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# Prediction of $pK_a$ Values for Oligo-methacrylic Acids Using Combined Classical and Quantum Approaches

### Haitao Dong, Hongbo Du, and Xianghong Qian\*

Department of Mechanical Engineering, Colorado State University, Fort Collins, Colorado 80523 Received: June 29, 2009; Revised Manuscript Received: August 26, 2009

The  $pK_a$  values for polymeric acids are very useful quantities for many applications including separations using ion-exchange membranes and catalysis using polymeric acids. However, the  $pK_a$  value of a polymeric acid is typically different from the corresponding monomer value and is generally unknown. The  $pK_a$  value of a particular acid group is strongly dependent on the local environment of the dissociating acid group and the broad dielectric medium. The  $pK_a$  values for oligo-methacrylic acids were systematically determined as a function of degree of polymerization using combined classical and quantum mechanical approaches. The atomic charges were determined quantum mechanically, whereas the  $pK_a$  values were determined solving the Poisson—Boltzmann equation. The  $pK_a$  values were found to increase as the degree of polymerization (DP) increases and converge to a stable value after DP reaches 8. The predicted  $pK_a$  values agree very well with experimental results.

### Introduction

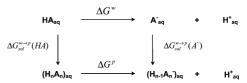
The acidity constant for macromolecules such as proteins and polymeric acids with multiple acid groups is complex due to each acid group's unique electrostatic environment. 1-4 Polymeric acids with multiple acid groups have wide applications in specific bioseparations and catalysis. The  $pK_a$  values of the acid groups in a polymeric acid (e.g., poly(methacrylic acid), PMAA) are typically different from their corresponding monomer value due to the change in their electrostatic environment. Forsyth et al. show that two different carboxyl groups in the same protein can have  $pK_a$  values of 2 and 9.5 Since the  $pK_a$  values of the polymeric acids are typically unknown and expected to be different from their monomer values, it is therefore important to determine the  $pK_a$  values of polymeric acids used for ionexchange-based separations (e.g., PMMA) and for catalysis (polysulfonic acids). The present work is an attempt to investigate the  $pK_a$  dependence on the chain length of the short oligomers of methacrylic acids (MAAs).

The classical continuum dielectric model based on the Poisson—Boltzmann equation (PBE) was used in this work to determine the  $pK_a$  values of the oligo-methacrylic acids.<sup>6–9</sup> Georgescu et al. used this method to calculate the  $pK_a$  values of 166 ionizable groups in 12 proteins. The mean square error of their calculated  $pK_a$  values was 0.83 pH units, and only 3% of the calculated  $pK_a$  values are more than 2 pH units away from the corresponding experimental values.<sup>10</sup> Our current work is to our best knowledge the first attempt to predict the  $pK_a$  values for polymeric acids, and their dependence on the degree of polymerization (DP).

### Method

(1) Thermodynamic Cycle. The acidity constant,  $pK_a$ , of an acid group (HA) is determined by the free energy change of its

# SCHEME 1: Thermodynamic Cycle for Determining the Free Energy Change of Proton Dissociation of the Carboxyl Groups in Oligo-MAA in Water



proton dissociation process in water,  $\Delta G^{\text{w}}$ :

$$pK_{a} = \frac{1}{2.303RT} (\Delta G^{W}(HA \to A^{-} + H^{+}))$$
 (1)

In this study, a thermodynamic cycle (shown in Scheme 1) was used to calculate the relative  $pK_a$  change of MAA from the corresponding monomer value.

The free energy change  $\Delta G^p$  for proton dissociation of the oligo-MAA (bottom reaction in Scheme 1) in water can be determined on the basis of the value of free energy change  $\Delta G^w$  of the monomer, and the solvation free energy differences between the monomeric and oligomeric acids and their conjugate bases. The p $K_a$  value of the oligo-MAA is

$$pK_{a,n} = pK_{a,1} + \frac{1}{2.303RT} (\Delta G_{sol}^{w \to p}(A^{-}) - \Delta G_{sol}^{w \to p}(HA))$$

where p $K_{a,1}$  is the acid constant of the monomer MAA, where the experimental acidity constant is used with p $K_{a,1} = \Delta G^{\text{w}}/2.303RT$ .

