

93101Q



NEW ZEALAND QUALIFICATIONS AUTHORITY
MANA TOHU MĀTAURANGA O AOTEAROA

Scholarship 2014 Biology

2.00 pm Tuesday 18 November 2014
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 2–6 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: BULLDOGS

There are over 200 breeds of domesticated dog, *Canis lupus familiaris*, which are all descended from the grey wolf, *Canis lupus*. All domesticated dogs and the grey wolf have 78 chromosomes and will produce fertile offspring if they interbreed, which has not been known to happen in the wild. Dogs were domesticated from wolves, possibly as early as 30 000 years ago.

Over thousands of years, humans have selectively bred all the breeds known today from a small population of original dogs. While some breeds were developed hundreds, or even thousands of years ago, most breeds have been developed only in the last 100 years. One of the older breeds is the British bulldog, which was first recorded in 1500.

The bulldog was originally used to drive cattle. They were also used to subdue animals by latching onto them at their snout and pinning them to the ground by the force of their powerful bite. To be able to do this, the bulldog needed to be very ferocious and almost insensitive to pain. This practice was then developed into a 'sport' known as bull-baiting. A bulldog and a bull were placed together in a small enclosure and the bulldog would try and subdue the bull, which would defend itself with its horns mainly by trying to toss the bulldog out of the enclosure. Bull-baiting was outlawed in 1835.

By 1860 bulldogs began appearing in dog shows. Bulldogs, like all breeds, have a breed standard that specifies the phenotypic features they are judged against. For the bulldog these include:

- thick-set, low in stature, but broad and powerful, with stout muscular legs
- face extremely short with the skin deeply and closely wrinkled; muzzle very broad, blunt and inclined upwards
- a passive, non-aggressive temperament.

Today bulldogs are found as gentle family pets. While the bulldog has been bred for its phenotypic features, this breeding has also resulted in an increased incidence or predisposition to certain inherited disorders. These include:

- Brachycephalic syndrome (BS) – respiratory difficulties due to obstruction of their airways. This is caused by a face that has a very short distance between the tip of the nose and where it is set deep between the eyes.
- Hip dysplasia – occurs when the 'ball' at the top of the femur is not held firmly into the 'socket' of the pelvis and slides part way out. This disorder is a result of polygenic inheritance (caused by many different genes).



Grey wolf.

<http://jon-atkinson.com/Large%20Images%201/Grey%20Wolf%203.jpg>



Bulldog.

<http://animalkingdomz00.com/images/bulldog-10.jpg>

- Ventricular septal defect (VSD) – occurs when there is a hole in the muscular wall of the heart (the septum) that separates the right and left ventricles. Inheritance is autosomal recessive.
- Cryptorchidism – occurs when one or both of a dog's testicles have not descended into the scrotum. It is an autosomal dominant trait.
- Dermatitis – occurs when there is inflammation of the skin due to excessive skin folds or wrinkles which rub and trap moisture in the folds, and which commonly lead to bacterial infections. Wrinkling is considered to be an autosomal dominant trait.

It would be desirable if these disorders could be eliminated while still maintaining the bulldog standard.

Question

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

- how humans may have manipulated the evolution of bulldogs from wolves
- how further selective breeding could be used to try to eliminate EACH of the named disorders AND evaluate how effective this might be.

QUESTION TWO: NORTH ISLAND WETA

Weta are flightless, nocturnal insects. Their abdomen has stridulatory ridges that are used to make sounds. There are over 70 species of weta endemic to New Zealand, found in a wide range of habitats.

Recent analysis of mitochondrial DNA supports the hypothesis that New Zealand weta have been genetically isolated from Australian weta for more than 82 million years. Mitochondrial DNA also suggests that many new species have arisen in New Zealand since that time.

