Deuterium–Protium Fractionation in Solutions of Methoxide Ion in Mixtures of Methanol and Dimethyl Sulphoxide

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The fractionation factor of the methoxide ion (ϕ_{OMe}) † has been determined in mixtures of methanol and dimethyl sulphoxide (DMSO). By using ^1H n.m.r. data of very high precision it has been possible to use solutions of three different atom fractions of deuterium making the usual assumption about the chemical shift of the counterion (Na^+) unnecessary. ϕ_{OMe} has been found to decrease from 0.74 (MeOH) to 0.38 (75 mol % DMSO). The variation of ϕ_{OMe} is discussed in terms of increasing symmetry in the hydrogen bonds to the methoxide ion as the desolvation of the methoxide ion proceeds.

SOLVENT isotope effects on rate and equilibria are conveniently interpreted in terms of the fractionation factor theory.[1-5] A particularly important class of reactants in a number of reactions are the lyonium and lyate ions in water and alcohols. Focusing on the methoxide-catalysed reactions the fractionation factor of the methoxide ion, ϕ_{OMe}, has been of importance in understanding the role of solvating molecules on the rate of reactions in methanol.[6] It continuously plays an important role in the interpretation of solvent isotope effects in terms of solvation of transition states in methanol and it may be of help in understanding more quantitatively the role of hydrogen-bonding in methoxide-catalysed reactions in mixtures of methanol and DMSO.

The fractionation factor of the methoxide ion in methanol is generally accepted to be slightly above 0.70 at room temperature. It was determined by Gold and Grist [7] to be 0.74 but certain assumptions that were not without objections had to be made,[8] and in a recent study Jones *et al.* in attempting to remove the necessity of these assumptions redetermined ϕ_{OMe} in methanol [9] to be 0.7 although a loss in precision had to be endured.

The fractionation factor theory was developed by Gold [1] and Kresge [2] in terms of the isotopic exchange equilibrium between specific hydrogen positions and the bulk of the solvent, the equilibrium constant, ϕ_i, being defined as $([D]/[H])_i/([D]/[H])_{bulk}$, the ratio of ratios of deuterium to protium concentrations in the ith position and in bulk solvent. The magnitude of ϕ is determined by the difference in potential well of the hydrogen in the bulk and that in the hydrogen-bonded or covalently bonded position. Consequently, ϕ in itself can provide information about the environment of a hydrogen position. The determination of fractionation factors is conveniently done by a standard n.m.r. method.[10,11] In short, confining the discussion to solutes with non-exchangeable hydrogens, the chemical shift Δ of the hydroxy-protons of a hydroxylic solvent relative to some standard, is the weighted average of all kinds of exchangeable protons in the solution. Addition of a solute gives rise to a certain fraction of protons with the characteristics of the solvation shell of the solute, and Δ is shifted accordingly.

The complete formula describing the dependence of the chemical shift (Δ) on the concentration of a solute with non-exchangeable protons in methanol is (1) where

$$\Delta = a\sum_{i=1}^{\nu}\delta_i + \Delta_{OH} \qquad (1)$$

$a = [CH_3ONa]/[CH_3OH]$ and $\delta_i = \delta_i' - \Delta_{OH}$, δ_i' being the chemical shift of the proton in the ith position of the solvation shell, and Δ_{OH} is the shift of unperturbed bulk protons. The symbol ν denotes the number of hydrogens in the solvation shell. The corresponding formula, valid for low values of a, is (2).

$$\Delta = a\sum_{i=1}^{\nu}Q_i\delta_i + \Delta_{OH} \qquad (2)$$

In (2) $a = [CH_3ONa]/[CH_3OL]$ (L denoting H or D). Q_i is related to the fractionation factor ϕ_i according to equation (3).

$$Q_i = (1 - x + x\phi_i)^{-1} \qquad (3)$$

(For a complete derivation of the above formulae see ref. 9.)

