td>72</td>
<td>78</td>
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<td>White, %</td>
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<td>89</td>
<td>82</td>
<td>91</td>
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<td>85</td>
<td>82</td>
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<tr>
<td>Black, %</td>
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<td>Hispanic, %</td>
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<td>2</td>
<td>8</td>
<td>3</td>
<td>9</td>
<td>2</td>
<td>13</td>
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<tr>
<td>Other, %</td>
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<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>5</td>
<td>3</td>
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<td>Ever smoker, %</td>
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<td>53</td>
<td>67</td>
<td>56</td>
<td>68</td>
<td>65</td>
<td>61</td>
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<td>History of heavy alcohol use, %</td>
<td>51</td>
<td>53</td>
<td>51</td>
<td>42</td>
<td>57</td>
<td>52</td>
<td>51</td>
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<td>Diabetes Mellitus, %</td>
<td>13</td>
<td>9</td>
<td>15</td>
<td>6</td>
<td>17</td>
<td>13</td>
<td>13</td>
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<td>HCV RNA &gt;500,000, IU/mL, %</td>
<td>47</td>
<td>53</td>
<td>44</td>
<td>53</td>
<td>43</td>
<td>45</td>
<td>49</td>
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<td>Genotype 1, %</td>
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<td>64</td>
<td>62</td>
<td>55</td>
<td>68</td>
<td>58</td>
<td>70</td>
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<tr>
<td>AST, U/L</td>
<td>115.3(73.8)</td>
<td>110.8(88.1)</td>
<td>117.0(67.8)</td>
<td>103.4(64.6)</td>
<td>122.5(78.2)</td>
<td>106.3(59.1)</td>
<td>128.7(90.4)</td>
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<td>ALT, U/L</td>
<td>139.4(113.0)</td>
<td>134.1(111.0)</td>
<td>131.5(114.1)</td>
<td>142.4(118.6)</td>
<td>137.6(109.9)</td>
<td>129.1(98.5)</td>
<td>154.8(130.7)</td>
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<td>Albumin, g/dL</td>
<td>3.8(0.5)</td>
<td>3.8(0.4)</td>
<td>3.8(0.6)</td>
<td>3.9(0.5)</td>
<td>3.7(0.5)</td>
<td>3.8(0.5)</td>
<td>3.7(0.5)</td>
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<tr>
<td>Creatinine, mg/dL</td>
<td>0.9(0.5)</td>
<td>1.0(0.8)</td>
<td>0.9(0.2)</td>
<td>0.9(0.2)</td>
<td>0.9(0.5)</td>
<td>1.0(0.6)</td>
<td>0.9(0.2)</td>
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<tr>
<td>Total Bilirubin, mg/dL</td>
<td>0.9(1.1)</td>
<td>0.7(0.4)</td>
<td>0.9(1.2)</td>
<td>0.66(0.3)</td>
<td>1.0(1.3)</td>
<td>0.9(1.3)</td>
<td>0.8(0.5)</td>
</tr>
<tr>
<td>Platelets x 1000/mm³</td>
<td>152.4(59.4)</td>
<td>170.0(49.5)</td>
<td>145.8(61.7)</td>
<td>161.3(59.8)</td>
<td>146.6(58.8)</td>
<td>156.1(60.8)</td>
<td>146.5(57.1)</td>
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Child-Pugh Class

<table>
<thead>
<tr>
<th></th>
<th>Entire cohort</th>
<th>EGF AA</th>
<th>EGF AG/GG</th>
<th>IL28B CC</th>
<th>IL28B CT/TT</th>
<th>PNPLA3 CC</th>
<th>PNPLA3 CG/GG</th>
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</thead>
<tbody>
<tr>
<td>A, %</td>
<td>82</td>
<td>91</td>
<td>78</td>
<td>82</td>
<td>82</td>
<td>81</td>
<td>82</td>
</tr>
<tr>
<td>B, %</td>
<td>7</td>
<td>2</td>
<td>8</td>
<td>2</td>
<td>10</td>
<td>7</td>
<td>6</td>
</tr>
<tr>
<td>Unknown, %</td>
<td>12</td>
<td>7</td>
<td>14</td>
<td>17</td>
<td>9</td>
<td>12</td>
<td>12</td>
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Continuous Variables are presented as mean (SD).

doi:10.1371/journal.pone.0114747.t001

Table 2. Cox proportional Hazards Model for Clinical Deterioration.

