Appendix

This appendix provides a list of the equipment and supplies necessary for running each laboratory. Because many of the experiments described use the same equipment and supplies these are listed only once. Recipes for the solutions are also given for each exercise. Each recipe is listed only once for the laboratory when it is first required.

DNA Purification

Equipment and supplies

1. 8HQ (8-hydroxyquinoline) free base (Sigma Co., no. H6878). Do not use hemisulfate salt of the 8HQ.

2. Sterilized 15 ml and 50 ml conical polypropylene centrifuge tubes (e.g. Corning, nos 25319-15 and 25330-50).

3. Corex 25 ml centrifuge tubes with Teflon-lined caps (Corex, no. 8446-25).

4. EDTA (ethylenediaminetetra-acetic acid) (0.5 M at pH 8.0) (Ambion Inc., no. 9261).

5. Glass hooks. Glass hooks are made from Pasteur pipettes in the following way. First, place the end of a pipette horizontally into a Bunsen flame and seal it. Next, holding the pipette at a 45° angle, insert 0.5 cm of the tip into the flame. The end of the pipette will slowly drop under gravity forming a hook.

6. Ten times PBS (pH 7.4) (Ambion, no. 9625). The pH of the PBS solution is critical for collecting cheek cells. Preparation of this solution from basic ingredients is not recommended.

7. Redistilled, water-saturated phenol (Ambion Inc., no. 9712). Watersaturated phenol is preferable to the crystalline form because it is easier and safer to prepare buffered phenol from it. Water-saturated phenol can be stored indefinitely in a tightly closed, dark bottle at -70° C.

8. Proteinase K (Ambion Inc., no. 2546). Ambion Inc. is a low-cost source

of proteinase K. The enzyme is supplied in storage buffer containing 50 percent glycerol at a concentration of $20 \,\mathrm{mg\,ml^{-1}}$. Proteinase K solution should be stored at -20° C. Proteinase K remains active for several years at -20° C.

9. DNase-free ribonuclease A (Sigma, no. R4642). RNase is supplied in storage buffer with 50 percent glycerol at a concentration of 10 mg ml^{-1} . The enzyme can be stored indefinitely in a -20° C freezer.

10. DNase-free ribonuclease T1 (Ambion Inc., no. 2280). The enzyme is supplied in a storage buffer with 50 percent glycerol at concentration of 2000 units ml^{-1} and can be stored indefinitely in a -20° C freezer.

11. Sarcosyl (N-lauroylsarcosine) sodium salt (Sigma, no. L 5125).

Solutions to prepare

1. CIA (chloroform : isoamyl alcohol). Mix 24 volumes of chloroform with 1 volume of isoamyl alcohol. Because chloroform is light sensitive and very volatile, the CIA solution should be stored in a brown glass bottle, preferably in a fume hood.

2. Dilution buffer: 20 mM Tris-HCl (pH 8.5) and 100 mM Na₂ EDTA (pH 8.0). Prepare as described for lysis buffer.

3. Lysis buffer: 20 mM Tris (pH 8.5), 100 mM Na₂ EDTA (pH 8.0), 120 mM NaCl, and 1.2 percent Sarcosyl. Add the appropriate amount of 1M Tris–HCl stock solution and 0.5 M EDTA stock to the water. Check the pH of the lysis buffer and titrate it to pH 8.5 with concentrated NaOH if necessary. Add NaCl and sterilize by autoclaving for 20 minutes. Do not add Sarcosyl to the stock solution. It will be added after resuspension of the cells. Store at 4°C.

4. Phenol 8HQ. Water-saturated, twice-distilled phenol is equilibrated with an equal volume of 0.1 M sodium borate. Sodium borate should be used rather than the customary 0.1 M Tris solution because of its superior buffering capacity at pH 8.5, its low cost, its antioxidant properties, and its ability to remove oxidation products during the equilibration procedure. Mix an equal volume of a water-saturated phenol with 0.1 M sodium borate in a separation funnel. Shake until the solution turns milky. Wait for the phases to separate and then collect the bottom phenol phase. Add 8HQ to the phenol at a final concentration 0.1 percent (v/w). Phenol 8HQ can be stored in a dark bottle at 4°C for several weeks. Store at -70° C for long-term storage. The solution can be stored for several years at -70° C.

5. Twenty percent (w/v) Sarcosyl stock. Dissolve 40 g of Sarcosyl in 100 ml of double-distilled or deionized water. Adjust to 200 ml with double-distilled or deionized water. Sterilize by filtration through a $0.22 \,\mu m$ filter. Store at room temperature.

6. Sodium acetate (3 M). Sterilize the solution by autoclaving and store at 4°C.

Appendix

DNA Fingerprinting: Multi-locus Analysis

Equipment and supplies

1. Agarose powder SeaKemTM LE (FMC BioProducts, no. 50001) or equivalent.

2. Anti-DIG (digoxigenin) alkaline phosphatase (750 uml^{-1}) (Roche Molecular Biochemicals, no. 1093 274). The stock solution should not be frozen. Store at 4°C.