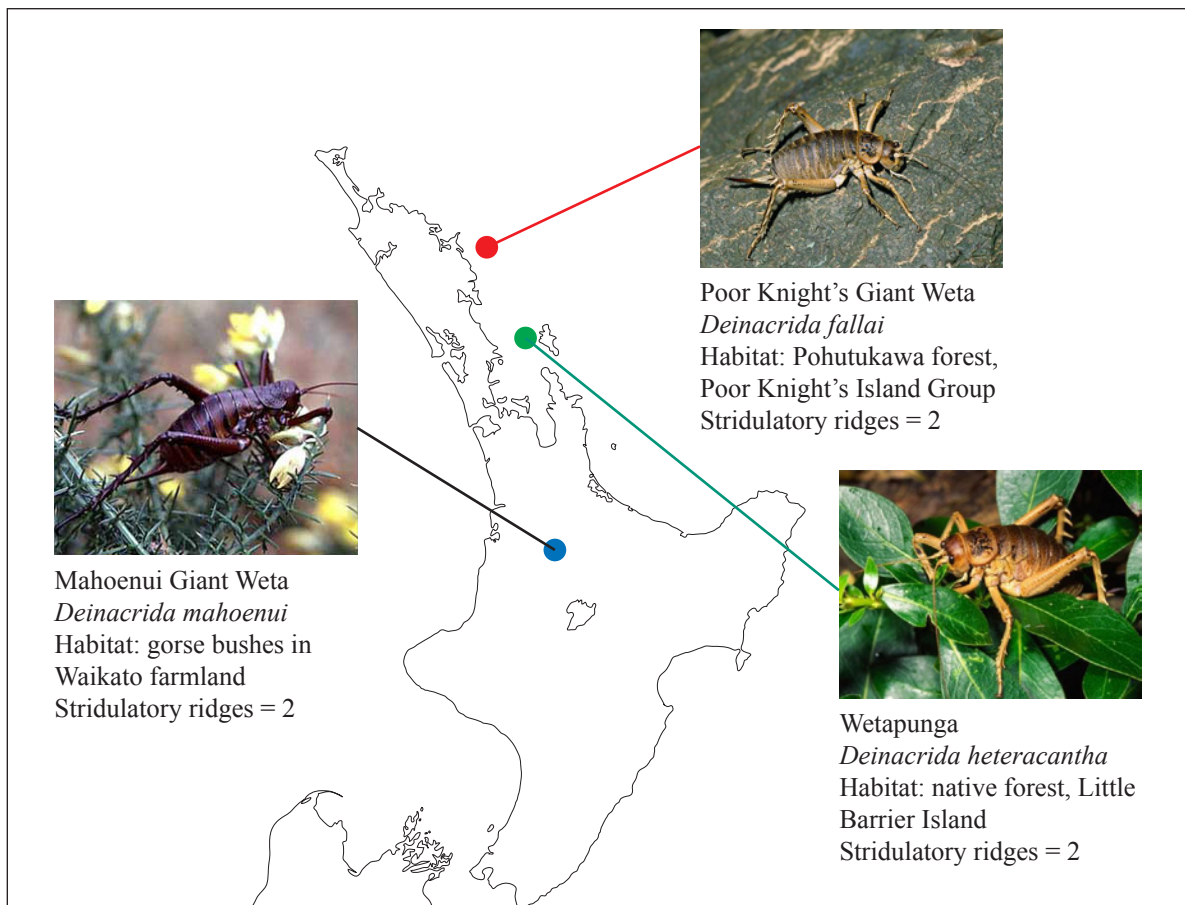
Two of the groups of New Zealand weta are:

- tree weta (genus: *Hemideina*, 7 species)
- giant weta (genus: *Deinacrida*, 11 species).

Tree weta and giant weta likely shared a common ancestor between two and five million years ago.

Giant weta are thought to have once been widespread throughout the North Island, but now only three species remain, existing as isolated populations. *Deinacrida fallai* and *D. heteracantha* are found in lowland forest, while *D. mahoenui* was believed to be extinct, but a remnant population has been found surviving in gorse bushes on farmland.

Deinacrida distribution



Map showing the main populations of the three giant weta species in the North Island.

<http://cdn1.arkive.org/media/7F/7F7EE67C-A26D-4A12-BCA0-C9366C608408/Presentation.Large/Poor-Knights-weta.jpg>

<http://1.bp.blogspot.com/-rG19rm7A7Ig/Tu5YVCBsrAI/AAAAAAAAAMBc/fGEPqdHJgsw/s1600/Deinacrida%2Bheteracantha04.jpg>

http://cfs2.tistory.com/upload_control/download.blog?fhandle=YmxvZzgwMzMxQGZzMj50aXN0b3J5LmNvbTovYXR0YWN0LzAvMDUwMDAwMDAwMDA2LmpwZw%3D%3

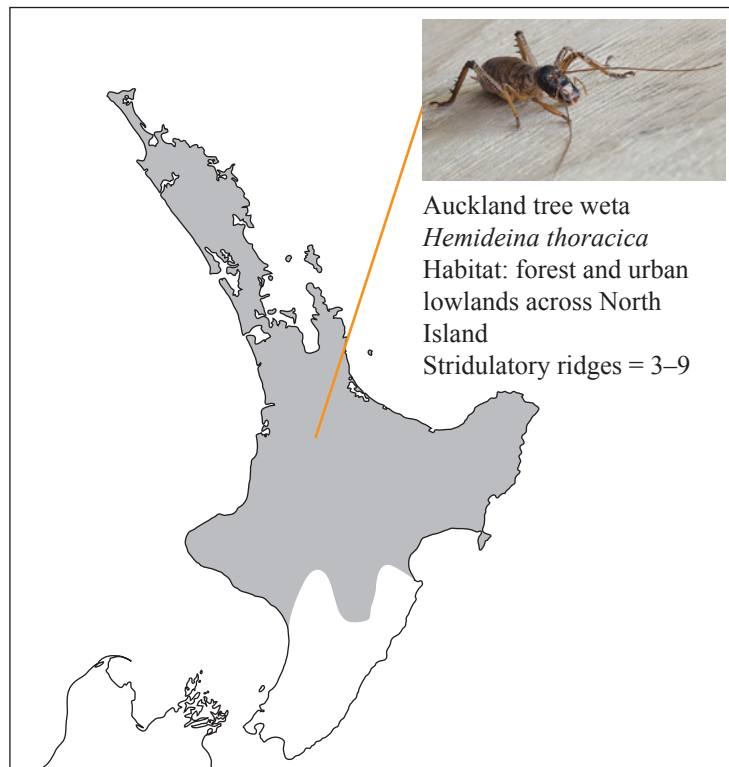
These three species are the largest of the giant weta species, with females being significantly larger than the males. They are often found at night, eating the tender new leaves and fruit of a wide variety of plants, or depositing eggs on the forest floor. They move relatively slowly, cannot jump, and when disturbed they 'freeze', making them easy to pick up. During the day, giant weta sit very still under tree leaves or loose bark.

