Using DNA Barcoding to Verify the Ingredients of Snack Foods

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Abstract:

With the gradual development of society, snacks have become an important part of people's daily life. But are the ingredients in all kinds of snacks on the market really as simple as those in the ingredient list? With the use of DNA barcoding technology, we can simply identify the substances contained in the common snacks, then make comparison and identify the authenticity of the information in the snacks' composition list. In the experiment, we use Kit Method and silica method to extract DNA from samples. Through PCR, gel electrophoresis and DNA sequencing, we gain the DNA sequence of different substance contain in food. Finally, DNA barcoding is used to find out the what types of animals own these DNA, and we find out that some of the substances contained in the products were extremely inconsistent with the ingredient list, and most of the snacks were mixed meat products instead of pure meat.

Introduction:

Animal derived products play an important role in human life. Snacks derived from meat products are the one of the most popular consumer goods. For instance: dried pork slice and dried beef cubes and so forth.

But there are lawbreakers driven by profits in which adulteration of snack products was carried out by various means. The definition of adulteration means deliberately replacing meat raw materials or tampering with meat food ingredient labels. These behaviors may create some hidden danger to safety. There were plenty of news reports about anaphylactic shock caused by adulteration. So we need pay attention on this situation. According to that, we ask the question about that and use DNA Barcoding to address the question.

We selected seven samples from the store.

Method:

1.There are two basic criteria for our selection:1. The raw materials in the ingredient list on the outer package of processed food should not be too similar in order to avoid this kind of situation, we chose roughly four kinds of processed food: fish(lionfish / Pterois volitans), pig (Sus), cattle (Bovine) and chicken (Gallus gallus domesticus) , so the results can be more comprehensive.

2. The processed food should not contain excessive oil or pungent smell, so that we can extract small pieces of sample in the experiment easily, we collected the samples twice, the first on August 2, 2020 and the second on August 4, 2020. the number of samples purchased for the first time was 16, which were divided into Group 1 and Group 2. The number of samples for the second purchase was 6, three samples were purchased repeatedly, and three new samples were purchased. The three new samples are all coded into the Group 3. Attachment: we bought all our samples in the local supermarket nearby.

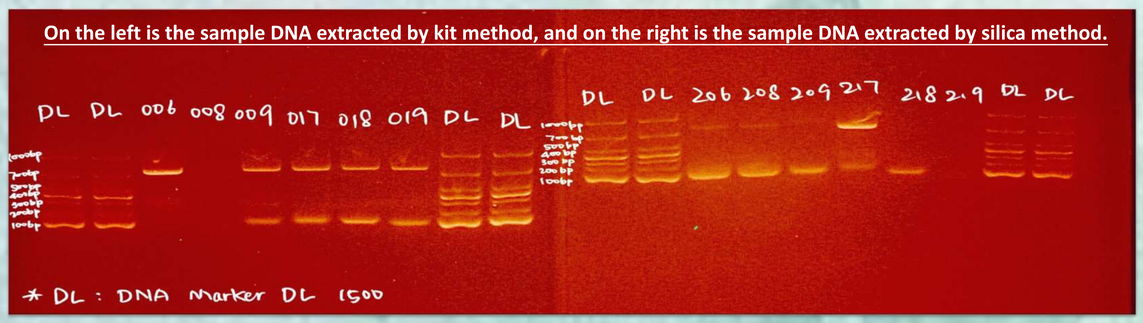

Figure 1: The gel electrophoretic results of the samples using kit method and silica method.

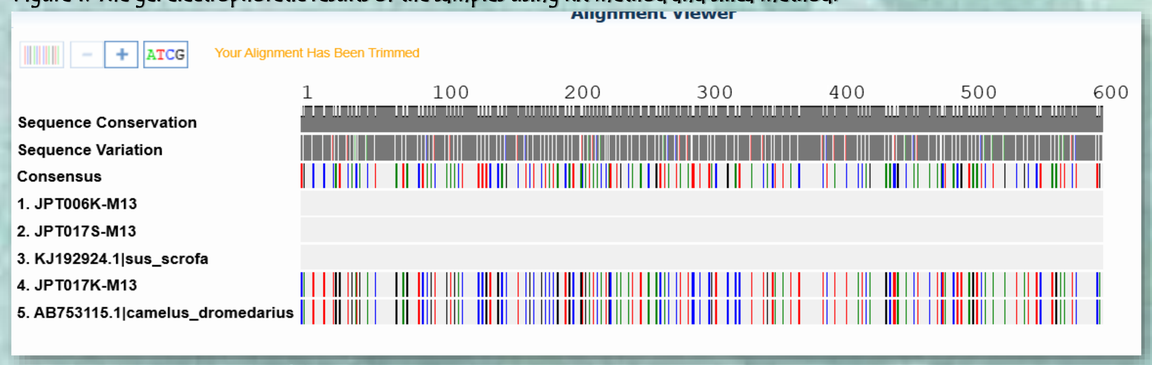

Figure 2: The muscle result of the sample JPT – 006, JPT – 017K and JPT – 017S.

