



HAL
open science

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

Sylvie Clerjon, Guilhem Pagès, Nour El Sabbagh, Amidou Traoré, J.-M. Bonny

► To cite this version:

Sylvie Clerjon, Guilhem Pagès, Nour El Sabbagh, Amidou Traoré, J.-M. Bonny. Characterization of sodium relaxation in food: a mandatory step to reach quantitative sodium images. 15. International Conference on the Applications of Magnetic Resonance in Food Science, Jun 2022, Aarhus, Denmark. hal-03757121

HAL Id: hal-03757121

<https://hal.inrae.fr/hal-03757121v1>

Submitted on 22 Aug 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

INRAE, QuaPA, F-63122 St Genes Champanelle, France
INRAE, PROBE research infrastructure, AgroResonance facility, F-63122 St Genes Champanelle, France

Sylvie Clerjon, Guilhem Pagès, Nour El Sabbagh, Amidou Traore, Jean-Marie Bonny

- Local quantification of ^{23}Na in food is critical to
- understand the relations between salt distribution (and relaxation) and sensory properties
 - construct mathematical models to optimize the salting processes.

The challenge of quantitative sodium MRI deals with

- the poor sensitivity of sodium nuclei
- the quadrupolar interactions
- the short T_2 relaxation times
- B_0 and B_1^+ inhomogeneities (similarly to other nuclei).

The present poster deals with the relaxation issues.

Sodium imaging quantification usually assumes that a single population is present in a voxel and that 3/5 of this population is invisible due to the short T_2 relaxation times compared to imaging TE. This hypothesis is true if all the sodium nuclei exhibit a biexponential super-lorentzian-like spectrum (type c) [1]. Even considering this invisibility factor, significant errors may persist [2]. That is why, we describe here an approach to check this assumption in different food matrices.

A double quantum filter experiment (DQF) was first acquired on fish, gels and carrot. **All samples exhibit double quantum coherences** (i.e. slow motion sodium).

This information is not a sufficient prerequisite to ensure quantitative MRI. A **relaxometry** study of SQ coherences has been added to check if all sodium presents a biexponential behaviour, i.e. type c [1].

Fish samples

Relaxometry experiments were performed on a Bruker 9.4 T magnet with a 30 mm volumetric insert. A CPMG ($TE=175 \mu\text{s}$, 256 echoes, $TR=500 \text{ ms}$) was recorded and the signal decay was fitted using a discrete biexponential model.

Reference gels

Relaxometry experiments were performed on a Bruker 9.4 T magnet with a 5 mm BBO coil. A CPMG ($TE=160 \mu\text{s}$, 4096 echoes, $TR=400 \text{ ms}$) was recorded and the signal decay was fitted using a discrete biexponential model.

