

**Assessment Schedule – 2012****Scholarship Biology (93101)****Evidence Statement****Question One Blackcaps: Evidence Statement**Migratory behaviour (**M**)

<b>MM</b>	A mutation has occurred resulting in some of the blackcaps migrating NW / to Britain.	<b>MM<sub>J</sub></b>	Results in the disruption of the navigation mechanism / named mechanism (s) resulting in change of direction.
<b>MH</b>	Migration is genetically controlled / innate.	<b>MH<sub>J</sub></b>	Migration is genetically controlled / innate as hybrid birds migrate in an intermediate direction.
<b>MA</b>	British migrants fly a shorter distance / not over the alps.	<b>MA<sub>J</sub></b>	Birds that have migrated to Britain have energy savings so they have increased survival / breeding chances.
		<b>MS<sub>J</sub></b>	Birds from Britain return earlier so will mate with other British migrants (not Spanish migrants).
<b>MF</b>	Food supplemented in Britain by humans in the form of (bird) seed.	<b>MF<sub>J</sub></b>	More nutritious / abundant food has enabled survival of the British migrants OR increased energy increases chances of successful migration(to Germany).
<b>MC</b>	Reduced (intraspecific) competition for food / resources in Britain.	<b>MC<sub>J</sub></b>	Abundant food / resources (with small population) reduces competition so increases survival chances of British migrants.

## Evolution (E)

<b>EP</b>	different selection pressures / natural selection in the environments of Spain and Britain.	<b>EP<sub>J</sub></b>	Results in changes in allele frequency between the two migrant groups.
<b>EB</b>	British beaks are longer and narrower to better access seeds / feeders.	<b>EB<sub>J</sub></b>	Change in beak shape linked to change in diet (from berries and fruits) in Spain to (primarily) seeds in Britain.
<b>EW</b>	British wings are rounder and more manoeuvrable to allow successful food gathering around bird feeder / urban gardens / avoiding (bird) predation NOT flying in the wind / over sea during migration.	<b>EW<sub>J</sub></b>	Change in wing shape linked to a change in flying need in Britain compared to Spain.eg change in predators / habitat / food.
		<b>EA<sub>J</sub></b>	Increase in frequency of alleles for phenotype differences / longer beaks / rounder wings. (not colour) Students can only get ONE of <b>EP<sub>J</sub></b> and <b>EA<sub>J</sub></b>
		<b>EL<sub>J</sub></b>	Colour genes are <b>linked</b> to other genes selected for.(may be wing / beak genes).
<b>EG</b>	Small British (Founder) population has increased likelihood of genetic drift	<b>EG<sub>J</sub></b>	This is the likely cause of the higher frequency of brown alleles / different colour in the British migrants.
<b>ER</b>	Reproductive isolating mechanisms / lack of gene flow are described in terms of two distinct breeding groups.	<b>ER<sub>J1</sub></b>	(Temporal) reproductive isolation due to birds from Britain arriving earlier than Spanish migrants to the breeding grounds in Germany so breed within their group.
		<b>ER<sub>J2</sub></b>	(Behavioural) reproductive isolation due to mate selection based on colour / courtship rituals.
<b>EH</b>	Migrating hybrids are unlikely to survive as get lost over ocean / can't find suitable environment / food supply.	<b>EH<sub>J</sub></b>	Maintains genetic isolation / selects against interbreeding between the two migrant groups.
<b>ED</b>	Divergent evolution/population are diverging.		
<b>ES</b>	Sympatric speciation may be occurring.	<b>ES<sub>J</sub></b>	The blackcaps are not geographically isolated as they breed / co-exist in the same area / Germany.

**Judgement statement (2 areas are M and E )**

<b>8</b>	8J's and 1 description OR 7J's and 3 descriptions Must have 3 J's from each area
<b>7</b>	7J's and 1 description OR 6J's and 3 descriptions Must have 2 J's from each area
<b>6</b>	6J's and 1 description OR 5J's and 3 descriptions OR 4J's and 5 descriptions Must have 1 J from each area
<b>5</b>	5J's and 1 descriptions OR 4J's and 3 descriptions OR 3 J's and 5 descriptions Must have 1 J from each area
<b>4</b>	4J's and 1 description OR 3J's and 3 descriptions OR 2 J's and 5 descriptions
<b>3</b>	3J's and 1 descriptions OR 2 J's and 3 descriptions OR 1 J and 5 descriptions
<b>2</b>	2J's and 1 description OR 1J and 3 descriptions OR 5 descriptions
<b>1</b>	1J OR 2 descriptions
<b>0</b>	Lack of relevant evidence

