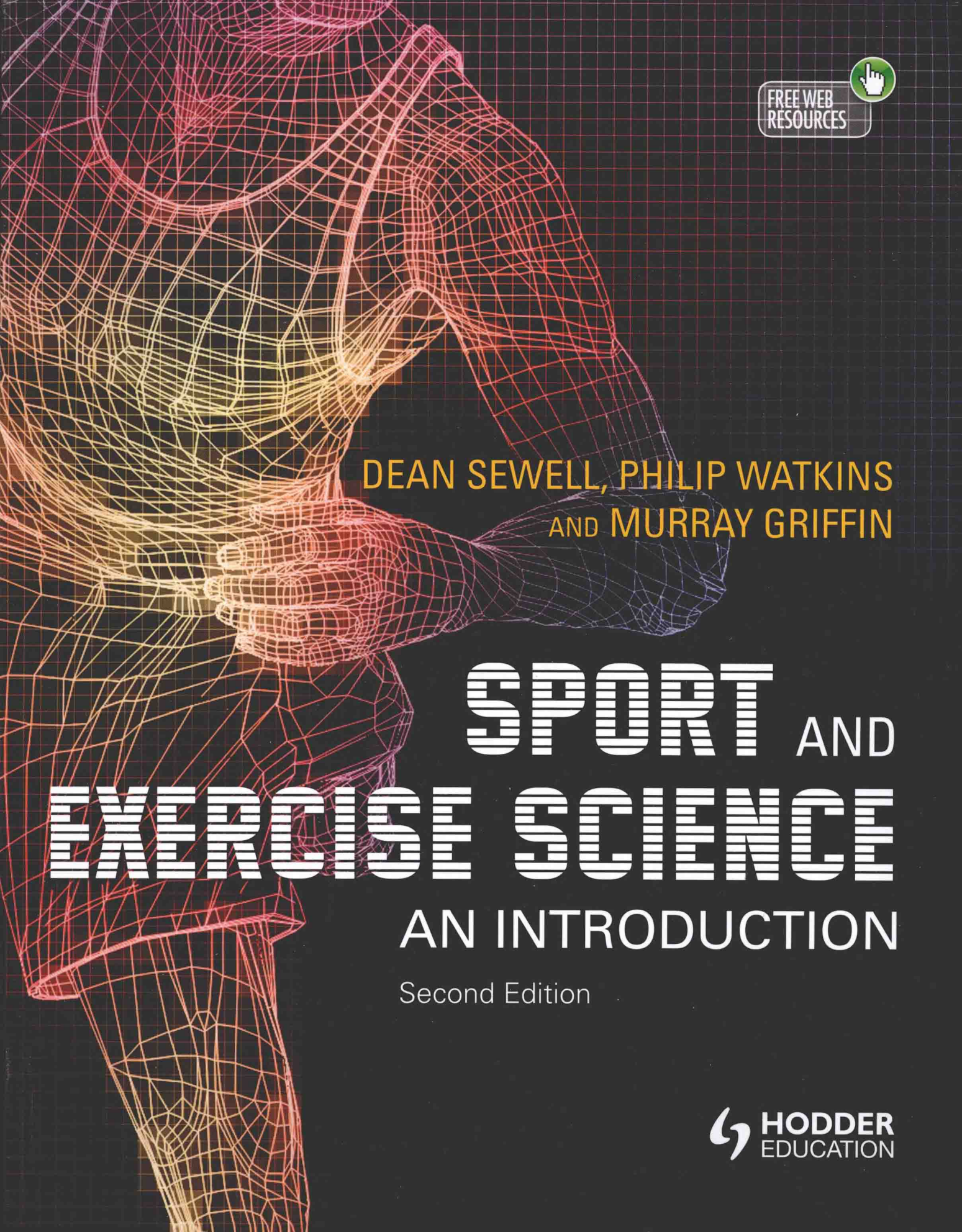

DEAN SEWELL, PHILIP WATKINS AND MURRAY GRIFFIN

SPORT AND EXERCISE SCIENCE

AN INTRODUCTION

Second Edition

HODDER EDUCATION

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HODDER EDUCATION
AN HACHETTE UK COMPANY

Dean Sewell

The making of the editions of this book has not simply been the coming together and commitment of three authors, but also the hard work and patience of a publishing team, including editors and artists. I would like to thank them for making the book a reality. The knowledge and understanding contained in this book has been gained by scientists over many decades, so it is to the scientific community that we should be grateful. I would also like to thank the excellent physiologists that I have had the privilege to meet and work with (EH being one of them, who passed away in 2011), my academic friends, colleagues and students, past and present for their inspiration and patience with me as a teacher and a researcher. And time with one's family is always compromised in completing these endeavours, so to Victoria, Amy and Jack I am thankful for your patience and support, too.

Philip Watkins

To my parents and to Heather.

Murray Griffin

I would like to thank my colleagues for their forbearance, my students for their comments, and my son Jack who, if he was able to speak, would probably tell me to stop writing and come and play some music.

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INTRODUCTION

Ever since humans have had a competitive edge, the need to improve performance and athletic ability has been an area of intense study. The last decade in particular has seen significant growth in course and student numbers in the discipline of sport and exercise science.

