

## **MARK SCHEME for the May/June 2014 series**

### **9700 BIOLOGY**

**9700/52**

Paper 5 (Planning, Analysis and Evaluation),  
maximum raw mark 30

This mark scheme is published as an aid to teachers and candidates, to indicate the requirements of the examination. It shows the basis on which Examiners were instructed to award marks. It does not indicate the details of the discussions that took place at an Examiners' meeting before marking began, which would have considered the acceptability of alternative answers.

Mark schemes should be read in conjunction with the question paper and the Principal Examiner Report for Teachers.

Cambridge will not enter into discussions about these mark schemes.

Cambridge is publishing the mark schemes for the May/June 2014 series for most IGCSE, GCE Advanced Level and Advanced Subsidiary Level components and some Ordinary Level components.

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Mark scheme abbreviations:

<b>;</b>	separates marking points
<b>/</b>	alternatives answers for the same point
<b>R</b>	reject
<b>A</b>	accept (for answers correctly cued by the question, or extra guidance)
<b>AW</b>	alternative wording (where responses vary more than usual)
<b><u>underline</u></b>	actual word given must be used by candidate (grammatical variants accepted)
<b>max</b>	indicates the maximum number of marks that can be given
<b>ora</b>	or reverse argument
<b>ecf</b>	error carried forward
<b>I</b>	ignore
<b>mp</b>	marking point (with relevant number)

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Question	Expected answer	Extra guidance	
1 (a) (i)	<i>idea that the detergent disrupts (named) <u>membranes</u> / <u>phospholipids</u> (and proteins) ;</i>	<b>A</b> make membrane permeable / destroys membrane <b>R</b> enzymes in detergent disrupt membrane <b>I</b> other feature of seeds included, e.g. testa / seed coat, etc. / cell walls / ref. to pH or alkaline	[1]
(ii)	<i>idea of inhibiting / denaturing <u>enzymes</u> ;</i>	<b>A</b> stops enzyme activity <b>I</b> denaturing DNA / melting DNA / extraction of DNA / strand separation of DNA <b>I</b> reference of constant temperature / cell membranes <b>I</b> kills microbes	[1]
(iii)	<i>idea of removing / trapping / separating (cellular / <b>AW</b>) debris <b>or</b> separating the DNA from the debris / <b>AW</b> ;</i>	<b>A</b> examples of cell debris / solids / cell walls <b>I</b> peas / particles / components / organelles / cell contents unqualified <b>R</b> impurities / precipitate / detergent / salt	[max 1]
(iv)	<i>idea of breaking down some of the proteins or histones associated with DNA or chromosomes ;</i>	<b>I</b> general ref. to function of proteases	[1]
(b)	any 5 of:  ref. to making / using agarose gel ;  ref. to using wells / channels / chambers / <b>AW</b> to place samples ;	<b>A</b> from diagrams as appropriate  <b>A</b> agar, (poly)acrylamide, agarose <b>R</b> starch gels <b>I</b> the support used e.g. microscope slides <b>A</b> e.g. pits / slits / chambers / holes / use of a comb	

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Question	Expected answer	Extra guidance	
	<p>ref. to wells / samples / <b>AW</b> being placed at or connected to the negative electrode / cathode / negative end (of gel) ; <b>ora</b></p> <p>ref. to any detail of adding samples (to wells) ;</p> <p>ref. to adding buffer ;</p> <p>ref. to applying potential difference / voltage difference ;</p> <p>ref. to a method of staining <b>and</b> observing the DNA ;</p> <p>ref. to hazard <b>and</b> suitable safety precaution ;</p>	<p><b>A</b> wells, in / on / near, the cathode</p> <p>e.g. adding (loading) dye or stain to each sample / adding (glycerine) to sink DNA / use of <u>micropipette</u> / e.g. of care in loading such as preventing sideways movement / putting different DNA sample in different lanes / using separate (micro) pipettes or tips.</p> <p><b>A</b> Gilson / Finn timer as a micropipette</p> <p><b>I</b> any specified volumes</p> <p><b>A</b> ref. to passing a current (between electrodes).</p> <p><b>A</b> any description of connecting or using a battery / power pack (to supply a current) or using direct current</p> <p><b>I</b> electricity unqualified / charge / electrons</p> <p>e.g. staining the DNA <b>and</b> using uv or fluorescent light / using pre-stained gels. Stains need not be named, but must be correct if given, e.g. methylene blue / ethidium bromide / crystal violet / sybr green / acridine orange / fluorescein</p> <p><b>A</b> idea of DNA samples that are already radioactive (at start) <b>and</b> then autoradiography (either directly from gel or indirectly from transfer) or take X-ray</p> <p><b>I</b> Southern blotting / radioactive or fluorescent probes / VNTRs</p> <p>e.g. electrical <b>and</b> not touching connectors or wear gloves</p> <p>stains / named stains / buffer are toxic / irritant / harmful <b>and</b> wear gloves / goggles / mask</p> <p>UV light <b>and</b> wear goggles</p> <p><b>A</b> allergy to stains / gel / buffer and wear gloves / goggles / mask</p> <p><b>I</b> low risk</p>	[max 5]

