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Reaction Mechanism for Direct Proton Transfer from Carbonic Acid to a Strong Base in Aqueous Solution II: Solvent Coordinate-Dependent Reaction Path

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Abstract

The protonation of methylamine base CH_3NH_2 by carbonic acid H_2CO_3 within a hydrogen (H)-bonded complex in aqueous solution was studied via Car–Parrinello dynamics in the preceding paper (Daschakraborty, S.; Kiefer, P. M.; Miller, Y.; Motro, Y.; Pines, D.; Pines, E.; Hynes, J. T. *J. Phys. Chem. B* **2016**, DOI: 10.1021/acs.jpcb.5b12742). Here some important further details of the reaction path are presented, with specific emphasis on the water solvent's role. The overall reaction is barrierless and very rapid, on an ~ 100 fs time scale, with the proton transfer (PT) event itself being very sudden (< 10 fs). This transfer is preceded by the acid–base H-bond's compression, while the water solvent changes little until the actual PT occurrence; this results from the very strong driving force for the reaction, as indicated by the very favorable acid–protonated base $\text{p}K_a$ difference. Further solvent rearrangement follows immediately the sudden PT's production of an incipient contact ion pair, stabilizing it by establishment of equilibrium solvation. The solvent water's short time scale ~ 120 fs response to the incipient ion pair formation is primarily associated with librational modes and H-bond compression of water molecules around the carboxylate anion and the protonated base. This is consistent with this stabilization involving

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Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acs.jpcb.5b12744. First, details of the energy gap coordinate E construction are collected. Next, the energy gap E coordinates for 10 individual trajectories for the carbonic acid PT to methylamine base in aqueous solution are presented. E and its vacuum component E_v analysis details are offered next, followed by a section discussing how proton-bending modes are related to E_v fluctuations. We then discuss the possible attempts for dissociation of the carboxylate-protonated methylamine contact ion pair during several reaction trajectories. Finally, we present structural and hydrogen bonding aspects of the aqueous solvent relaxation, including discussion of dynamics of H-bond distance and angle rearrangement of water molecules around two key sites of the complex subsequent to PT. (PDF)

Notes

The authors declare no competing financial interest.

significant increase in H-bonding of hydration shell waters to the negatively charged carboxylate group oxygens' (especially the former H_2CO_3 donor oxygen) and the nitrogen of the positively charged protonated base's NH_3^+ .

Graphical abstract

1. INTRODUCTION

In the preceding paper,¹ hereafter denoted as I, the protonation of the strong base methylamine CH_3NH_2 by carbonic acid H_2CO_3 in aqueous solution was studied via Car–Parrinello molecular dynamics (CP MD).^{2,3}

This proton transfer (PT) reaction within a hydrogen (H)-bonded complex was found to be barrierless and very rapid, consistent with the strong thermodynamic driving force inferred from the difference in acid strengths of H_2CO_3 and the base's conjugate acid CH_3NH_3^+ , a reactivity result of relevance for our proposal described in more detail elsewhere,⁴ that H_2CO_3 has the potential of being a major protonating agent of, for example, nitrogen bases in the blood.⁵

Primary attention was focused in I on the time evolution of the proton coordinate, the hydrogen bond coordinate $R_{\text{O}_A\text{N}}$ and the charge distribution's change between the original acid–base pair and the product contact ion pair. The important influence of the aqueous solvent in the reaction was invoked at assorted points in the analysis, but this was not analyzed in detail. In the present paper, we continue our analysis of this PT reaction by presenting a detailed analysis of the reaction path, with a specific and explicit focus on the role of the water solvent.

The outline for the remainder of this paper is as follows. Section 2 details the methodology for our analysis of the reaction path in terms of the H-bond coordinate and an energy gap which has two components, one which involves the aqueous solvent contribution, which serves as a solvent coordinate, and a second contribution which serves as a coordinate related to reaction-induced geometry changes within the H-bonded complex. Section 3 analyzes the reaction path, in terms of the coordinates just mentioned, prior to the PT

occurrence and for a short period of ~50 fs thereafter, in which a necessary angular aspect of the complex's internal H-bonding is completed, the nascent contact ion pair charge distribution evolves to its final form and solvent stabilization of the ion pair is ensured. A detailed analysis of the full aqueous solvation relaxation after the PT occurrence is then given in section 4. Here we also provide insights on the contributions to this relaxation from solvent water- ion pair atomic site H-bond changes in number and strength, for the sites where the largest charge change in the PT reaction occurs. Concluding remarks are offered in section 5.

2. TRAJECTORY ANALYSIS DETAILS

We have used the same simulated carbonic acid–methylamine PT reaction trajectories as in I, to which the reader is referred for details including construction of the simulation box containing the aqueous solution of the H-bonded acid–base pair complex, the method of preparing and collecting 10 CP MD reaction trajectories, and the obtaining of reference water solvent structures for isolated species (carbonic acid, bicarbonate, methylamine, and protonated methylamine) in aqueous solution. In the following, we describe the energy gap coordinate analysis that we will use for exploration of the reaction path with the inclusion of the water solvent.

2.1. Energy Gap Coordinate E Analysis Method

In I, we focused on dynamic evolution of the proton coordinate and the H-bond separation of the acidic oxygen and basic nitrogen in our geometric description of the reaction. In order to include the water solvent in the dynamical description (and as in previous activated PT studies^{6–10}), we employ an energy gap coordinate E . This will prove useful, despite the present PT reaction's lack of any activation barrier. The more specialized details of this E construction are relegated to the Supporting Information in section S1. For simplicity, only the salient features of the E analysis are presented here. Of particular interest is that this gap is defined to include not only a solvent contribution (also familiar from solvation dynamics studies^{11–28}) but also a reacting pair vibrational contribution, which depends upon the acid–base complex's geometry (not however including the proton stretch). Since E , and its solvent and vibrational components defined below, only depend on the geometries of the complex and the surrounding water solvent molecules, they can be evaluated at each time step during a trajectory. The reaction path presented in section 3 will be constructed in terms of these E components from an average of the 10 trajectories' E time dependence.

The gap E is defined to be the interaction energy difference between the two diabatic valence bond (VB) potentials (neutral pair minus ion pair), in the presence of the water solvent; these are representative of the limiting neutral and ion pair H-bonded complexes of eq 1, and each is evaluated at its potential minimum with respect to the proton coordinate. E is

$$\Delta E(\mathbf{Q}, \mathbf{S}) = V_N(q_{N,\min}, \mathbf{Q}, \mathbf{S}) - V_I(q_{I,\min}, \mathbf{Q}, \mathbf{S}) \quad (2)$$

where $q_{N,\min}$ and $q_{I,\min}$ are the respective fixed proton location minima of the O_A-H_A and H_A-N vibrational stretches and $\mathbf{Q}$ represents the H-bonded complex's intermolecular coordinates including the H-bond separation $R_{O_A N}$ and bend angles defined below.²⁹ $\mathbf{S}$ represents the solvent configuration, that is, the coordinates of all the solvent water molecules.

