Direct detection of methamphetamine and MDMA in human urine by APCI-Ion Trap Mass Spectrometry

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AIMS: Drug abuse is one of the most serious social problems around the world. The most abused drug in Japan is methamphetamine, which accounts for 80-90% of all drug offenders. In addition, recently there has been a considerable increase in the number of seizures of tablets containing 3,4-methylenedioxymethamphetamine (MDMA). The current way to identify illicit drugs in urine requires time-consuming sample pretreatment and separation step (i.e., gas chromatography or liquid chromatography), followed by mass spectrometry (MS). We developed a novel method for direct detection of drugs of abuse in samples by atmospheric pressure chemical ionization (APCI) and ion trap MS without any sample pretreatment or separation step. In the present study, the mass spectrometer was applied for detection of drugs and their metabolites in urine samples.

METHODS: Experiments were performed using a Hitachi DS-1000N ion-trap mass spectrometer equipped with an APCI ion source, a heater unit (set at about 230°C) and an air pump for sample introduction to the ion source. Fifty microliters of urine samples spiked with and without known amounts of drugs (methamphetamine, amphetamine, MDMA or MDA) were put on a cellulose cloth, which was then mounted in a plain metal frame. The mounted samples were vaporized at the heater unit, and introduced to the APCI ion source through a transfer line heated at about 230°C, by constant air flow at about 0.5 L/min using the air pump. Ions generated by corona discharge were introduced to the ion trap mass spectro-meter operated under the MS and MS/MS modes. Helium was used as the collision gas. After setting the mounted sample on the tray, analysis was performed automatically. Matrix effect was evaluated by comparing ion intensities of the drugs obtained from their aqueous solutions to those from their spiked urine samples (drug concentration of 2 µg/mL). Each experiment was performed in triplicate.

RESULTS: The major ions were observed at *m/z* 150 and 136 in the full-scan mass spectrum obtained from a urine sample spiked with methamphetamine and amphetamine, corresponding to their protonated molecules. In the MS/MS mode, dissociation of the ion at *m/z* 150 produced a characteristic fragment peak at *m/z* 119, derived from cleavage of the methylamino group from the protonated molecule of methamphetamine. Dissociation of the ion at *m/z* 136 (the protonated molecule of amphetamine) also produced a fragment peak at *m/z* 119. Combination of the MS and MS/MS mode provided accurate identification of the drugs in urine samples. In the same manner, MDMA and MDA in a urine sample produced ions at *m/z* 194 and 180 in the MS mode, and ions at *m/z* 163 in the MS/MS mode. The ion intensities of methamphetamine, amphetamine, MDMA and MDA were decreased by 71.5%, 92.2%, 88.8% and 91.4% (the averages of 5 individual urine samples), respectively, due to matrix effect. However, lower limits of detection for methamphetamine, amphetamine, MDMA and MDA

were 0.3, 0.5, 0.3 and 0.5 µg/mL in urine, respectively, when 50 µL samples were used for analysis. Analysis time required was only 20 seconds per sample.

CONCLUSIONS: Direct APCI MS without any sample pretreatment or sparation step was applied for analysis of drugs in urine samples. The method was simple, rapid and sensitive enough to perform drug screening in urine.

KEYWORDS: *Drugs of abuse, Urine, Direct Detection, Ion Trap Mass Spectrometry, APCI, Methamphetamine, MDMA*

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