(2) Poisson-Boltzmann Equation. PBE solves for the electrostatic potential  $\varphi(\vec{r})$  at position  $\vec{r}$  from contributions of all the charges in the system using Boltzmann distribution,

<sup>\*</sup> Corresponding author. E-mail: xhqian@engr.colostate.edu.

$$\nabla \cdot \varepsilon(\vec{r}) \nabla \varphi(\vec{r}) = -4\pi \rho_0(\vec{r}) - 4\pi \sum_{\lambda} q_{\lambda} \rho_{\lambda} \exp[-\beta q_{\lambda} \varphi(\vec{r})]$$
(3)

where  $\varepsilon(\vec{r})$  is the position dependent dielectric constant,  $\rho_0$  the charge distribution of the solute, and  $q_\lambda$  and  $\rho_\lambda$  the charge and concentration of salt ion  $\lambda$ , respectively. It has been shown that PBE can accurately predict the p $K_a$  values of proteins. <sup>6,10–13</sup> Using the continuum dielectric model under PBE, the system is divided into the solute and structureless solvent parts. The solvation free energy of the solute comes from all of the electrostatic interactions including the Coulombic interactions between the solute and the induced charges in solvent, and any additional interactions due to the presence of an external field and any salt in solution,

$$\Delta G_{\rm sol} = \sum_{j} q_{j} \varphi_{\rm coul}(\vec{r}_{j}) + \sum_{j} q_{j} \varphi_{\rm react}(\vec{r}_{j}) + \sum_{j} q_{j} \varphi_{\rm solv}(\vec{r}_{j})$$
(4)

In this study, the PBE was solved for both the neutral oligomers and their conjugate bases. Only the intrinsic  $pK_a$  values of the oligo-MAAs are determined; i.e., only one acid group is ionized, while all other acid groups are at their neutral states. With one acid group in the ionized state, further ionizations become increasingly more difficult due to electrostatic repulsions, and thus are not expected to contribute significantly to the acid strength. Moreover, as the DP value increases, the number of calculations needed to determine the atomic charges quantum mechanically increases dramatically for double or multiple ionizations. These more complex situations will be subject to future investigations.

(3) Computational Details. The PBE of the oligo-MAA was solved numerically using the Delphi code. <sup>14</sup> It utilizes a finite-deferential method and is capable of treating multiple solvent media with different dielectric constants. In order to take into account the conformations of oligo-MAA, the multiconformation continuum electrostatics (MCCE) program based on the Delphi code developed by Gunner's group is used. <sup>6,15</sup> The structures and atomic charges of oligo-MAA were obtained by using the Car—Parrinello molecular dynamics (CPMD) simulations. <sup>16</sup> For oligomers with DP  $\geq$  10, charges from the 8-mer were used. The details of atomic charge calculations are given in the Supporting Information.

In MCCE, each of the oligo-MAAs is divided into three types of residues: CH<sub>3</sub>-capped, H-capped, and middle residue, as shown in Figure 1. The COOH group in the residues was allowed to rotate. The solvent is a mixture of water with a dielectric constant ( $\varepsilon$ ) of 80 and the oligomers have  $\varepsilon=3$ . The latter value was taken from the dielectric constants of small carboxylic acids, which are in a range of 2.58-3.44.<sup>17</sup>

## **Results and Discussion**

Table 1 lists the calculated  $pK_a$  values for oligo-MAA with DP = 2–20. Also listed for comparison are the  $pK_a$  values for the dimer and trimer in our earlier study using *ab initio* calculations. <sup>18</sup> Our earlier studies yield  $pK_a$  values of 6.08 and 5.27 for the CH<sub>3</sub>-capped and H-capped residues, respectively, for the dimer. The  $pK_a$  values calculated using MCCE are 5.22 and 5.23, respectively, in good agreement with our previous results. For the two end residues of the MAA trimer, the MCCE  $pK_a$  values of 6.51 and 6.90 are larger than the previously

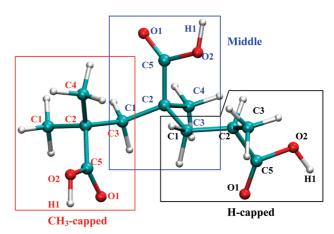


Figure 1. Residues of the MAA trimer.