What one is actually studying is the chemical shift, Δ, as a function of a and the aim is to determine the slope $d\Delta/da$. From measurements in solutions of varying degree of deuteriation it is in principle possible to gain information about ϕ_i. The difficulty encountered here is that addition of a solute gives rise to a number of different hydrogen positions, whereas the number of experimentally obtainable observables is limited. Careful balancing is required between the experimental limitations and the choice of chemical model. More thorough discussions on this dilemma are to be found in refs. 7—9. Gold and Grist [7] assumed that the only fractionating species in solution was the methoxide ion and that the influence on the chemical shift of the sodium ion (δ_{Na^+} 3 p.p.m./mole fraction) [7] could be taken as that determined from a low temperature freezing-out experiment,[12] all other contributions being neglected. From the above discussion, then, it is clear that they needed to determine two unknowns, δ_{OMe} and ϕ_{OMe}, which was done from two series of experiments, one in completely protiated methanol and one in predominantly deuteriated

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† Strictly speaking the fractionation factor is that of the hydrogens in the solvation shell of the methoxide ion.

methanol. From four series of experiments, Jones *et al.* determined these two constants and, in addition, the resultant chemical shift, δ_0, of all protons in non-fractionating positions. Apart from the two series of Gold and Grist,[7] two more could be produced by adding tritiated methanol to solutions that were otherwise analogous to those of the first two series and determining the slope $d\Delta/da$ by means of tritium n.m.r. In the latter investigation, a discrepancy was found between δ_0 and δ_{Na^+} [7] which was attributed to a contribution by the second solvation shell of the methoxide ion. The underlying assumption was that the only fractionating species in the solution was the methoxide ion.

The use of tritium n.m.r. is not required if ^1H n.m.r. data of very high precision can be obtained. This is of some importance today since powerful spectrometers with superconducting magnets are now fairly frequent whereas tritium n.m.r. is reserved for specialized laboratories.

We present here an investigation of the fractionation factor of the methoxide ion in methanol and in mixtures of methanol and DMSO. Through use of a Bruker WH 270 n.m.r. spectrometer data of sufficiently high precision are obtained to permit the use of slopes $d\Delta/da$ determined in these solvents at *three* different atom fractions of deuterium, thereby facilitating the determination of the same constants as in the foregoing investigation.[9] The determination of at least three constants, δ_0, δ_{OMe}, and ϕ_{OMe} is essential to the determination in DMSO mixtures since chemical models of species in mixed solvents are very uncertain. ϕ_{OMe} in these mixtures provides information about the solvation of the methoxide ion and permits the use of kinetic solvent isotope effects in mixed media. The use of kinetic solvent isotope effects on methoxide-catalysed reactions in mixtures of methanol and DMSO may be of interest in quantitative studies of the solvation of such reactions since these isotope effects are due to hydrogen-bonding types of interactions. It would be of great interest to the discussion of rate enhancements in dipolar aprotic solvents if the effects of hydrogen bonding could be separated from other effects. It should be pointed out at this point that although the major part of the rate enhancement is generally attributed to the destabilization of the methoxide ion,[13] the difference in rate increase between methoxide-catalysed reactions involving different substrates may be considerable due to differences in solvation of different transition states.[14,15]

EXPERIMENTAL

The solvents of listed quality were purchased from the following manufacturers and used without further purification: methanol, anhydrous, $H_2O < 0.01\%$ w/w, May and Baker; dimethyl sulphoxide, $H_2O < 0.01\%$ w/w, Riedel de Haën AG; methan[^{2}H]ol, 99.7 atom % D and ultra high purity 99.9 atom % D, Ciba-Geigy; [$^2H_6$]dimethyl sulphoxide, 99.5 atom % D, Ciba-Geigy. Methanol was analysed by Karl Fischer titration and exhibited 0.012% w/w water.

Special care was taken to clean and dry all glassware used. Whenever possible transfer of solutions was carried out using pipettes with disposable plastic tips. Solutions were prepared and weighed in gas-tight vials and all work with the solutions took place under dry nitrogen.

