-SQA- SCOTTISH QUALIFICATIONS AUTHORITY

HIGHER NATIONAL UNIT SPECIFICATION

GENERAL INFORMATION

-Unit Number- **7611846**

-Superclass- **RH**

-Title- **INTRODUCTION TO GENETICS**

-DESCRIPTION-

GENERAL COMPETENCE FOR UNIT: Explaining the structure of DNA. Explaining simple and dihybrid inheritance and describing the principles and techniques of molecular genetics.

OUTCOMES

1. explain DNA structure with regard to cell division;

2. explain simple inheritance in terms of genetics;

3. explain dihybrid inheritance in terms of genetics;

4. describe the principles and techniques of molecular genetics with respect to recombinant DNA technology.

CREDIT VALUE: 1 HN Credit

ACCESS STATEMENT: Standard Grade at 3 in Biology, or equivalent.

For further information contact: Committee and Administration Unit, SQA, Hanover House, 24 Douglas Street, Glasgow G2 7NQ.

Additional copies of this unit may be purchased from SQA (Sales and Despatch section). At the time of publication, the cost is £1.50 (minimum order £5).

HIGHER NATIONAL UNIT SPECIFICATION

STATEMENT OF STANDARDS

UNIT NUMBER: 7611846

UNIT TITLE: INTRODUCTION TO GENETICS

Acceptable performance in this unit will be the satisfactory achievement of the standards set out in this part of the specification. All sections of the statement of standards are mandatory and cannot be altered without reference to SQA.

OUTCOME

1. EXPLAIN DNA STRUCTURE WITH REGARD TO CELL DIVISION

PERFORMANCE CRITERIA

(a) The explanation of DNA structure and method of replication is correct.
(b) The comparison of mitosis and meiosis is correct.
(c) The explanation of mutation is correct.

RANGE STATEMENT

DNA: nucleotide; polynucleotide; double helix; semi-conservative replication.

Mitosis: stages; structures involved.

Mutations: chromosomal alterations; point mutations; changes in chromosomal number.

Meiosis: stages; structures; ploidy; fertilization and variation.

EVIDENCE REQUIREMENTS

Written evidence to include diagrammatic comparison of mitosis and meiosis.

OUTCOME

2. EXPLAIN SIMPLE INHERITANCE IN TERMS OF GENETICS

PERFORMANCE CRITERIA

(a) The explanation of a monohybrid cross using a Punnett square is correct.
(b) The explanation of co-dominance, multiple alleles and polygenic inheritance using a Punnett square is correct.

RANGE STATEMENT

Monohybrid: homozygous crosses; test crosses.

EVIDENCE REQUIREMENTS

Written evidence using Punnett squares to explain a monohybrid cross, codominance, multiple alleles and polygenic inheritance.

OUTCOME

3. EXPLAIN DIHYBRID INHERITANCE IN TERMS OF GENETICS

PERFORMANCE CRITERIA

(a) The explanation of a dihybrid cross using a Punnett square is correct.
(b) The calculation of the fitness of theoretical ratios relating to independently assorted genes using chi-squared test is correct.
(c) The calculation of the relative position of linked genes based on recombination data is correct.
(d) The calculation of the results of crosses involving sex linkage are correct.

RANGE STATEMENT

Dihybrid: independently assorted genes; linked genes.

Sex linkage: haemophilia; red/green colour blindness.

EVIDENCE REQUIREMENTS

Written evidence using a Punnett square to explain dihybrid crosses and sex linkage. Written evidence of ability to calculate fitness of theoretical ratios and relative positions of linked genes.

OUTCOME

4. DESCRIBE THE PRINCIPLES AND TECHNIQUES OF MOLECULAR GENETICS WITH RESPECT TO RECOMBINANT DNA TECHNOLOGY

PERFORMANCE CRITERIA

(a) The description of gene action is correct with regard to polypeptide synthesis and its control.
(b) The description of methods used in recombinant DNA technology, and their applications are correct.

RANGE STATEMENT

Gene action: Jacob/monod hypothesis transcription; RNA polymerase; mRNA; translation; polypeptide.

Applications: laboratory methods; industrial applications.

EVIDENCE REQUIREMENTS

Written evidence describing gene action with regard to polypeptide synthesis. Written evidence describing recombinant DNA technology with regard to laboratory methods and industrial applications.

MERIT To gain a pass in this unit, a candidate must meet the standards set out in the outcomes, performance criteria, range statements and evidence requirements.

To achieve a merit in this unit a candidate must demonstrate a superior or more sophisticated level of performance. This would be demonstrated by two of the following:

- an in-depth comparison of mitosis and meiosis;
- an in-depth explanation of mutation;
- the correct calculation of the results of complex dihybrid crosses involving sex linkage.

ASSESSMENT

In order to achieve this unit, candidates are required to present sufficient evidence that they have met all the performance criteria for each outcome within the range specified. Details of these requirements are given for each outcome. The assessment instruments used should follow the general guidance offered by the SQA assessment model and an integrative approach to assessment is encouraged. (See references at the end of support notes.)

Accurate records should be made of the assessment instruments used showing how evidence is generated for each outcome and giving marking schemes and/or checklists, etc. Records of candidates' achievements should also be kept. These records will be required for external verification.

SPECIAL NEEDS

Proposals to modify outcomes, range statements or agreed assessment arrangements should be discussed in the first place with the external verifier.

HIGHER NATIONAL UNIT SPECIFICATION

SUPPORT NOTES

UNIT NUMBER: 7611846

UNIT TITLE: INTRODUCTION GENETICS

SUPPORT NOTES: This part of the unit specification is offered as guidance. None of the sections of the support notes is mandatory.

NOTIONAL DESIGN LENGTH: SQA allocates a notional design length to a unit on the basis of the time estimated for achievement of the stated standards by a candidate whose starting point is as described in the access statement. The notional design length for this unit is 40 hours. The use of notional design length for programme design and timetabling is advisory only. The division of these outcomes is recommended to be: Outcome 1 - 10 hours; Outcome 2 - 7 hours; Outcome 3 - 13 hours; Outcome 4 - 10 hours.

PURPOSE This unit would most likely be used early on in HNC and HND programmes in Biology or other Science awards. It is designed to provide a base on which further units may build

CONTENT/CONTEXT Corresponding to outcomes:

Chromosomal alterations: deletion, inversion, translocation.

Point mutations: duplication; insertion; deletion; inversion substitution.

Changes in chromosome number: Down's; Turner's; Klinefelter's syndrome.

Multiple alleles: human blood groups.

Polygenic inheritance: continuous variation; height; skin colour.

Outcome 4 could be integrated with a communication unit providing subject matter for a talk or oral presentation by the candidate.

APPROACHES TO GENERATING EVIDENCE Lecturing approach:

In terms of building on prior knowledge this unit has been constructed in a logical order. Therefore it is suggested that lecturers presenting "Introduction to Genetics" begin with Outcome 1 and work through to Outcome 4.

REFERENCES

1. Guide to unit writing.
2. For a fuller discussion on assessment issues, please refer to SQA's Guide to Assessment.
3. Information for centres on SQA's operating procedures is contained in SQA's Guide to Procedures.
4. For details of other SQA publications, please consult SQA's publications list.