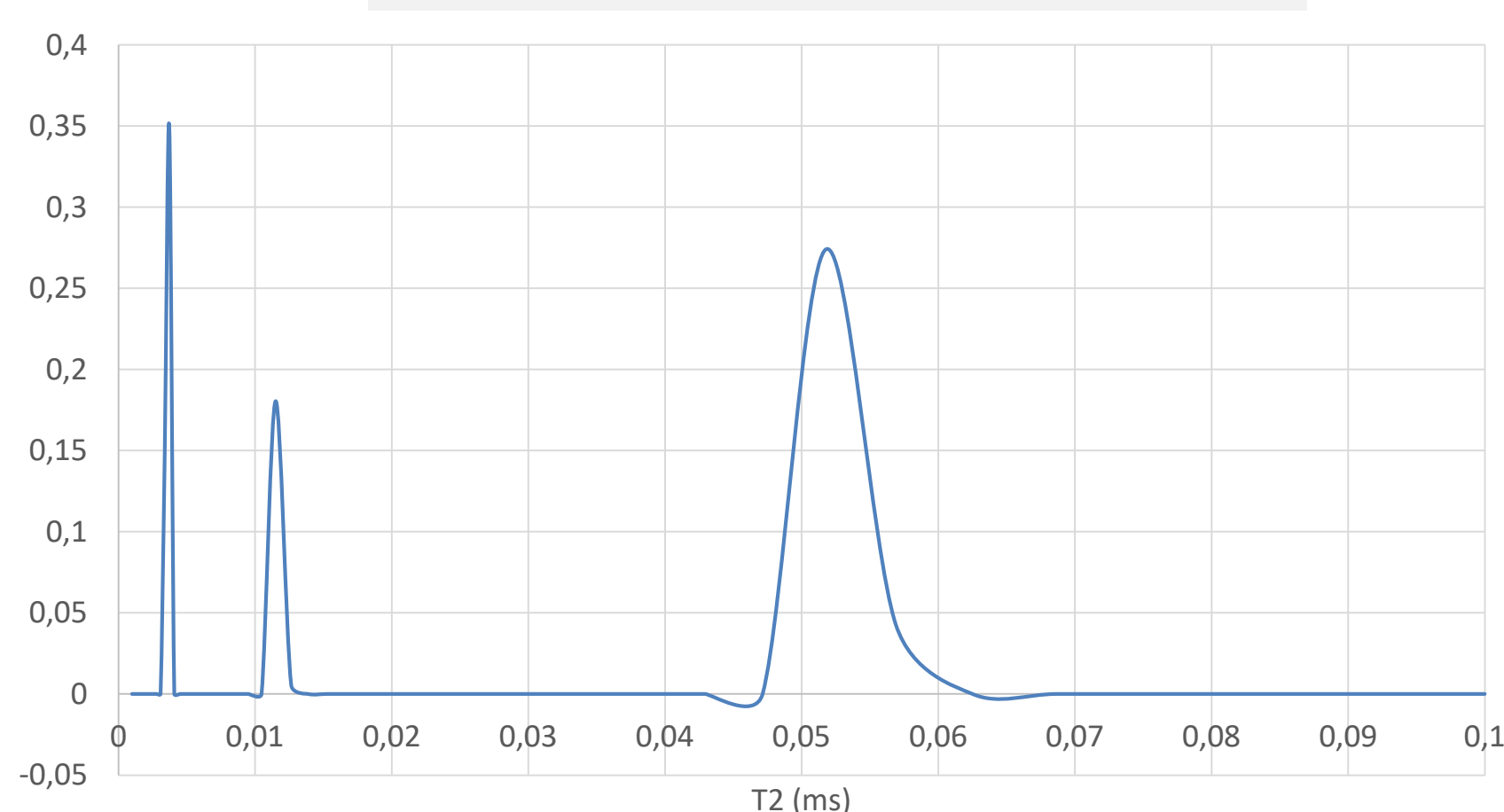
Carrot samples

	Fish	Gel	Carrot
T_{2fast}	5 ms	7.8 ms	4.6 ms
Amplitude (T_{2fast})	62.2%	3.6%	37.8%
T_{2slow}	48.3 ms	21.4 ms	24.9 ms
Amplitude (T_{2slow})	37.8%	96.4%	62.2%

The fish is the only sample exhibiting a biexponential behaviour with the theoretical amplitudes of 3/5 and 2/5 [1].

