

Resolution in mass spectrometry

One aspect for classifying mass analysers is **resolution** (R) – the capability to distinguish between ions with similar m/z value. Resolution is defined as:

$$R = \frac{m}{\Delta m}$$

where m is the mass of the component corresponding to the first peak (or the mean of the masses of the components of the two peaks under observation) and Δm is the difference of mass for the two peaks under consideration.

Mass analysers with **low resolution (LR)** offer unit resolution. This means that the analyser is only capable of differentiating the nominal m/z value of ions (see Fig. 1a). At the same time, **high resolution (HR)** mass analysers are capable in distinguishing ions with very similar m/z values from each other (see Fig. 1b). E.g. in Fig. 1, a section from the LR and HR mass spectra of dammar resin are compared. In the LR spectrum only one peak (at m/z 525.3) is visible, whereas in the HR spectrum three peaks (at m/z 525.28170, m/z 525.31815, m/z 525.35449) can be found.

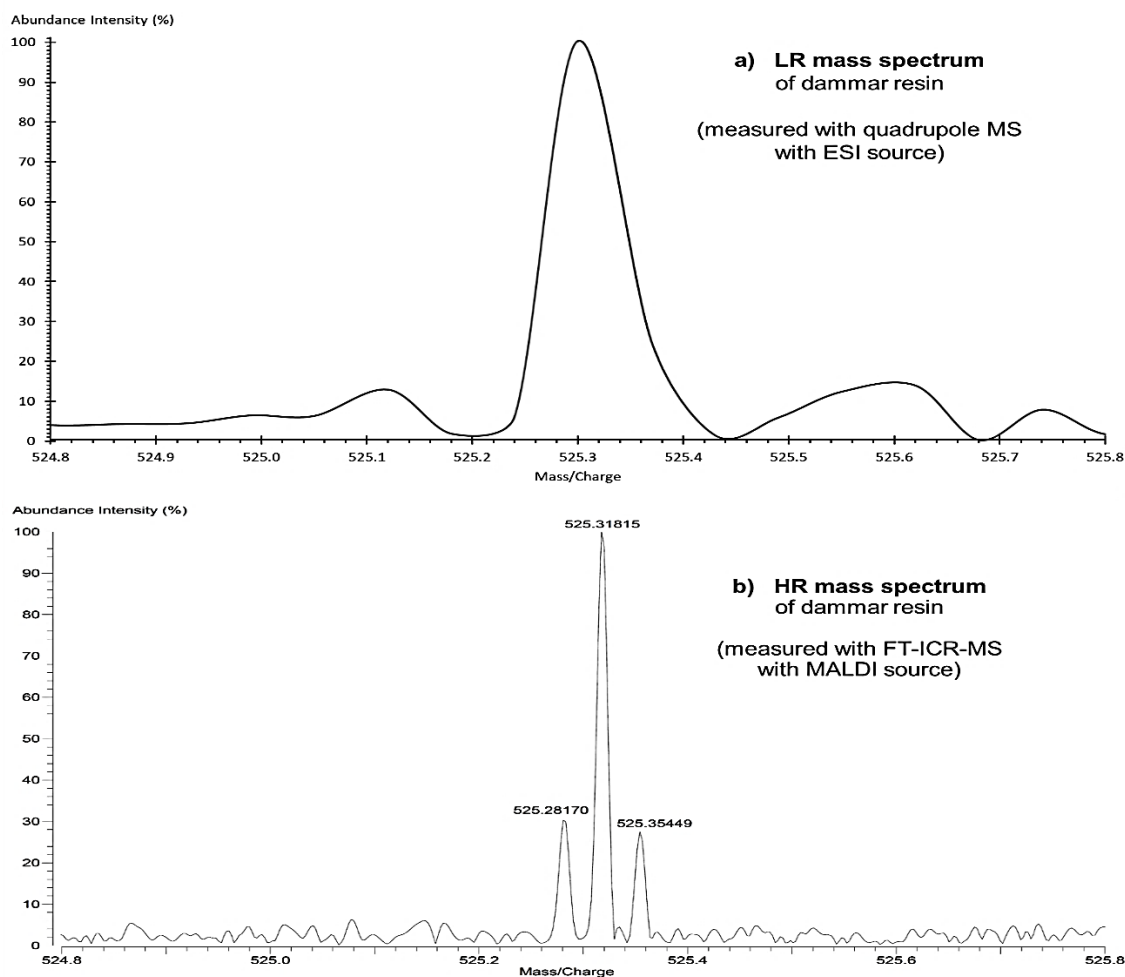


Fig. 1. Comparison of LR and HR mass spectra (selected range) of dammar resin.