Sodium methoxide was prepared from freshly cut, cleaned sodium metal (puriss, 99.5% Kistner). Stock solutions, *ca.* 0.25M, were prepared immediately before use. The stock solutions were carefully titrated against dried potassium hydrogen phthalate, diluted by weight and the base concentrations calculated using accessible density data [16] under the reasonable assumption that the small isotope effect on molar volume is independent of base concentration. The upper limits of the base concentrations used in 25, 50, and 75 mol % DMSO were 0.2, 0.1, and 0.05M, respectively.

The n.m.r. spectra were recorded on a Bruker WH 270 Fourier transform spectrometer. Field locking signals were provided by [$^2H_6$]DMSO, methan[^{2}H]ol, or [$^2H_6$]acetone, the latter solvent being in the inner tube when coaxial n.m.r. tubes had to be used. The probe was thermostatted to 25 °C. To achieve maximum resolution the spectral width was set to 1 000 Hz which in connection with an 8K computer memory capacity used for the real part of the spectrum provided a theoretical resolution of 0.12 Hz, corresponding to 0.0004 p.p.m. The aim was that no spectrum should be passed until two consecutive determinations gave chemical shifts differing by no more than 0.12 Hz. This could not be altogether fulfilled, probably because of the temperature instability of the probe, but the large majority nevertheless met this requirement. In view of the temperature dependence of the hydroxylic signal this appears to be a good demonstration of the thermostatting capacity of the n.m.r. spectrometer. A positive shift is downfield to conform to the commonly used δ scale. It should be noted that refs. 7 and 9 use the τ convention. That means that there will be a difference in sign between the values given there and in the present investigation.

In 75 mol % DMSO in methanol the isotopic exchange reaction at the methyl groups of the DMSO molecule is very fast [17] when catalysed by the methoxide ion.* In order to minimize deviations in atom fraction of deuterium in the solution a DMSO mixture was prepared of roughly the same isotopic composition as the methanol and the spectra were recorded within 2 h of the preparation of the base solution. In spite of a systematic variation of the time between mixing and the recording of the spectrum within the time limit of 2 h no systematic deviation could be detected in the plots.

RESULTS

Parameters obtained from plots of chemical shift of the hydroxylic methanol protons *versus* $a = [CH_3ONa]/[CH_3OL]$, are presented in Table 1.† For the methanolic runs values for comparison are provided by the literature. The slope in light methanol, +24.40 p.p.m./a (Table 1, for sign see Experimental section) is somewhat less in the present paper than in those reported earlier, −25.41 [7] and −25.0,[9] the literature values being in good mutual agreement when it is taken into consideration that the latter value refers to a plot of shift *versus* a whereas the former refers to the use

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* Assuming no kinetic isotope effect a half-life of 120 min may be estimated for the reaction at highest base concentration (0.05M).

† No deviations from linearity could be detected over the concentration ranges (see Experimental section) used.

of mole fractions. In the predominantly deuteriated system the atom fractions of deuterium do not agree between the different investigations but qualitatively the results are analogous to those in the light system. The reason that our slopes are slightly less than the others is not understood by us but the possibility that it should arise from a difference in water content is ruled out by the following argument. To six solutions constituting a run in methanol of deuterium content $x = 0.995$ *ca.* 1% (w/w) water was added and the parameters of the linear dependence of shift on a were evaluated in the usual way. When due allowance for difference in base concentration and deuterium content had been made no significant difference in slope could be detected between the run with added water and that without, although the limits of error were considerably larger in the former case (±0.6 units). The small effects on the slope and intercept by added water make it unlikely that fortuitous water is the cause of the discrepancy. The intercepts (Table 1), corresponding to the chemical shifts in pure methanol are in good agreement with those reported in ref. 7 if the temperature difference is taken into account. The solvent isotope effect on the chemical shifts is reproduced.