Giant weta are usually observed alone, or else with a single male close by a female; the male is thought to be attracted to the female by pheromones. It is not clear if stridulatory sounds are important in giant weta mating. *D. mahoenui* have been seen mating during the day on a gorse bush, tightly locked together for four hours and moving sluggishly afterwards.

There is little genetic variation within the *Deinacrida* genus.

Unlike giant weta, tree weta have flourished in New Zealand. The Auckland tree weta, *Hemideina thoracica*, is abundant and distributed throughout most of the North Island. *H. thoracica* inhabits lowland forests, including urban gardens.

***Hemideina thoracica* distribution**



http://farm7.staticflickr.com/6099/6294575874_de0d4d0684_z.jpg

Males have a distinctively dark, enlarged head with powerful jaws. These weta react aggressively if threatened, raising their spiked legs over their head and opening their jaws. Their bite is painful and they can jump considerable distances. Tree weta spend the day hidden in holes (burrows) in tree trunks. They emerge at night to feed on lichens, leaves and fruit.

At the end of spring, males attract multiple females to their burrow, possibly through a mixture of pheromones and mating sounds made by rubbing their back legs against the stridulatory ridges on their abdomen. Males have been seen defending their 'harem' of females aggressively from other males. Mating occurs throughout early summer, and up to 300 eggs per female are deposited in the ground.

There is a large degree of genetic variation within the *Hemideina thoracica* species.

Question

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

- the evolutionary patterns and processes that have resulted in the two groups of New Zealand giant weta and tree weta, each with many different species
- why the Auckland tree weta has a widespread distribution while the three species of North Island giant weta exist only as small isolated populations.

QUESTION THREE: DNA ANALYSIS IN HUMAN EVOLUTION

Since the successful sequencing of human DNA in the Human Genome Project (HGP) in 2003, genome analysis, using both nuclear DNA and mitochondrial DNA, has become a standard research tool. This is providing valuable evidence for the evolution of *Homo sapiens*. The most accepted hypothesis is that *H. sapiens* emerged in Africa about 200 000 years ago and subsequently dispersed throughout Europe, Asia, and then the rest of the world.

Since 2003, the genomes of chimpanzees, gorillas, Neanderthals, and Denisovans have all been sequenced and can be compared to that of *H. sapiens* living today. Comparisons indicate that many mutations have occurred within our genome in both the coding and non-coding regions of DNA. Some non-coding regions of DNA act as the switches that turn genes on and off, therefore determining which genes are expressed. To date, several hundred mutations have been identified that are likely to have had a significant effect on the evolution of *H. sapiens*. These include:

- A mutation in the MYH16 gene, which resulted in the weakening of jaw muscles. A decrease in the muscle mass resulted in a decrease in the bone mass, allowing for skull expansion. The mutation occurred at least 2.4 mya.
- The SRGAP2 gene has duplicated twice, first about 3.4 mya and again about 2.4 mya. This gene causes neurons in the developing brain of embryos to form connections to neighbouring neurons. Individuals with the duplicated versions of the gene have neurons which can extend further distances and make new connections with other neurons. This occurs in the regions of the brain that control language, communication, abstract thought, and memory.
- The FOXP2 gene is active in our brain during embryonic development. Mutation(s) in the FOXP2 gene occurred in our evolution, resulting in two different amino acids in the protein coded for, compared to the same protein in chimpanzees. We share this variant of the gene with both Neanderthals and Denisovans. The latest research indicates that this variant is important in learning that specific vocal movements generate certain sounds – and possibly even how to sequence sounds into an understandable sentence.
- Compared to chimpanzees and gorillas, humans have slightly different switches for two genes that code for the glucose transporters in the membranes of cells in the brain and muscle tissue respectively. Mutations in these switches have resulted in more glucose transporters in our brain tissue and less in our muscle tissue.
- The HACNS1 region of DNA has undergone 16 mutations since the hominin and hominid lines diverged. This region is associated with switching on genes that are associated with limb development in the embryo, in particular the wrist and thumb in humans.
- Chimpanzees have two copies of the gene that codes for the production of salivary amylase, which has a key role in the digestion of starch into simple sugars. In human evolution this gene has repeatedly duplicated, so that present day humans have on average six copies of the gene, with some individuals having as many as fifteen copies. These duplications are likely to have occurred within the last 100 000 years.

Question

Analyse the information provided in the resource material and integrate it with your biological knowledge to discuss how these mutations have contributed to the biological AND cultural evolution of *H. sapiens*.