Results :

We tested 19 different samples, used two different DNA extraction methods (Kit Method and silica method), and conducted two experiments. The gel electrophoresis of the first experiment showed that only one sample (JPT - 003) DNA was successfully amplified by PCR. But in the subsequent DNA sequencing, JPT - 003 did not have a clear DNA sequence. After second gel electrophoresis experiments, the results were more ideal. Kit method successfully extracted five different samples' DNA, and silica method successfully extracted one sample's DNA. (The results of gel electrophoresis are shown in Figure 1: Diagram of gel electrophoresis.). The DNA of six successful samples in the second experiment were also successfully sequenced.(The results of DNA sequencing and interspecific comparison are shown in Figure 2: the diagram of the DNA barcoding result.)

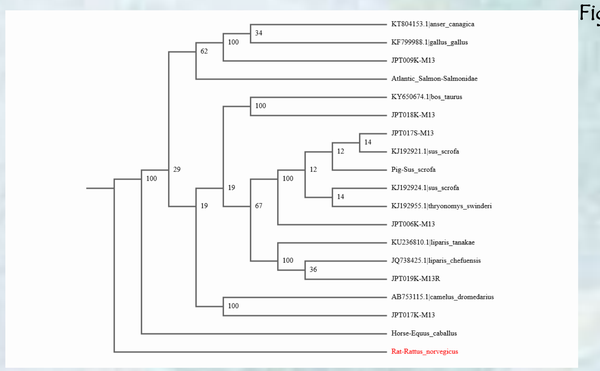

Figure 3: The PHYLIP NL result of the six successful samples.

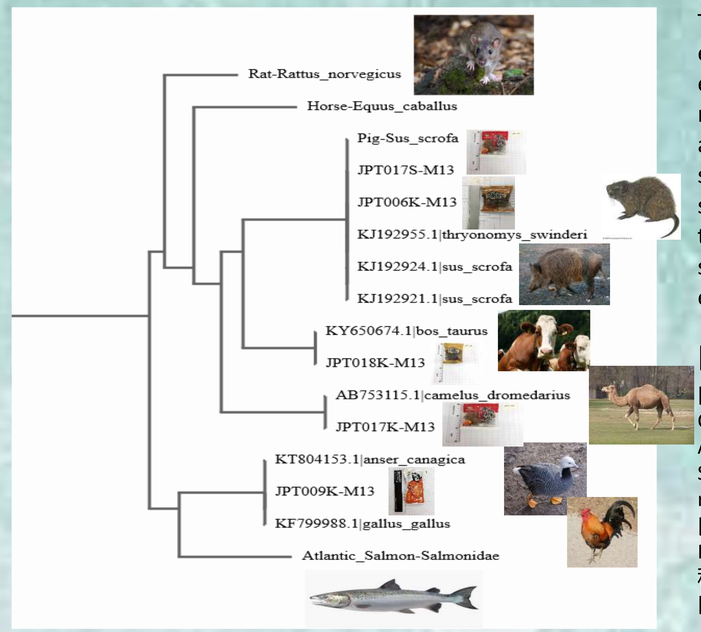

Figure 4: The PHYLIP ML result of the six successful samples.

Results :

Two phylogenetic trees (NL and ML) showed that the COI region of the sample JPT – 006's DNA is similar to rats and pigs' DNA, which was different from the ingredients list of sample JPT - 006. Similarly, the COI region of the sample JPT – 017's DNA is highly similar to camel DNA, which was inconsistent with the information on its ingredient list too. The DNA in the remaining three samples (JPT - 019, JPT - 009 and JPT - 18) roughly matched the information in the ingredient list.

Discussion:

Actually, our experiments show that some foods in the market do adulterate. Take the sixth sample as the example, according to its ingredients table which shows only to contain beef and shrimp. In fact, it does not only have these things, but also have other compositions that pork *(Sus scrofa)* and rat meat *(Thryonomys swinderi)*. This kind of situation and behavior will greatly threaten our physical and mental health, because there have been many cases of allergy or even shock death caused by the ingredients not marked by the business, and this makes the confidence of customers for food greatly reduced, so we should pay attention to and severely punish this kind of behavior. Using DNA barcoding to verify the ingredients of snacks food which can make full use of it to identify the nature of species, this method is fast and has high credibility, through this method we can greatly reduce the behavior of adulteration in food, and it has certain protection for the health to it. In fact, we failed in our first experiment. At that time, we selected 16 samples, and only one was successful. Unfortunately, it was not detected when we sent it for sequencing, so the first experiment ended in failure. The main reason is that the reagents we use may be expired reagents that are ineffective. In the second experiment, we only selected six samples, and used new reagents, and two different methods were used at the same time. Finally, amplification and sequencing were successful. It's a pity that we didn't select many samples in the second experiment, so there were only six successful samples. Therefore, it is suggested to select more samples in future experiments and check the shelf life of reagents.

References:

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