NUCLEAR MAGNETIC RELAXATION OF AQUEOUS SOLUTIONS OF PROTEINS, BLOOD PLASMA, ERYTHROCYTES, AND WHOLE BLOOD


KEY WORDS: proton relaxation; protein solutions; blood plasma.

Interest in the study of nuclear magnetic relaxation (NMR) of blood and biological fluids [2, 11] is due to the wide opportunities presented by the method for studying the properties of blood and its rapid analysis. The parameters of NMR which can be measured, namely the spin-lattice ($T_1$) and spin-spin ($T_2$) relaxation times of the protons of water, in fact depend on the rheologic properties of the blood, dynamic changes in water in the membranes, diffusion of water molecules, protein hydration, the biochemical composition of the plasma, and the state of the erythrocytes.

It is thus possible in principle to carry out a comprehensive rapid analysis of whole blood and its components and, in addition, to record pathological changes associated with various diseases [7, 15]. It has been shown that the spin-lattice relaxation time of blood depends essentially on the frequency of NMR [12]. For instance, at frequencies of under 5 MHz and over 15 MHz, constancy of the relaxation rate is observed, and that at low frequencies its value is almost 4 times greater. Frequency correlations have been found between the measured properties and concentrations of individual blood components, namely for solutions of hemoglobin (Hb) [12, 15] depending on pH and temperature, including when pathological changes are present [13], and also for solutions of plasma and blood serum [10].

In our view, analysis of the blood ought to be based on a separate study of the relaxation relationships of serum, plasma, solutions of erythrocytes, and hemoglobin, and on the construction of a general model which will take account of changes in the relaxation time of water protons relative to all its components as a single physiological system. On that basis, the aim of the investigation was to study the components of blood, which could serve as the basis for construction of a relaxation model of whole blood.

EXPERIMENTAL METHOD

Serum was obtained by centrifuging blood at 1000 g for 10 min; plasma was obtained by stabilizing blood with heparin; after centrifugation the erythrocytes were washed 3 times in Ringer's solution. Tests were carried out for 1 h after the blood was taken. Relaxation measurements were made on the Minispinekho instrument at 25°C and with a frequency of NMR of 5 MHz [1]. The $T_1$ relaxation time was measured by Khan's method, and $T_2$ by the method in [3]. Altogether 143 blood samples were tested. Blood serum was investigated in 22 healthy women and 12 pregnant women with toxemia. As the comparison solution we used physiological saline (0.9% NaCl solution), whose relaxation velocity ($T_{1,2}$)$^{-1}$ was 0.42 sec (for bidistilled water 0.40 sec$^{-1}$). For human serum and a solution of human albumin, relaxation time was a linear function of concentration of the component in physiological saline. For whole erythrocytes, amplitude was a biexponential function of time, with short and long relaxation time ($T_1$, $T_2$); relaxation time, moreover, was a linear function of hemoglobin concentration. The measured values of relaxation time lay within the following limits:

- for blood $T_1$ is 0.4-0.7 sec, $T_2$ 0.05-0.4 sec;
- for plasma, 0.7-1.1 and 0.05-0.5 sec respectively;
- for erythrocytes 0.25-0.5 and 0.03-0.3 sec respectively.
EXPERIMENTAL RESULTS

The principle of the technique of construction of a model reflecting dependence of relaxation velocities \((T_{1,2})^{-1}\) of protons of water molecules on the composition of the solution to be analyzed, is one of additiveness of the measured property for all sorts (types) of water protons, and allowing for their concentration. The effect of the different proteins and of other components of the blood on the relaxation characteristics of water molecules differs, and this is reflected in the change in the values of the parameters in response to a change in the qualitative and quantitative composition of the blood. Taking the above considerations into account, it is best to begin an investigation of the multicomponent system with model solutions, simulating changes in the concentration of the principal blood components. The effect of each component on the property measured is described by the equation:

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(T_{1,2})^{-1} = \sum_{i} K_{e1,2}^{i} \cdot C_{i} \cdot \alpha_{s}
\]

where \(K_{e1,2}^{i}\) is a coefficient of proportionality, characterizing the contribution of the i-th component to acceleration of relaxation of water protons; \(C_{i}\) and \(\alpha_{s}\) denote its concentration and fraction respectively.

In accordance with the approach in [2], describing at least two sorts of water molecules ("bound" and "unbound"), a proportional relationship can be expected between the relaxation velocity and protein concentration. In fact, a linear relationship is observed not only for model solutions containing albumin (Fig. 1), but also for solutions obtained by diluting blood serum with different total protein concentrations and different relative proportions of the albumin and