Figure 2. Plot representation of the number of transitions (×) and transversions (∆) versus of the genetic distance calculated with the Tamura–Nei model (TN93) among all pairwised strains of TTSuV genogroups 1 (A) and 2 (B). Solid lines indicate the best fit found in each mutational type. The "s" and "v" represented the number of transitions (x) and transversions (∆), respectively.