Characterization of sodium relaxation in food: a mandatory step to reach quantitative sodium images

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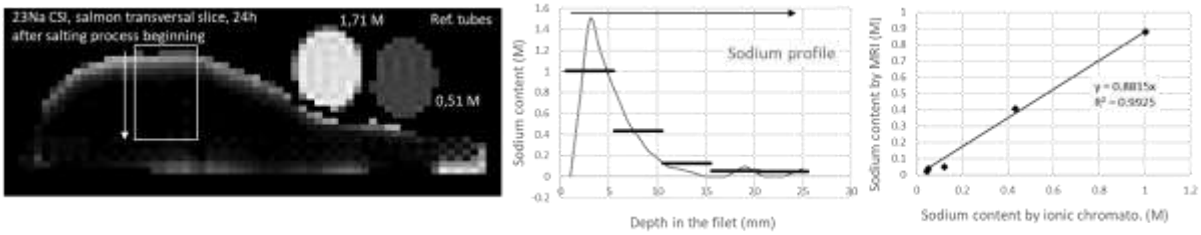
Local quantification of ^{23}Na is critical to (i) understand the relations between salt distribution (and relaxation) and sensory properties and (ii) construct mathematical models of the salting processes. The challenge of quantitative sodium MRI deals with (i) the nuclei low gyromagnetic ratio, (ii) the quadrupolar interactions, (iii) the short T_2 relaxation times and (iv) similarly to other nuclei, B_0 and B_1^+ inhomogeneities. Sodium quantification usually assumes that a single population is present in a voxel and that 3/5 of its population is invisible due to short T_2 relaxation times. This hypothesis is true if all the sodium nuclei experienced, at the NMR timescale, quadrupolar interactions [1]. However, even considering this invisibility factor, significant errors may persist [2]. That is why, we describe here an original approach to check that all sodium presents weak quadrupolar interactions, i.e. type c [1]. When valid, this information was used to map the sodium content.

Filets were salted on the upper side with 6% in weight of dry salt during 6 hours at 8°C. Then, they underwent 6 hours at 24°C (smoking) and were stored at 5°C. A 16 g sample and an entire filet were used for the relaxometry and imaging experiments, respectively. Relaxometry experiments were performed on a Bruker 9.4 T magnet with a 30 mm volumetric insert. A double quantum filter experiment (DQF) was first acquired. Then, a CPMG (TE=175 µs, 256 echoes, TR=500 ms) was recorded and the signal decay was adjusted using a biexponential model. Imaging experiments were performed on a horizontal Biospec 4.7 T system equipped with a DOTY 20 cm ^{1}H/^{23}Na quadrature-polarized coil. Sodium acquisitions were achieved with a CSI (TR=100 ms, voxel volume = 3 × 2 × 8 mm^3, acquisition time = 1h). The FIDs were fitted voxelwise with a single Lorentzian lineshape for estimating the relaxation-corrected amplitudes and correcting B_0 inhomogeneities. Emission RF-field variations were not corrected as the B_1^+ maps showed weak variations.

A DQF signal was detected. Moreover, the CPMG decay showed a biexponential behavior with relative amplitudes of 2/5 and 3/5 for the slow and fast components, respectively. Both demonstrated that all the sodium was of type c, the same type than gelatin (ref. tubes) [3]. ^{23}Na CSI maps showed that at 24h, salt is not yet homogenized (Figure). The sodium profile exhibited the sodium gradient concentration in the thick part of the filet. The sodium content matched with sodium content measured by ion chromatography (black lines on the profile).



Surprisingly, analysis on other foods, e.g. carrot and pasta cooked in salted water, exhibited a different relaxation behavior: slow and fast fractions ratio differing from 2/5 and 3/5. These results suggest the presence of different sodium pools and may explain the errors previously observed.

Funded by the European FEAMP project InnoSalt driven by the CITPPMP (FEA470018FA1000012 2019-2022)

References

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