<table>
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<tr>
<th>Genotype</th>
<th>Cases/Person-Years</th>
<th>Age, sex, race-Adjusted Hazard Ratio (95%CI)</th>
<th>P value</th>
<th>Multivariable Adjusted Hazard Ratio* (95% CI)</th>
<th>P value</th>
</tr>
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<tbody>
<tr>
<td>EGF AA</td>
<td>9/390</td>
<td>1.00</td>
<td></td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>EGF non-AA</td>
<td>57/812</td>
<td>3.20 (1.57–6.52)</td>
<td>0.001</td>
<td>2.87 (1.31–6.25)</td>
<td>0.008</td>
</tr>
<tr>
<td>IL28B CC</td>
<td>19/506</td>
<td>1.00</td>
<td></td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>IL28B non-CC</td>
<td>47/697</td>
<td>1.78 (1.03–3.06)</td>
<td>0.04</td>
<td>1.38 (0.71–2.68)</td>
<td>0.34</td>
</tr>
<tr>
<td>PNPLA3 CC</td>
<td>32/752</td>
<td>1.00</td>
<td></td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>PNPLA3 non-CC</td>
<td>34/451</td>
<td>1.79 (1.10–2.90)</td>
<td>0.02</td>
<td>1.45 (0.85–2.47)</td>
<td>0.17</td>
</tr>
</tbody>
</table>

*Adjusted for age, sex, race, and baseline total bilirubin, albumin, and platelets.
EGF: Epidermal Growth Factor; IL28B: interleukin-28B; PNPLA3: patatin-like phospholipase domain-containing protein 3; CI: confidence interval.

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analyses restricted to those with Child-Pugh Class A cirrhosis, and found that EGF non-AA genotype was associated with the risk of clinical deterioration in Child-Pugh Class A subjects (age, sex, race-adjusted HR=3.30; 95%CI 1.46–7.35; p=0.004). The significant association between PNPLA3 genotype and risk of clinical deterioration also persisted (age, sex, race-adjusted HR=2.04; 95%CI 1.16–3.60; p=0.01 for non-CC compared with CC). The association between IL28B genotype and risk of clinical deterioration did not remain statistically significant (age, sex, race-adjusted HR=1.81; 95%CI 0.95–3.48; p=0.07 for non-CC compared with CC).

One hundred twenty-six patients (75%) received some course of antiviral therapy with either interferon alfa alone or interferon alfa and ribavirin following the index biopsy. Among these, forty patients (32%) achieved a SVR to antiviral therapy. Among these forty patients, only 3 patients developed clinical deterioration. One patient had an episode of variceal hemorrhage and two patients developed HCC. When we incorporated achievement of SVR into the age, sex, and race-adjusted model, EGF non-AA genotype remained a significant predictor of increased risk of clinical deterioration (HR=2.74; 95%CI 1.32–5.67; p=0.007). There were no longer significant associations between IL28B genotype (age, sex, race-adjusted HR=1.61; 95%CI 0.93–2.79; p=0.09 for non-CC compared with CC) and PNPLA3 genotype (age, sex, and race-adjusted HR 1.56; 95%CI 0.96–2.56; p=0.07 for non-CC compared with CC) and clinical deterioration. The addition of SVR to the age, sex, and race-adjusted model with all 3 loci did not materially alter the results.

### Table 3. Combined genotype model.

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Cases/Person-Years</th>
<th>Age, sex, race-Adjusted Hazard Ratio (95%CI)</th>
<th>P value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/1 unfavorable genotypes*</td>
<td>18/569</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>2 unfavorable genotypes</td>
<td>23/424</td>
<td>1.79 (0.96–3.35)</td>
<td>0.07</td>
</tr>
<tr>
<td>3 unfavorable genotypes</td>
<td>25/209</td>
<td>4.03 (2.13–7.62)</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>

*P_linear trend<0.0001.

*unfavorable genotypes include EGF non-AA, IL28B non-CC, and PNPLA3 non-CC.

EGF: Epidermal Growth Factor; IL28B: interleukin-28B; PNPLA3: patatin-like phospholipase domain-containing protein 3; CI: confidence interval.
Discussion

We found significant associations between EGF, IL28B, and PNPLA3 genotypes and the risk of clinical deterioration in patients with HCV-related cirrhosis. The risk associated with EGF genotype persisted, even after adjustment for known clinical predictors of progression, including albumin, bilirubin, and platelets. These results suggest that genetic variation at the EGF locus is independently associated with clinical deterioration in patients with CHC and provides prognostic information beyond known clinical predictors. In contrast, genetic variations at IL28B and PNPLA3 loci were associated with prognosis in age, sex, and race-adjusted models, but the association was no longer statistically significant after adjustment for albumin, bilirubin, and platelets. This may reflect either a weaker association of these polymorphisms with clinical deterioration compared with the EGF polymorphism or the possibility that the effect of the IL28B and PNPLA3 polymorphisms on clinical deterioration may be mediated by these clinical factors. Thus, controlling for these variables may mask a true biological relation. Our combined analysis shows that the risk of clinical deterioration significantly increases with the presence of each unfavorable genotype and suggests that all three SNPs in concert could be useful in predicting disease progression.

Our findings are consistent with prior data regarding the EGF locus and clinical outcome in liver disease. We previously found that the EGF AG and GG genotypes are associated with a two to four-fold increased risk for HCC [10]. Moreover, EGF expression, as assessed in a gene expression signature in non-tumoral liver tissue, is associated with poor survival in HCC patients after resection and with progression to advanced cirrhosis, HCC development and poor survival in HCV-related early-stage cirrhosis [20,21]. Our findings extend the results of these studies by identifying a role for the EGF locus independently or in concert with two additional SNPs in not only the development of HCC but also the progression of HCV-related cirrhosis. Consistent with these results is a cross-sectional study showing that the G allele of EGF rs4444903 is associated with higher degrees of liver fibrosis in younger subjects with CHC [12].