Figure 1 qualitatively depicts the gap E between the neutral V_N and ionic V_I VB potentials. The VB potentials themselves, as well as the adiabatic proton potential that results from their electronic mixing (solid line), are also displayed. For PT reactions,^{4–10} this E gap reflects the proton potential's evolving asymmetry; here negative E values correspond to reactant configurations with the proton bound to the carbonic acid, while positive E values correspond to product configurations with the proton bound to the methylamine base.

The total energy gap E coordinate can be instructively decomposed into a H-bond, vacuum gap contribution E_v (which will depend on the internal coordinates of the H-bond complex) and a solvent contribution E_s

$$\Delta E = \Delta E_v + \Delta E_s \quad (3)$$

E and its components are to be evaluated for each time point along each trajectory. But E cannot be evaluated in the CP MD simulations using eq 2 because the VB potentials are not known. We will circumvent this difficulty and describe here an approximate E evaluation protocol that, as we shall later see in section 3, provides a clear picture for the nascent reaction path in terms of coordinates that affect this asymmetry coordinate. This method utilizes electronic structure calculations of the H-bonded complex in the surrounding water solvent's field for each time point. Two such calculations are performed for system configurations for each time point, corresponding to the two limiting VB structures, now described in more detail.

2.1.1. Diabatic Proton Positions—The two VB reference structures require assignment of the proton position in each of them. These two reference proton positions are to be determined for each configuration along a trajectory and the difference between them is just the proton position. All the other nuclei, including solvent molecules, remain at their coordinates given by that trajectory time point. The reference proton positions are defined respectively as 1 Å away from the carbonic acid O_A in the O_A-H_A direction for the $HOCOOH \cdots NH_2CH_3$ complex in its neutral VB state and 1 Å away from the protonated base in the $H_A-NH_2^+$ direction for the ionic VB state $HOCOO^- \cdots ^+HNH_2CH_3$.²⁹ These two positions are therefore determined from the coordinates O_A , H_A , and N . Since the H-bond complex's internal coordinates $\mathbf{Q}$, which include the H-bond length $R_{O_A N}$, vary throughout the trajectory, so too will these reference proton positions. The result is an energy difference that is $\mathbf{Q}$ -dependent, consistent with the eq 2 definition.

2.1.2. Total Energy Gap E —With these two reference H-bond complex VB structure configurations defined for each time point, we can now turn to details of the electronic structure information necessary for E 's evaluation. We employ quantum chemistry

calculations (B3LYP/6-311+G**) for the carbonic acid–nitrogen base pair, with the surrounding water molecules treated as point charges (SPC/E charges: -0.8476 for O_W and 0.4238 for H_W).³⁰ Accordingly, E is the difference (neutral minus ionic) in electronic energy (B3LYP/6-311+G**) of the H-bonded complex in the field of the surrounding water molecules for the two reference proton positions indicated above.²⁹

2.1.3. Vacuum Energy Gap Contribution E_v — E_v in eq 3 is the E energy gap in the absence of the water solvent. Hence, E_v is evaluated in the manner just described for E , except that the water molecules' reaction field is ignored. E_v is then the difference in electronic energy (B3LYP/6-311+G**) of the H-bonded complex, in the absence of the surrounding water molecules' point charges, for the two reference proton positions indicated above.

2.1.4. Solvent Energy Gap Contribution E_s —The solvent contribution E_s can obviously be obtained as the difference between E and E_v via eq 3. An alternate and potentially more instructive route which we will also use is to calculate E_s by an electrostatic method similar to procedures in traditional evaluations of solvent response.^{12,15,23,24} It has the appeal of analytic simplicity and will allow us to conveniently calculate aspects of the dynamic hydration around desired atoms within the H-bonded acid–base complex.³¹

In the electrostatic method, E_s is taken as the difference in electrostatic interaction between the different charge distributions characteristic of the neutral and ionic VB states and the surrounding water molecules' charge distribution. For its evaluation, ESP point charges for each atom in the acid–base pair are obtained from electronic structure calculations of a series of before PT H-bonded complexes taken from the CP MD equilibration trajectory and a set of structures from the ion pair after PT. The charges are modified to remove any charge transfer between the carbonic acid proton donor and the methylamine base proton acceptor.³² The resulting charges are given in Table 1. With our definitions, the only configurational, structural difference between the neutral and ionic VB states is the proton position (just as with the E (E_v) calculation described above). Since the complex's charges reside on the H-bonded complex's individual nuclei whose positions change with time, E_s is a function of the intermolecular H-bond coordinates Q .

3. REACTION MECHANISM

We now turn our attention to aspects of the reaction mechanism, extending those described in I, with a specific emphasis on how key reactive coordinates including the solvent contribute to the reaction path. Our coordinate selection focuses especially on the acid–base H-bond coordinate $R_{O_A N}$ and the solvent energy gap coordinate E_s (see subsection 2.1). Our basic perspective is that, as discussed in I, the proton vibrational dynamics is faster than either of these coordinates, and the proton vibration typically adiabatically adjusts to them. However, for completeness and clarity, we also include the proton coordinate in our presentation. The reaction path is first presented in terms of these $R_{O_A N}$ and E_s coordinates utilizing an average over all 10 trajectories. The time dependence of these reaction

coordinates, with attention also to the proton coordinate, is then analyzed utilizing the related energy gap coordinate E analysis of subsection 2.1.

3.1. Reaction Path

We begin by presenting the reaction path for the carbonic acid-methylamine PT in Figure 2b, which plots the averages of the solvent coordinate $\langle E_S \rangle$ and H-bond coordinate $\langle R_{O_A N} \rangle$ against each other along the trajectory, with $t = 0$ defined for $x_{PT} = 0$, the location of the PT's occurrence (the same trajectory average scheme as that used to produce Figures 1c and 3 of I). The corresponding average proton's position is displayed in Figure 2a. Plotting both coordinates' time dependence at the same time relative to the PT occurrence yields Figure 2b. The connection of the complex's H-bond dynamics with the variation of the H-bond length-dependent E component, the vacuum potential asymmetry E_v is made in Figure 2c, which displays the trajectory-averaged $\langle E_v \rangle$ versus the average H-bond coordinate $\langle R_{O_A N} \rangle$ (the averaging is similar to that for $\langle E_S \rangle$).