3. Capillary tubes (25 µl) (Idaho Technology, no. 1709).

4. CDP-Star solution (Tropix Co., no. MS100R). Store the solution in the dark at 4°C. CDP-Star is easily destroyed by ubiquitous alkaline phosphatase. Wear gloves and use sterilized tips when handling CDP-Star solution.

5. Dig Easy Hyb solution (Roche Molecular Biochemicals, no. 1603 558).

6. Dig Wash and Block Buffer Set (Roche Molecular Biochemicals, no. 1585 762). It is possible to prepare each reagent from basic ingredients, but the cost of it will be higher than the cost of the kit.

7. Ten times DIG-dUTP labeling mixture (Roche Molecular Biochemicals, no. 1 227 065).

8. DIG-labeled control DNA (Roche Molecular Bichemicals, no. 1093 657).

9. DNA Ladder (1 kb) (Life Technologies, no. 15615-016).

10. Ten times dNTP mix for an air cycler (Idaho Technology, no. 1774).

11. Ethidium bromide (Sigma Co., no. E 8751).

12. Ficoll 400 (Sigma Co., no. F 4375).

13. Gel electrophoresis apparatus (minimum $13 \text{ cm} \times 20 \text{ cm}$ gel size) with power supply (e.g. Owl Scientific, no. A1). One per group.

14. *Hae*III restriction enzyme (NEB, no. 108S or equivalent).

15. Male and female human genomic DNA (Sigma, nos D-3160, D-3035, or equivalent).

16. Hybridization bottles (150 mm × 35 mm) (e.g. HyBaid Co., no. H9084 or equivalent).

17. A hybridization oven (e.g. HyBaid Co., no. H9320 or equivalent). The oven should be capable of rotation at variable speeds.

18. M13mp RF1 DNA (Amersham Pharmacia Biotech, no. 27-1547-01).

19. MagnaGraph nylon membrane (0.22 μ pore size) (Osmonics/MSI., no. NJTHY00010).

20. NBT solution (Roche Molecular Biochemicals, no. 1383213).

21. Ten times PCR (polymerase chain reaction) buffer mix for the air cycler (Idaho Technology, no. 1781).

- **22.** A plastic bag sealer (Fisher Scientific, no. 01-812-13 or equivalent).
 - **23.** Plastic bags (e.g. Kapak Co., no. 402 or Roche Molecular Biochemicals, no. 1666 649).

24. Primers: M13 V F, GGTACATGGGTTCCTATT and M13 V R, CCCTTATTAGCGTTTGCCAT.

- **25.** Pyrex glass dishes (two per group).
- 26. Rotary platform shakers.

27. A Stratalinker[®] ultraviolet (UV) oven (Stratagen Co., no. 400071 or equivalent). In order to cross-link DNA to the nylon membrane efficiently the UV source should be capable of delivering 120 mJ cm⁻². Excessive cross-linking will decrease the hybridization efficiency.

28. Taq DNA polymerase.

- 29. Whatman 3MM chromatography paper (Whatman Co., no. 3030917).
- 30. X-phosphate solution (Roche Molecular Biochemicals, no. 1 383 221).

31. X-ray film BioMax Light (Kodak, 8×10 in no. 178–8207 or equivalent).

Solutions to prepare

1. Buffer A. Add 100 ml of buffer 1 (Roche Molecular Biochemicals Set) to 900 ml of sterilized distilled water. Store at 4°C.

2. Buffer B (blocking solution). Add 10 ml of blocking solution (Dig Wash and Block Buffer Set, Roche Molecular Biochemicals) to 80 ml of sterilized distilled water. Add 10 ml of maleic acid buffer (bottle 2, Dig Wash and Block Buffer Set, Roche Molecular Biochemicals). Always prepare freshly.

3. Buffer C (detection buffer): 0.1 M Tris-HCl (pH 9.5) and 0.1 M NaCl.

4. Denaturation solution: 0.5 N NaOH and 1.5 M NaCl. Prepare the solution using 10 N NaOH. The solution can be stored at room temperature for a few months. If a white precipitate forms, the solution should be discarded.

5. Depurination solution: 0.5 N HCl.

6. Ethidium bromide stock. (5 mg ml⁻¹): 100 mg ethidium bromide and 20 ml water. Dissolve the powder in the water by stirring under a chemical hood. Store at room temperature in a tightly closed, dark bottle.

7. Neutralization solution: 0.5 M Trisma base and 1.5 M NaCl. Add 60.5 g of Trisma base and 87.45 g of NaCl to 850 ml of deionized water. Dissolve the salts and adjust the pH to 7.5 with concentrated HCl. Fill with water to 1000 ml. Store at 4°C.