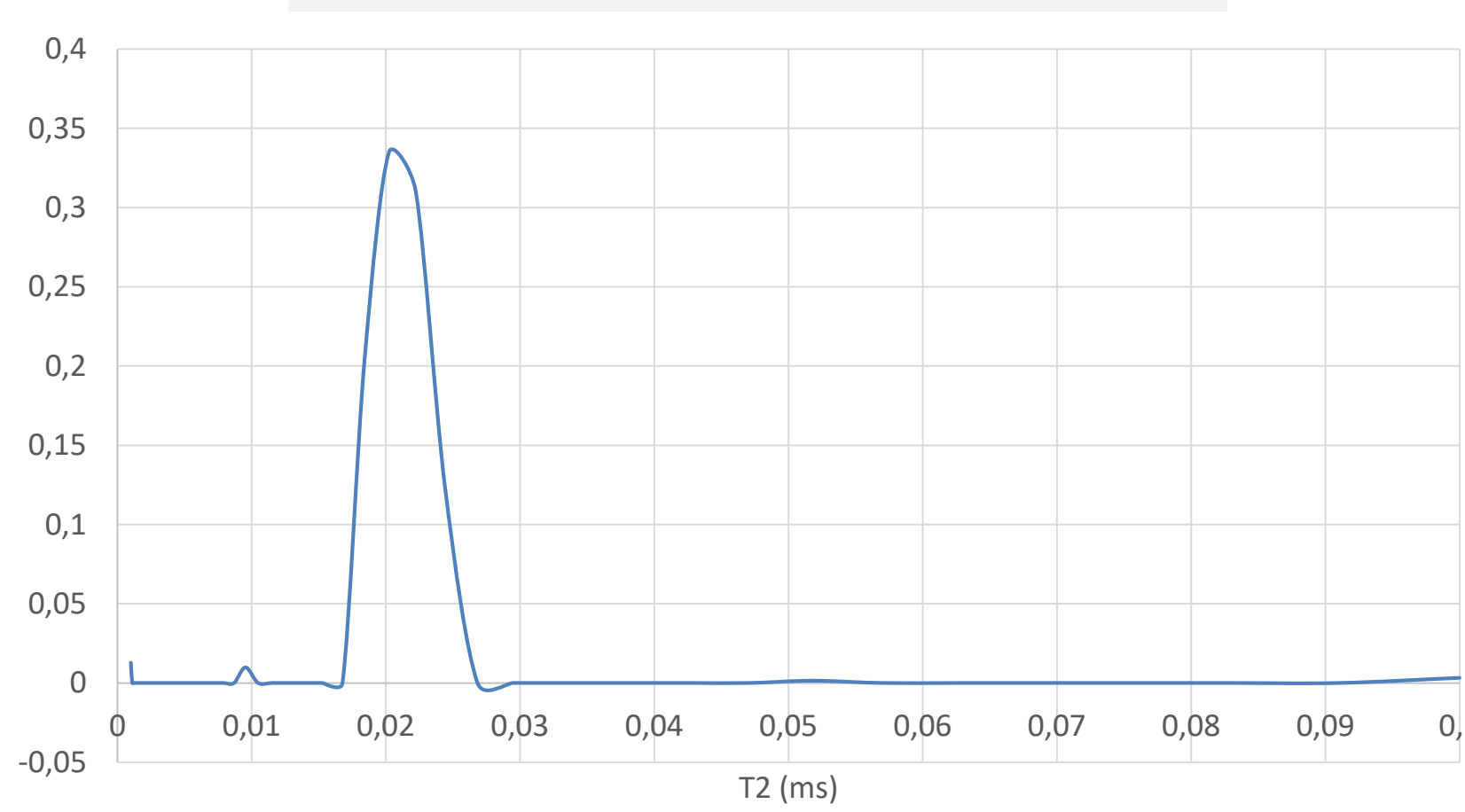
This first conclusion shows that biexponential discrete analysis is an unfair strategy for appreciating complex relaxation behavior. Hence, signal decay was then adjusted using a continuous inversion with L2-regularization [3].