Our results are consistent with the functional nature of EGF rs4444903. We have previously reported increased stability of EGF 61*G allele transcripts compared to EGF 61*A allele transcripts in human hepatoma cell lines and primary human hepatocytes as well as increased levels of serum and liver EGF in subjects with cirrhosis who have the EGF GG versus AA genotype [10]. Additionally, the EGF receptor (EGFR) [22] and its HRas signaling pathway have been identified as host factors for HCV cellular entry [23]. HCV infection also induces EGFR signaling in cell culture models [24] and increases EGFR expression in HCV-infected patients [23]. Taken together with our study, these findings support a key role for EGF in the mediation of CHC-related liver damage.

Our finding of an association between increased risk of clinical deterioration and the IL28B non-CC genotype in age, sex, and race-adjusted analysis is supported by evidence that carriage of the T allele is associated with fibrosis
severity, cirrhosis and HCC in CHC [7, 9]. In contrast to our results, however, one

group showed that the CC genotype was associated with increased risk for adverse
clinical outcomes [8]. This group also found no association between IL28B
genotype and fibrosis progression. The difference in our findings may be related
to the fact that their cohort consisted of patients who were prior non-responders
to interferon and ribavirin and had advanced fibrosis or cirrhosis. Of note, the
association between IL28B genotype and clinical deterioration was not significant
in our analysis when restricted to Child Pugh Class A subjects or after excluding
HCC from the definition of the primary outcome. This may reflect limited power
in this smaller cohort and potentially a more limited role for the IL28B genotype
in hepatic decompensation compared with development of HCC. The association
between IL28B genotype and clinical deterioration was also no longer significant
after adjustment for SVR. This likely reflects the fact that the impact of IL28B on
clinical deterioration is mediated through response to therapy or potentially
limited power to detect the association in the larger model.

Our results showing an association between PNPLA3 non-CC genotype and
risk of clinical deterioration in age, sex, and race-adjusted analysis is supported by
a study showing an association between the PNPLA3 C>G polymorphism and
fibrosis progression in CHC [14] and a meta-analysis showing an association
between this polymorphism and hepatocarcinogenesis in subjects of European
descent [16].

Our study has several limitations. First, we excluded sixteen subjects from the
multivariable model adjusting for known predictors of disease progression due to
missing laboratory variables. This may have limited our power to detect the
association between the PNPLA3 and IL28B polymorphisms and clinical
deterioration in analyses adjusted for established laboratory predictors of
outcome. Second, we did not have information on disease duration prior to the
biopsy. However, no patients had evidence of decompensated liver disease prior to
the biopsy and our results were consistent even among those with Child-Pugh
Class A disease. Third, because the index biopsies were performed between 1990
and 2007, we did not have reliable information quantifying the amount of
steatosis on each biopsy, and thus could not incorporate this into our
multivariable model. While steatosis has been shown to predict fibrosis
progression prior to the development of cirrhosis, it has not been shown to
predict decompensation once cirrhosis has occurred. Fourth, our population was
predominantly Caucasian males, limiting the external generalizability of our
findings. However, recent meta-analyses revealed that although allele frequencies
of the EGF polymorphism vary according to race, the association between EGF
genotype and HCC risk appears independent of race [25, 26]. Nonetheless, further
studies are required to validate our findings in more diverse cohorts. Last, we only
examined clinical deterioration among individuals with hepatitis C-related
cirrhosis. It is unknown if our findings would be similar among patients with
other etiologies of cirrhosis. However, a recent study reported an association
between carriage of the EGF G allele and cirrhosis in 62 subjects with chronic HBV
infection [27].
In conclusion, our findings support a role for EGF and possibly IL28B and PNPLA3 genotyping in identifying persons with CHC at high risk for disease progression. In light of our group’s finding that pharmacological inhibition of EGFR with erlotinib prevented progression of cirrhosis and regressed fibrosis in animal models of progressive cirrhosis [28], EGFR inhibition may be a promising therapeutic approach for reduction of fibrogenesis and prevention of HCC in high risk patients. Taken together with the known association of genetic variation in the EGF gene with EGF levels, our data support the potential for EGF genotyping to identify patients who may be candidates for strategies to modulate EGF.

Author Contributions
Conceived and designed the experiments: LK KJ KC KT BF RC. Performed the experiments: LK KJ TA NU LW BF. Analyzed the data: LK KJ HZ LW KC AC KT YH TB BF RC. Contributed reagents/materials/analysis tools: LW TG KT BF RC. Wrote the paper: LK KJ AC BF RC. Critical Revision of the Manuscript for Important Intellectual Content: YH KC TA TB AC KT BF RC.

References