TABLE 1

Parameters from least-squares analysis of plots of chemical shift (Δ) *versus* $a = [CH_3ONa]/[CH_3OL]$. The methyl protons of methanol have been used as an internal reference. Error limits are standard deviations of the mean

Atom fraction D	($d\Delta/da$) (p.p.m. a^{-1})	Intercept (p.p.m.)	Number of experiments
	Methanol		
0	24.40 ± 0.24	1.535 ± 0.002	15
0.502—0.512	28.91 ± 0.15	1.527 ± 0.001	24
0.995—0.999	34.78 ± 0.26	1.518 ± 0.002	15
	25 mol % DMSO–75 mol % methanol		
0	24.68 ± 0.19	1.154 ± 0.002	16
0.500—0.508	28.65 ± 0.19	1.150 ± 0.001	23
0.997	34.19 ± 0.20	1.153 ± 0.001	11
	50 mol % DMSO–50 mol % methanol		
0	23.20 ± 0.19	0.972 ± 0.002	8
0.500	25.67 ± 0.23	0.973 ± 0.002	8
0.997	30.38 ± 0.18	0.976 ± 0.002	8
	75 mol % DMSO–25 mol % methanol		
0	20.35 ± 0.08	0.895 ± 0.001	8
0.502	22.27 ± 0.27	0.907 ± 0.002	7
0.995	27.24 ± 0.22	0.903 ± 0.002	5

Evaluation of ϕ_{OMe} is done by a modification of the procedure suggested in ref. 9. Under the assumption that the only fractionating species in the solution is the methoxide ion, $d\Delta/da$ is given by equation (4) where δ_0 is the sum of

$$d\Delta/da = \delta_0 + Q_{OMe}\delta_{OMe} \qquad (4)$$

shifts of all protons in non-fractionating positions and δ_{OMe} is the corresponding sum for fractionating positions.

For different values of x, the atom fraction of deuterium in the solution, Q [equation (3)] assumes different magnitudes and a plot of $d\Delta/da$ *versus* Q yields a straight line with slope δ_{OMe} and the intercept δ_0. In practice, different values of ϕ are tested and the one giving a straight line is taken as the correct one. Three isotopic compositions are employed, 0, 50, and 99 atom % D. The plots for different solvent compositions are shown in Figure 1. The resulting fractionation factors are given in Table 2 and the parameters δ_{OMe} and δ_0 in Table 3. In the case of methanol the fractionation factor of this paper reproduces very nicely the widely accepted one of ref. 7, 0.74, a value which is strongly supported by solvent isotope effects on rates and equilibria involving the methoxide ion in methanol. ϕ_{OMe} is given in ref. 9 as 0.7 and that value is thus also in line with the cited chemical evidence. It should be pointed out that the graphical procedure is extremely sensitive to small changes

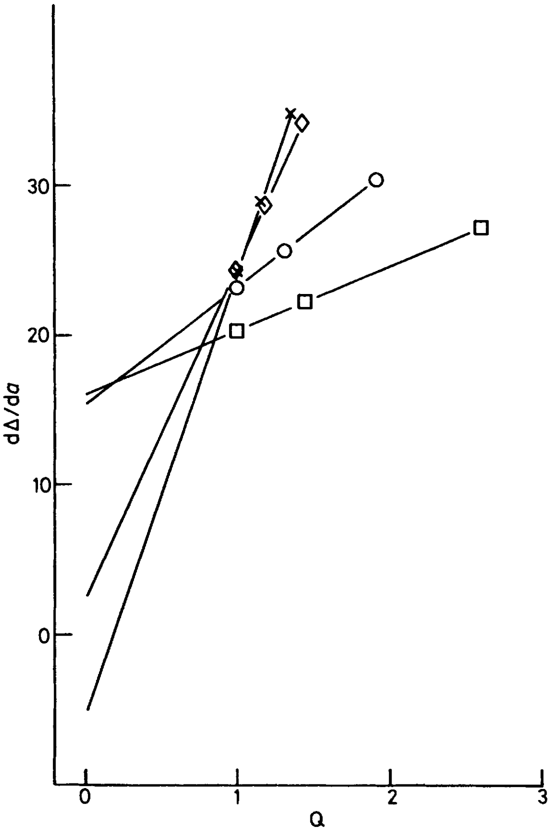


FIGURE 1 Determination of the fractionation factor of the methoxide ion according to the formula $d\Delta/da = \delta_0 + Q_{OMe}\delta_{OMe}$. The symbols refer to the following solvent compositions: ×, methanol; ◇, $x_{DMSO} = 0.25$; ○, $x_{DMSO} = 0.50$; □, $x_{DMSO} = 0.75$

