From Bloch Equation to MR Contrasts: Relaxation & Physical Bases of Tissue Contrast

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INTRODUCTION

Tissue relaxation represents the most utilized contrast mechanism in MRI. Nuclear spin relaxation is caused by the interactions experiences by the nuclear spins in the strong magnetic field. It is not only dependent on the magnitude of these interactions but also on their rate of fluctuation. Although it is possible to derive relaxation terms from the basic NMR quantum mechanics principles, it is customary to use classical physics approach in the form of phenomenological Bloch equations which are intuitive yet sufficient to describe complex relaxation phenomena in heterogeneous media. This simplified approach is further justified since quantum approach can only explain relaxation behaviour is relatively simple systems such as water or water solutions but is basically useless in describing more complex relaxation phenomena in heterogonous tissue compromised of multiple water physical compartments which further complicated the interaction between water and protons associated with molecules such as lipids and proteins.

T1 & T2 RELAXATION

The RF excitation pulse disturbs the thermal equilibrium of the spin system (or magnetization, M) which is eventually restored by the process known as spin-lattice relaxation (or longitudinal relaxation). This process depends on the energy exchange between the spin system and surrounding thermal reservoir ("lattice"). The equilibrium is characterized by the state of magnetization M_0 oriented along the main magnetic field, B_0. The phenomenogical equation describing this process is given by:

$$\frac{dM_z}{dt} = -(M_z - M_0)R_1 \qquad (1)$$

Where M_z is the longitudinal component of the total magnetization, M_0 denotes the equilibrium magnetization and R_1 is the longitudinal relaxation rate constant equal to $1/T_1$ (T_1 is defined as longitudinal relaxation time). Equation 1 is readily solvable for given initial conditions. For the standard T_1 relaxation time assessment the inversion recovery sequence is used (Fig.1a). The 180° pulse inverts the equilibrium magnetization, M_0 and the longitudinal magnetization recovery is described as:

$$M_z(t = TI) = M_0[1 - 2e^{-TIR_1}] \qquad (2)$$

Where TI is an inversion recovery time.

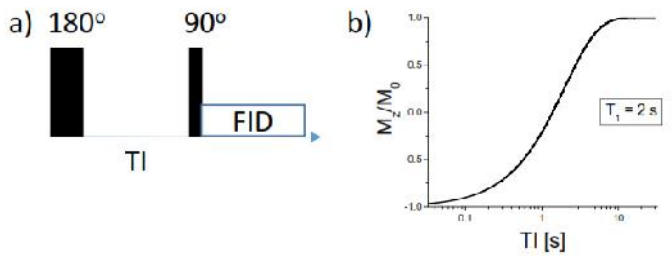

Figure 1. *Inversion recovery (IR) sequence –a) and corresponding longitudinal relaxation behaviour as a function of recovery time, TI for T_1=2s –b). 180°pulse followed by inversion time delay, TI. 90°pulse allows to tip the longitudinal magnetization into the transverse plane allowing for magnetization read-out.*

The behaviour of magnetization in transverse plane, $M_{x,y}$ is characterized by a different time constant – transverse relaxation time, T_2 and results from the loss of signal coherence related of time fluctuations of the magnetic field (also called spin-spin

relaxation) which cases the spins to dephase. In consequence the behaviour of total magnetization in the rotating frame can be described by following Bloch equation:

$$\frac{d}{dt}\begin{bmatrix}M_x\\M_y\\M_z\end{bmatrix}=\begin{bmatrix}-R_2 & \gamma(B_0-\frac{\omega}{\gamma}) & 0\\ -\gamma(B_0-\frac{\omega}{\gamma}) & -R_2 & \gamma B_1\\ 0 & -\gamma B_1 & -R_1\end{bmatrix}\begin{bmatrix}M_x\\M_y\\M_z\end{bmatrix}+\begin{bmatrix}0\\0\\M_0\end{bmatrix} \quad (3)$$

Where γ is a gyromagnetic ratio and B_1 is the amplitude of the RF pulse and ω is the offset frequency. Eq. 3 describes the behaviour of magnetization during the RF excitation and provides a valuable general reference in describing many phenomena important in MRI.

Equation 3. describes the behaviour of magnetization in relatively simple system in which all the spins are equivalent in terms of their physical and chemical properties which results in mono-exponential longitudinal recovery (T_1) and transverse decay (T_2). This is rarely the case in tissues in which water protons exhibit different interactions depending on their physical and chemical environment. Figure 2. presents complex water environment in which the presence of different physical compartments (intra-, extra cellular) is further complicated by the presence of macromolecules (pools) which can also interact with water protons and in consequence alter their relaxation properties.