In this subsection, we only give a first discussion of the reaction path's main features in order to provide an overview. We then turn to further details concerning the path in the remainder of section 3 and, for later times, in section 4.

The reaction path begins with a compression of the H-bond separation within the neutral carbonic acid-methylamine base pair complex until the point of PT occurrence ($t = 0$). The averaged H-bond contribution $\langle E_v \rangle$ in Figure 2c increases during the H-bond compression; in any event, this is in the direction favoring the ion pair, and as we explain in subsection 3.2, this is related to the fact that $\langle E_v \rangle$ is anticorrelated with the average H-bond length coordinate $\langle E_v \rangle$. During the rapid $\langle R_{O_A N} \rangle$ compression, the water solvent has little changed (see Figure 2b), evidenced by the nearly constant $\langle E_S \rangle$, but does change rapidly in the PT occurrence region, directly favoring the ion pair product right in the neighborhood of the proton occurrence at $t = 0$, a phenomenon related to establishment of a symmetric proton potential (see Figure 2b of I).

For the first 50 fs after the PT occurrence, which itself takes place after the first minimum of the H-bond compression (see Figure 1 of I) and in which the H-bond coordinate $\langle R_{O_A N} \rangle$ is increasing, $\langle E_v \rangle$'s behavior in Figure 2b is associated with the proton bending H_A-N-CH_3 angle adjusting to become that appropriate to the protonated methylamine base, and the solvent coordinate $\langle E_S \rangle$ in Figure 2b increases slightly during this H-bond expansion, corresponding to the continuing initial solvent stabilization; these aspects will be further discussed in subsection 3.2. After this 50 fs period, $\langle E_S \rangle$ increases significantly with time, as solvent stabilization of the ion pair increases (whose time scale will be discussed further in section 4), while $\langle R_{O_A N} \rangle$ fluctuates about the ion pair separation, and $\langle E_v \rangle$ primarily fluctuates around a constant value associated with the now established ion pair average structure.

3.2. Time Dependence of E

In order to put the Figure 2 reaction path into a more extended perspective, we now turn to detailed analyses of the total energy gap E and its vacuum and solvent components E_v and E_s (see eq 3). We give the analyses from the perspective of a single trajectory first and then of a trajectory average.

3.2.1. Single Trajectory Analysis of E —Figure 3a presents the full energy gap coordinate E evaluated for the fourth reaction trajectory. The other two Figure 3 panels display the trajectory's vacuum and solvent gap components. Clearly all of these coordinates change considerably during the reaction, with major changes in the PT occurrence's neighborhood, indicated by the dashed line. The corresponding results for all ten reaction trajectories are presented in Figure S1 of SI. In what follows, the general behavior for single trajectories is analyzed, using the fourth trajectory as a representative.

Total Energy Gap E : It will be useful to bear in mind Figure 2 of I which displays the evolution of the proton potential in solution for key points in the reaction progress. We recall that our E definition convention, proton potential in aqueous solution for the acid–base H-bond complex neutral pair minus that for ion pair, is such that with the proton localized within the acid, E is negative, since the neutral potential minimum is below that of the ionic potential. The opposite situation occurs where the ion pair is more stable than the neutral pair. Thus, Figure 3a shows that E is initially negative, with the proton being localized near the carbonic acid's carbonyl group acidic oxygen; the transition from negative to positive E occurs near $x_{PT} = 0$, and after the occurrence of PT the proton is bound to the nitrogen of the methylamine base and E is positive.

H-Bond Contribution E_v : The H-bond complex's vacuum contribution E_v 's evolution for the fourth trajectory is presented in Figure 3b. Apart from the evident higher frequency oscillations, E_v within and after the PT occurrence region is strongly anticorrelated with the H-bond length $R_{O_A N}$, also plotted there: E_v is more (less) negative for larger (shorter) $R_{O_A N}$ separations. The origin of this $\Delta E_v - R_{O_A N}$ connection will now be pursued, as will the high frequency oscillations in Figure 3b (and Figure 2c), which will be shown to originate from acid–base complex bending vibrations (as previewed in subsection 3.1).

We first provide some useful physical background for the vacuum gap E_v . At infinite separation of the PT products, E_v is just the *negative* of the proton affinity difference PA for methylamine and bicarbonate, which is the vacuum reaction free energy G_{RXN} for PT from carbonic acid to methylamine. The resulting value $E_v = -PA = -125 \text{ kcal/mol}$ ^{33–35} is extremely negative, so that this PT reaction is extremely difficult to effect in vacuum. This E_v value increases (becomes less negative) upon formation of the H-bonded complex at the given H-bond geometry. This motivates our decomposition of E_v into two contributions

$$\Delta E_v(Q) = \Delta_Q(Q) - \Delta PA \quad (4)$$

where $\alpha(Q)$ is the vacuum E contribution for the formation of the neutral and ionic complexes at a given geometry Q , from the isolated species; it and therefore E_v are Q -dependent, that is, dependent on the H-bond separation $R_{O_A N}$ and angles.²⁹ (For the aqueous solution problem of interest, those coordinates will be those relevant for that problem; see below.) From the E_v values in Figure 3b and $PA = -125$ kcal/mol, $Q \sim 100$ kcal/mol, a large positive value reflecting the stronger interaction in the ion pair.³⁶ Further, as the H-bond coordinate is reduced, the electrostatic ion pair interaction becomes stronger, and Q increases. The result is that E_v is less negative as the H-bond length decreases, as is seen in Figure 3b upon carboxylate-protonated methylamine pair formation.

The detailed H-bond distance and proton bending angle impacts in Figure 3b can be understood via a further, extended discussion of the H-bond geometry Q dependence of E_v . We begin with influence of the O_A -N H-bond separation $R_{O_A N}$, and for this purpose consider the on-contact carbonic acid-methylamine pair in vacuum. We obtained several of these vacuum complexes by optimizing, within a B3LYP/6-311+G** level of theory and basis set calculation, the on-contact neutral pair in vacuum by constraining $R_{O_A N}$ at different values. Proton potentials at several different H-bond lengths were generated for each of these complexes, by evaluating the electronic energy (B3LYP/6-311+G**) for several proton H_A positions along the O_A - H_A direction.

