CHAPTER 5

CONCLUSION

In this thesis, plasma samples from MDD (n = 48) and the normal (n = 20) groups were analyzed by 2DE, and followed by MALDI-TOF MS. The proteins in plasma, either before or after depletion of albumin and IgG, were successfully separated into spots by IEF and SDS-PAGE in the first and second dimensions, respectively. In comparison, the 2DE gel staining with colloidal Coomassie blue G-250 was the most informative, and this staining process was selected for the entire gels carried out in this thesis. According to %V comparison of the matched spots, the expression levels of α1-antitrypsin, fibrinogen, haptoglobin, transcritption factor, apo AI, apo AII, apo E, HDL associated protein, IgG light chain and C3 were significantly higher in MDD than in the normal. Therefore, these proteins are possible biomarker candidates in plasma for differentiating MDD from the normal, though the controversy of high expressions of apo AI, apo AII and C3 in MDD is needed to be validated. In comparison among NR, FR and SR, the expressions of α1-antitrypsin, apo AI, C3, haptoglobin and IgG light chain were significantly highest in NR, whereas, that of transcription factor and Rap 1A were significantly lowest in NR. These proteins in particular Rap 1A are biomarker candidates in plasma for early prediction of the responsiveness to fluoxetine and, may be, other SSIRs.