8. Ten percent SDS (sodium deodecyl sulfate) stock. Add 10 g of powder to 70 ml of distilled water and dissolve by slow stirring. Add water to a final volume of 100 ml and sterilize by filtration through a 0.45 μ filter. Do not autoclave. Store at room temperature.

9. Ten times SSC: 1.5 M NaCl and 0.15 M sodium citrate. Dissolve 87.5 g of NaCl and 44.1 g of sodium citrate in 850 ml of distilled or deionized water. Adjust the pH to 7.5 with 10N NaOH and add water to 1,000 ml. Store at 4°C.

218

10. Standard DNA: 1 kb 100 μl Ladder DNA, 700 μl TE buffer, and 200 μl loading dye solution.

11. Stop solution (loading dye): 15 percent Ficoll 400, 5 M urea, 0.1 M sodium EDTA (pH 8.0), 0.01 percent bromophenol blue, and 0.01 percent xylene cyanol. Prepare at least 10 ml of the solution. Dissolve an appropriate amount of Ficoll powder in double-distilled or deionized water by stirring at 40–50°C. Add a stock solution of EDTA, powdered urea, and dyes and aliquot approximately $500 \,\mu$ l into microfuge tubes and store at -20° C.

12. Fifty times TAE (Tris–acetate EDTA) electrophoresis buffer: 2M Trisma base, 1M acetic acid, and 50 mM Na_2 EDTA (pH 8.0). Weigh 242 g of Trisma base and add to 800 ml of double-distilled or deionized water. Add 57.1 ml of glacial acetic acid and 100 ml of 0.5 M EDTA stock solution (pH 8.0). Dissolve the powder by continuous stirring for 30 minutes and add water to a final volume of 11. Do not autoclave. Store tightly closed at room temperature.

13. Washing solution II: two times SSC and 0.1 percent SDS.

14. Washing solution III: one times SSC and 0.1 percent SDS.

DNA Fingerprinting: Single-locus Analysis

Equipment and supplies

- 1. D2S44 probe (Promega, no. DK263A or equivalent).
- 2. MetaPhorTM agarose (FNC BioProducts, no. 501810).

Solutions to prepare

1. Hybridization solution: 0.5 m sodium phosphate (pH 7.2), 0.5 percent (v/v) Tween 20, and 1 percent casein (Hammerstein grade) or blocker casein in PBS (Pierce, no. 37528).

2. Twenty times SSC: 3 M NaCl and 0.3 M sodium citrate. Dissolve 175 g of NaCl and 88.2 g of sodium citrate in 900 ml of distilled or deionized water. Adjust the pH to 7.5 with 10 N NaOH and add water to 1,000 ml. Store at 4°C.

3. Stripping solution: 0.4N NaOH and 0.1 percent SDS. The solution should be freshly prepared.

4. Ten times TBE (Tris–borate EDTA) electrophoresis buffer: 890mM Tris base, 890mM boric acid, and 20mM EDTA. Dissolve the Tris and boric acid in deionized water and add the appropriate amount of 0.5 M EDTA (pH 8.0). Store at room temperature.

5. Ten times wash buffer I: 0.5 M sodium phosphate (pH 7.2) and 5 percent (v/v) Tween 20.

220 Out of Africa: Origin of Modern Humans

Equipment and supplies

1. Acetamide (Sigma Co., no. A 0500).

2. *Alu* primers: *Alu* F, CCTTCCACAGTGTATTGTGTC and *Alu* R, TAGAAATGTGTGGGACAGTTC.

3. Capillary tubes (10µl) (Idaho Technology, no. 1705).

4. Low molecular weight DNA standard (BioMarker Low Bioventure Inc.).

5. Ten times high magnesium PCR buffer mix for an air cycler (Idaho Technology, no. 1781).

6. Ten times low magnesium PCR buffer mix for an air cycler (Idaho Technology, no. 1783).

7. TT Primers: TT F, TAATTGTTGGAGTCGCAAGCTGAAC and TT R, GCCTGAGTGACAGAGTGAGAACC.

Solutions to prepare

1. Fifty percent acetamide.

2. Low DNA standard: 150µl (BioMarker Low), 70µl TE buffer, and 40µl BioTracker tracking dye. Store at –20°C.

DNA Sequencing

Equipment and supplies

1. An AeroMist disposable inhalator–nebulizer (Inhalation Plastic Inc., no. 4207).

2. Ampicillin, sodium salt (Sigma Co., no. A 9518).

3. ATP (100 mM) (Roche Molecular Biochemicals, no. 1 140 965 or equivalent).

4. DNA Sequencing Kit v2 (PE Biosystems, no. 4314417).

5. ElectroMax *Escherichia coli* cells DH 10B (Life Technologies Inc., no. 318290015).

6. Electroporation cuvettes (0.1 mm gap) (Invitrogen Inc., no. P410-50).

7. Filtration cartridges (Edge Biosystem Inc., no. 42453 or equivalent).

8. Oak Ridge polypropylene 50ml centrifuge tubes with caps (e.g. Nalgene[®] no. 21009).

9. PLG (Phase Lock Gel) I tubes (Eppendorf, no. 0032007953).

- **10.** PCI (Phenol: CIA) mixture (Ambion, no. 9732).
- 11. Polypropylene culture tubes (Falcon, no. 2059 or equivalent). The

Appendix

"Falcon 2059" tube of Becton Dickson Co. is the standard for transformation experiments. Other equivalent brands are acceptable, but batches of tubes are occasionally contaminated with surfactants that inhibit transformation.

