

DNA gives new perspectives to understand the mysteries of nature

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What caused the extinction of the woolly rhinoceros ten thousand years ago from an area in Europe covering the coasts of the Arctic Ocean in the north to the coasts of the Mediterranean in the south? What caused the extinction of the mammoth while other ice age mammals like the musk ox just barely survived to present day. A new scientific methodological approach to detect genetic material will help researchers to solve the many mysteries of the past.

"I'm confident that the new methodological approach, will be of great importance to molecular biology", says Professor Eske Willerslev at the Centre for Ancient Genetics, University of Copenhagen, Denmark. One of his PhD students recently came up with a brilliant idea. What usually has taken the DNA-researchers several years of laboratory work can now be done in just a few hours thanks to this breakthrough enabling researchers to get a full view of total ecosystems or populations dating thousands of years back in time.

The automation of a long research process

Professor Eske Willerslev and his team find DNA traces of ancient life for their research in areas where the ground is permanently frozen like in Siberia or Alaska. Here, inside the frozen ground, traces of ancient DNA are preserved and by bringing back earth samples drilled from the permafrost of Siberia and Canada, the team is able to find ancient DNA material from the animals and the plants that used to live in the area

thousands of years ago. In order to detect the types of DNA material in a sample, the researchers are normally using a DNA primer - a kind of 'fishing hook' attaching itself to a specific piece of the DNA. That particular piece of DNA is then being multiplied, cloned and sequenced, which makes it possible to be identified by the researchers. However, this present procedure is slow, and it takes years just to identify a fraction of the most common animals and plants available from the DNA in the many samples.

A new sequencing machine (454 parallel sequencing, GS20, Roche/454 Life Sciences) capable of interpreting millions of pieces of DNA in just a few hours was recently introduced. The machine alone brought in a revolution to the field, but have certain disadvantages and shortcomings. Firstly, an analysis made by the machine is quite expensive. Each analysis costs approximately DKK 45 000 (equivalent to \$ 7 500) and although the machine reads extensive amounts of DNA material, the cost is still considerable to a research project. Secondly, a vital problem arises when researchers try to benefit from the machine's enormous capacity by analyzing samples from multiple locations or specimens in a single run in order to reduce costs. The machine simply cannot separate more than 16 samples from each other.

Eske Willerslev went to check out the machine for himself at the Danish Cattle Research Centre in Foulum – the only place in Denmark, which operates the new sequencing machine. He realized to his great disappointment that the researchers at the University of Copenhagen could not make use of the machine for their respective projects due to the disadvantages mentioned above. Not being able to benefit from the technology available to make their work easier, faster and even much more efficient was naturally a major upset to his team

A simple but brilliant idea

Then Jonas Binladen, a PhD student from his team, came up with a simple but brilliant idea: By putting a 'finger-print' attached to the fishing hooks (tagged primers) used to amplify DNA from each sample, one should in theory be able to localize each of the million sequences produced in each run, to its original sample or specimen. By making it possible to process amplification products from multiple samples or specimens in the same run, the team could make use of the machine's great capacity.

The research team now wanted to test the idea. And it really did work! Amplification product marked with a particular tag during the traditional amplification step where dispatched to the centre in Foulum for a run on their 454 machine. When receiving the great news, Jonas Binladen remembers: "I was extremely happy, but actually not that surprised. I was in a way certain, that it would work out".

The results are now being published in the scientific web magazine *PLoS ONE* Publication.

According to Eske Willerslev, the new approach discovered by the team at the Centre for Ancient Genetics have great scientific potentials:

"Today, when using conventional methods to detect ancient DNA, we are only able to carry out a limited number of samples providing us with a somewhat random image of life in the past. This new approach helps us to give more complete and accurate performances in research. By combining information about the species of animals with the vegetation of the area, we are able to find out more about the climate and the ecosystem through different periods of time and see the changes. As a result, our knowledge will be put into a whole new perspective. For instance, finding out if species became endangered due to a dramatic change in the climate or if the decline in numbers started many years earlier than we originally thought or estimated," he says.

Eske Willerslev also hopes to find answers to the many mysteries of nature in ancient times.

Source: University of Copenhagen

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