A clinical prediction model predicted absence of significant fibrosis in chronic hepatitis B


Clinical impact ratings Internal medicine ★★★★★★ Gastroenterology ★★★★★★

**Q** In patients with chronic hepatitis B, what clinical and laboratory variables predict liver fibrosis?

**METHODS**

Design: cohort study with independent derivation and validation sets.

Setting: Prince of Wales Hospital, Hong Kong.

Patients: 235 patients (mean age 39 y, 77% men) who had HBV-DNA concentrations >10^5 copies/ml and were treatment-naive. Alanine transaminase (ALT) concentrations were 1.5–10 x the upper limit of normal; ALT concentrations were not part of the inclusion criteria for cirrhotic patients. 150 patients formed the derivation set, and 85 patients formed the validation set.

**Description of prediction guide:** predictive models were developed by using univariate analysis to obtain significant variables; these were entered in a multivariate stepwise logistic regression. The diagnostic value of each regression model was evaluated by area under the receiver operating characteristic (AUROC) curve.

**Outcomes:** significant fibrosis (Ishak score ≥3 [presence of bridging fibrosis or cirrhosis]) found on liver biopsy.

**MAIN RESULTS**

26% of patients had significant fibrosis. 12 variables were associated with significant fibrosis in univariate analysis: age, body mass index (BMI), serum albumin, total bilirubin, alkaline phosphatase, aspartate transaminase (AST), ALT/AST ratio, α fetoprotein, platelet count, international normalised ratio, HBcAg positivity, and HBV-DNA. 2 sensitive models for predicting fibrosis had comparable AUROCs, and 1 model was preferred because it had only 4 variables (BMI, bilirubin, albumin, and platelet count). The table shows the diagnostic performance of this model. The model is described on the Evidence-Based Medicine website (www.evidence-basedmedicine.com).

**CONCLUSION**

In patients with chronic hepatitis B, a clinical prediction model comprising body mass index and 3 routine laboratory tests (bilirubin, albumin, and platelet count) was accurate for predicting absence of significant fibrosis.

**Commentary**

Non-invasive assessment of fibrosis is a hot topic: patients hate liver biopsies, liver biopsies have their complications, and they are costly. Therefore, replacement of this invasive procedure by a surrogate fibrosis marker is highly desirable. Essentially, 3 different types of surrogate markers are currently being evaluated: (1) scores derived by logistic regression analysis from a variety of clinical and laboratory parameters based on features associated with advanced liver disease, such as platelet count, albumin, bilirubin, or fibrogenic factors including insulin resistance, or BMI; (2) fibrosis markers sensu strictu measuring part of the extracellular matrix in blood (eg, different procollagens, hyaluronate, laminin, and many others); and (3) probing the liver’s elasticity with ultrasonography (Fibroscan®). Hui et al settled for the first approach and identified BMI, platelet count, bilirubin, and albumin as strong predictors of fibrosis, like so many scores and fibrosis markers, the negative predictive value was strong (0.92) while the positive predictive value was weak (0.41 to 0.63).

I do not share the authors’ belief that a score has to be sought for each and every liver disease; this is reinforced by the parameters selected for their analysis: most of them appear in other scores derived from patients with hepatitis C or populations with cirrhosis of any aetiology. What is needed now is a well powered, prospective study comparing the many proposed scores. Hopefully, physicians will then decide on the best one and use it in clinical decision making.

Will such a fibrosis score replace liver biopsy for good? I do not believe so since liver biopsy gives more information than just extent of fibrosis. But a reliable score will certainly reduce the frequency with which such a procedure is performed—and this already will earn us our patients’ gratitude.

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<table>
<thead>
<tr>
<th>Patient group</th>
<th>Predictive probability cutpoint†</th>
<th>Sensitivity (95% CI)</th>
<th>Specificity (CI)</th>
<th>+LR</th>
<th>−LR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training set</td>
<td>&gt;0.15</td>
<td>93% (85 to 100)</td>
<td>49% (40 to 59)</td>
<td>1.8</td>
<td>0.14</td>
</tr>
<tr>
<td></td>
<td>&gt;0.5</td>
<td>41% (26 to 57)</td>
<td>90% (85 to 96)</td>
<td>4.1</td>
<td>0.65</td>
</tr>
<tr>
<td>Derivation set</td>
<td>&gt;0.15</td>
<td>75% (54 to 96)</td>
<td>53% (40 to 65)</td>
<td>1.6</td>
<td>0.47</td>
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<tr>
<td></td>
<td>&gt;0.5</td>
<td>25% (4 to 46)</td>
<td>85% (76 to 94)</td>
<td>1.7</td>
<td>0.88</td>
</tr>
</tbody>
</table>

*Diagnostic terms defined in glossary; LR calculated from data in article.
†Model for calculating predictive probability available on website (www.evidence-basedmedicine.com).