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# The challenge to get MRI metabolic maps in fleshy fruit: tomato example

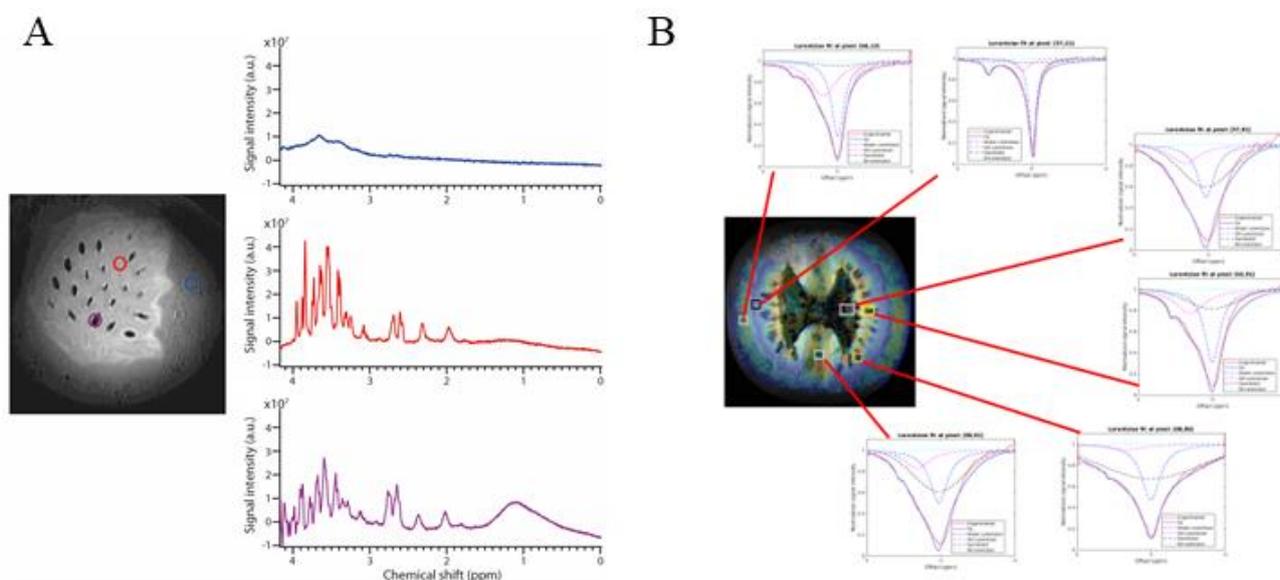
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Besides its classical water-related images, MRI is able to give metabolic information mainly thanks to two approaches. The first one is classical magnetic resonance spectroscopy imaging (MRSI) which leads to one NMR spectrum per image voxel. The second one is chemical exchange saturation transfer (CEST) contrast which gives a map weighed by the metabolite exchangeable protons. CEST MRI monitors the water signal intensity in function of the saturation frequency in a so-called z-spectrum. Saturating the signal at the frequency of exchangeable protons partially saturates the water signal leading to its decrease. Each contrast presents its own advantages and drawbacks. However, both methods have the same limitation, which concerns the excellent homogeneity of the magnetic field required over the entire image.

Fruits are complex organs consisting in different tissues for which the development and metabolism are coordinated. In fleshy fruits, the properties of the different tissues change along fruit development including their microstructure, juiciness and biochemical composition. It is then critical to have a method providing spatial information about these properties non-destructively. MRI is then a tool of choice. To test MRSI and CEST-MRI approaches in such complex biological contexts, we chose the tomato as a model of fleshy fruit containing several compartments with different magnetic properties [1]. In this work, we aimed at comparing MRSI and CEST-MRI in red-ripe tomato fruit.

MRI acquisitions were performed on a 11.7-T Bruker Biospec equipped with a 72-mm circular polarizer coil and piloted by ParaVision 6.0.1. Moneymaker variety tomatoes were studied at a red-ripe stage. MRSI and CEST-MRI data were analyzed based on CSIapo software [2] and home-written MATLAB scripts, respectively. CEST maps were generated by fitting for each voxel the z-spectra with a 4-pool model. The experimental protocol is detailed in [1].



**Figure 1** –Illustration of metabolic MRI results obtained using (A) MRSI and (B) CEST contrasts on red-ripe tomato fruit and corresponding NMR and z-spectra. For both metabolic MRI methods, data quality is tissue-dependent. Contrary to MRSI, CEST contrast measures metabolic information over the entire image.

Figure 1 illustrates results obtained by MRSI (A) or CEST-MRI (B) contrast. The quality of the MRSI spectra is highly dependent on voxel position. For voxels set in locular tissue (red) or seed (purple), the NMR spectra were readily exploitable, and carbohydrates, citrate, glutamate, GABA and lipids were identified. However, in pericarp (blue) the NMR spectrum displayed only broad signals and was not exploitable demonstrating the difficulty to use this method for the entire fruit imaging. The CEST map was carefully analyzed by plotting the z-spectrum for voxels belonging to different tissues. Clearly, the broadness of the direct water saturation, i.e. the main attenuation on the z-spectrum centered at 0 ppm, depended on the tissue as illustrated by the three top z-spectra. To take into account these variations, the CEST maps were generated by adjusting a model containing three Lorentzian pools (water, hydroxyl and amine moieties) and an extra Gaussian pool belonging to the semi-solid macromolecules [3]. This fitting approach allowed to accurately model the z-spectrum in each voxel and then to obtain a CEST map of the different pools for the whole fruit.

In conclusion, we demonstrated that MRSI is not an appropriate approach to image fruit metabolites. However, a CEST-MRI method combined with a careful data analysis based on model adjustments is an interesting alternative solution.

## References

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