

○ clonal Δ less sib — with in isolate
 □ super sib ▽ unrelated between isolates (same year) ● 2008 ● 2010
 ◇ sibs × other between isolates (different year) ● 2009 ● 2011

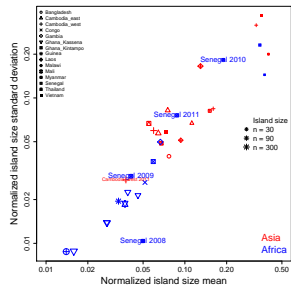


Figure 2 is a line graph showing the cumulative frequencies of genotype errors for two methods, DEploid and DEploidIBD, across three levels of relatedness: Low, Moderate, and High. The x-axis represents the Genotype Error (ranging from 0.00 to 0.05), and the y-axis represents the Cumulative frequencies (ranging from 0.0 to 1.0). The legend indicates that dashed lines represent DEploidIBD and solid lines represent DEploid. The colors represent the relatedness levels: blue for Low, green for Moderate, and red for High. In all cases, DEploidIBD (dashed lines) shows higher cumulative frequencies (lower error rates) compared to DEploid (solid lines). The performance difference is most significant for high relatedness data (red lines), where DEploidIBD reaches a cumulative frequency of 1.0 at a lower error rate than DEploid.