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Correction to Differential Stabilities and Sequence-Dependent Base Pair Opening Dynamics of Watson-Crick Base Pairs with 5-Hydroxymethylcytosine, 5-Formylcytosine, or 5-Carboxylcytosine

Marta W. Szulik, Pradeep S. Pallan, Boguslaw Nocek, Markus Voebler, Surajit Banerjee, Sonja Brooks, Andrzej Joachimiak, Martin Egli, Brandt F. Eichman, and Michael P. Stone

In our recently published article on the structures and base pair opening dynamics of Dickerson–Drew dodecamer (DDD) duplexes with incorporated 5-hydroxymethylcytosine (5hmC), 5-formylcytosine (5fC), or 5-carboxylcytosine (5caC), we inadvertently failed to reference two publications by others who had reported structures of the DDD with single 5hmC residues inserted per strand. Spingler and co-workers¹ reported the structures of DDDs with 5hmC replacing either C³ (5'- dCG-5hmC-GAATTCGCG-3'; two crystal forms) or C⁹ (5'- dCGCGAATT-5hmC-GCG-3') at resolutions of between 1.66 and 1.99 Å. Schofield and co-workers² subsequently published a structure of the DDD with 5hmC replacing C⁹ at greater resolution (1.3 Å) and assessed the water structure around and conformational variations of the 5hmC hydroxyl moiety. Our structure of the modified DDD 5'-dCGCGAATT-5hmC-GCG-3' had a resolution of 1.02 Å. Similar to the structures published before, the presence of 5hmC had negligible effects on the global and local geometry of the DDD using the native duplex as a reference. We apologize for the omission. There is also a typographical error in the right-hand column on p 1297. The sentence in question should read “At the neighbor C³:G¹⁰ base pair, the G¹⁰ N1H resonance remained detectable at 55 °C, also exhibiting broadening.”

REFERENCES

1. Renciuik D, Blacque O, Vorlickova M, Spingler B. Crystal structures of B-DNA dodecamer containing the epigenetic modifications 5-hydroxymethylcytosine or 5-methylcytosine. *Nucleic Acids Res.* 2013; 41:9891–9900. [PubMed: 23963698]
2. Lercher L, McDonough MA, El-Sagheer AH, Thalhammer A, Kriaucionis S, Brown T, Schofield CJ. Structural insights into how 5-hydroxymethylation influences transcription factor binding. *Chem. Commun.* 2014; 50:1794–1796.