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Data Article

Data on the optimization of a GC–MS procedure for the determination of total plasma myo-inositol



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ABSTRACT

Myo-inositol (MI) is one of the stereoisomers of hexahydroxycyclohexane, which plays an important role in intracellular signal pathway. Derivatization is an indispensable step in both external and internal standard method during the chromatography-mass spectrometer (GC–MS) detection, as MI can't be ionized directly. It is valuable to optimize the derivative process and the detection volume for clinical detection. This article contains optimization data related to research publication "Quantification of plasma myo-inositol using gas chromatography-mass spectrometry" [1]. Here we introduce the data on the optimized derivatization volume, temperature, duration and the detection volume.

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Specifications Table

Subject area	Chemistry
More specific subject area	Analytical Chemistry, Chromatography-Mass Spectrometer
Type of data	Table, graph
How data was acquired	GC-MS
Data format	Raw
Experimental factors	Extraction reagents were added to the plasma and evaporated to be dry before derivatization; experimental factors include the derivatization volume, temperature, duration and the detection volume.
Experimental features	7890A Gas Chromatography equipment a fused silica HP- 5 MS capillary column (Agilent Technologies, USA) was used for the GC separation.
Data source location	Beijing, China
Data accessibility	Data with this article

Value of the data

- The data for the optimized derivatization volume, temperature, duration and the detection volume is presented;
- Periphery blood is enough for the detection of plasma MI;
- The optimized derivatization condition for MI analysis could be used not only for biological specimens, but also for food and others.

1. Data

This data consist of the optimal derivatization condition of MI, including amount of derivatization reagent, derivative temperature and derivative time (Figs. 1 and 2). Furthermore, the detection volume of the plasma was minimized (Table 1).

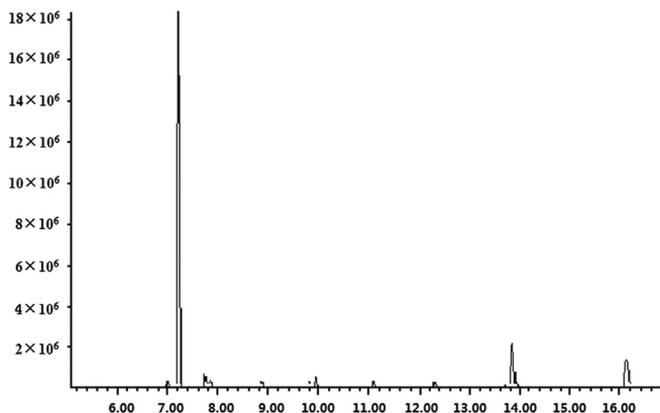


Fig. 1. Total ion chromatogram (TIC) profiles of GC-MS results.

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