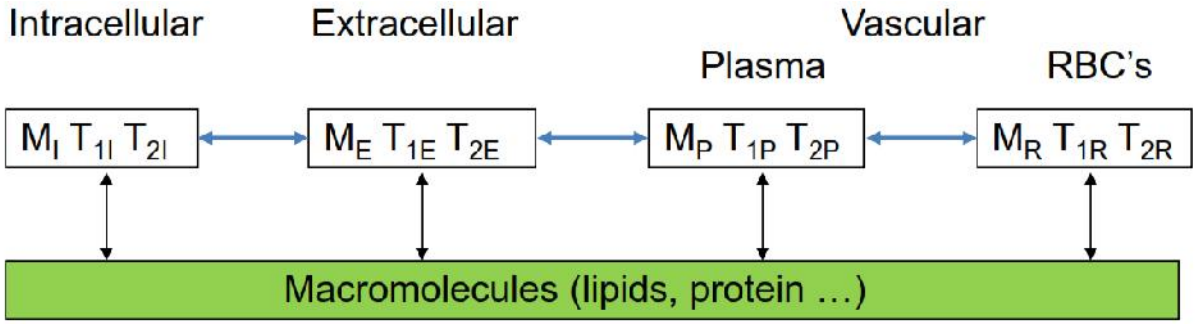

Figure 2. *Schematic representation of tissue comprised of three compartments (intracellular, extracellular and vascular). Vascular compartment is further divided into plasma and red blood cell (RBC). Water in each compartment is characterized by its own initial magnetization and T1 and T2 relaxation. Since cellular and vascular membranes are permeable to water the diffusion motion of water allows for water exchange between compartments (diffusional exchange). The presence of protons associated with other molecules (such as lipids and proteins) may also alternated water behaviour due to chemical or physical exchange between water and molecular protons.*

As a consequence of tissue heterogeneity T_1 and T_2 relaxation are rarely mono-exponential, although due to diffusional exchange they are not simply a sum of relaxation processes in different compartments. Incorporation of the exchange processes is relatively straightforward: Fig.3 shows a schematic of two exchanging compartments whereas Eq. 4 presents the modified Bloch equations:

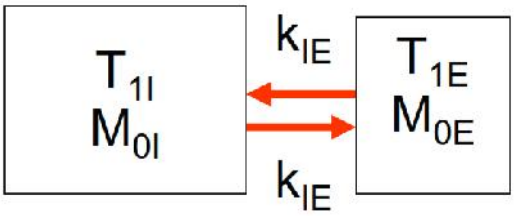

Figure 3. *Schematic of two-compartmental exchange of T1 relaxation. Intra (I) and extracellular (E) compartments exhibit different initial magnetizations, M_0 and different relaxation times. There are two exchange rate constants k_{IE} and k_{EI} denoting movement of water between compartments.*

Similar model and can be defined for T2 relaxation. The behaviour of magnetization due to exchange can be described as follows:

$$\frac{dM_{x,yI}}{dt} = -k_{IE}M_{zI} + k_{EI}M_{zE}$$
$$\frac{dM_{x,yE}}{dt} = \frac{M_{0E} - M_{zE}}{T1_E} - k_{EI}M_{zE} + k_{IE}M_{zI} \quad (4)$$

In order to preserve the total number of water protons in each compartment exchange rates need to satisfy the following condition:

$$k_{IE}M_{0I} = k_{EI}M_{0E}$$

The intra-extracellular exchange rate, k_{IE} is directly linked to cell membrane permeability Λ and surface to volume ratio S/V and its inverse τ is a mean residence time of water inside the cell:

$$k_{IE} = \Lambda\frac{S}{V} \qquad {}^2{}_I = 1/k_{IE}$$

Since exchange rate, k_{IE} is dependent both on cell membrane permeability and surface-to-volume ratio is significantly varies between different types of cells: from quite slow rate of ~ 0.3 s^{-1} for large neuron to ~ 80 s^{-1} for red blood cells. For comparison Table 1. lists surface to volume ratio and calculated mean residence times for typical cells.

TABLE 1

cell type	cell shape	diameter (μm)	surface/volume ratio (μm-1)	τ (ms) for Λ = 0.5 (10^{-3} cm s^{-1})	τ (ms) for Λ = 3.0 (10^{-3} cm s^{-1})
RBC	biconcave disk	6.4	0.79	72	12
Axon	cylinder	2.6	2.6	50	8
Neuron (cell body)	sphere	100	0.06	3333	557
Glial cell	sphere	2.9	1.0	200	33

Bloch equations (Eq.4) can be readily solved demonstrating counter-intuitive behaviour of tissue relaxation. Figure 4 shows the T2 relaxation in white matter as measured experimentally (Fig.4a) and in hypothetical case of no exchange (Fig.4c). Although experimental T2 relaxation shows two relaxing components their relative amplitudes and relaxation times are not correspond to intrinsic values of myelin and intra/extracellular water since the presence of exchange significantly alters these values.

