

which is traced to be derived from the mother map.

The methodology includes the examination and selection of cartographic features to ascertain and arrange a sampling sequence. This method groups the identified unique traits or map-genetic elements for tracing through variant maps of the period. These elements are identified, arranged, compared, and traced in a cartographic-genetic element table (Table 1), which lists the major chronological maps determined to be variants in this study. The primary conditions for establishing the connectivity of the number of unique elements from the mother map, which have been discovered in the variant maps, follows the identification of unique features, such as the double row of trees, and misspelled nomenclature.

boundary line of the

To determine if similar values were present in the related maps, and which of the maps were related as directly influenced by the Herrman's map, further analysis is required. This analysis determines shape and size of the sequence of maps to standardize comparisons. Longitude corrections for the various maps can be calculated. The calculation of percentage of error between the control points of the various maps can be applied to further facilitate the analysis in making comparisons. Additional research can develop other criteria used to help identify the prototype variants, and