

93101Q





QUALIFY FOR THE FUTURE WORLD KIA NOHO TAKATŪ KI TŌ ĀMUA AO!

Scholarship 2015 Biology

9.30 a.m. Tuesday 10 November 2015 Time allowed: Three hours Total marks: 24

QUESTION BOOKLET

There are THREE questions in this booklet. Answer ALL questions.

Write your answers in Answer Booklet 93101A.

Start your answer to each question on a new page. Carefully number each question.

Check that this booklet has pages 2–7 in the correct order and that none of these pages is blank.

YOU MAY KEEP THIS BOOKLET AT THE END OF THE EXAMINATION.

QUESTION ONE: MOA A GOER?

Extinction is part of the evolutionary life cycle of a species. Researchers have calculated that the natural rate of extinction in the past was about 0.1 species per year per million species. However, the extinction rate today has been calculated as being between 100 and 1000 species per year per million species. The New Zealand moa became extinct about 600 years ago. Moa were endemic flightless birds found throughout New Zealand, inhabiting forests, shrublands, and grasslands from coastal to subalpine regions. Moa would have been the dominant herbivores within New Zealand's ecosystems. At least nine species have been identified, which display a wide range of size.



www.TeAra.govt.nz/en/diagram/11364/moa-diversity

Trevor Mallard, the Member of Parliament for Wainuiomata, caused controversy in July 2014 when he expressed a desire to see moa again roaming through the Rimutaka Forest Park, near Wellington. Mr Mallard was quoted as saying, 'I'm absolutely certain that at some point in the future, a whole pile of species that are currently extinct will be brought back to life ("de-extinction") ... the moa will be a goer but we're talking 50 - 100 years out.' He did not want a 240 kg, 3.5 m moa roaming the forest but a small one that 'don't weigh much more than turkeys ... ones that I could pat on the head rather than ones that are going to bowl us over ...' For copyright reasons, this resource cannot be reproduced here.

Adapted from: www.google.co.nz/maps

Question

Analyse the information provided in the resource material and integrate it with your biological knowledge to discuss:

- the evolutionary and ecological factors that contribute to declining population numbers that may result in the extinction of species AND account for the very large increase in the rate of extinction of species in modern times. Use named examples to support your discussion
- how humans could manipulate the transfer of moa DNA to restore a moa population to the Rimutaka Forest Park AND analyse the biological implications of this. Give your justified opinion on whether the 'moa is a goer'.

QUESTION TWO: HUMAN DISPERSAL

Evidence from the fossil record and DNA analysis indicates that there were three distinct groups of hominins living in Eurasia about 50000 years ago. Genome analysis indicates that some degree of interbreeding occurred between the groups as shown in the figure below.





Adapted from http://newscenter.berkeley.edu/wp-content/uploads/2013/12/earlyhumans400.jpg

The genome of *Homo sapiens* contains a gene known as EPAS1 which regulates the production of haemoglobin, the oxygen transporting molecule in red blood cells. When oxygen levels in the blood drop, EPAS1 is switched on, resulting in the increased production of haemoglobin.

Air at high altitudes has much less oxygen per unit volume than air at sea level. This makes it harder for humans to breathe and so oxygenate the blood. The common variants of the EPAS1 gene that are found in most human populations mean that when people move from sea level to high altitudes, their bodies overproduce haemoglobin. More red blood cells are produced which thicken the blood, resulting in problems such as hypertension, increased risk of strokes and heart attacks, difficulty in conceiving, low birth weight, and increased mortality.

Recent genome analysis has identified a rare variant of the EPAS1 gene. This variant is found in a significant frequency in only two modern human populations – Tibetans and Han Chinese. (Han Chinese are the oldest ethnic group in China.) The rare variant has also been identified in a few Mongolians and Nepalese Sherpas. It has not been found in any modern human populations outside East Asia, including those that live at high altitude.



Location of Tibetan Plateau and Altai Mountains

http://tibettruth.files.wordpress.com/2010/01/themap1.gif?w=646

Tibetan people live permanently at altitudes of about 4000 m on the Tibetan Plateau, where the air has about 40% less oxygen than at sea level. Researchers have found that 87% of the Tibetan population have the rare variant of EPAS1. These individuals do not overproduce haemoglobin and red blood cells at high altitudes so do not experience thickened blood and the resultant problems. The variant has spread rapidly through the Tibetan population. In addition, 9% of the Han Chinese who live in lowland China also have the variant.

The rare variant of the EPAS1 gene has also been found in the genome of the long extinct Denisovans, a group of hominins that lived in the Altai Mountains in east-central Asia approximately 80 000 to 40 000 years ago.

Question

Analyse the information provided in the resource material and integrate it with your biological knowledge to account for the presence AND distribution of the rare variant of the EPAS1 gene in modern human populations.

QUESTION THREE: HAWAIIAN HONEYCREEPERS

The Hawaiian Islands are a very young group of islands in the Pacific Ocean and are the most isolated island group in the world. The group comprises four main islands (Kaua'i, O'ahu, Maui, and Hawai'i) and several other smaller islands. They are all volcanic in origin and formed from erupting magma as the Earth's crust moved over a hotspot. The oldest of the main islands is Kaua'i, which formed about 5 million years ago (mya). The newest is Hawai'i, which formed less than 1 mya.



http://earthsky.org/earth/the-march-2011-tsunami-toll-on-wildlife-at-the-midway-atoll

The Hawaiian honeycreepers (also known as Hawaiian finches) are birds that are endemic to the Hawaiian Islands. At least 56 species of honeycreepers are known to have existed, of which 18 (possibly 19 as the Poouli has not been seen since 2004, but has not yet been classified as extinct) have survived to the present day. There is great phenotypic diversity between the species, especially in body colour, and size and shape of the beak.

Some of the diversity in colour and beaks between different species of honeycreeper is shown below:

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Akialoa (extinct)

Akiapolaau

Maui parrotbill

Maui creeper

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Poouli

DNA analysis has indicated the Hawaiian Islands were colonised by a common ancestor of both rosefinches (*Carpodacus* sp.) and Hawaiian honeycreepers (*Drepanidinae* sp.) that arrived from Asia between 7 and 5 mya. Subsequent rapid evolution occurred, resulting in many species of Hawaiian honeycreepers occupying a wide variety of ecological niches on the various islands.

The diagram below is a phylogenetic tree of the living species of honeycreeper (and the common rosefinch).

- The grey circles indicate which of the four main islands each species is found on. In addition to this the Nihoa finch is found only on Nihoa Island, while the Laysan finch is found only on Laysan Island.
- The width of the vertical arrows indicates the time of formation of the named islands.

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Adapted from: http://nationalzoo.si.edu/SCBI/CCEG/news/LernerHoneycreeperRadiationCurrBiol2011.pdf

Question

Analyse the information provided in the resource material and integrate it with your biological knowledge to discuss the evolutionary processes that have resulted in the distribution and diversity of honeycreepers on the Hawaiian Islands.

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