Supporting Information for: Interplay between Hydroxyl Radical Attack and H-bond Stability in Guanine-Cytosine.

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Supporting Information

As noted in the text, the influence of diffuse function has been assessed by performing two approaches:

- Method 1: PCM single-point calculations at M06-2X/6-311G(d,p):B97D/6-31G(d):PM6 level on the M06-2X/6-311G(d,p):B97D/6-31G(d):PM6 optimized geometries.
- Method 2: PCM single-point calculations at M06-2X/6-311++G(d,p):B97D/6-31+G(d):PM6 level on the M06-2X/6-311G(d,p):B97D/6-31G(d):PM6 optimized geometries.

As listed in Table 1 the energy difference is small (< 1 kcal mol⁻¹). Despite this minor effect, the energies discussed in our paper have been computed within the Method 2 aiming to provide the most accurate results.

	3bp	o-0w	3bp	3bp-5w		
Structure	Method1	Method 2	Method 1	Method 2		
G(80H):C	0.00	0.00	0.00	0.00		
G(8OH):C-1ts ^a			10.36	10.52		
G(8OH):C-1 ^a			8.76	7.77		
G(8OH):C-2ts	16.57	17.07	11.44	10.56		
G(8OH):C-2	7.95	8.42	12.00	11.09		
G(8OH):C-3ts ^b			18.37	18.78		
G(8OH):C-3 ^b			12.62	12.78		
G:C(6OH)	0.00	0.00	0.00	0.00		
$G:C(6OH)-1ts^{C}$						
G:C(6OH)-1 ^c						
G:C(6OH)-2ts	12.10	12.35	9.08	9.07		
G:C(6OH)-2	2.50	2.73	5.51	5.19		
G:C(6OH)-3ts ^b			15.70	16.14		
G:C(6OH)-3 ^b			10.04	10.10		

Table 1: Relative Energies (in kcal mol^{-1}) Calculated for the Tautomeric Equilibria in theEmbedded G:C-OH Adducts.

^{*a*} No stable structure in the 3bp-0w model.

^{*b*} Structure only accessible in the 3bp-5w model.

^c No stable structure neither in the 3bp-0w nor in the 3bp-5w models.

 Table 2: Imaginary Vibrational Frequencies (ν/cm^{-1}) Calculated for the Transitions States
 and Normal Mode Analysis.

	3bp-0w		3	3bp-5w	
Structure	v	assignment ^a	v	assignment ^a	
G(8OH):C-1ts ^b			1144i	H1	
G(8OH):C-2ts	1339i	H1 + H4	651i	H4	
$G(8OH):C-3ts^{c}$			764i	H4'	
G:C(6OH)-2ts	1271	H1 + H4	1278i	H4	
G:C(6OH)-3ts ^b			677i	H4'	

^a Protons involved in the stretching mode.
^b No stable structure in the 3bp-0w model.
^b Structure only accessible in the 3bp-5w model.
^c No stable structure neither in the 3bp-0w nor in the 3bp-5w models.

Since the low layer is modeled at the semiempirical PM6 method, it is technically not possible to perform the ESP analysis within the proposed ONIOM partition. Accordingly, we extracted the high layer, namely the hydrated hydroxy GC adducts, from the 3bp-5w model to compute the ESP of the atoms interacting with the water molecules around the O6(G)-N4(C) H-bond. As can be seen in Table 3, N7(G) and H4' atoms are less negative in the G(8OH):C-2 structure than in canonical G(8OH):C form, while no variation is observed for the O6(G) atom. This result is consistent with Mulliken's analysis and indicates the origin of the extra destabilization of the G(8OH):C-2 when going from the 3bp-0w to the 3bp-5w model. However, we underline that Mulliken and ESP schemes differ for the evolution of the H4 proton charge. More especially, with ESP H4' becomes less positive following the PT reactions.

Table 3: ESP charges (|e|) Predicted for Undamaged DNA and G:C–OH Radical Adducts.

Structure	N7(G)	O6(G)	H4	H4'	H1
G:C (undamaged)	-0.52	-0.63	0.59	0.58	0.28
G(8OH):C	-0.71	-0.58	0.56	0.58	0.31
G(8OH):C-1ts	-0.76	-0.55	0.55	0.58	0.21
G(8OH):C-1	-0.61	-0.64	0.47	0.54	0.25
G(8OH):C-2ts	-0.59	-0.61	0.49	0.51	0.29
G(8OH):C-2	-0.58	-0.58	0.47	0.49	0.29
G(8OH):C-3ts	-0.63	-0.58	0.39	0.57	0.26
G(8OH):C-3	-0.58	-0.61	0.44	0.45	0.19
G:C(6OH)	-0.32	-0.63	0.53	0.54	0.26
G:C(6OH)-2ts	-0.35	-0.63	0.53	0.52	0.22
G:C(6OH)-2	-0.32	-0.66	0.54	0.50	0.27
G:C(6OH)-3ts	-0.45	-0.66	0.48	0.53	0.20
G:C(6OH)-3	-0.46	-0.62	0.49	0.44	0.19