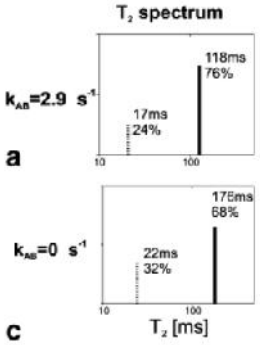

Figure 4. *Experimental –a and hypothetical –c) T2 relaxation spectrum in the presence of myelin-intra/extracellular exchange (a). c) shows the theoretical spectrum and intrinsic T2 relaxation of water within myelin and in intra/extracellular space. Note that due to exchange the T2 components are shifted towards shorter T2 values and that the amplitude of short T2 component at 17ms (a) is no longer equal to the relative amount of water in myelin compartment.*

RELAXATION VS. B_0 FIELD.

Quantitative evaluation of tissue relaxation times is very helpful in identifying and characterizing tissue pathologies, optimizing imaging sequences for improved tissue contrast and to compare results from different studies. It is therefore surprising that the reported values of both T1 and T2 relaxation times may significantly differ from one study to the other. In part this is related to systematic errors caused by field inhomogeneities, RF pulse imperfections etc. Moreover, due to non-monoexponential nature of tissue relaxation its estimates may depend on the choice of sequence parameters (inversion recovery time or echo time TE) In the case of T1 relaxation there is added complexity since T1 relaxation, by definition, increases with the magnetic field B_0. By definition, the transverse relaxation time, T2, results from time-dependent variations of the effective magnetic field "seen" by an average proton in the measured system. This classic T2 characteristic (intrinsic T2 relaxation time) takes into account rotational and diffusional motion of protons in tissue. It does not, however, include *spatially* varying magnetic fields. In particular, the presence of paramagnetic or supermagnetic (iron) particles or altered tissue susceptibility result in microscopic field variations that may not be easily compensated by spin echo (or CPMG) sequence. Therefore, measured T2 relaxation time may depend on the external magnetic field and, more importantly on the echo time, TE. It is not surprising, therefore, to observe some decrease in measured literature T2 values at sufficiently long echo times. Therefore while comparing relaxation values measured by different laboratories it is also important to take into account experimental parameters (if they are comparable T2 relaxation appear very similar at different fields – Table 2).

Table 2. Adapted from [1]

T_2 and T_1 Relaxation Times at 3T and 1.5T Measured at 37°C. Literature data is also shown.

Tissue	T_2—3 T [ms]		T_1—3 T [ms]		T_2—1.5 T [ms]		T_1—1.5 T [ms]	
	This study	Literature	This study	Literature	This study	Literature	This study	Literature
Liver	42 ± 3		812 ± 64		46 ± 6	54 ± 8[35]	576 ± 30	~600[23]
Skeletal muscle	50 ± 4	32 ± 2[25]	1412 ± 13	1420 ± 38[25]	44 ± 6	35 ± 4[25]	1008 ± 20	1060 ± 155[25]
Heart	47 ± 11		1471 ± 31		40 ± 6	44 ± 6[36]	1030 ± 34	
Kidney	56 ± 4		1194 ± 27		55 ± 3	61 ± 11[37]	690 ± 30	709 ± 60[37]
Cartilage 0°	27 ± 3	37 ± 4[25]	1158 ± 18	~1240[25]	30 ± 4	42 ± 7[25]	1024 ± 70	~1060[25]
Cartilage 55°	43 ± 2	45 ± 67[20]	1156 ± 10		44 ± 5		1038 ± 67	
White matter	69 ± 3	56 ± 4[27]	1084 ± 45	1110 ± 45[29]	72 ± 4	79 ± 8[38]	884 ± 50	778 ± 84[38]
Gray matter	99 ± 7	71 ± 10[27]	1820 ± 114	1470 ± 50[29]	95 ± 8	~95[39]	1124 ± 50	1066 ± 228[38]
Optic nerve	78 ± 5		1083 ± 39		77 ± 9		815 ± 30	
Spinal cord	78 ± 2		993 ± 47		74 ± 6		745 ± 37	
Blood	275 ± 50		1932 ± 85	~1550[30]	290 ± 30	327 ± 40[14]	1441 ± 120	~1200[3C]

1. Stanisz et al. MRM 2005 **54**(3) 507-512