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(c) (i)	<i>idea of</i> (relative) distance moved by fragments / pieces of DNA / segments of DNA / lengths of DNA <b>or</b> number of fragments ;	<b>A</b> if it is clear they are measuring ‘how far’ the DNA fragments have moved. <b>A</b> position of fragment / <b>AW</b> <b>I</b> reference to bands / lines / stripes  <b>A</b> identify length or size of fragments using known size standard markers ;	[max 1]
(ii)	Any 2 of :  <u>volume</u> of DNA / sample (added to the wells) ;  <i>idea of</i> time / distance allowed for the samples to run (on the gel) ;  pH / (type of) buffer / electrolyte ;  volume of buffer / electrolyte ;  potential difference / voltage difference / current (used for the electrophoresis) ;  (type of) stain / time allowed for staining ;  type / thickness / consistency / volume / concentration / pore size of gel ;  temperature ;	<b>I</b> size of wells <b>I</b> mass / amount / quantity / stated figure  <b>I</b> time unqualified <b>I</b> distance anode and cathode  <b>A</b> named buffer, e.g. EDTA / Tris  <b>A</b> enough buffer to cover gel  <b>A</b> number of batteries  <b>I</b> volume / amount, of stain  <b>I</b> amount	[max 2]

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(d) (i)	<p><i>more restriction sites for Eco RI than for Hin dIII</i></p> <p>any 1 of:</p> <p><i>idea of the total number of fragments / <b>AW</b>, from Eco RI is greater ;</i></p> <p><i>idea of more shorter (length) fragments for Eco RI ;</i></p>	<p><b>A</b> bands / lines / stripes / sections, <b>AW</b></p> <p><b>A</b> numbers for Eco RI and for Hin dIII, but Eco RI must have more</p>	[max 1]
	<p><i>some Eco RI sites within fragments produced by Hin dIII</i></p> <p>any 1 of:</p> <p><i>idea of (some) fragment(s) for Hin dIII / Eco RI not present in mixed cut ;</i></p> <p><i>idea of mixed cut has many more (shorter) fragments ;</i></p>	<p><b>I</b> some fragments disappear unqualified</p> <p><b>A</b> more total number of fragments / bands in the mixed cut not present in the separate cuts</p> <p><b>A</b> <i>idea of</i> any new or different fragments</p>	[max 1]
(ii)	<p>any 1 of:</p> <p><i>idea of cannot tell if the extra / new (short) fragments are due to Hin dIII sites within Eco RI fragments ; ora</i></p> <p><i>idea of difficulty in distinguishing the bands (as they are faint or close together) ;</i></p>	<p><b>A</b> cannot tell where extra bands in mixed cut have come from / cannot assume that all the new fragments are from Eco RI cutting Hin dIII site <b>ora</b></p> <p><b>I</b> any ref. to insufficient data / repeats / replicates</p>	[max 1]
(e) (i)	(3') CCGAATGACCCAGATT (5') ;		[1]