These vacuum proton potentials are displayed in Figure 4a, which shows that, as $R_{O_A N}$ decreases, there is a decrease in the relative energy for the shoulder/well, with the proton located 1 Å away from N with respect to the potential minimum. The consequence of this potential variation is the fairly linear decrease in E_v with increasing $R_{O_A N}$ seen in Figure 4b for each of the optimized vacuum complexes.³⁷

The angular dependence of the vacuum gap E_v is also relevant in Figure 3b. In particular, the time scale for the high frequency fluctuations (~ 20 fs) of E_v in Figure 3b suggests their association with a proton bending mode within the H-bond acid-base complex (it cannot be due to the proton stretch: the 2 VB states' proton positions are already fixed at 1 Å from either O_A or N). To explore this issue, we select the $R_{O_A N} = 2.7$ Å vacuum complex and evaluate E_v for different proton bending H_A - O_A -C angles; this is displayed in Figure 4c. The observed nearly harmonic bend angle behavior indicates the coupling between E_v and fluctuations of this H_A - O_A -C bend mode, and indeed the E_v minimum at $\sim 103^\circ$ closely corresponds to the equilibrium bend angle $\sim 108^\circ$. The high frequency fluctuation of E_v in Figure 3b before PT occurrence is evidently due to such H_A - O_A -C proton bend oscillations.

In order to analyze the situation further for the aqueous reaction of interest, it is most convenient to examine the trajectory-averaged Figure 4d and e. The former displays the H-bond evolution previously discussed, while the latter details the evolving proton angles: $\angle CO_A H_A$, which is most relevant for the reactant neutral pair, and the second angle $\angle H_A N CH_3$, which is most relevant for the product contact ion pair. Both angles can obviously be defined during the reaction, but their relative importance clearly changes as the proton is transferred from the carbonic acid's oxygen to the nitrogen of the methylamine

base. To come back to our primary purpose of interpreting the vacuum gap coordinate's behavior, Figure 4e also exhibits the average $\langle E_v \rangle$ during the PT reaction. Its behavior before PT is argued in Supporting Information section S4 to be the result of the combination of the H-bond coordinate and reactant angle $\angle \text{CO}_A\text{H}_A$ (although this is a somewhat subtle effect); it is also argued there that after PT occurrence, $\langle E_v \rangle$'s rather pronounced oscillatory behavior in Figure 4e can be understood in terms of the combination of the anticorrelated H-bond and ion pair product angle $\angle \text{H}_A\text{NCH}_3$.

Water Solvent Contribution E_S : We now turn to the important water solvent contribution E_S to the total energy gap E . Figure 3c displays the solvent coordinate E_S results calculated via the electrostatic method described in subsection 2.1, plotted for the fourth trajectory as the dashed line. (E_S results for all 10 trajectories are plotted in Supporting Information Figure S3.) Comparison of the three panels in Figure 3 indicates, as per our expectation given the formation of an ion pair in the PT reaction, that the aqueous solvent makes a considerable contribution to E during the PT reaction trajectory. An alternate E_S is also displayed in Figure 3c as the solid line. This is simply the eq 3 E_S definition, the difference of $E - E_v$ from Figure 3a and b. The temporal behavior for each method is similar—even extending to the common fluctuations. This similarity yields similar solvent relaxation times for the two, as discussed below in subsection 4.1. The offset visible in Figure 5c between the two methods' is due to the errors associated with each method, as outlined in Supporting Information section S3.

3.2.2. Trajectory-Averaged Analysis of E —We now analyze the time dependence of the 10 trajectory averages for the total energy gap coordinate E and its components used to generate Figure 2. The averages are taken in the same manner as that for the generation of Figure 1c of I; each E is averaged over the trajectories for every time point relative to the PT occurrence time. The results are shown in Figure 5, with the E and E_v averages given in Figure 5a and the two E_S evaluations, as in Figure 3c, are given in Figure 5b. The key features and their origin will already be familiar from our earlier discussion of the single trajectory results, so that we can be relatively brief.

The negative to positive transition for E , depicting the acid–base neutral pair to contact ion pair transition, is clearly evident in Figure 5a, as is the negative E_v contribution due to the intrinsic acidity measure PA . The positive solvent coordinate E_S contribution of Figure 5b is relatively flat before occurrence of the PT and rises just during the occurrence and continues thereafter, reflecting the aqueous solvent rearrangement stabilizing the bicarbonate-protonated amine contact ion pair; clearly the major portion of the stabilization is post the PT occurrence. (One indication of a small water-complex H-bonding changes during the proton occurrence may be found in Figure S9a and b of SI.)

Finally, we can use Figure 5 to characterize the initial energy gap response, i.e. in the first 50 fs after PT response, pointed out in subsection 3.1, to the suddenly produced contact ion pair. This response includes both proton bend adjustment and water solvent relaxation (see Figure 2). Immediately after the PT occurrence, the H-bond expands and $\langle E_v \rangle$ becomes less negative, and exhibits an H-bond vibrational period pattern (see Figure 3b). The Figure 5b dip at ~ 20 fs in $\langle E \rangle$ and $\langle E_v \rangle$ is consistent with this. But in Figure 5a, a higher

frequency motion is also apparent after the PT occurrence. The initial rise ($t \sim 10$ fs) and oscillation in $\langle E_v \rangle$ (and $\langle E \rangle$) after this occurrence is due to alignment of the O_A-H_A-N H-bond, becoming nearly linear, which is coupled with proton bending modes, which before the PT occurrence, was carbonic acid's H_A-O_A-C proton bending mode and after it is the protonated amine's H_A-N-CH_3 proton bending mode. (Details are given in Supporting Information section S4.) The steady increase of the solvent coordinate contribution $\langle E_S \rangle$ to the energy gap after the sudden PT amounts to a sort of solvation dynamics for the newly created bicarbonate-protonated amine contact ion pair. But while the PT occurrence itself is sudden, Figure 2a shows that the produced ion pair's charge distribution continues to develop during the initial 50 fs. The Figure 5b solvation dynamics in this period is thus occurring in an evolving charge distribution; this is an important difference from standard solvation dynamics discussions.^{11–28} Thereafter, $\langle E_S \rangle$ continues to progress and further stabilize the ion pair in the presence of its now established fixed charge distribution. This relaxation continues beyond the confines of Figure 5b and is more fully characterized in the next section.

The analysis of the reaction path in this section has covered the basic essentials for the carbonic acid-methylamine PT reaction. We can, however, push the analysis to longer times in the next Section in order to probe several further interesting reaction aspects, in particular site-specific effects in the water solvent.

