OL-043 Multiple drug resistance from single lamivudine therapy after adefovir treatment failure in chronic hepatitis B patients

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Objectives: To investigate the multiple drug resistance (MDR) profiles in patients who took sequential therapy after adefovir treatment failure.
Methods: 210 patients' clinical data and serum samples who took sequential lamivudine therapy as rescue therapy after adefovir treatment failure were collected from 5 hospitals in China during December 2007 to December 2009. PCR product population sequencing was used for screening MDR. PCR product cloning sequencing were used for further analyzing resistance profiles.
Results: 3 MDR patients were identified with population sequencing. All 3 patients are genotype C patients. Population sequencing showed rtM204V + rtL180M +rtA181V mutation in all 3 patients. And 64 clones were get from 3 patients. Cloning sequencing results were showed in Chart1. All clones carried mutations resistant to lamivudine and adefovir. rtM204V + rtL180M +rtA181V is the major mutation type in 3 MDR patients (67.2%). Besides, all 3 patients carried clones with entecavir resistance mutation (rtM250V/H, rtS202I, rtI169V), though in minority (23.4%).
Conclusions: Single lamivudine as rescue therapy for adefovir treatment failure may cause MDR. rtM204V + rtL180M + rtA181V is the major form of mutation in these patients. Entecavir resistance mutation maybe induced with sequential therapy.

Chart 1. Cloning sequencing of 3 MDR chronic hepatitis B patients

Treatment history	Mutations	Number
ADV(36m) → LAM(12m)	M204V+A181V+L180M	19
	M204I+A181T	
	M204V+A181T	1
	M204V+A181V+L180M+M250V	11
ADV(36m) → LAM(15m)	M204V+A181V+L180M	8
	M204V+A181V+L180M+S202I	1
	M204I+A181T	1
	M204V+A181V	1
ADV(12m) → LAM(12m)	M204V+A181V+L180M	16
	M204V+A181V+L180M+I169V	1
	M204V+A181V+L180M+M250V	1
	M204V+A181V+L180M+M250H	1
	M204V+A181I	1

OL-044 Comparison of MELD, Mayo, MESO, CTP and MELD-Na scores for predicting 3-month mortality in patients with acute-on-chronic hepatitis B liver failure

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Aim: To investigate the model for end-stage liver disease (MELD), Child–Turcotte–Pugh (CTP), Mayo, end-stage liver disease score to serum sodium ratio (MESO) and MELD with incorporation of serum sodium (MELD-Na) score in predicting the short-term prognosis of patients with ACHBLF.
Methods: Data from 226 patients admitted due to ACHBLF were reviewed. The ability of five score systems to predict the prognosis of ACHBLF were compared with the receive operating characteristic curve (ROC).
Result: The MELD, CTP, Mayo, MESO, MELD-Na scores in death group (30.2±9.2, 11.3±1.4, 10.4±1.2, 2.3±0.7 and 38.0±11.8, respectively) were higher than those in survival group (21.0±6.8, 10.6±1.6, 9.0±1.6, 1.5±0.5 and 22.5±8.2, respectively) (all $P < 0.01$). The area under the ROC (AUC) of five score systems were 0.809, 0.616, 0.759, 0.828 and 0.874, respectively (Figure 1, Table 1). The Youden's indexes were 0.501, 0.183, 0.413, 0.520 and 0.632, respectively.
Conclusion: MELD-Na is more appropriate in predicting short-term mortality, but larger scale studies are needed to confirm the superiority of MELD-Na to MELD, Mayo, MESO and CTP in patients with ACHBLF.

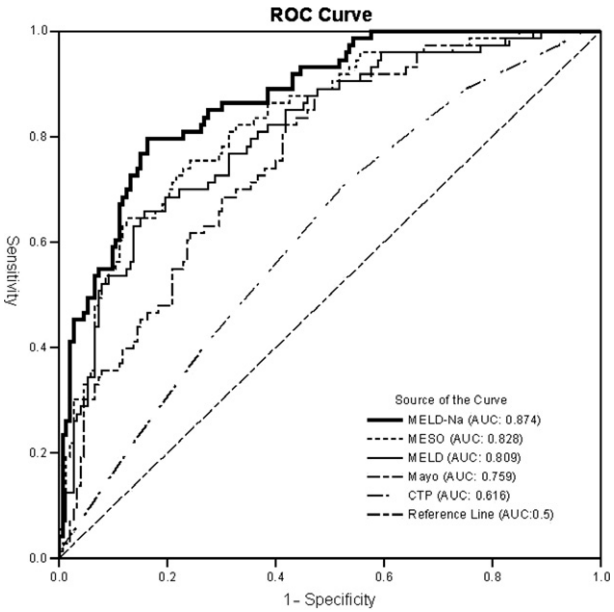

Figure 1. Comparison of the predictive accuracy of the five models to predict 3-month mortality of acute-on-chronic hepatitis B liver failure.

Table 1

Items	Z statistics	P value
CTP vs. Mayo	4.32	<0.001
CTP vs. MELD	4.20	<0.001
CTP vs. MELD-Na	6.16	<0.001
CTP vs. MESO	4.76	<0.001
Mayo vs. MELD	1.38	0.168
Mayo vs. MELD-Na	3.44	0.001
Mayo vs. MESO	1.99	0.046
MELD vs. MELD-Na	3.14	0.002
MELD vs. MESO	2.70	0.007
MESO vs. MELD-Na	2.83	0.005