**Question Two: Evidence Statement****Origins and inheritance patterns ie the Genetics (G) of the dry earwax allele**

<b>Evidence of Origin and Inheritance</b>		<b>Justification</b>	
<b>GP</b>	Dry earwax allele is the result of a gene / point mutation.	<b>G<sub>J1</sub></b>	Only one gene is affected/not a chromosomal mutation.
<b>GM</b>	Missense mutation / only one amino acid has changed in the protein/a different amino acid coded for.	<b>G<sub>J2</sub></b>	Substitution (point) mutation as base G (in wet earwax allele) is replaced by A (in dry earwax allele).
<b>GF</b>	Functional protein still produced by wet earwax gene / allele.	<b>G<sub>J3</sub></b>	The protein has altered biological function that controls transport of secretory products across membranes / changes in secretory products means earwax dry rather than wet.
<b>GG</b>	Mutation occurred in gamete-producing cell / meiosis / germline	<b>GG<sub>J</sub></b>	Mutation was then inherited AND entered the gene pool/population
<b>GC</b>	Mutation / dry ear wax is autosomal / not sex linked as gene is located on chromosome number 16 / not sex chromosome (X or Y)		
<b>GR</b>	Mutation / dry ear wax allele is recessive <b>OR</b> wet ear wax allele is dominant	<b>GR<sub>J</sub></b>	Two A alleles / AA genotype needed for individual to have dry earwax. Heterozygote / GA (and GG) shows wet earwax. Could use a clearly-labelled Punnett.

**Distribution (D) of both types of earwax**

Evidence of distribution		Justification	
<b>DD</b>	Mutation occurred after dispersal of <i>Homo sapiens</i> from Africa / when <i>Homo sapiens</i> arrived in China.	<b>DD<sub>j1</sub></b>	Accounts for the low percentage of dry earwax allele/high percentage of wet earwax allele in Europe / Africa (as a result of dispersal from Africa).
		<b>DD<sub>j2</sub></b>	Accounts for 100% dry earwax in Chinese populations / high percentage of dry earwax allele in Asian populations.
<b>DF</b>	Founder population of <i>Homo sapiens</i> that reached / settled in China had the mutant allele. Accept bottleneck effect as alternative.	<b>DF<sub>j</sub></b>	Genetic drift / chance has eliminated the dominant / wet earwax allele from the population / fixed the recessive / dry earwax allele in the population.
<b>DG1</b>	Significant <b>gene flow</b> from China to adjacent Countries / Japan / India.	<b>DG<sub>j1</sub></b>	Migration / dispersal from China/ interbreeding with India / Japan populations accounts for intermediate frequency (54% and 69%) of dry ear wax allele in these countries.
<b>DG2</b>	Minimal / no <b>gene flow</b> from China to Europe / Russia / Africa.	<b>DG<sub>j2</sub></b>	Minimal / no migration / dispersal from China / interbreeding with European / Russian / African populations accounts for the low frequency (<3- 5%) of dry ear wax allele in these countries.
<b>DN</b>	Native North Americans resulted from migration across the Bering Strait land bridge from Asia.	<b>DN<sub>j1</sub></b>	The lower (30%) frequency of the dry earwax allele in native Americans compared to Asians results from interbreeding with non-native Americans (recently e.g last 500 years).
		<b>DN<sub>j2</sub></b>	Founder population had lower frequency of dry earwax allele / genetic drift caused random change in frequency of dry earwax allele.
<b>DA</b>	(Recent) immigration from Europe / Africa accounts for the low (1%) percentage of dry earwax allele in non-native Americans.		
<b>DL</b>	Allele for dry earwax may be linked to an allele / gene that has strong selection pressures.	<b>DL<sub>j</sub></b>	Dry earwax allele is inherited along with the allele that is selected for and so is present in all of the population.
<b>DS</b>	No obvious selection pressures for dry earwax.		