12. pUC18 SmaI/BAP (Amersham Pharmacia Biotech, no. 27-4860-01).

13. Rapid DNA Ligation Kit (Roche Molecular Biochemicals, no. 1 635 379 or equivalent).

14. T4 DNA polymerase (NEB, no. 203S).

15. T4 polynucleotide kinase (NEB, no. 201S).

16. Transformation apparatus *E. coli* pulser (Bio-Rad, no. 3 165-2101 or equivalent).

17. Universal M13/pUC sequencing primer (NEB, no. 3 1211 or equivalent).

Solutions to prepare

1. Ammonium acetate (7.5 M). Dissolve 57.8 g of ammonium acetate in 60 ml of double-distilled or deionized water. Stir until the salt is fully dissolved. Do not heat to facilitate dissolving. Fill up to 100 ml and sterilize by filtration. Store tightly closed at 4°C. The solution can be stored for one to two months under these conditions. Long-term storage is possible at -70° C.

2. One thousand times ampicillin: 500 mg ampicillin and distilled or deionized water. Add 500 mg of ampicillin to 5 ml of distilled water. Sterilize by filtration and store in small aliquots at -20° C.

3. ATP (0.5 mM). Dilute 5 mM ATP solution ten times. Add $2 \mu l$ of 5 mM ATP stock solution to $18 \mu l$ of sterile water. Prepare the solution freshly. Do not store.

4. ATP (5 mM). Prepare 100 μ l of solution. Add 5 μ l of stock ATP solution to 95 μ l of sterile 5 mM Tris–HCl (pH 7.5). Store at –20°C.

5. Seventy percent ethanol. Add 25 ml of double-distilled or deionized water to 70 ml of 95 percent ethanol. Never use 100 percent ethanol because it contains an additive that can inhibit the activities of some enzymes. Store in $a-20^{\circ}$ C freezer.

6. IPTG (25 mg ml⁻¹): 2.5 percent IPTG. Dissolve 250 mg of IPTG in sterilized water. Store at –20°C.

7. LB agar amp plates: 1 percent Bacto Tryptone, 0.5 percent yeast extract, 0.5 percent NaCl, 1.5 percent Difco agar, and $100 \mu g m l^{-1}$ ampicillin. Add the first three ingredients to 11 of distilled water in a 21 Erlenmeyer flask. Stir to dissolve all the ingredients completely. Adjust the pH to 7.5 with 1 N NaOH. This will take approximately 4 ml of 1 N NaOH. Add the Difco agar and sterilize by autoclaving for 20 minutes. Cool the medium to 60–65 °C and add 1 ml of ampicillin stock solution. Mix by swirling the flask and pour the plates. This will make 25–30 plates. The plates can be stored for two to three weeks at 4°C.

9. Solution II (plasmid preparation): 0.2 N NaOH and 10 percent SDS. Prepare freshly before use.

10. Terrific broth medium (TB): 1.2 percent Bacto Tryptone, 2.4 percent yeast extract, 0.4 percent glycerol, and ten times phosphate stock solution. Mix the first three ingredients in 900 ml of deionized water and autoclave for 20 minutes to cool to room temperature and add 100 ml of phosphate stock solution. Store at 4°C.

11. X-gal (20 mg ml⁻¹): 2 percent X-gal and DMSO. Dissolve 200 mg of X-gal in 10 ml of DMSO. Store in the dark at –20°C. DMSO is used instead of the commonly used DMF (dimethylformamide) for X-gal preparation because DMF is very toxic.

Determination of Human Telomere Length

Equipment and supplies

1. Wizard Genomic Purification Kit (Promega, no. TM050).

- 2. *Hinf*I restriction endonuclease (NEB, no. 155S or equivalent).
- 3. RsaI restriction endonuclease (NEB, no. 167S or equivalent).

4. Telo TAGGG Telomere Length Assay (Roche Molecular Biochemicals, no. 2 209 136).

5. TurboBlotters (one per group) (Midwest Scientific Co., no. 10-439-012).

RT-PCR of Human Genes

Equipment and supplies

- 1. RNaseZapTM solution (Ambion, no. 9780 or equivalent).
- 2. RNAwizTM solution (Ambion, no. 9736 or equivalent).
- 3. RNAsecureTM resuspensiton solution (Ambion, no. 7010 or equivalent).
- 4. Formaldehyde load dye (Ambion, no. 3 8552).