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(ii)	<p>any 3 of:</p> <p>identify that start is where shortest / lightest fragment is located ;</p> <p><i>idea that</i> the sequence (of nucleotides / bases) are identified by colour or from the key / <b>AW</b> ;</p> <p><i>idea that</i> (strand synthesised) by (complementary) base pairing ;</p> <p><i>idea that</i> the template (sequence) is antiparallel (to the fragment) ;</p>	<p><i>need to make a link to the idea of a starting point at the 3' end of the original / template DNA which is where the shortest fragments are located.</i></p> <p><b>A</b> read the sequence of the fragment from the right to left / from the anode end / opposite direction to electrophoresis.</p> <p><b>I</b> if just restate the key</p> <p><b>A</b> named base pairs</p> <p><b>A</b> 5' end of the fragment DNA is the 3' end of the template (and so sequence is read in reverse)</p> <p><b>I</b> the fragment is complementary to the template</p>	<p>[max 3]</p> <p><b>[Total: 19]</b></p>

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2 (a) (i)	nitrogen supplied / present (in the medium) ;  variety of <u>Sorghum</u> ;	<b>A</b> concentration / amount / quantity of nitrogen / high and low nitrogen / with and without nitrogen (in the medium) <b>I</b> mass / volume / nitrogen unqualified <b>I</b> high and low nitrogen plants  <b>R</b> plant / species <b>A</b> cultivar / type	[2]
(ii)	eight / several / many / large number replicates of <u>each</u> variety ;	<b>I</b> more than one of each variety / enough if number quote must be 8 or 16 replicates of each variety	[1]
(b) (i)	83 % ; ;  <i>working:</i> $19.8 - 3.3 (= 16.5)$  <b>or</b> $\frac{16.5}{19.8} \times 100$  <b>or</b> wrong data (x) $\frac{(16.4 - 2.0)}{16.4} \times 100$	<b>A ecf</b> for answer from incorrect arithmetic to max 1  <b>A ecf</b> for wrong data with correct working and answer to max 1	[2]



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(ii)	<p>standard error is an estimate of the reliability of the <u>mean</u> (of a population)  <b>or</b>  shows the reliability of the <u>mean</u> ;</p> <p>a small standard error indicates the <u>mean</u> value is close to the <u>actual</u> (population) <u>mean</u>  <b>or</b>  small standard error indicates that <u>mean</u> is more reliable ;</p>	<p><i>must ref. to <math>S_M</math> and not <math>s</math>, so must ref. to the reliability of the <u>mean</u>, not the data</i></p> <p><b>A</b> shows the closeness of the calculated mean (of a sample) to the actual mean (of a population)</p> <p><b>A</b> the accuracy of the calculated mean value (in relation to the actual mean)</p> <p><b>A</b> the spread of the sample means from the actual mean</p> <p><b>A</b> examples from Table 2.1 e.g.:  PEP carboxylase / Rubisco smaller <math>S_M</math> so sample <u>mean</u> is closer to <u>actual mean</u></p> <p>NADP malate dehydrogenase very large <math>S_M</math> so sample <u>mean</u> not very close to <u>actual mean</u></p>	[2]
(c) (i)	<p><b>X</b> and <b>Z</b> ;</p> <p>ranges overlap / <math>S_M</math> values overlap (between <b>X</b> and <b>Z</b>) ;</p>	I error bars overlap	[2]
(ii)	<p><i>idea of 8 replicates / samples for each strain and subtracting 1 from each ;</i></p>	<p><b>A</b> as a formula <math>(8 - 1) + (8 - 1) / 16 - 2</math></p> <p><b>R</b> <math>(n - 1) + (n - 1)</math> unless the value of <math>n</math> is given</p>	[1]

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(d)	<p><b>W and</b></p> <p>comparing low nitrogen to high nitrogen shows there is an increase in activity of PEP carboxylase <b>and</b> the other varieties show a fall</p> <p><b>or</b></p> <p>comparing low nitrogen to high nitrogen shows there is a fall in activity of NADP –malate dehydrogenase <b>and</b> the other varieties show an increase ;</p>	<p><b>A ora</b> for either enzyme</p> <p>I does not follow the trend unless qualified</p> <p><b>A</b> between high to low nitrogen PEP carboxylase / NADP show a different or opposite effect to the others</p>	<p>[max. 1]</p>
			[Total: 11]