Fish samples



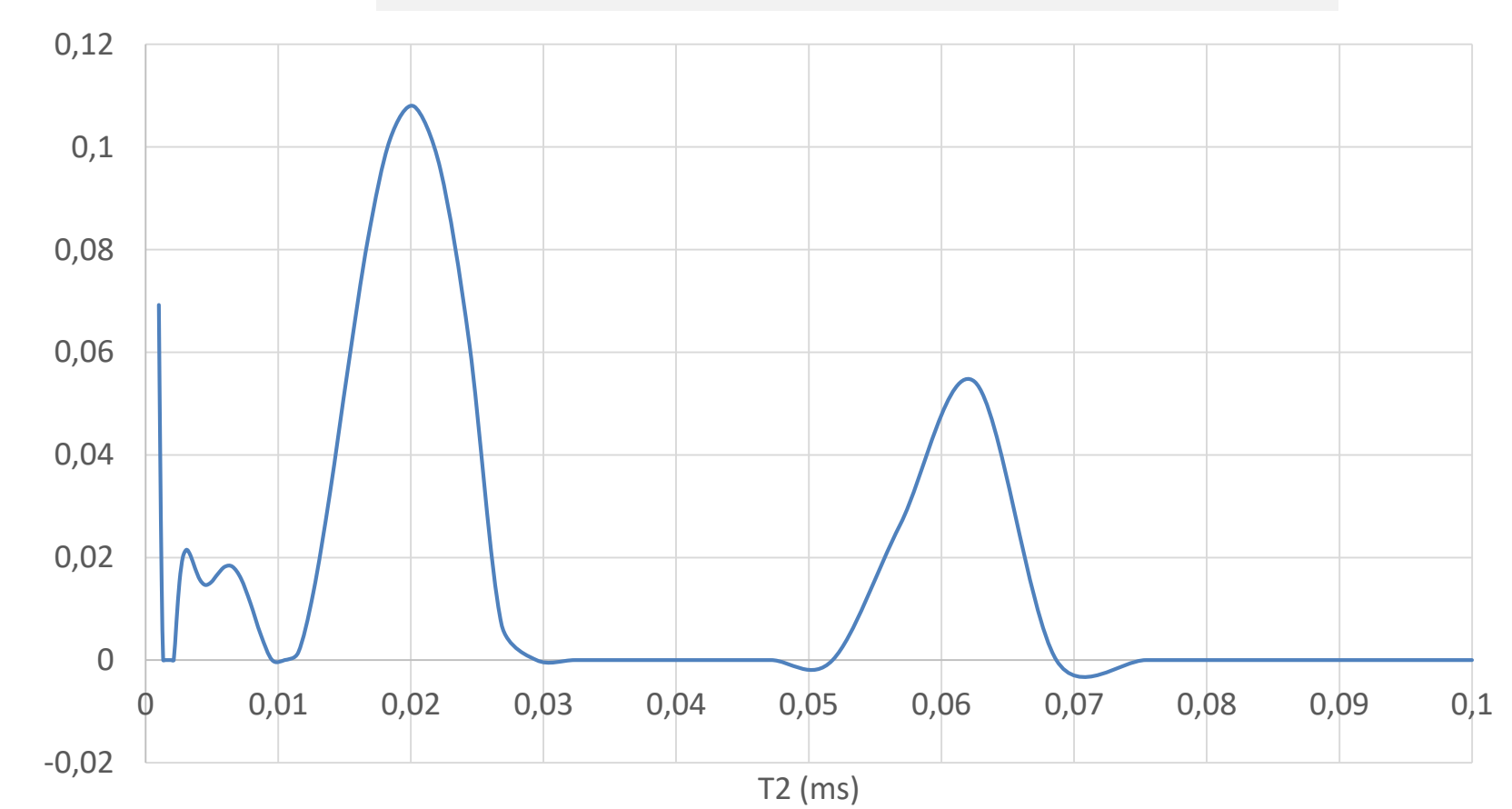
Fish sample exhibits short T_2 pools between 4 ms and 11 ms, and a slow population with a T_2 around 52 ms.

Reference gels



Gels exhibit a minor short T_2 pool at 10 ms and a slow population with a T_2 around 21 ms.

Carrot samples



Carrot sample exhibits more than two pools: 2 short T_2 pools between 2 ms and 9 ms, the main population around 24 ms and a free pool around 62 ms.

Key takeaways

- MR spectroscopy at high field allows to finely analyze the DQ and SQ relaxation of sodium in our food matrices
- SQ analysis reveals more complex relaxations than those suggested by DQ experiments
- Continuous inversion can be conducted on ^{23}Na decay. However it should be interpreted with caution due to low SNR and the possible mix of several populations in heterogeneous systems (carrot, fish...)

Consequences for quantitative sodium MRI

- Reference gels and food matrices showed contrasted behaviors and thus probable different invisibility factors. These factors need to be evaluated to construct quantitative sodium images
- Because of low SNR, adjustment using a continuous inversion with L2-regularization must be repeated on many samples for robust results
- Because food are heterogeneous, MR spectroscopy should be performed on several parts of the food (the edge, the core, the fat, the lean ...)

Application to sensory properties

Fine analysis of sodium relaxation in food matrices is important

- to build quantitative ^{23}Na MRI and then measure sodium location/diffusion in food
- to characterize sodium-matrices interaction

because both location and interaction could be correlated with the sensory availability of sodium in food. One of the purposes of the ANR project Sal&Mieux is to demonstrate this correlation and to suggest solutions to prepare food with less salt without altering the salty taste.

References

- Rooney, W. D. and C. S. Springer (1991). NMR in Biomedicine 4(5).
- Vellyulin, E. and I. G. Aursand (2007). Journal of the Science of Food and Agriculture 87(14).
- Whittall, K. P. and A. L. MacKay (1989). Journal of Magnetic Resonance (1969) 84(1): 134-152.