5. TitanTM One Tube RT-PCR Kit (Roche Molecular Biochemicals, no. 1 939 823).

6. Human β -actin primers: forward, CCAAGGCCAACCGCGAGAA-GATGAC and reverse, AGGGTACATGGTGGTGCCGCCAGAC.

Index

Page numbers in *italics* refer to Figures; those in **bold** to Tables.

ABI 3700 sequencer, 134-6 affinity matrix application, 131 agarose, definition of, 30 agarose gel electrophoresis Alu amplification, 90-1 buffers, 31-2 in fingerprinting, 29-35, 104 in plasmid preparation for DNA sequencing, 133-4, 135 principle of, 29-31 RT-PCR of human genes, 204-7, 206, 211 telomere length determination and, 177 - 9alignment sequences, 143-7 with BLAST, 158-9 alkaline lysis, in plasmid preparation for DNA sequencing, 130-1 alkaline transfer of DNA, 37-8 allele frequencies, single-locus DNA fingerprinting, 70 Alu amplification, reaction stock mixture for, 85 Alu primers, agarose gel electrophoresis, 92 Alu SINE element, 159 Alu STR haplotypes in world populations, 82 ammonium acetate solution DNA precipitation, 8 in plasmid preparation for DNA sequencing, 131 amplification rapid cycle, 84 STR primers, 92 ATP concentration, in DNA sequencing, 118 aurintricarboxylic acid (ATA), 199

autoradiography, DNA probe preparation and, 43-4 avian myoblastosis virus (AMV), 211 bacteria, transformation by electroporation, 121 - 9band-sharing coefficients, DNA fingerprinting, 59 base content analysis, single-sequence analysis and, 162 Basic Local Alignment Search Tool (BLAST), 139, 147-50 sequence alignment with, 158-9 versus FASTA, 150-1 beta-lactamase gene, DNA sequencing, 113 bins, single-locus DNA fingerprinting, 71 biotin, DNA probe preparation, 44 BLAST see Basic Local Alignment Search Tool blunt-end cloning, 115 blunt-end ligation in DNA sequencing, 118 repair of ends of sheared DNA, 107 boiling lysis, in plasmid preparation for DNA sequencing, 131 buffers, in electrophoresis, 31-2 capillary nebulization channel size, 102 capillary transfer, 37-8 CD4 STR alleles, 80 cheek cells absorption spectrum of DNA, 18 breakage, 3 collection of, 13, 171, 202 chemiluminescent detection, DNA probe

preparation, 44

chloroform: isoamyl alcohol (CIA) Marmur method, 5 repair of ends of sheared DNA, 106-7 safety precautions, 11 chromatograms, editing, 155-6 chromosome 2, DNA single-locus analysis and, 62 chromosomes position of query sequence, 159-60 telomeric structure on, 167 cloning blunt-end, 115 preparation of plasmid for, 114-15 principle of, 111-12 vectors, 112-14 colormetric detection, DNA probe preparation, 44 complementary strands, DNA hybridization, 46 computer analysis of sequencing data, 139-63 base content analysis, 162 BLAST, 147-50, 150-1, 158-9 chromosome position of query sequence, 159-60 databases accessible through Internet, 141 dot matrix analysis, 152-4, 153, 162-3 dynamic programming decision matrix, 145 EMBL sequence file format, 143 FASTA, 143, 150-1 formats, 140-3 GenBank DNA sequence file format, 142 global alignment principles, 146 local alignment principles, 146 restriction enzyme site analysis, 162 sequence alignments, 143-7, 158-9 single-sequence analysis, 151-2, 161-3 TRF length analysis, 193-4 concatameric ligation, DNA sequencing, 116cycle sequencing, 134-6 D2S44 alleles, single-locus DNA fingerprinting, 74 in Simpson trial, 74-5 data analysis, 59-61, 69-71 database option, in BLAST, 149 databases, sequence formats and, 140-3 DDBJ, 140-2

deproteinization, 3-6, 170-3

enzymes, 6 Kirby method, 4 Marmur method, 4 organic solvents, 3-5 detection buffer, single-locus DNA fingerprinting, 67 - 8chemiluminescent, 44 colorimetric, 44 membrane preparation for, 56-7 signal procedure, 58-9 dideoxy terminators, removal in DNA sequencing, 137 diethyl pyrocarbonate (DEPC), 199-200 DIG, see digoxigenin Dig Easy Hyb solution, 49 digestion, restriction enzyme, 25-8 digoxigenin (DIG), 43, 164 DNA fingerprinting, 51 preparation of probe, 51, 51-3 dissociation, DNA hybridization and, 46 DNA absorption spectrum of, 18 alkaline transfer, 37-8 amplification, 84, 92 cell breakage, 3 cell composition, 2 cheek cell collection and, 11-19 circular DNA, nebulization, 103 cloning, principle of, 111-12 concentration, 7-9, 17-18, 174 deproteinization and, 3-6 end-repair reaction, 108 fingerprinting, see fingerprinting hybridization, see hybridization isolation procedure, 2, 170-3 precipitation of, 7-9, 16-17 preparation of, 1-19 purification of, 9-19, 171-3, 174 quantity and, 9-10 replication, at ends of linear molecules, 168 RNA removal and, 6-7 sequencing, see sequencing shearing by nebulization, 100-10 DNA polymerase, random priming and, 45 DNase contamination, 12 DNASIS program, single-sequence analysis and, 162 dot matrix analysis, 152-4 principle of, 153 single-sequence analysis and, 162-3

