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ASSESSMENT and QUALIFICATIONS ALLIANCE

General Certificate of Education

Biology 5416
Specification B

BYB2 Genes and genetic Engineering

Mark Scheme

2006 examination – June series

Mark schemes are prepared by the Principal Examiner and considered, together with the relevant questions, by a panel of subject teachers. This mark scheme includes any amendments made at the standardisation meeting attended by all examiners and is the scheme which was used by them in this examination. The standardisation meeting ensures that the mark scheme covers the candidates' responses to questions and that every examiner understands and applies it in the same correct way. As preparation for the standardisation meeting each examiner analyses a number of candidates' scripts: alternative answers not already covered by the mark scheme are discussed at the meeting and legislated for. If, after this meeting, examiners encounter unusual answers which have not been discussed at the meeting they are required to refer these to the Principal Examiner.

It must be stressed that a mark scheme is a working document, in many cases further developed and expanded on the basis of candidates' reactions to a particular paper. Assumptions about future mark schemes on the basis of one year's document should be avoided; whilst the guiding principles of assessment remain constant, details will change, depending on the content of a particular examination paper.

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General Guidance for the Mark Scheme

The following conventions are used in the mark scheme:

- A semicolon (;) separates each mark point
- An oblique stroke (/) separates alternatives within a mark point
- Underlining of a word or phrase means that the term must be used by candidates
- Brackets are used to indicate contexts for which a mark point is valid, but which may just be implied by a candidate's answer
- '*Accept*' and '*reject*' show answers which should be allowed or not allowed.
- Additional instructions may be shown in *italics*

The scheme shows the minimum acceptable answer(s) for each mark point - better, more detailed, or more advanced answers are always accepted, provided that they cover the same key ideas. Occasionally, a candidate will give a biologically correct answer that has not come up at standardising. If it is equivalent in standard to the mark scheme answers, it may be credited.

In some cases a mark may be awarded for understanding of a general principle, even though the detailed mark points on the scheme have not been made. This will be indicated on the mark scheme.

All mark points are awarded independently, unless a link between points is specified in the scheme.

Converse answers are normally acceptable, unless the wording of the question rules this out.

Disqualifiers

A correct point is disqualified when the candidate contradicts it in the same answer.

The list rule

When a question asks for a specific number of points, and the candidate gives more, any wrong answer cancels a correct answer. For example, if a question asks for two points and three answers are given, two correct and one clearly wrong, the mark awarded is one, whatever the order of the answers.

Valid points from **diagrams** are credited, if they are not duplicated in the text.

Where a question asks for **differences** between X and Y, the mark may be awarded for a feature of X without the converse for Y, if it is absolutely clear which is being referred to.

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BYB2 Genes and Genetic Engineering

Question 1

(a) produced by mitosis;
genetically identical; 2
(accept identical genes/ same genotype/DNA/genetic information)
(reject same genes, same genetic code)

(b) cells lost ability to control development / no longer totipotent /
cells have differentiated/become specialised; 1

(c) (many) offspring with favourable characteristics / high meat/milk yield;
pedigree embryos into non-pedigree mothers / not risking pedigree mothers / rare breeds conserved;
sex/gender selection; 2 max

Total 5

Question 2

(a) (i) (D) B E A C; 1

(ii) metaphase; 1

(b) interphase/S phase; 1

(c) (i) 0.06 x 100;
6(%); 2
(correct answer 2 marks)

(ii) more (cancer cells) killed, cancer cells divide more (often) (so are more likely to be killed, more susceptible); 1

(iii) longer time to recover;
reduced rate of mitosis / divide more slowly/increased doubling time; 2

Total 8

Question 3

(a) (i) join/attach nucleotides, to form a strand/along backbone/ phosphodiester bonds; 1
(*reject reference to H bonds, complementary base pairing)*

(ii) ribosome/RER; 1

(b) (i) CGTTACCAA; 1

(ii) CGU UAC CAA; 1

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(c) substitution; 1

(d) (i) alanine; 1

(ii) (mutation 1)
no change (to sequence of amino acids);
codon for alanine/degenerate codon/same amino acid coded for; 2

(mutation 2)
(change in sequence) valine replaced by alanine/codon for alanine;
folding/shape/tertiary structure/position of bonds may change; 2
(*reject peptide bonds)*

Total 10

Question 4

(a) each strand copied/acts as a template;
(daughter) DNA one new strand and one original/parent strand; 2

(b) (i) ^{15}N/ tube **B** (DNA), more/greater density;
(reject heavier) 1

(ii) DNA with one heavy and one light strand;
new/synthesised strand, made with ^{14}N/ light strand; 2

(c) 32;
28 32 26; 2

Total 7

Question 5

(a) haploid cells produced/halves chromosome number;
fertilisation/fusion of gametes, diploid number restored;
chromosome number constant at each generation; 2 max

(b) principle of 2 chromosomes per cell;
4 correct combinations, long with short; 2

(c) (i) 8;

(ii) 8; 2

(d) (in males) more gametes produced / rapid gamete production / more lost; 1

Total 7

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Question 6

(a)	(i)	transfer/carry genes from one organism to another/into bacteria/cells;	1
	(ii)	cut open plasmid; cut donor DNA, to remove gene/length of DNA; cut donor DNA and plasmid with the same enzyme/enzyme that cuts at the same base sequence; sticky ends/(overhanging) ends with, single strand/bases exposed; association/attachment/pairing of complementary strand;	2 max
	(iii)	annealing/splicing/backbones joined/phosphodiester bonds;	1
(b)	(i)	L and M;	1
	(ii)	fragments 64 and 36 (kilobases obtained)	1
			Total 6

Question 7

(a)	1.	DNA heated to 90 to 95°C;	
	2.	strands separate;	
	3.	cooled / to temperature below 70°C	
	4.	primers bind;	
	5.	nucleotides attach;	
	6.	by complementary base pairing;	
	7.	temperature 70 - 75°C;	
	8.	DNA polymerase joins nucleotides together;	
	9.	cycle repeated;	6 max
(b)	1.	percentage risk is too high for human application;	
	2.	incorrect mRNA;	
	3.	different tRNA/tRNA brings incorrect amino acid;	
	4.	structure of protein synthesised unknown/sequence of amino acids changed/ incorrect shape/folding of polypeptide changed;	
	5.	produce a toxic/harmful protein;	
	6.	protein non-functional / chloride ions not transported / thick mucus results;	4 max
			Total 10
			QWC 1

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