CORRECTIONS

Importance of Exocyclic Base Functional Groups of Central Core Guanosines for Hammerhead Ribozyme Activity, by Thomas Tuschl, Mabel M. P. Ng, Wolfgang Pieken, Fritz Benseler, and Fritz Eckstein*, Volume 32, Number 43, November 2, 1993, pages 11658–11668.

Page 11665. In column 2, paragraph 2, six slants were incorrectly inserted and should be deleted. The paragraph should read as follows:

G/A Mispairs. The question remains as to what interactions these guanosines are involved in. It has been postulated that the A9/G12 and G8/A13 residues, adjacent to stem II of the hammerhead, are capable of forming G/A double-mismatched base pairs (Li et al., 1991a; Slim & Gait, 1992). G/A mismatches are conformationally variable and can exist in four different structures, all of which involve normal base tautomers with guanosine in the anti conformation (Figure 3a–d) (Li et al., 1991a). Protonation of adenosine under acidic conditions allows additional G(syn)/A(anti) pairing (Figure 3e) (Gao & Patel, 1988; Leonard et al., 1990). Three of the unprotonated structures (Figure 3a–c) have been observed experimentally (Li et al., 1991). While single G/A pairs destabilize duplex structures, adjacent 5′-GA-3′ mismatches can reach stabilities similar to fully Watson–Crick base-paired duplexes (Ebel et al., 1992; Li et al., 1991b; SantaLucia et al., 1990). Tandem G/A mismatches in the sequence context of d(5′-RGAN-3′) adopt the imino pairing scheme (Figure 3a,b) and do not require the participation of the guanosine 2-amino group. G/A to I/A substitution in this sequence context is not duplex destabilizing (Ebel et al., 1992). In contrast, deoxyinosine substitution in the d(5′-YGAR-3′) sequence produces relatively unstable tandem I/A mismatches, indicating that the 2-amino group of guanosine is crucial for stability in this stacking environment (Figure 3c,d) (Ebel et al., 1992; Li et al., 1991a; Lane et al., 1992). RNA duplexes with the G/A double mismatch in the sequence extent of 5′-CAGG-3′ and 5′-CGAG-3′ displayed similar stability (SantaLucia et al., 1990), but the high stability of the reversed mismatch sequence 5′-AG-3′ in RNA is unusual (Ebel et al., 1992; Li et al., 1991b). NMR and functional group modification studies on these RNA duplexes support two distinct types of base pairing, the A/G sequence that involves hydrogen-bonded imino protons (Figure 3a) and the G/A sequence that does not (SantaLucia et al., 1990, 1991). The substitution of adenine by purine reduces drastically the loop stability of the G/A as well as the A/G sequence, whereas the guanosine to inosine substitution has a slightly stabilizing effect.

0006-2960/94/0433-848$04.50/0