224

144 - 5graph of, 145 EDTA, heavy metals and, 12-13 electrophoresis, see agarose gel electrophoresis electroporation, transformation of bacteria by, 121–9 EMBL, see European Molecular Biology Laboratory end-repair reaction, 108 end-replication problem, telomere length and, 167 ENTREZ, 140 enzymatic procedures, RNA removal and, 6 - 7enzyme digestion, restriction, 25-8, 174-7 enzyme-alkaline phosphatase, 62 enzymes deproteinization, 6 restriction digestion, 25-8, 174-7 Escherichia coli, nick translation, 44-5 EST, see Expressed Sequence Tag ethanol, DNA precipitation, 7-9 ethidium bromide, 13 eucaryotic chromosomes, telomeres and, 165 European Molecular Biology Laboratory (EMBL), 140-3 sequence file format, 143 expect value option in BLAST, 149-50 Expressed Sequence Tag (EST), 139 expressed sequences, search for, in BLAST, 159 FASTA, 147, 150 sequence file format, 142, 143, 143 versus BLAST, 150-1 filter option, in BLAST, 148-9 fingerprinting agarose gel electrophoresis, 29-35

alkaline transfer in, 37 digoxigenin-labelled probe, **51**

endonuclease, 25-8

56-7

217 - 18

hybridization, 43-54

membrane preparation for detection,

mismatched hybrid removal and, 56-7

multi-locus analysis, 20-61, 21, 60,

probe preparation, 43-54

dynamic programming decision matrix,

signal detection procedure, 58–9 single-locus analysis, 62–75, 64, 218– 19 Southern blotting, 37–41, 40 fixed bins, single-locus DNA fingerprinting, 71 floating bins, single-locus DNA fingerprinting, 71 fluorescent tags, DNA probe preparation and, 44 forensic profiling, single-locus DNA fingerprinting, 65, 71 formamide concentration, hybridization

restriction enzyme digestion in, 25-8

gel electrophoresis, *see* electrophoresis gel size, DNA fingerprinting and, 32 gel staining, DNA fingerprinting and, 33 gels, photographing, 33–4 GenBank database, 139 DNA sequence file format, 140–2, *142* global alignments, principle of, *146* guanidinium hot-phenol method, 200 guanidinium isothiocynate, 201

reaction solution, 49

hapten-like molecules, DNA probe preparation and, 44 haptens, DNA probe preparation and, 44 high-salt lithium chloride method, 200 high-scoring segment pairs (HSPs), 148 high stringency washes, washing reaction and, 50 Homo erectus, 77 Homo sapiens, 77 human genomic DNA, see DNA human sequencing library plate, 129 humans, modern, origin of, 76-93 hybridization, 46, 185-6, 187-9 DNA probe preparation, 43–54 pre-hybridization, 53-4 reaction solution, 49-50 removal of mismatched hybrids, 56 temperature, 47-8 time in, 48-9 hydrodynamic shearing, avoidance of, 11 - 12

Intelligenetic sequence entry format, 143 Internet, sequence databases accessible through, **141** isoamyl alcohol, Marmur method, 5

225

	isolation procedure, schematic outline of, 2
-	isopropanol, DNA precipitation, 7–9
	Kirby method of deproteinization, 4
	KTUP values, 150
	laminar flow, 101
	ligation reactions in DNA sequencing, 111–21, 119
	linear molecules, DNA replication at end of, 168
	linkage disequilibrium, definition of, 78
	living cells, composition of, 2
	loading dye solutions, DNA fingerprinting and, 32–3
	local alignment analysis programs, 139–63 principle of, <i>146</i>
	lysis by boiling, in plasmid preparation for
	DNA sequencing, 131
	macaloid, RT–PCR of human genes, 199
	Marmur method of deproteinization, 4
	chloroform:isoamyl alcohol and, 5
	master mix 1 (MX1), RT–PCR of human
	genes, 213
	master mix 2 (MX2), RT–PCR of human
	genes, 213
	master reaction mixture, in DNA
	sequencing, 119 match windows, single-locus DNA
	fingerprinting, 72, 74
	maximal-scoring segment pairs (MSPs),
	148
	melting, DNA hybridization and, 46, 47
	membrane detection, and hybridization,
	187–8
	membrane preparation, for detection, 56–7
	membrane stripping
	DNA single-locus analysis and, 62 single-locus DNA fingerprinting, 66, 73
	MetaPhor TM agarose, 89–90
	micro-satellites, in multi-locus DNA
	fingerprinting, 22
	mini-satellites
	in multi-locus DNA fingerprinting, 22
	in single-locus DNA fingerprinting, 63
	mitochondrial Eve data, and modern human
	origin, 78
	modern human origin
	Alu amplification, 90–1
	Alu STR haplotypes in world
	populations, 82

