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Fish sauce is an important seasoning in Asian countries like Vietnam and China. It contains biogenic amines which contributes to the smell and taste of fermented foods like cheese, meat products and the fish sauce. Prior studies that uses techniques like gene clone libraries and DGGE to determine the microorganism’s community that produces the biogenic amines is too slow to produce result for complex bacterial community. To combat such issue, this paper uses the recent developed technique of high-throughput sequencing to analysis the bacterial community in fish sauces with improved speed. The author acquired and analyzed the biogenic amines composition of fish sauce from Guangdong, China. The author also sequenced the DNA for the bacteria community in the fish sauce. Using such data, the author is able to perform statistical analysis and determine that histamine, tyramine, cadaverine and putrescine are the four major biogenic amines in the fish sauce. Tyramine quantity is positively correlated to the quantity of histamine(R=0.0113). DNA analysis shows the change of bacterial community during different stage of fish sauce. The finding of this study provides improve ways to analysis fish sauce and can be useful for fish sauce production.

In the paper, the author uses the PCA to analysis the data from the free amino acids concentration data set (table 2). Using such method, the author studies the relationship between each amino acid and the extracted principal component. In the paper, the author finds out that principal component 1(PC1) and principal component 2(PC2) accounted for most of the variance in the dataset (85.87%). They also find out that the PC1 was positively related to amino acids like aspartic acid, glutamic acid, histidine, leucine, lysine, Tetragenococcus, and Halomonas. PC1 also negatively relates to the amount of histamine, putrescine, tyramine, cadaverine, Photobacterium, and Halanaerobium. They find out, on the other hand, most amino acids are on the PC2 positive side except Tetragenococcus which shows the significance difference between this specific acid and the rest of the amino acid. In my attempt to replicate the PCA in the paper, I failed to achieve the same result as the author of the paper did. However, my analysis also finds out that the PC1 and PC2 are accounts for most of the variance (99.69%) with nearly no variance left for any other possible principle component. My PCA shows seemingly random grouping in PC1 just as the paper. It also shows a very strong grouping behavior for a large chunk of the amino acid in PC2 which also agrees with the paper. This shows a clear similarity between most of the amino acid that is within the free amino acids in the Yu-lu.

One possible reason for the difference between mine and the author’s PCA is that the data provided by the paper contains standard deviation and I did not taking in to account for that. It is possible for the author to adjust each amino acid value within the standard deviation to shift the result into the positive and negative side. The similarity in mine and the paper’s grouping pattern is a good proof.

