

Figure 1. Saturation test of 16S gene fragments. Relationships of uncorrected p-distances between pairs of taxa with the number of transitional or transversional changes. Regression analysis demonstrates that both transitions ($R^2 = 0.7141$) and transversions ($R^2 = 0.6604$) are approximately linear in distribution.

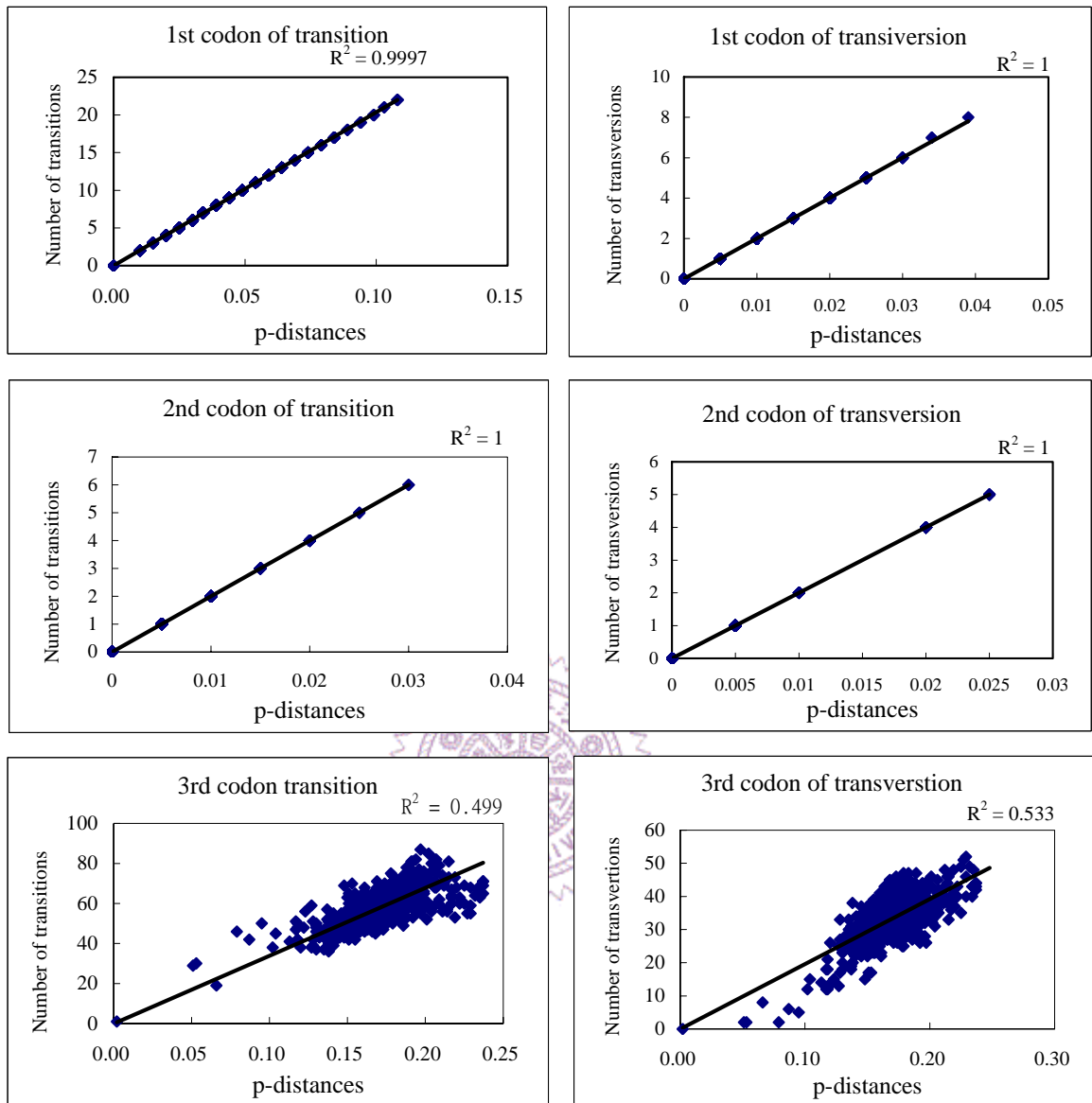


Figure 2. Saturation test of COI genefragments. Relationships of uncorrected p-distances between pairs of taxa and the number of transitional and transversional changes. At third codon position of transitional changes, saturation tendency was shown to reach a plateau at p-distance above 20%.