Alu(-)STRs in world populations, 81 agarose gel electrophoresis of amplification, 92 amplification of human genomic DNA using STR primers, 92 data analysis, 91 experiment schematic, 77 high resolution agarose electrophoresis, 89-90 multiple-origin model, 77 polymorphic markers at CD4 locus on chromosome 12, 80 rapid cycle DNA amplification, 84 reaction stock mixture, 85, 86 running PCRs, 85-7, 86 STR primers, 92 TT amplification, 89-90 multi-locus analysis, DNA fingerprinting, 20-61, 21, 217-18 principle of, 23 multiple cloning site, DNA cloning, 113 NBRF sequence entry format, 143

nebulization shearing of DNA, 100–6 Needleman–Wunsch algorithm, 145 nick translation, 44–5 NIH Image, TRF length analysis and, 191, 193, 194 non-radioactive reporters, DNA probe preparation and, 44 nr database search, BLAST and, 158–9 nucleation reaction, DNA hybridization and, 46

Oligo(dT)12–18 primer, RT–PCR of human genes, 211 organic solvents, deproteinization and, 3–5 out-of-Africa replacement (OAR) hypothesis, 77, 78

pairwise alignment analysis, 153 PCI reagent, repair of ends of sheared DNA, 106–7 PCR reaction kinetics, 81–4 phenol in deproteinization, 4 repair of ends of sheared DNA, 106–7 RT–PCR of human genes, 201 safety precautions, 11 phosphodiester bonds, heavy metals and, 12–13 photo-oxidation, 13

226

phylogenetic analysis, 77 plasmid preparation for cloning, 114-15 for DNA sequencing, 130-4 plasmid sequences, removal of, 154 polymerase chain reaction (PCR) amplification, in ABI 3700 sequencing, 134-6 multi-locus DNA fingerprinting, 24 probe preparation, 45-6 rapid cycle DNA amplification, 84 running, 85-7, 86 see also RT-PCR PCR STR reaction (RSMT), modern human origin, 85-6 polymorphic loci, definition of, 78 polymorphism, single-locus DNA fingerprinting and, 63 polynucleotide kinase removal, 108 positive selection marker, DNA sequencing, 113 pre-hybridization, 53-4, 186 single-locus DNA fingerprinting, 66 precipitation of DNA, 16-17 probes, 45-6 preparation, and hybridization, 43-4 product rule, single-locus DNA fingerprinting, 71 programming, dynamic, 144-5, 145 protein denaturation agents, 199 protein removal, see deproteinization protein RNase inhibitors, 199 protein, salting out, 170-3 purification, 13-15, 16-19 determination of DNA purity and quantity, 9-10, 17-18, 171-3, 174 of plasmids for DNA sequencing, 130 of total RNA, 198-203

quantity determination of DNA, 9–10 query sequence, chromosome position of, 159–60

radioactive reporters, DNA probe preparation and, 43–4 random fragment sequencing, 95 random hexanucleotide primers, RT–PCR of human genes, 212 random priming, 45 random strategies (shotgun strategies), 95, 97 rapid cycle DNA amplification, 84 re-annealing reaction, DNA hybridization, 46 re-association, DNA hybridization, 46 reaction stock mixture for Alu amplification (RSMA), 85 in DNA sequencing, 119, 136 hybridization and, 49-50 STR (RSMT), modern human origin, 86 READSEQ program, 143 recirculization, DNA sequencing and, 116 removal of mismatched hybrid, 56 renaturation, DNA hybridization and, 46 repair reaction, repair of ends of sheared DNA, 107 replicative history, telomere length, 168 replicon, ligation to sequencing vector, 112, 113 reporter enzyme-alkaline phosphatase, 62 reporters non-radioactive, 44 radioactive, 43-4 restriction endonuclease, in DNA fingerprinting, 25-8 restriction enzyme digestion, 25-8, 27, 174-7 restriction enzyme site analysis, 162 restriction reactions, preparation of, 176 resuspension of cells, in plasmid preparation for DNA sequencing, 131 reverse transcriptase reaction, RT-PCR of human genes, 210-12 RNA, 196-214 agarose gel electrophoresis, 204-7 isolation, 200 purification of, 198-203 removal from DNA preparations, 6-7 RNaseOff solution, RT-PCR of human genes, 200 RNases, elimination of, 199-200 RNaseZapTM, RT-PCR of human genes, 200 RNasin, RT-PCR of human genes, 199 RNAwizTM, RT-PCR of human genes, 201 RT-PCR, 96-214 analysis of results, 214 human cheek cell collection, 202 master mix1 (MX1), 213 master mix2 (MX2), 213 procedures schematic, 197 reverse transcriptases, 210-12 RNA agarose gel electrophoresis, 204-7, 206,211

