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THE QUALITATIVE ANALYSIS OF TRIACYLGLYCERIDES USING ELECTROSPRAY MASS SPECTROMETRY

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The analysis of triacylglycerides (TGs) from a biological sample provides a challenge for mass spectrometry. These neutral lipids are not efficiently ionized under ESI conditions, which generally require a basic, or acidic, site to generate MH^+ , or $[M-H]^-$, ions. In addition, these lipids are may be present as part of a complex mixture of different molecular species with various acyl side chains and numerous isobaric species. While GC-MS is useful in quantifying the fatty acids resulting from the hydrolysis of TGs, the method cannot determine the identity of the precursor TGs.

The addition of NH_4^+ ions to TG mixtures allows molecular adducts, $TG-NH_4^+$, to be formed under ESI conditions. Typically these molecular adducts are very stable allowing the molecular weight of the TG to be readily determined. Collision induced dissociation of $TG-NH_4^+$ adducts result in characteristic neutral losses forming diacylglyceride fragment ions, DG^+ . A tandem mass spectrometer, operating in the neutral loss scanning mode, can then rapidly identify isobaric TGs containing a specific acyl chain. Successive scanning of all neutral losses characteristic of potential acyl side chains leads to a profile of possible TG molecular species. The further fragmentation of the DG^+ ion, in a MS^3 experiment, results in ions characteristic of the remaining acyl chains (e.g. acylium ions), allowing unequivocal identification of TGs. Here we report the qualitative analysis of TGs in the RAW 264.7 macrophage using ESI mass spectrometry.