TABLE 1: Calculated  $pK_a$  Values for Methacrylic Acid Oligomers with DP = 2-20 Given by the Multiconformation Continuum Electrostatics (MCCE) Program

			$pK_a$	
		CH <sub>3</sub> -capped	H-capped	mid (average)
dimer	MCCE	5.22	5.23	
	Gaussian	6.08	5.27	
trimer	MCCE	6.51	6.90	5.52
	Gaussian	5.46	5.37	5.64
4-mer		6.06	5.92	5.68
5-mer		7.61	6.74	6.26
6-mer		6.71	6.88	6.16
7-mer		7.36	8.24	6.88
8-mer		7.14	8.46	6.99
12-mer		7.05	8.54	7.42
16-mer		7.40	8.84	7.50
20-mer		7.86	8.79	7.44
exp.	7.3			

predicted values of 5.46 and 5.37. However, the  $pK_a$  values for the middle residue agree well (5.52 and 5.64, respectively).

The overall agreement between the two methods indicates that the continuum dielectric model of the PBE can adequately describe the electrostatic environment of oligo-MAA at an accuracy level similar to *ab initio* methods. Both methods predict an increase in the  $pK_a$  values for the oligo-MAA. In our previous study, the calculated  $pK_a$  value of methacrylic acid was 4.83 (exp. = 4.65). The calculated  $pK_a$  values for the dimer and trimer using the same method are 0.73 higher on average. In this work, the experimental  $pK_a$  value of 5.03 for pivalic acid was used as the monomer value for comparison. For the H-capped residue, 2-methyl propanoic acid ( $pK_a$  = 4.83) was used instead. For the CH<sub>3</sub>-capped and middle residues in the dimer and trimer, MCCE calculations predict an average of 0.72 increase in the  $pK_a$  values. For the H-capped residues, the shift is 0.69. These results are in excellent agreement with our earlier data.

The p $K_a$  values for the oligo-MAA with DP = 4–20 by MCCE are also listed in Table 1. Their p $K_a$  values are all higher than their respective monomer values. Figure 2 shows the p $K_a$  values averaged over all residues (blue diamonds) for the oligo-MAA with DP = 2–20. The average p $K_a$  values show a significant increase from the dimer (p $K_a$  = 5.22) to 7-mer (p $K_a$  = 7.14). This near 2 p $K_a$  unit increase suggests that the electrostatic environments of the ionizing carboxyl groups become very different upon polymerization. Further DP increase has no apparent additional impact on the p $K_a$  values. The p $K_a$  values averaged over all middle residues (light blue triangles in Figure 2) show a similar trend. Both series of calculated p $K_a$ 

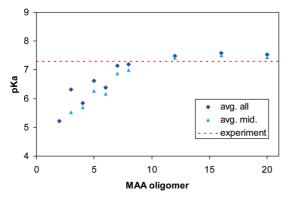


Figure 2. Average  $pK_a$  values for methacrylic acid oligomers with DP = 2-20 given by the multiconformation continuum electrostatics (MCCE) program. The red dotted line represents the experimental p $K_a$ of PMAA (p $K_a = 7.3$ ).

values converge to 7.5, which is in excellent agreement with the experimental  $pK_a$  value of 7.3 for PMAA (the red dotted line in Figure 2).19

The  $pK_a$  values by MCCE show that the proton dissociation process of the oligo-MAA becomes less favorable upon polymerization. The electrostatic effect of increasing the DP value is to shift the ionization equilibrium further to the direction of disfavoring the anions up to DP 7.