4. LONGER TIME ASPECTS OF THE PT REACTION: SITE-SPECIFIC SOLVATION ASPECTS OF THE PT REACTION

As we just noted, section 3 has completed the description of the major nuclear motion aspects of the $H_2CO_3-NH_2CH_3$ PT reaction. We can nonetheless glean further information about the reaction process by extending our study to longer times in this section. In particular, we wish to address what is happening in the water solvent at a molecular level for the PT reaction. It is the acquisition of this level of detail that requires attention to longer times than examined in previous sections, beginning with establishment of the aqueous solvent relaxation time scale.

The electrostatic version of the solvent coordinate E_S is utilized in this Section (as in the bold line in Figure 5b); the alternate difference version analyzed in Supporting Information section S3 yields a similar time scale (see Figure S4 of SI). The pairwise nature of E_S 's electrostatic version allows identification of contributions from each hydration shell water molecule, so that we can then analyze the solvent structure associated with the PT reaction around key sites of the acid–base H-bonded complex.

4.1. Water Solvent Relaxation Time Scale

To begin the establishment of the water solvent relaxation time scale, we replot in Figure 6a the electrostatic solvent coordinate $\langle E_S \rangle$ for a longer time window than in Figure 5b, beginning with $t = 0$ (defined for each trajectory's PT occurrence when the proton coordinate $x_{PT} = 0$); this coincides with the $\langle E_S(t) \rangle$'s increase due to the emergence of the ion pair.

In order to clarify the behavior in Figure 6a, we employ the normalized nonequilibrium response function to characterize the $\langle E_S(t) \rangle$ time dependence^{14–17,23}

$$\Delta(t) = \frac{\langle \Delta E_S(t) \rangle - \langle \Delta E_S(\infty) \rangle}{\langle \Delta E_S(0) \rangle - \langle \Delta E_S(\infty) \rangle} \quad (5)$$

shown in Figure 6b. This characterizes the water solvent relaxation from the initial value $\langle E_S(0) \rangle$, where the solvent is equilibrated with the neutral pair $\text{HOCOOH} \cdots \text{NH}_2\text{CH}_3$ before PT, to its equilibrium value $\langle E_S(\infty) \rangle$ for the ion pair $\text{HOCOO}^- \cdots ^+\text{HNNH}_2\text{CH}_3$; from Figure 6a, we extract the limiting averages $\langle E_S(0) \rangle$ and $\langle E_S(\infty) \rangle$ before and after PT as 17 and 45 kcal/mol.

We recall from the end of section 3 that a period of ~ 50 fs after the PT occurrence at $t = 0$ is required for full development of the charge distribution in the product carboxylate-protonated methylamine contact ion pair. This initial evolution period automatically makes our relaxation function $\Delta(t)$ in Figure 6b different, at least at short times, from standard water^{11–22} and other^{23–28} solvation dynamics theory^{12,13,15,17,20–28} and experiment.^{11,14,16,18,19} Here we make the simplest estimate of the water relaxation time for our carbonic acid PT problem by simply fitting $\Delta(t)$ in Figure 6b with a single exponential function, which yields a relaxation time $\tau_S \sim 120$ fs.

For perspective, experimental analysis of water dynamics in a nonreactive setting yields trimodal behavior, comprising a Gaussian with an ~ 50 fs (45%) time constant and a biexponential functions, with one time scale of ~ 130 fs (20%) and the other at ~ 1 ps (35%).¹¹ The Gaussian originates from inertial motion of water molecules, while the other two are associated with libration and slower rotation of water molecules, respectively.^{11–22} Even though there is a solute charge-evolution perturbation on the ~ 50 fs time scale in our PT case, it seems reasonable to associate the $\Delta(t)$ in Figure 6b time scale ~ 120 fs to a significant degree, especially in view of the large body of information on the characteristic time scale for these motions, with water librations, that is, hindered rotations. We will see that we should also include H-bond compressions in the interpretation.

Due to our limited run time of 1 ps after PT occurrence, any slower exponential component at ~ 1 ps such as found in water solvation dynamics experiments^{11,14,16,18,19} is missed. A key reason for this restriction is that the ion pair attempts to dissociate at that time scale. Such attempts were observed in two of our 10 trajectories (for details, see Supporting Information section S5). Since these dissociation attempts affect E_S , all data past the point of the attempts were discarded in the trajectory averaging for $\langle E_S(t) \rangle$.

4.2. Site-Specific Solvent Rearrangement

With the time scale ~ 120 fs of the water solvent relaxation after PT occurrence now established, we can now ask what the contribution to these dynamics is from various sites on the reaction product carboxylate-protonated methylamine contact ion pair. We focus on three key sites, with the numbering from Scheme 1: the O_A and O_C oxygens on the bicarbonate and the NH_3 moiety carrying the transferred proton on the protonated methylamine; Table 1

shows that these have the largest charge change in the PT reaction: the proton-donating O_A and the neighboring carboxylic O_C which is in resonance with it carry the majority of the negative charge increase in the anion, and the NH_3 moiety carries the majority of the increased positive charge in the protonated base.

Figure 7a displays the trajectory-averaged solvent coordinate $\langle E_S \rangle$, again evaluated via the electrostatic method due to the interaction with six water molecules, the two nearest water solvent molecules for each of the three sites. (The choice of two molecules follows from the determination that the coordination numbers around these sites are approximately two after the PT reaction (see Supporting Information section S6).) $\langle E_S \rangle$ increases for each site, as expected from the increased charge magnitudes. The contribution for the O_A site is dominant for the initial increase of $\langle E_S \rangle$; the water solvent molecules around O_A respond quickly after the PT occurrence, within ~ 30 fs. This initial $\langle E_S \rangle$ increase in the ~ 50 fs interval reflects the initial stabilization of the transferred proton in the incipient ion pair product, as pointed out in subsection 4.1. The O_A site contribution continues to evolve past the initial period and the other site contributions increase as well. The NH_3 site contribution in particular becomes of comparable magnitude to that of the O_A site, while the contribution O_C site, with its smaller charge change, remains less important.

These contact ion pair site-specific effects clearly should be related to H-bonds of these sites to water molecules in the pair's hydration shell. That this is indeed the case is detailed in Supporting Information section S6 via an examination of appropriate radial distribution functions, as well as of H-bond numbers and lengths (as a measure of H-bond strength). In brief, it is shown there that, with the notable exception of the proton-donating oxygen O_A , which after PT occurrence picks up a new H-bond with a water molecule, the predominant aqueous solvent effects for the other two sites result from the strengthening of water molecule-ion pair site H-bonds already present in the carbonic acid-methylamine neutral contact pair.

