# 1.4 Genetic Information, Variation and Relationships: 1-hour Pack

Total Marks

AQA 7402 · Calculator allowed · about 60 minutes

Name: _____ Date: ____ / ____ / _____

**Answer ALL questions. Show all your working.**

**1** This question is about meiosis and genetic variation.

**(a)** State the number of chromosomes present in a human somatic (body) cell and in a human gamete. **(2)**

**(b)** Describe how independent assortment during meiosis I contributes to genetic variation. **(3)**

**(c)** Calculate the number of genetically different gamete combinations (due to independent assortment alone) that can be produced by a species with a diploid number of 8. **(2)**

**(d)** Explain how crossing over during prophase I further increases genetic variation, beyond that produced by independent assortment alone. **(3)**

**(Total for Question 1 is 10 marks)**


© Revision Library | revisionlibrary.co.uk

**2** A group of students investigated the biodiversity of a rocky shore habitat using a 0.25 $m^2$ quadrat placed at 10 random points along a 20 m transect. They counted the number of individuals of each species present. Their results are shown below.

Species A (limpet): 24 individuals

Species B (barnacle): 56 individuals

Species C (dog whelk): 8 individuals

Species D (periwinkle): 12 individuals

Total (N) = 100 individuals

| Species | Number of individuals |
|---|---|
| Species A (limpet) | 24 |
| Species B (barnacle) | 56 |
| Species C (dog whelk) | 8 |
| Species D (periwinkle) | 12 |
| Total (N) | 100 |

**(a)** Describe how the students could have used random sampling to choose the position of each quadrat along the transect, ensuring their method avoided bias. **(3)**

**(b)** Simpson's Index of Diversity can be calculated using the formula: **(4)**

$D = 1 - [ \text{sum}( n/N )^2 ]$

where n = number of individuals of one species and N = total number of individuals of all species.

Calculate the Index of Diversity, D, for this habitat using the data given. Give your answer to 3 significant figures.

**(c)** A second, more disturbed area of the same shore was found to have an Index of Diversity of 0.31. Using this value and your answer to part (b), explain which of the two areas has the higher biodiversity and suggest one possible reason for the difference. **(3)**


© Revision Library | revisionlibrary.co.uk

**(d)** State two variables, other than species number and abundance, that the students should have kept the same when comparing the two areas to make the comparison valid. **(2)**

**(Total for Question 2 is 12 marks)**

---

**3** This question is about species, taxonomy and evidence of evolutionary relationships.

**(a)** The taxonomic hierarchy used to classify organisms, from largest to smallest group, is: Domain, Kingdom, ___, Class, Order, Family, Genus, Species. Name the missing group. **(1)**

**(b)** State the biological definition of a species. **(2)**

**(c)** Explain why courtship behaviour between two organisms is used as evidence that they belong to the same species. **(3)**

**(d)** Scientists compare the base sequence of a specific gene (for example, the gene coding for cytochrome c) in different species to assess how closely related they are. Explain how the number of differences in the base sequence between two species can be used to determine how recently they diverged from a common ancestor. **(3)**

**(Total for Question 3 is 9 marks)**


© Revision Library | revisionlibrary.co.uk

**4** In a population of 500 ladybirds, a single gene controls wing case colour, with allele M (melanic/black) dominant to allele m (red). Genotyping of the population gave the following results: MM = 20, Mm = 160, mm = 320.

**(a)** Define the term 'gene pool'. **(1)**

**(b)** Calculate the frequency of the m allele in this population. **(3)**

**(c)** Suggest and explain one factor, other than mutation, that could reduce the genetic diversity of this ladybird population in the future. **(3)**

**(d)** Explain why natural selection acting on this population could not occur without genetic diversity. **(2)**

**(Total for Question 4 is 9 marks)**

---

**5** Molecular phylogenetics and molecular clock. Two species X and Y have mitochondrial gene sequences that differ by 120 nucleotide substitutions over a 1500 base gene. If the neutral substitution rate for this gene is estimated at $1.5 \times 10^{-8}$ substitutions per site per year per lineage, estimate the time since the two species diverged in millions of years. Show working and give answer to two significant figures. Assume a molecular clock with two independent lineages accumulating substitutions.

**(a)** Write the equation relating total substitutions $S = 2 \mu t L$ where $\mu$ is rate per site per year per lineage, L is sequence length and t is divergence time in years. Rearrange to give t. **(2)**

**(b)** Calculate t in millions of years using $S = 120$, $\mu = 1.5 \times 10^{-8}$, $L = 1500$. Give answer to two significant figures. **(6)**

**(Total for Question 5 is 8 marks)**


© Revision Library | revisionlibrary.co.uk

# Mark scheme · 1.4 Genetic Information, Variation and Relationships: 1-hour Pack

## Question 1

(a) 46 (23 pairs) in a somatic cell **B1**

(a) 23 in a gamete **B1**

**(a) Answer: 46 in a somatic cell; 23 in a gamete.**

(b) homologous pairs of chromosomes line up in a random orientation at the equator during metaphase I **B1**

(b) each pair consists of one maternal and one paternal chromosome, and either can end up in either daughter cell independently of how other pairs orientate **B1**

(b) this creates many different possible combinations of maternal and paternal chromosomes in the resulting gametes **B1**

**(b) Answer: Random orientation of homologous pairs at metaphase I produces many chromosome combinations in gametes.**

(c) haploid number n = 8 / 2 = 4 **M1**

(c) $2^4$ = 16 cao **A1**

**(c) Answer: 16 different gamete combinations**

(d) non-sister chromatids of homologous chromosomes pair up (forming a bivalent) and become twisted around each other at points called chiasmata **B1**

(d) sections of chromatids (alleles) are exchanged/swapped between the non-sister chromatids **B1**

