SVRScore: A Novel and Highly Predictive Score for SVR Prediction in Chronic Hepatitis C Genotype 1 Infected Patients

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Introduction

Recent studies have demonstrated that changes in HCV RNA levels compared to baseline values during therapy are useful for predicting response and may aid decisions about the duration of treatment. Discontinuation of therapy can be considered for those patients with genotype 1 when an early virological response (EVR) is not achieved. However, limitations exist regarding interpretation of EVR and treatment decisions must be individualized, particularly when other endpoints of therapy, such as histological response or treatment of extrahepatic manifestations, are being considered. **Pretreatment HCV RNA levels and week 4 appears to be interesting in predicting response**. No study was done in combination of these values in an individualized highly predicting score.

Aim

We looked at pre-treatment (BL) VL, and week 4 VL (W4) to assess a predictive score achieving probability of sustained virological response (SVR) in CHC genotype 1 patients: the SVRScore.

Patients & Methods

Patients:

113 CHC genotype 1 patients were included from MODULOPEG study. Among these patients, 86 achieved complete 48 weeks treatment (54 had an SVR). All patients were treated with Peginterferon alfa-2a (40kD) + Ribavirin.

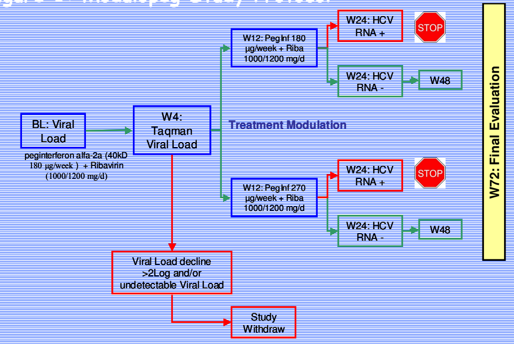
Methods:

Serum HCV RNA was measured using COBAS TaqMan HCV Test (TaqMan HCV; Roche Molecular Systems Inc., Branchburg, N.J.).

Satistical Analysis

Chi-square test or Fisher's exact test were used to compare proportions. Binary logistic regression analysis was assessed with BL VL and W4 VL as predictors of SVR, to obtain the SVRScore. A p-value less than 0.05 was considered as statistically significant.

Figure 1: Modulopeg Study Protocol



Results

- Preliminary results showed no difference of SVR rate between patients with modulated treatment and patients with classical treatment.
- In univariate analysis BL VL and W4 VL were both associated with SVR ($p<.0001$ and $p<.01$ respectively). In multivariate analysis, BL VL and W4 VL were both independent predictors of SVR (respective odds ratio 0.29 (95% CI 0.09-0.95), and 0.39 (0.24-0.63) (Table 1).

Table 1: Multivariate Analysis for Prediction of SVR. Negative HCV RNA was the probability modeled.

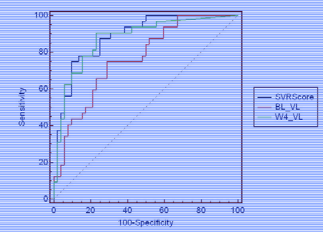
Variables in Model	Odds Ratio	95% CI	*P*-value
Log_{10}BL_VL	0.288	[0.087-0.950]	0.04
Log_{10}W4_VL	0.386	[0.236-0.633]	<0.01

- From the binary logistic regression, we calculated the SVRScore combining BL VL and W4 VL:

$$SVRScore = \frac{EXP[11.8031 - 1.2443(\log_{10} BL\_VL) - 0.9509(\log_{10} W4\_VL)]}{1 + EXP[11.8031 - 1.2443(\log_{10} BL\_VL) - 0.9509(\log_{10} W4\_VL)]}$$

- SVRScore area under the ROC curve for SVR prediction was of 0.89 (significantly higher than that from BL, 0.77 (p=0.008), but not from W4, 0.88) (Figure 2).

Figure 2: Roc curve of SVRScore, Baseline, and Week 4 for SVR prediction



- Positive predictive value of SVRScore for SVR prediction was **86%** (44/52) vs. 70% (53/76) for SVR prediction of Week_12 viral load (p=0.06).

Conclusions

We developed the SVRScore, a new, simple, and highly predictive score for SVR prediction in CHC genotype 1 infected patients. With high predictive values the SVRScore remains useful for the treatment management patients with CHC. Further studies should be conducted to validate this score on independent cohorts.

Aknowledgments

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