TABLE 2

Fractionation factor of the methoxide ion in mixtures of methanol and DMSO

x_{DMSO}	a [a]	b [b]
0	0.74 ± 0.06	0.73
0.25	0.70 ± 0.07	0.72
0.50	0.52 ± 0.08	0.76
0.75	0.38 ± 0.05	0.75

[a] According to the general treatment. See text. By assuming normal distribution of $d\Delta/da$ given in Table 1 a probability of a particular ϕ can be obtained as the product of the probabilities of $d\Delta/da$ calculated at the three isotopic Q values. The two ϕ values defining the area that is roughly 2/3 of the total integrated area of the so obtained probability function are given as the limits of error in ϕ, in analogy with the definition of the standard deviation. [b] With the assumption that δ_{Na^+} has the experimental value [7] in methanol and is otherwise zero.

in the experimentally determined parameters of Table 1. Nevertheless it is reassuring to find such a good correspondence to the literature data in methanol and it lends support to our belief that the general procedure is correct and that the method is practicable in methanol–DMSO mixtures. In such systems literature reports are, to our knowledge, missing and comparisons can therefore not be made. Returning to the question of the sensitivity of the determinations to experimental errors, the graphical method seems safer, the lower the value of ϕ_{OMe}, as in mixtures of methanol and DMSO of increasing DMSO content.

TABLE 3

Chemical shifts of protons in the solvation shell of sodium methoxide

x_{DMSO}	δ_{OMe} [a] (p.p.m. a^{-1})	δ_0 [b] (p.p.m. a^{-1})
0	29.7	−5.3
0.25	22.3	2.4
0.50	7.8	15.4
0.75	4.3	16.1

[a] The sum of shifts of all protons in fractionating positions.
[b] The sum of shifts of all protons in non-fractionating positions.

Our results (Table 3) do not accord with those of ref. 9. For a discussion of this see below. Preparation of a series of base solutions by weight from a stock solution requires that the titration is done with care. Any error in the concentration of the stock solution appears as roughly the same relative error in the slope of shift *versus a*. Such a relative error will give rise to a systematic error in the slope which will not be discovered unless more than one stock solution is used for the same solvent system. It is therefore comforting to find that our results in methanol and 25 mol % DMSO, where at least two different stock solutions have been used for each isotopic composition, show such good precision.

A consequence of diluting by weight is that the mole fraction of DMSO will not as a rule be exactly what it is intended to be and corrections will have to be made. For this purpose the chemical shift of pure methanol in DMSO as a function of the DMSO content has been determined (Figure 2) and the chemical shifts in the solutions of deviating DMSO fraction have been corrected to one referring to the desired mole fraction. The underlying assumption is here that there is no salt effect on the solvent effect on the chemical shift. It is unlikely that any serious error should arise in this way unless the deviation is so large that in the deuteriated solutions a significantly different ϕ_{OMe} exists in which case the simple correction will not be sufficient.

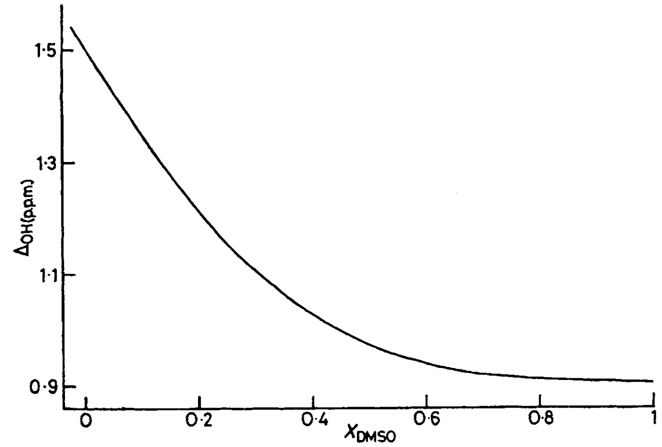


FIGURE 2 Chemical shift of hydroxylic protons in methanol relative to that of the methyl protons of methanol as a function of DMSO content

