was low. Further, the result needs to be verified by other laboratory diagnosis methods in case of Pott's disease.

OL-039 Can *Mycobacterium tuberculosis* DNA be detected in plasma/serum samples from tuberculosis patients?

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Background: Tests based on PCR have shown promise for the detection of *M. tuberculosis* in different clinical samples except plasma/serum. The purpose of this study was to know that whether *M. tuberculosis* DNA can be detected in plasma/serum samples.
Methods: 43 serums and 94 plasma were collected from 124 clinical diagnosed TB patients. Four different *M. tuberculosis* DNA extraction methods, including phenol-chloroform method, Qiagen kit, Omega kit and magnetic bead method were compared to get higher sensitivity. One quantitative fluorescent PCR designed by this study was used for the detection of *M. tuberculosis* DNA.
Results: The highest DNA extraction efficiency (52.8%) and the best reproducibility (CV = 26.7%) were seen in the magnetic bead method. And *M. tuberculosis* DNA can really be detected in some samples, and 39 of the 124 (31.5%) TB patients showed *M. tuberculosis* DNA positive in plasma/serum samples. Interestingly, 35.3% (12/34) smear negative cases demonstrate *M. tuberculosis* DNA positive.
Conclusion: In conclusion, this is the first study to report the existence of circulating *M. tuberculosis* DNA in plasma/serum from tuberculosis patients and showed that the detection of *M. tuberculosis* DNA may provide valuable information for the diagnosis of AFB negative TB patients.

OL-040 Rapid identification and molecular characterization of drug resistant *Mycobacterium tuberculosis* isolates circulating in China by multilocus PCR and electrospray ionization mass spectrometry

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Objective: The emergence of multidrug-resistant (MDR)-TB and more recently, of extensively drug-resistant (XDR)-TB is a real threat to achieve TB control and elimination. Quick detection of drug resistance is an urgent clinical need for personalized treatment to control MDR-TB or XDR-TB.
Methods: We used multilocus PCR and electrospray ionization mass spectrometry (PCR/ESI-MS) to determine the genotype and drug resistance profiles for 96 *Mycobacterium tuberculosis* isolates circulating in low and high endemic regions (Shanghai, n = 49; Chongqing, n = 47) in China.
Results: The mutation profiles obtained by the PCR/ESI-MS assay indicated that Principal Genetic Group 1 (PGG1) profile (87.5%) was dominant across the isolates tested in China. The results revealed that a cluster of 11 isolates with *katG* S315T & *inhA* promoter C-15T, *rpoB* S531L, and *embB* M306I in Chongqing, the high TB endemic region, which was not observed in Shanghai, the low endemic region. In addition, another resistance mutation profile with *katG* S315T & *inhA* promoter T-8C, *rpoB* D516G & P564R/A, was detected in 10 isolates in high endemic region in comparison to one in low endemic region. Drug-resistant gene mutations were more diversified in the low endemic region than in the high endemic region.
Conclusion: PCR/ESI-MS can provide another rapid and accurate laboratory diagnostic tool for antituberculosis drug resistance determination. This new technique has potential to facilitate rapid determination of MDR-TB in China, allowing timely guidance for individualized treatment.

Free Paper Presentation 6: Hepatitis B
Saturday, July 16, 2011, 15:30–17:00
Meeting Room 310

PL-006 HBV infection modeling and numerical simulation for anti-HBV infection personalized combination therapy

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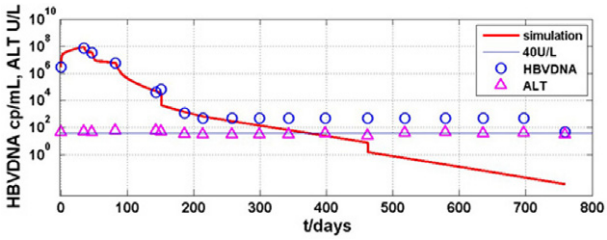
Background: Some chronic HBV (CHB) patients have normal ALTs and hepatic injuries. Chinese herbal medicine and nucleosides combination treatments may be effective for some of such kind patients. It needs to develop an anti-HBV infection treatment model to interpret the mechanism for curable CHB patients with near normal liver functions.
Methods: A 57 years old male chronic HBeAg positive patient (nucleosides-native) received Chinese Herbal Medicine (CHM 15–23 ingredients, 450–600 g) treatment two times daily for 24 weeks, switched to CHM + Adefovir Dipivoxil for 53 weeks, then switched to CHM + Entecavir for 21 weeks. A new differential equation model is introduced to describe the dynamics of anti-HBV infection treatment, in which a *term* is in charge of killing virus rather than infected hepatocytes.
Results: His HBeAg got seroconversion at week 98. The numerical simulation of the model and his HBV DNA, ALT are shown in following figure.
Conclusions: Analysis shows that a treated CHB patient with infective number $R_0 < 1$ will eventually be cured. Large value of that *term* makes patient's virus be eventually cleared without damaging hepatocytes.
Acknowledgment: This work is supported by the 11–5 Key Special Project of China (No. 2008ZX10005–006).



OL-041 Evaluation of serum level changes of sCD26 & sCD30 before and after treatment with interferon among naive chronic hepatitis B patients

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Propose: To evaluate the role of serum levels of sCD26 and sCD30 in predicting the outcome of therapy with IFNα among naïve chronic hepatitis B patients.