(d) this produces new/recombinant combinations of alleles on a chromosome not present in either parent, increasing variation beyond that from independent assortment alone (which only shuffles whole chromosomes) **B1**

**(d) Answer: Crossing over exchanges sections between non-sister chromatids, creating new allele combinations on chromosomes.**

## Question 2

(a) divide the transect into a numbered grid/sections (using a tape measure marked at regular intervals) **B1**

(a) use a random number generator/table to generate coordinate or position numbers **B1**

(a) place the quadrat at the positions given by the random numbers, rather than the students choosing where to place it, avoiding the students unconsciously selecting areas with more or fewer visible organisms **B1**

**(a) Answer: Number the transect, generate random positions, place quadrats only at those positions.**

(b) calculates n/N for each species (0.24, 0.56, 0.08, 0.12) **M1**

(b) squares each proportion and sums them: 0.0576 + 0.3136 + 0.0064 + 0.0144 = 0.392 **M1**

(b) subtracts sum from 1: D = 1 - 0.392 **dM1**

(b) D = 0.608 (3 sf) cao **A1**

**(b) Answer: D = 0.608**

(c) ft the first area (D = 0.608, or candidate's value from (b)) has the higher biodiversity, because a value of D closer to 1 indicates greater species diversity/a more even distribution of species **B1**

(c) a valid suggested reason, e.g. the disturbed area may have been affected by trampling/pollution, or a dominant coloniser species may be outcompeting others, reducing the number of species or making one species very dominant **B1**

(c) further valid development, e.g. lower diversity reduces the community's stability/resilience to further environmental change **B1**

**(c) Answer: The first area has higher biodiversity (D closer to 1); disturbance likely reduced species evenness/richness in the second area.**

(d) quadrat size (area sampled) **B1**

(d) number of sample points/quadrats used (sampling effort); accept time of year, tide height or time spent searching **B1**

**(d) Answer: Quadrat size and number of samples (accept time of year/tide height).**


© Revision Library | revisionlibrary.co.uk

## Question 3

(a) Phylum **B1**

**(a) Answer: Phylum**

(b) a group of organisms with similar characteristics/morphology (and genetics) **B1**

(b) that can interbreed to produce fertile offspring **B1**

**(b) Answer: A group of similar organisms able to interbreed and produce fertile offspring.**

(c) courtship behaviour is species-specific: it involves a stereotyped, recognisable sequence of behaviours unique to a species **B1**

(c) if two organisms recognise and respond correctly to each other's courtship behaviour (and successfully mate), this suggests they are of the same species (able to interbreed) **B1**

(c) courtship behaviour also ensures individuals identify a mate of the correct species, preventing hybridisation or wasted reproductive effort **B1**

**(c) Answer: Courtship behaviour is species-specific, so mutual recognition indicates the organisms are the same, interbreeding species.**

(d) the fewer the differences in the DNA base sequence (or the amino acid sequence of the coded protein) between two species, the more closely related they are **B1**

(d) mutations accumulate in DNA over time at a roughly constant/measurable rate, so more differences indicate a greater length of time since the two species diverged from a common ancestor **B1**

(d) this evidence can be used to construct or confirm phylogenetic trees showing evolutionary relationships, supporting or independent of evidence from physical characteristics **B1**

**(d) Answer: More sequence differences indicate more time (and mutations) since divergence, allowing construction of phylogenetic trees.**

## Question 4

(a) all the alleles of all the genes present in a population at a given time **B1**

**(a) Answer: The complete set of alleles present in a population at a given time.**

(b) total number of alleles = 500 x 2 = 1000 **M1**

(b) number of m alleles = (320 x 2) + (160 x 1) = 800 **M1**

(b) frequency = 800 / 1000 = 0.8 cao **A1**

**(b) Answer: Allele frequency of m = 0.8 (80%)**

(c) identifies a valid factor, e.g. a genetic bottleneck (a dramatic reduction in population size, due to disease or habitat loss) or a founder effect (a small number of individuals colonising a new isolated habitat) **B1**

(c) explains that only a small, potentially non-representative, sample of the alleles present in the original gene pool would survive/be passed on **B1**

(c) so some alleles may be lost completely (allele frequencies change), reducing overall genetic diversity and increasing the risk of extinction/reducing the ability to adapt to future environmental change **B1**

**(c) Answer: A genetic bottleneck or founder effect would reduce diversity because only a small, unrepresentative sample of alleles would survive/found the new population.**

(d) natural selection depends on differences (variation) between individuals in their alleles/phenotypes, giving some individuals a selective (survival/reproductive) advantage over others in a given environment **B1**

(d) without genetic diversity, all individuals would be genetically identical/equally suited (or unsuited) to the environment, so there would be nothing for selection pressures to act on and allele frequencies could not change over time **B1**

**(d) Answer: Without variation there is no differential survival/reproduction for selection to act on, so allele frequencies cannot change.**

## Question 5

(a) state S = 2 μ L t or equivalent **M1**

(a) rearrange t = S / (2 μ L) cao **A1**

**(a) Answer: t = S / (2 μ L)**

(b) substitute values: $t = 120 / (2 \times 1.5 \times 10^{-8} \times 1500)$ **M1**

(b) compute denominator: $2 \times 1.5 \times 10^{-8} \times 1500 = 4.5 \times 10^{-5}$ **M1**

(b) compute $t = 120 / 4.5 \times 10^{-5} = 2.666... \times 10^{6}$ years **M1**

(b) convert to millions of years = $2.67 \times 10^{0}$ Myr **M1**

(b) round to two significant figures **M1**

(b) 2.7 million years cao **A1**

**(b) Answer: 2.7 million years**


© Revision Library | revisionlibrary.co.uk