



Figure 2.- Principal component projection of 12 samples of *Peromyscus* with the minimum spanning tree network superimposed. Identification of sample numbers as in Figure 1 and Appendix.

The multivariate analyses (UPGMA cluster analysis, PCA, and minimum spanning tree) produced similar arrangements of the samples as in the univariate analysis (Figs. 2 and 3). The sample of *P. boylii rowleyi* (1) was clearly distinct from the samples of *P. simulus* which were arranged into three groups: a coastal (2) and three inland (4, 7, and 12) samples from the northern part of the species range in Sinaloa (except for sample 7 for the Sinaloa/Nayarit border); two samples from southern Sinaloa (3 and 5), and three samples from Nayarit (8, 9, and 10), of which all but samples 8 and 10 are from inland localities; and two coastal samples from southern Sinaloa (6) and southern Nayarit (11).