Finally, Figure 7b displays the averaged total solvent coordinate $\langle E_S \rangle$ and the sum Σ of the three Figure 7a site-specific contributions to $\langle E_S \rangle$ and that for the solvation nearest the nonreactive hydroxyl oxygen O_{na} (see Scheme 1). The contributions in Σ for these four sites (O_A , O_C , O_{na} , and NH_3) can be used to operationally define a "first hydration shell" for the water solvent relaxation for the carboxylate-protonated methylamine ion pair complex. The $\langle E_S \rangle - \Sigma$ difference then provides an estimate of the second solvation shell and beyond contribution to $\langle E_S \rangle$. While the time scales for the $\langle E_S \rangle$ and Σ are similar beyond the initial period, the amplitude of the first solvation shell contribution is clearly more significant, but solvation of the ion pair by outer shells is not entirely negligible.

Finally, in order to understand the solvent relaxation around the product ion pair complex in more molecular detail, we have followed the time evolution of the parameters for the H-bond rearrangement of waters next to the key sites of the complex. These key sites are O_A and the NH_2 grouping which has the maximum hydration occurring after PT occurrence, as we have already observed in Figure 7. The detailed analysis in Supporting Information subsection S6.3, which analyzes the time behavior of two angles and two H-bond distances, related to the H-bonds between the acidic O_A and a single nearest water molecule and between the

base's hydrogens N each with a single nearest water. The analysis shows that these H bond rearrangements, which are basically strong H-bond formations, occur on a time scale of 200 fs or so, with fitted exponential decay times of ~ 170 fs. These observations are consistent with the 200 fs predominant solvent relaxation shown in Figure 6b and its associated average solvent energy gap coordinate in Figure 6a. The angular and H-bond distance dynamics in Supporting Information subsection S6.3 indicate that the key water solvent motions on this time scale, when the relaxation has significantly completed, are (certainly coupled) water librational motions and H-bond distance compressions associated with the formation of strong H-bonds between these water molecules and the two charge sites of the product ion pair complex.

5. CONCLUDING REMARKS

In this Article, we have detailed, beyond the geometric and charge evolution description of paper I, the reaction path for the rapid, barrierless proton transfer (PT) from carbonic acid (H_2CO_3) to the strong base methylamine (CH_3NH_2) within a hydrogen (H)-bonded complex in aqueous solution, described by Car–Parrinello molecular dynamics simulations. This path demonstrates the special importance of the H-bond coordinate distance $R_{\text{O}_\text{A}\text{N}}$ between H_2CO_3 's proton-donating oxygen O_A and the proton-accepting nitrogen of CH_3NH_2 and aqueous solvation here described by an energy gap solvent coordinate.

Compression of $R_{\text{O}_\text{A}\text{N}}$ coordinate is a key for the reaction path prior to the PT occurrence, while water solvent rearrangement assisting this PT commences only during that occurrence. Further H-bond and particularly solvent motion helps to stabilize the nascent carboxylate-protonated methylamine contact ion pair just after this, in a transient period of ~ 50 fs, during which the final charge distribution of the pair is being established. In this transient period, there is also a contribution to the reaction path from the total energy gap coordinate contribution arising from the participation of the $\text{C}-\text{O}_\text{A}-\text{H}$ or equivalently the $\text{O}_\text{A}-\text{H}-\text{N}$ angle change associated with the transfer of the proton. The complete further stabilization of the product contact ion pair is characterized by a time scale of ~ 120 fs, implicating, for example, the water librational motions in the process. A site-specific analysis of the aqueous solvent relaxation after the PT occurrence indicates that the major solvent rearrangement occurs around the proton-donating oxygen O_A of carbonic acid and the NH_3 moiety of the protonated methylamine base, an aspect also analyzed in terms of changes in the number and strength of the H-bonds between solvent water molecules and these H-bond acceptor sites. The time scales observed account for most of the water solvent relaxation and analysis shows that not only water librations are involved, but also H-bond compressions, both motions being key in the formation of new strong H-bonds of water to the two sites.

An aspect of the reaction mechanism we have not examined here or in I is issues of intramolecular and intermolecular energy transfer for vibrations in the produced ion pair. A proper treatment would require a quantization of the proton and possibly other vibrational degrees of freedom, for example, the protonated methylamine and perhaps its anion partner. This might be attempted, perhaps via existing methodology³⁸ at some later date, but goes far beyond the scope of the present study.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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References

1. Daschakraborty S, Kiefer PM, Miller Y, Motro Y, Pines D, Pines E, Hynes JT. Mechanism of Direct Proton Transfer from Carbonic Acid to a Strong Base in Aqueous Solution I: Acid and Base Coordinate and Charge Dynamics. *J Phys Chem B*. 2016; doi: 10.1021/acs.jpcc.5b12742
2. Car R, Parrinello M. Unified Approach for Molecular Dynamics and Density-Functional Theory. *Phys Rev Lett*. 1985; 55:2471–2474. [PubMed: 10032153]
3. Grimme SJ. Accurate Description of van der Waals Complexes by Density Functional Theory Including Empirical Corrections. *J Comput Chem*. 2004; 25:1463–1473. [PubMed: 15224390]
4. Pines D, Ditkovich J, Mukra T, Miller Y, Kiefer PM, Daschakraborty S, Hynes JT, Pines E. How Acidic Is Carbonic Acid? *J Phys Chem B*. 2016; doi: 10.1021/acs.jpcc.5b12428
5. Schmidt, RF., Thews, G. Human Physiology. Springer-Verlag; Berlin: 1980.
6. Ando K, Hynes JT. Molecular Mechanism of HCl Acid Ionization in Water Solvent. *Ab initio* Potential Energy Surfaces and Monte Carlo Simulations. *J Phys Chem B*. 1997; 101:10464–10478.
7. Andot K, Hynes JT. HCl Acid Ionization in Water Solvent: A Theoretical Molecular Modelling. *J Mol Liq*. 1995; 64:25–37.
8. Ando K, Hynes JT. Molecular Mechanism of HF Acid Ionization in Water: An Electronic Structure-Monte Carlo Study. *J Phys Chem A*. 1999; 103:10398–10408.
9. Kiefer PM, Hynes JT. Nonlinear Free Energy Relations for Adiabatic Proton Transfer Reactions in a Polar Environment. II. Inclusion of the Hydrogen Bond Vibration. *J Phys Chem A*. 2002; 106:1850–1861.
10. Kiefer, PM., Hynes, JT. Theoretical Aspects of Proton Transfer Reactions in a Polar Environment. In: Hynes, JT.Klinman, JP.Limbach, H-H., Schowen, RL., editors. Hydrogen-Transfer Reactions. Wiley-VCH; Weinheim, Germany: 2006. p. 303-348.Ch. 10
11. Jimenez R, Fleming GR, Kumar PV, Maroncelli M. Femtosecond Solvation Dynamics of Water. *Nature*. 1994; 369:471–473.
12. Rey R, Hynes JT. Solvation Dynamics in Liquid Water. 1. Ultrafast Energy Fluxes. *J Phys Chem B*. 2015; 119:7558–7570. [PubMed: 25635521]
13. Roy S, Bagchi B. Solvation Dynamics in Liquid Water. A Novel Interplay Between Librational and Diffusive Modes. *J Chem Phys*. 1993; 99:9938–9943.
14. Jarz ba W, Walker GC, Johnson AE, Kahlow MA, Barbara PF. Femtosecond Microscopic Solvation Dynamics of Aqueous Solutions. *J Phys Chem*. 1988; 92:7039–7041.
15. Petersen J, Møller KB, Rey R, Hynes JT. Ultrafast Librational Relaxation of H₂O in Liquid Water. *J Phys Chem B*. 2013; 117:4541–4552. [PubMed: 23131075]
16. Horng ML, Gardecki ML, Papazyan A, Maroncelli M. Sub-Picosecond Measurements of Polar Solvation Dynamics: Coumarin 153 Revisited. *J Phys Chem*. 1995; 99:17311–17337.
17. Maroncelli M, Fleming G. Computer Simulation of the Dynamics of Aqueous Solvation. *J Chem Phys*. 1988; 89:5044–5069.
18. Maroncelli M. The Dynamics of Solvation in Polar Liquids. *J Mol Liq*. 1993; 57:1–37.
19. Maroncelli M, Fleming GR. Picosecond Solvation Dynamics of Coumarin 153: The Importance of Molecular Aspects of Solvation. *J Chem Phys*. 1987; 86:6221–6239.