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<b>1</b>	1J OR 2 descriptions
<b>0</b>	Lack of relevant evidence

**Question Three. Evidence for saddlebacks****Aspects of niche (N) and human impact/intervention**

<b>NN</b>	Saddlebacks were successful / well-adapted in their niche prior to human intervention / introduced mammalian predators		
<b>NP</b>	Saddleback numbers were reduced significantly / cannot survive to reproduce as a result of introduced mammalian predators / named predators	<b>NP<sub>J</sub></b>	Aspects of their niche that made them vulnerable to predators. TWO of: <ul style="list-style-type: none"> <li>• ground feeding</li> <li>• nesting on ground</li> <li>• poor flying</li> <li>• fledglings on the ground</li> </ul>
<b>NC1</b>	Saddleback numbers were reduced significantly / cannot survive to reproduce as a result of <ul style="list-style-type: none"> <li>• Introduced (mammalian) competitors / named competitors.</li> </ul>	<b>NC<sub>J</sub></b>	Introduced competitors / deforestation resulted in a reduction in nest sites / food / territories.  <b>Can only be given once.</b>
<b>NC2</b>	<ul style="list-style-type: none"> <li>• Deforestation / habitat destruction by humans.</li> </ul>		
<b>NF</b>	Saddleback food sources are diverse / omnivorous (invertebrates, fruits, nectar)	<b>NF<sub>J</sub></b>	Saddlebacks can survive successfully in a variety of (new islands) habitats / reduces interspecific competition (with other birds)
<b>NR</b>	Saddlebacks reproductive strategies are successful as a result of ONE of: <ul style="list-style-type: none"> <li>• Long breeding lives (1–17 years).</li> <li>• large numbers of offspring yearly (up to 3 young in three clutches).</li> </ul>	<b>NR<sub>J</sub></b>	The high reproductive rate / natality means populations can be established quickly on new islands / in an absence of predators / bottleneck recovery / numbers were maintained on Hen Island
		<b>NM<sub>J</sub></b>	Monogamy became a disadvantage limiting reproductive success once predators present as if one parent killed breeding stops.

<b>NT</b>	Saddlebacks pairs establish year-round territories so only the birds with territories breed.	<b>NT<sub>J</sub></b>	Therefore the favourable alleles will increase in frequency/weaker alleles will decrease in frequency from the gene pool.
<b>NB</b>	<b>Bottleneck effect</b> as huge reduction in numbers / only 500 birds on Hen island.	<b>NB<sub>J</sub></b>	So allele frequency not representative of original population / genetic diversity reduced.

### Implications for future conservation (C) management of the Saddleback

	<b>Implication for future</b>		<b>Justification</b>
<b>CR</b>	Most songs are unique to / heard only on one island (70%)	<b>CR<sub>J</sub></b>	Therefore acts as a reproductive isolating mechanism (RIM) / very little gene flow which could lead to speciation in the saddlebacks.
<b>CA</b>	<b>Allopatric</b> speciation could result from geographical isolation (on islands).	<b>CA<sub>J</sub></b>	different selection pressures (on islands) / saddlebacks poor flyers limiting gene flow between (islands) populations ( resulting in divergence / speciation).
<b>CS</b>	Moving saddlebacks from one population / island to another has resulted in different songs occurring <b>within the population on one island.</b>	<b>CS<sub>J1</sub></b>  <b>CS<sub>J2</sub></b>	Groups on one island with different songs will not breed / RIM leading to (sympatric) speciation / divergence  Need to take into account song differences and relocate only birds with same / recognizable song.
<b>CP</b>	All 3 versions of the noncoding region of DNA <b>are still present</b> on each island/relocated population.	<b>CP<sub>J</sub></b>	Indicating that genetic diversity has been maintained in relocated populations.
<b>CD</b>	There <b>are differences</b> in the frequency of the 3 different versions of noncoding region of DNA on each island / relocated population.	<b>CD<sub>J</sub></b>	Indicating that genetic drift has occurred/selection pressures may be different on each island / genetic diversity is decreasing (not increasing because eg the losing / reduction of the “black” DNA version in Kapiti / Zealandia).
<b>CF</b>	Moving a few / small number of individuals to a different island has caused a series of <b>Founder</b> populations.	<b>CF<sub>J</sub></b>	Therefore increased chance of genetic drift with increased chance of reduction in genetic diversity.
		<b>CC<sub>J</sub></b>	Continued translocations are advised in order to maintain genetic diversity / prevent reproductive isolation / speciation.



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