DISCUSSION

The choice of chemical model needs careful consideration and, possibly, independent experimental evidence to support it as illustrated by the present investigation. The introduction outlines how a balance must be reached between the amount of information which one wants to extract and the experimental limitations. The experimental information available are the plots of hydroxy proton chemical shifts *versus* some measure of the base concentration in solutions of different isotopic composition. Three compositions, 0, 50, and 99 atom % deuterium, and ^1H n.m.r. data of high precision make it possible to determine three unknowns. We are thus restricted to a model where only the first solvation shell of the methoxide ion fractionates. This seems a fairly reasonable model particularly in view of the value for $\phi_{Na^+} = 0.98$ (H_2O; 25 °C) estimated from electrochemical measurements.[4,18] Using the value for δ_{Na^+} [7] together with ϕ_{Na^+} does not affect the magnitude of ϕ_{OMe} since the correction lies well within the experimental uncertainty of $d\Delta/da$. In view of this we prefer to treat its solvation shell as if it were non-fractionating.

The choice of models may have a dramatic influence on the value of ϕ_{OMe} even if all the models seem to be reasonable from a chemical point of view. The method used in the present paper gives rise to the values of ϕ_{OMe} in Table 2, column a, whereas a chemical model with δ_0 taken as δ_{Na^+} in methanol and $\delta_0 = 0$ in the DMSO mixtures yields the values in Table 2, column b. The second model is not unreasonable since δ_0 is in fact very close to δ_{Na^+} in methanol and may be estimated to be close to zero in DMSO mixtures from the following argument. The protons that contribute to δ_0 are probably from the solvation shell of the sodium ion and the second shell of the methoxide ion. Taking Gutman's donor number [19] as a measure of solute–solvent interaction one would expect an extreme specific solvation of the sodium by DMSO. Under those circumstances DMSO would be expected to shut out the methanol from the close environment of the sodium ion, making the chemical shift independent of the concentration of sodium ions. In 25—75 mol % DMSO a second solvation shell would be completely different from one in pure hydroxylic solvents, that could affect chemical shifts by structure-making or -breaking types of behaviour. In these mixtures there are no solvent isotope effects on the chemical shift of methanol solutions (Table 1) and it seems natural to interpret this as if no strong hydrogen bonds exist, such bonds being essential to the existence of a second solvation shell. From these considerations, too, a value of $\delta_0 = 0$ in mixtures of DMSO and methanol appears quite conceivable. As the fractionation factors of the methoxide ion in these media are not easily predicted, clearly independent evidence is required to choose between the models. An extreme specific solvation of the sodium ion could probably be detected by using ^{23}Na n.m.r. in determining the ' iso-solvation point '.[20] In a separate investigation such a determination has been carried out,[21] and the sodium ion turned out to be to only a very small, if any, degree specifically solvated by DMSO, settling the matter conclusively and giving preference to the results in Table 2, column a. This demonstrates the improvement of the procedure in allowing determinations of fractionation factors in systems where chemical shifts of counterions are not known. The method is of course limited to solutions where only one site gives rise to fractionation.

