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I would like to make a test of three variables, I have done the statistics and I have obtained a conclusion, I would like to have someone to confirm this conclusion or this can also be a part of the conclusion or I can begin by a higher number of tests. Any suggestions? Many thanks in advance. A: I would do at least \$20-30\$ samples. The number of samples is not really relevant but rather the fact that you are attempting to do \$30\$ tests. In your case I would take \$20\$ and split my samples into two groups (maybe this is already what you did). I would then look at the correlation between the dependent and the independent variables. I would expect there to be something there (Correlation is a statistical assumption that there will be a weak relationship). If there is then this should help to reduce the chance of Type I errors in the conclusion (ie, you really did find something). If you are satisfied that there is something there then you would be free to proceed with your hypothesis testing. Finally, you could also repeat your process of splitting your samples into two groups and examine the correlations between the dependent and independent variables in the larger sample. It is quite easy to miss something if you are doing too few samples and the real variable has small correlations with the predictors. If there is a difference in the correlations in the larger sample then then it is possible that some real effects have been missed. -encoding sequences (16S rRNA) of the known phytopathogenic bacteria were obtained from the GenBank database. In order to find the phylogenetic relatives of these phytopathogenic bacteria in *T*. *soudanensis*, homologous sequences were used to screen for the phylogenetic neighbors with a standard bit-score cutoff of 30. An alignment of these homologous sequences was generated with MUSCLE \[@pone.0216779.ref052]. The alignment was trimmed with GBlocks \[@pone.0216779.ref053]. Phylogenetic trees were constructed from the alignment with the program RAxML \[@pone.0216779.ref054] under the maximum likelihood (ML) criterion. Bootstrap resampling was used to assess the statistical support for the inferred groups. Trees were visualized using TreeView \[@pone.0216779.ref055]. The sequences of *Pseud



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