20. Tran V, Schwartz BJ. Role of Nonpolar Forces in Aqueous Solvation: Computer Simulation Study of Solvation Dynamics in Water Following Changes in Solute Size, Shape and Charge. *J Phys Chem B*. 1999; 103:5570–5580.
21. Nandi N, Roy S, Bagchi B. Ionic and Dipolar Solvation Dynamics in Liquid Water. *Proc - Indian Acad Sci Chem Sci*. 1994; 106:1297–1306.
22. Nandi N, Roy S, Bagchi B. Ultrafast Solvation Dynamics in Water: Isotope Effects and Comparison with Experimental Results. *J Chem Phys*. 1995; 102:1390–1397.
23. Carter EA, Hynes JT. Solvation Dynamics for an Ion Pair in a Polar Solvent: Time Dependent Fluorescence and Photochemical Charge Transfer. *J Chem Phys*. 1991; 94:5961–5979.
24. Fonseca T, Ladanyi BM. Breakdown of Linear Response for Solvation Dynamics in Methanol. *J Phys Chem*. 1991; 95:2116–2219.
25. Bagchi B, Oxtoby DW, Fleming GR. Theory of the Time Development of the Stokes Shift in Polar Media. *Chem Phys*. 1984; 86:257–267.
26. Daschakraborty S, Biswas R. Ultrafast Solvation Response in Room Temperature Ionic Liquids: Possible Origin and Importance of the Collective and the Nearest Neighbour solvent Modes. *J Chem Phys*. 2012; 137:114501. [PubMed: 22998265]
27. Bagchi B, Biswas R. Polar and Nonpolar Solvation Dynamics, Ion Diffusion, and Vibrational Relaxation: Role of Biphasic Solvent Response in Chemical Dynamics. *Adv Chem Phys*. 1999; 109:207–433.
28. Bagchi B. Dynamics of Solvation and Charge Transfer Reactions in Dipolar Liquids. *Annu Rev Phys Chem*. 1989; 40:115–141.
29. The E definition eq 2 explicitly includes angular dependence related to bent H-bonds in the H-bonded complex. Our $q_{N, \min}$ and $q_{I, \min}$ definitions have the proton 1 Å away from the carbonic acid's acidic oxygen in the O_A-H direction for the neutral state and 1 Å away from the nitrogen in the $H-NH_2^+$ direction for the ionic state. The 1 Å distance choice derives from the features that the average reactant O_A-H_A and product H_A-N distances are 1.02 and 1.05 Å, respectively, as determined from the simulation of isolated species in aqueous solution (see section 2.3 of I). The reference separations required for the energy gap E are equilibrium VB electronically diabatic values, and are thus slightly smaller and closer to 1 Å than are these values.
30. Berendsen HJC, Grigera JR, Straatsma TP. The Missing Term in Effective Pair Potentials. *J Phys Chem*. 1987; 91:6269–6271.
31. On the other hand, the electrostatic point charges of the complex atoms should be benchmarked in some way, e.g., via calculation of some physical parameters these point charges and comparison with standard experimental values (Which is a standard force field development method). In the present work, we will use the comparison of the calculations of the electrostatic E_S and that resulting from the difference of E and E_v . See section 3.2.
32. The desired ESP charges refer to the limiting neutral and ionic states of the complex (see eq 1), for which there is no charge transfer between AH and B in the neutral pair and A^- and ^+HB in the ion pair. However, some charge transfer is present according to our electronic structure calculations; this transfer is deleted by changing the atomic charges on the O_A and N atoms so that the resulting net charges on AH and B are zero, and are -1 and $+1$ for A^- and ^+HB , respectively.
33. The proton affinity (PA) of HCO_3^- is 339 kcal/mol,³⁴ while that of CH_3NH_2 is 214 kcal/mol.³⁵
34. Squires RR. Gas-phase Thermochemical Properties of the Bicarbonate and Bisulfite Ions. *Int J Mass Spectrom Ion Processes*. 1992; 117:565–600.
35. Hunter EPL, Lias SG. Evaluated Gas Phase Basicities and Proton Affinities of Molecules: An Update. *J Phys Chem Ref Data*. 1998; 27:413–656.
36. A simple electrostatic calculation considering ion pair atoms as point charges yields an interaction energy of ~ 100 kcal/mol for the ion pair at its equilibrium separation. A similar value of ~ 90 kcal/mol has been observed for a cation–anion interaction. See Annapureddy HVR, Dang LX. Pairing Mechanism among Ionic Liquid Ions in Aqueous Solutions: A Molecular Dynamics Study. *J Phys Chem B*. 2013; 117:8555–8560. [PubMed: 23800046]
37. It is useful to note that similar behavior is exhibited for vacuum potentials in Figure 2 of I. Even though the proton potentials with water solvent interaction switch from a minimum near the acid to

a potential with a minimum near the base due to solvent stabilization of the ion pair product, the corresponding vacuum potentials always have a minimum near the acid.