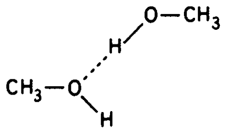
Turning to the fractionation factors of the methoxide ion we may compare our value of ϕ_{OMe} in methanol with the literature values. It agrees very well with that determined by Gold and Grist, 0.74,[7] although their work was carried out at a slightly higher temperature (33.5 °C) and it also agrees with the value 0.7 reported by Jones *et al.*[9] On addition of DMSO ϕ_{OMe} drops dramatically (Table 2, column a) and reaches a value of 0.38 in 75 mol % DMSO in methanol. The drop of fractionation factors seems to be a common type of behaviour [22] for hydrogen-bonded complexes on transfer from hydroxylic solvents to dipolar aprotic ones. A rough extrapolation of the present data to pure DMSO would give a fractionation factor in the neighbourhood of 0.3. Fractionation factors for homoconjugate complexes of *p*-nitrophenol and 3,5-dinitrobenzoic acid and some other compounds [22] are reported to be of about the same magnitude suggesting that in the limit when x_{DMSO} tends to unity the methoxide ion exists as the monosolvate. Recently it has been suggested that the gas-phase fractionation factor for the proton-bound dimer of methoxide ion is of the order of 0.2.[23] Kreevoy and Liang [22] suggest that the reason for the drop on going to dipolar aprotic solvents of the fractionation factor of homoconjugate complexes is a simultaneous desolvation of both anionic fragments resulting in a more symmetric hydrogen bond. A direct application of that model to the present system seems unnatural and we suggest that the gradual desolvation of the ion leads to more symmetric hydrogen bonds for those methanol molecules that are still in a hydrogen-bonded position, maybe through an inductive effect. Under the assumption that the trisolvate is a correct representation of the true nature of the solvated methoxide ion in methanol ϕ values can be assigned to the different solvates if the supposition is made that the magnitude of the isotopic free energy difference on transfer of a hydrogen from bulk solvent is linearly related to the number of solvating methanol molecules of the primary solvation shell of the methoxide ion. The trisolvate gives ϕ_{OMe} 0.74 and according to the extrapolation above the monosolvate gives ϕ_{OMe} 0.3. A hypothetical fractionation factor ϕ_{OMe} 0.47 may then be assigned to the disolvate. Such a value is exhibited by a solution with roughly 60 mol % DMSO and is consistent with the view that the methoxide ion is desolvated roughly linearly with the mole fraction of DMSO. The opposite has been suggested.[24]

The difficulty in comparing the different ϕ values of this work is that they refer to different solvents. It is obvious that the fractionation depends on the difference in nature between the solvating and bulk positions for the hydrogen and both are changed by addition of an aprotic solvent. Relating the ϕ values of this work to some common standard state is possible in principle but in practice the accuracy obtainable is not overwhelming compared to the precision in ϕ. We estimate, however, that the correction that should be applied to the experimental ϕ values for difference in bulk is rather small. From the commonly accepted knowledge that hydrogen bonds between DMSO and methanol are stronger than between methanol and methanol it follows that the measured ϕ values (Table 2, column a) represent the upper limit to the ' true ' ones that are hypothetically measured relative to methanol as the standard state. It may however be an oversimplification since this model does not account for the difference in librational frequencies, between methanol and methanol–DMSO.

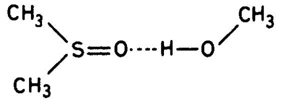
The parameters of Table 3 deserve some comment. Comparing the values of the methanolic ' run ' with those of the literature we find that our δ_0 is very close to the value of δ_{Na^+} used by Gold and Grist,[7] although they neglected any contribution from the second solvation shell of the methoxide ion. The present results thus suggest that the second solvation shell of the methoxide ion does not contribute very much to δ_0. This is in accord with the idea that methanol is not a very strongly structured solvent, at least not compared to water where the concept of a second solvation shell around the solutes is well founded. It has also been suggested that in methanol the solvent clusters predominantly exist as tetramers.[25] A trisolvated methoxide ion is probably not too dissimilar to such a four-membered cluster and the presence of solvated sodium methoxide may therefore be of little importance to the structure of liquid methanol. The importance of the second shell is stressed by Jones *et al.*[9] who obtained a value of -4 p.p.m./*a* for δ_0 (for sign see Experimental section), the difference, -7 p.p.m./*a*, between their value and δ_{Na^+} being assigned to such a shell. In our opinion -7 seems too big compared to that of the inner shell, -22. The present work yields $+29.7$ (for sign see Experimental section) for the methoxide ion, in good agreement with ref. 7.

In DMSO the situation is complex. On going from methanol to 75 mol % DMSO δ_{OMe} decreases from $+29.7$ to $+4.3$ a trend that is readily understood in terms of desolvation of the methoxide ion. Although it is difficult to tell about solution structure in mixed solvents it is possible that structures such as (I)—(V) could account for the observed shifts.