It is also interesting to examine the spatial variations of  $pK_a$ values along the oligo-MAA chains. The MCCE results show that the middle residue gives a slightly lower  $pK_a$  value than the two end residues. The  $pK_a$  difference between the middle residues and the CH<sub>3</sub>-capped residues becomes smaller as the DP increases. On the other hand, the  $pK_a$  value of the H-capped residue increases up to DP = 16. For DP > 8, the p $K_a$  values of the H-capped residues are above 8.4, which is higher than the other p $K_a$  values. This variation in p $K_a$  along the polymer chain indicates that the electrostatic environment around the ionizing residues is different depending on the position of the residues. As the chain becomes longer, this variation becomes less significant.

The agreement of MCCE-derived  $pK_a$  values with experimental measurements indicates that the continuum dielectric model is able to capture the essence of the electrostatic properties of the oligo-MAA. However, the conformations and the atomic charges of the oligo-MAA in our calculations were obtained from the gas phase. These may not reflect the true conformations and charges of oligomers in water. Here, the oligomers adopt a fully extended chain conformation. Also, only the intrinsic acidity constant of the ionizing group was considered in the present study. The more complex multiple ionization constants, which involve interactions between various neutral and ionized acid groups, were not studied.

### Conclusion

The continuum dielectric model of the Poisson-Boltzmann equation has been used to predict the intrinsic  $pK_a$  values of oligomers of methacrylic acid with DP = 2-20. The calculated  $pK_a$  values agree well with ab initio results for the dimer and trimer. A converged p $K_a$  value of 7.5 is reached for DP > 12. This value agrees well with the experimental measurement of 7.3. The results confirm that the acid strength of polymeric acids becomes weaker with respect to their corresponding monomer values.

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Supporting Information Available: Description of the CPMD calculation details and effects of the dielectric constant, table showing calculated  $pK_a$  values for methacrylic acid oligomers, and figure showing average  $pK_a$  values for methacrylic acid oligomers. This material is available free of charge via the Internet at http://pubs.acs.org.

#### References and Notes

- (1) Sharp, K. A.; Honig, B. Annu. Rev. Biophys. Biophys. Chem. 1990, 19, 301.
  - (2) Warshel, A. Acc. Chem. Res. 1981, 14, 284.
  - (3) Warshel, A. Biochemistry 1981, 20, 3167.
- (4) Warshel, A.; Aquist, J. Annu. Rev. Biophys. Biophys. Chem. 1991, 20, 267.
- (5) Forsyth, W. R.; Antosiewicz, J. M.; Robertson, A. D. Proteins: Struct., Funct., Genet. 2002, 48, 388.
  - (6) Alexov, E. G.; Gunner, M. R. Biophys. J. 1997, 74, 2075.
- (7) Antosiewicz, J. M.; McCammon, J. A.; Gilson, M. K. Biochemistry **1996**, 35, 7819.
- (8) Gilson, M. K.; Rashin, A.; Fine, R.; Honig, B. J. Mol. Biol. 1985, 184, 503.
  - (9) Warwicker, J.; Watson, H. C. J. Mol. Biol. 1982, 157, 671.
- (10) Georgescu, R. E.; Alexov, E. G.; Gunner, M. R. Biophys. J. 2002, 83, 1731.
  - (11) Bashford, D.; Karplus, M. Biochemistry 1990, 29, 10219.
  - (12) Demchuk, E.; Wade, R. C. J. Phys. Chem. 1996, 100, 17373.
- (13) Yang, A. S.; Gunner, M. R.; Sampogna, R.; Sharp, K. A.; Honig, B. Proteins 1993, 15, 252.
- (14) Rocchia, W.; Alexov, E. G.; Honig, B. J. Phys. Chem. B 2001, 105, 6507.
  - (15) Alexov, E. G.; Gunner, M. R. Biochemistry 1999, 38, 8253.
- (16) CPMD, http://www.cpmd.org/, Copyright IBM Corp 1990-2008, MPI fur Festkorperforschung Stuttgart 1997-2001.
- (17) Lange, N. A. Lange's Handbook of Chemistry, 16th ed.; McGraw-Hill: New York, 2005.
  - (18) Dong, H.; Du, H.; Qian, X. J. Phys. Chem. A 2008, 112, 12687.
- (19) Ikawa, T.; Abe, K.; Honda, K.; Tsuchida, E. J. Polym. Sci., Polym. Chem. Ed. 1975, 13, 1505.

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