38. Rey R, Hynes JT. Tracking Energy Transfer from Excited to Accepting Modes: Application to Water Bend Vibrational Relaxation. *Phys Chem Chem Phys*. 2012; 14:6332–6342. [PubMed: 22402668]

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Figure 1. Schematic energy gap ΔE definition in terms of the diabatic neutral and VB potentials for the acid–base H-bonded complex in interaction with the aqueous solvent. This figure is also intended to convey the idea that the VB states’ reference geometries have the proton coordinate positions fixed at their values at the minima of the respective potentials. The displayed situation is appropriate before, e.g., H-bond and solvent rearrangements permit the PT and ultimately an exothermic reaction situation. See Figure 2 of I.

Figure 2.

Trajectory-averaged (a) normalized proton coordinate x_{PT} (eq 3 of I), H-bond length $\langle R_{O_A N} \rangle$ (dashed line), total charges of methylamine and bicarbonate moieties (solid lines) as a function of time; (b) solvent coordinate $\langle E_S \rangle$ and (c) vacuum gap coordinate $\langle E_V \rangle$ paths versus the averaged H-bond length $\langle R_{O_A N} \rangle$. The green dashed vertical line in (a) indicates $t = 0$ the time for PT occurrence, and the time points along each path are indicated in panels (b) and (c), with $t = 0$ retaining this meaning.

Figure 3.

Total, vacuum and solvent energy gap coordinates versus time for the fourth reaction trajectory. The $t = 0$ value here is the time at which the equilibration constraints were turned off and the dashed vertical red lines in all panels indicate the PT occurrence time when the normalized proton coordinate (eq 3 of I) $x_{PT} = 0$. (a) The total energy gap E (solid line) and (b) vacuum gap E_v (solid line) values versus time for the fourth reaction trajectory. (c) The solvent contribution E_s versus time as calculated with the electrostatic method (dashed green line) and for the $E_s = E - E_v$ difference method (solid line). (Evaluation details for E and its components are given in subsection 2.1.) The normalized proton coordinate x_{PT} (dotted blue line) is also plotted in panels (a) and (c), while the H-bond coordinate R_{OAN} is also plotted in panel (b) (dashed blue line), with values given by the right-hand ordinate axis. Each panel's curves are rather noisy, due to thermal fluctuations for this single trajectory, especially due to the specific water solvent molecules in close proximity to the H-bonded complex. Nonetheless, we can identify specific H-bond complex vibrational motions in, e.g., panels (b) and (c); see the text.

Figure 4.

(a) Calculated vacuum potentials along the R_{OAN} proton stretch for the carbonic acid–methylamine complex for differing H-bond coordinate R_{OAN} values, indicating the relative destabilization of the ionic component with increasing R_{OAN} . The energy minimum for each potential is set to zero to aid in the comparison. These potentials were evaluated via B3LYP/6-311+G** electronic structure calculations. (In aqueous solution, the ionic portion of these curves is stabilized, in a fashion similar to what is seen in Figure 2c of I.) (b) The vacuum gap E_v versus R_{OAN} for the vacuum H-bonded acid–base complexes in panel (a). (c) E_v versus the H_A-O_A-C proton bend angle for the $R_{OAN} = 2.7$ Å vacuum H-bonded complex in

(a). Lines in (b) and (c) are linear interpolations between data points (○). See subsection 2.1 for details of the E_v calculation. (d) Trajectory-averaged H-bond coordinate $R_{O_A N}$ as a function of time. (e) Trajectory-averaged E_v (red line) and two bending angles: $\angle CO_A H_A$ (black line) and $\angle H_A NCH_3$ (blue line) versus time (the carbon of the protonated base's methyl group is labeled CH_3 in the Figure for convenience).

Figure 5.

Average over the 10 trajectories for (a) the total energy gap, $\langle \Delta E \rangle$ (black line), the vacuum contribution, $\langle \Delta E_v \rangle$ (blue line), and (b) the solvent coordinate contribution, $\langle \Delta E_s \rangle$, from the electrostatic (black line) and $\langle \Delta E_s \rangle = \langle \Delta E \rangle - \langle \Delta E_v \rangle$ difference (blue line) methods versus time; see the text for details.

Figure 6.

Average water solvent coordinate $\langle \Delta E_s \rangle$ as a function of time with $t=0$ set for the proton coordinate $x_{PT}=0$, locating the PT occurrence. (b) Trajectory-averaged water relaxation function $\Delta(t)$ in the presence of the $\text{H}_2\text{CO}_3\text{--CH}_3\text{NH}_2$ reaction system, eq 5, as a function of time (solid line) and its linear exponential fit (blue dashed line).

Figure 7.

(a) Ten trajectory averaged solvent coordinate $\langle E_S \rangle$ contributions (from the two nearest water molecules) for the three key sites (the proton-donating O_A , its neighboring oxygen O_C , and the NH_3 moiety for the protonated base). $t = 0$ is the time for the proton coordinate $x_{PT} = 0$, i.e., the PT occurrence, in each trajectory. (b) Comparison of total $\langle E_S \rangle$ and the sum of the contributions from these three key sites (O_A , O_{na} , O_C , and NH_3).

Scheme 1. Neutral *cis-cis* Conformer on-Contact Carbonic Acid–Methylamine Pair with the Atoms Labeled^a

^aLabels are maintained throughout the PT reaction producing the contact ion pair products.

Table 1

ESP Atomic Charges for the Carbonic Acid/Bicarbonate-Methylamine/Protonated Methylamine Acid–Base Complex, in Its Neutral Reactant and Ionic Product Forms, Used to Evaluate the Solvent Energy Gap

Coordinate E_S^a

atom/moiety	neutral pair charge (e)	ion pair charge (e)
C	1.00	1.04
O _A	−0.57	−0.88
O _C	−0.73	−0.88
O _{na}	−0.68	−0.80
H _{na}	0.53	0.51
HCO ₃ moiety	−0.45	−1.01
N	−0.64	−0.14
$\overline{H}_N^b$	0.25	0.28
CH ₃	−0.01	−0.21
$\overline{H}_C^c$	0.05	0.12
CH ₃ NH ₂ moiety	0.00	0.57
H _A	0.45	0.44

^a Atom labeling is that depicted Scheme 1.

^b The overbar indicates an overage over the two nitrogen hydrogens, both before and after PT (the transferring proton H_A's charge is accounted for separately).

^c The overbar indicates an overage over the three methyl hydrogens, both before and after PT.