In methanol the chemical shift of the solvation-shell protons of the methoxide ion is quite different from that of the bulk protons, due to hydrogen bonding, of course. On adding DMSO, a stronger hydrogen bond acceptor than methanol, the bulk protons experience stronger hydrogen-bonding and their chemical shift tends to be more like that of the solvation shell of the methoxide ion. The bulk solvent changes characteristics from those that would be expected from structure (I) to those of structure (II) which is closer to structure (III). This in addition to desolvation would explain the decrease in δ_{OMe}.



(I)



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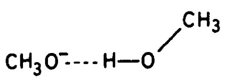
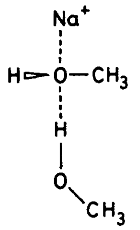
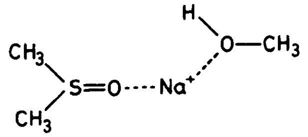


(III)



(IV)



(V)

The corresponding change for δ_0 is more difficult to rationalize. From -5.3 to $+16.1$ units the change is drastic on going into 75 mol % DMSO. From ^{23}Na n.m.r. experiments[21] it is evident that the composition of the primary solvation shell of the sodium ion resembles that of the bulk solvent. Consequently, the change is even more drastic than the numbers indicate, since the effect of added solutes on the chemical shift would again be expected to decrease as the solutes are desolvated with respect to methanol.

The chemical shift of the solvation-shell protons of the sodium ion in methanol is fairly similar to that of bulk protons as the sodium ion is rather poorly solvated in methanol (IV). As the DMSO content is increased the sodium ion appears in an environment such as in (V). A possible anisotropy effect of the S=O group (see below) makes it reasonable that the chemical shift of the hydroxy-protons in (V) should be very different from that in (II), giving rise to the great sensitivity of the chemical shift to added solute (Table 3).

The intercepts of plots of chemical shift *versus a* (Table 1) represent the chemical shift of the hydroxylic solvent–co-solvent in the absence of solute and is interesting in its own right. Chemical shifts of hydroxylic solvent protons have been used to study solute–solvent interactions but what we attempt here is also to draw some conclusions from the solvent isotope effect on the chemical shift of the hydroxylic protons in methanol and in DMSO mixtures. In pure methanol there is a solvent isotope effect on that shift (Table 1). The conclusion is inescapable that it depends on some hydrogen-bonding type of interaction between light and heavy methanol. In 25 mol % DMSO the isotope effect is gone and the intercepts are nearly identical, meaning that on the average much fewer methanol molecules are engaged in hydrogen bonding to each other, or, alternatively, that all methanol molecules are hydrogen bonded to DMSO molecules. It is interesting to note that at a relative abundance DMSO : methanol of 1 : 3 hydrogen bonding between methanol molecules is negligible and this seems to indicate that DMSO accepts hydrogen bonds from at least two methanol molecules at the same time.

The chemical shift of methanol hydroxylic protons in mixtures with DMSO experiences a dramatic change as compared with pure methanol (Figure 2). The major part of this change takes place on increasing the molar ratio of DMSO to 0.5. The direction of this change is in contrast to the generally accepted view that hydrogens in strong hydrogen bonds (II) resonate at a lower field than hydrogens in weaker hydrogen bonds (I). It is known, however, that a change to lower field in certain cases could be compensated by an anisotropy effect from a neighbouring group.[26] It is possible that the S=O group in the present case could play such a role.

It seems reasonable to assume that after the molar ratio has reached unity the magnetic environment of the hydroxylic protons does not change since all methanol molecules are tied up with DMSO. The implication is that structures in solution where two DMSO molecules are hydrogen-bonded to the same methanol molecule, do not exist to any appreciable extent. Slightly above 50 mol % DMSO the n.m.r. spectrum of methanol changes from two singlets to one doublet and one quartet in a manner that is seen also in absolutely dry methanol. Small amounts of water are capable of promoting fast hydrogen exchange between methanol molecules. This effect which is not observed at a little above the equimolar ratio indicates that all hydroxylic species in the solution must be hydrogen-bonded to DMSO molecules so strongly that they hardly encounter other hydroxylic solvent molecules.

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