227

RNA isolation methods, 200 RNA purification, 202-3 RNases elimination, 199-200 running of, 209-14 salt concentration, hybridization reaction solution, 49 salting out, of protein, 170-3 satellites, in multi-locus DNA fingerprinting, 22 Sequencher chromatogram editing, 155 single-sequence analysis and, 161-3 sequencing, 95-137, 220-2 ABI 3700 sequencer, 134-6 agarose gel electrophoresis in, 104, 133-4, 135 alignments, 143-7, 158-9 bacteria transformation by electroporation, 121-9 blunt-end ligation schematic, 107 cloning, 111-15 coverage, 99 data, computer analysis of, 139-63 databases, Internet access and, 141 dideoxy terminator removal, 137 electroporation in, 121-9 end-repair reaction in, 108 file format, 140-3 human sequencing library plate, 129 library, 97, 100-1, 129 ligation reaction and, 115-18, 119 ligation to sequencing vector, 111-21 master reaction mixture, 119 methods, 97-8 mini-gel electrophoresis, 133-4 nebulization shearing in, 100-6 plasmid preparation, 114-15, 130-4, 135 plasmid removal, 154 procedures schematic, 96 reaction mix, 136 repair reaction schematic, 107 shearing DNA, 100-10 strategies, 97, 98-9 transfer, TurboBlotter and, 183 transformation of bacteria by electroporation, 121-9 vector, ligation to, 111-21 short interspersed nuclear elements (SINEs), 139 short tandem repeats (STRs)

amplification of human genomic DNA using, 92 modern human origin and, 76, 79 multi-locus DNA fingerprinting, 24 signal detection DNA fingerprinting and, 58-9, 67-8 Simpson Trial D2S44 probe, 74-5 single-locus DNA fingerprinting, 22, 62-75, 218-19 allelic frequencies of D2S44 VNTR locus, 70 autogram of, 73 data analysis and, 69-71 membrane stripping, 66 outline schematic of, 63 pre-hybridization, 66-7 principle of, 64 signal detection, 67-8 Simpson Trial D2S44 probe, 74-5 washing reaction, 67 single-sequence analysis, 151-2, 161-3 sliding window filter, dot matrix analysis and. 153 Smith-Waterman algorithm, 145, 147 sodium acetate, DNA precipitation, 8 sodium chloride, DNA precipitation, 8 solution II, in plasmid preparation for DNA sequencing, 131, 132 Southern blotting, 37-41 preparation, 40 single-locus DNA fingerprinting, 63 telomere length determination, 180-4 specific oligonucleotide primers, 212 strand separation, DNA hybridization and, 46 STRs, see short tandem repeats subclone coverage, DNA sequencing and, 99 submarine gels, DNA fingerprinting and, supercoiled DNA, nebulization and, 103 T4 DNA polymerase, in DNA sequencing, 107 telomere length determination, 164-94, 222 activity, schematic of, 169 agarose gel electrophoresis, 177-9 average length of TRF region, 192, 193 chromosome end and, 167 collecting human cheek cells, 171 concentration of DNA, 174

228

deproteinization, 170-3 DNA replication at ends of linear molecules, 168 genomic DNA isolation, 170-3 hybridization and, 185-9 pre-hybridization and, 186 purification, 171-3, 174 restriction enzyme digestion, 174-7 restriction reaction preparation, 176 telomerase activity schematic, 169 outline of procedures schematic, 166 Southern transfer, 180-4 TRF length analysis and, 190-4 TurboBlotter and, 183 Telomere Reverse Transcriptase (TERT), telomere length and, 167 terminal restriction fragment (TRF), 164, 190 - 4determination of average length of region, 192 calculation of, 192-4 time, DNA hybridization and, 48-9 transformation, of bacteria by electroporation, 121-9 translation, nick, 44-5 TRF, see terminal restriction fragment TRI-ReagentTM, RT-PCR of human genes, 200

TT amplification, high resolution agarose electrophoresis, 89–90 TurboBlotting, telomere length determination and, 180, 181, *183*

uncertainty data, single-locus DNA fingerprinting, 74

vanadyl–ribonucleoside complexes, 199 variable number tandem repeat (VNTR) in multi-locus DNA fingerprinting, 22 in single-locus DNA fingerprinting, 63 vector sequences, removing, in dot matrix analysis, 156 vortexing, digoxigenin label concentration,

51

washing reaction DNA fingerprinting and, 50, 67 hybridization, 187 Wizard DNA purification kit, 170–3 word, definition of, 150 word size option, in BLAST, 148 world populations *Alu* STR haplotypes in, **82** *Alu*(–)STRs values in, **81**

zippering reaction, DNA hybridization, 46