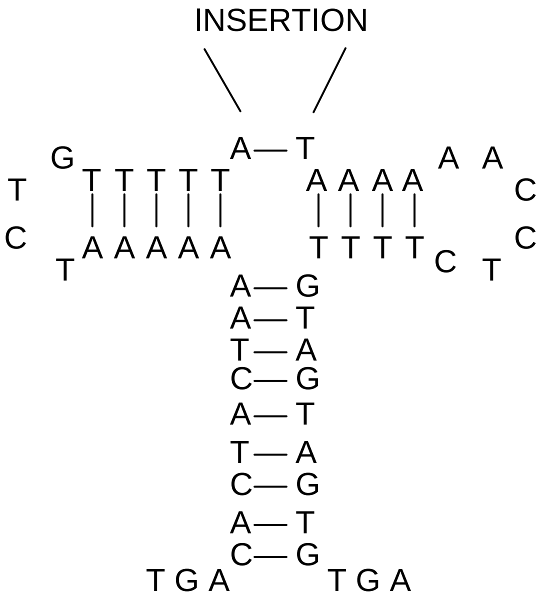

Supplemental Figure 5. Likely base paring and folding of the *Tgm-Express* inverted repeats flanked by the target site duplication (TGA). The differing bases in the repeats form the loops of the two hairpins. Except for this structure, the rest of the insertion in the *wp* mutant gene, does not have any similarity to other previously characterized soybean *Tgm* elements**.**