How can one define sport and exercise science? Sport and exercise science uses the scientific principles from the mainstream sciences, and applies them to the sport and exercise environment in order to, for example, improve performance or health, reduce injury or increase motivation. Sport science finds its ideal home firmly within the world of elite and professional sport. World-class athletes such as Usain Bolt and Paula Radcliffe, as talented as they are, would find it very difficult to achieve their significant levels of sporting excellence without the knowledge and support offered by sport science and sports medicine. Individual training programmes are designed so these athletes can train at the correct intensities, in the right frame of mind, recover appropriately, take in the correct nutrition at the optimum times, and produce their best performances when it matters. Producing top-level performances in modern sport, whether on the track, on the pitch or in the pool, requires an enormous team effort both on and off the field of play. National governing bodies (NGOs) such as the Football Association employ sport scientists (physiology, biomechanics, psychology), physiotherapists, doctors, strength and conditioning coaches and sports nutritionists to support the coaching staff and players in the quest for sporting excellence.

And it is not just in elite level sport where knowledge of sport and exercise science can be beneficial. Many employment opportunities exist in such areas as teaching, lecturing, research, coaching, fitness instructing, sports management and sports development (to name but a few). It is, of course, equally rewarding to study such an exciting and diverse subject area for its own sake at both undergraduate and postgraduate levels.

Historically in the UK, the sports-related courses of the early 1980s were based predominantly at the older and more traditional teacher-training establishments, the roots of which lay firmly in physical education. As a result, these courses were driven by a high practical sports element. Over time, courses became more laboratory-based as sport and exercise science courses were established in science divisions to counter the drop in student numbers on science-orientated courses. The foundations of sport and exercise science lie in the disciplines of physiology, biomechanics and psychology and so the science-based courses had a strong bias towards these subject areas.

However, institutions are now offering specialist pathways, modules and degree programmes in areas like sports injuries, sports therapy, strength and conditioning, sports coaching, nutrition for sport, exercise and health and sports medicine. There has also been a shift from sport to exercise science. This is not surprising in light of successive government drives to promote public health through physical activity, in an attempt to create a healthier nation and, consequently, reduce the burden on the National Health Service. Furthermore, the 2012 Olympic bid was partly built on the legacy of increased participation in sport and a more active population. Whether that is realistic is yet to be seen.

The first edition of **Sport and Exercise Science: An Introduction** was a groundbreaking new text and this second edition continues to fill a significant gap in the market, covering

the three key areas of Anatomy and Physiology, Biomechanics and Psychology required for early undergraduate study and beyond. Without a firm grounding in these disciplines at first-year level, progression cannot be made to the more specialist and applied subject areas usually available to students in their Middle and Honours years of their degree programmes. The development in schools during the late 1980s and early 1990s of exam-based A-Level Physical Education also forced some Higher Education establishments to increase the academic content of sports-related courses. The market has became swamped with various advanced level texts for sixth-formers studying physical education and sports-related courses but, until now, there has been little for undergraduates covering all three disciplines at the appropriate level.

In keeping with the above, the text has been divided into three clearly defined sections: Anatomy and Physiology, Biomechanics and Psychology. Each section is divided into separate chapters covering a particular theme or subject. Every chapter employs accessible and easy-to-follow examples, relevant diagrams and photographs from the sport and exercise arena to highlight specific principles that are grounded in academic theory. Time-out features are used to help bridge the gap between the practical and the theoretical, and to introduce the reader to recent experiments and developments within the field. Summaries, further reading suggestions and review questions provide the student with an excellent opportunity to extend their knowledge and promote critical thinking. Accompanying this textbook is a fully interactive, comprehensive and free companion website www.hodderplus.com/sport that complements and enhances student learning.

Sport and exercise science will continue to grow as a highly popular subject area to study at university. As these courses become more specialized and more prolific, and course titles change to satisfy the demands of employers or government policy (such as widening participation), **Sport and Exercise Science: An Introduction** will remain an excellent introductory core text for any student studying sport and exercise in Higher Education.

Dean Sewell
Philip Watkins
Murray Griffin

Guide to companion website

To support students in their learning, there is a companion website for this second edition of Sport *& Exercise Science*, providing free access to a range of invaluable resources such as:

- interactive multiple-choice questions to test students' progress
- revision questions and answers that reinforce students' understanding
- audio files that summarise key topics
- animations that demonstrate complex processes of exercise physiology and biomechanics
- glossary that explains key sport and exercise terminology clearly.

Terms in bold within the book can be found within the online glossary. To access the glossary and many other resources, go to www.hodderplus.com/sport.

CONTENTS

I Anatomy and Physiology

1 Sport and Exercise in the Life Sciences

Chapter Objectives

In this chapter you will learn about:

- The genomic era, 60 years after the structure of DNA was revealed.
- The feats of scientific endeavour and human performance that have advanced considerably and are set to continue to do so.
- The basic structure of the cell and its function in relation to exercise and health.
- The basic features of DNA structure and information transfer.
- The role of reactions and enzymes in metabolism and the basic function of molecules and macromolecules.

Introduction

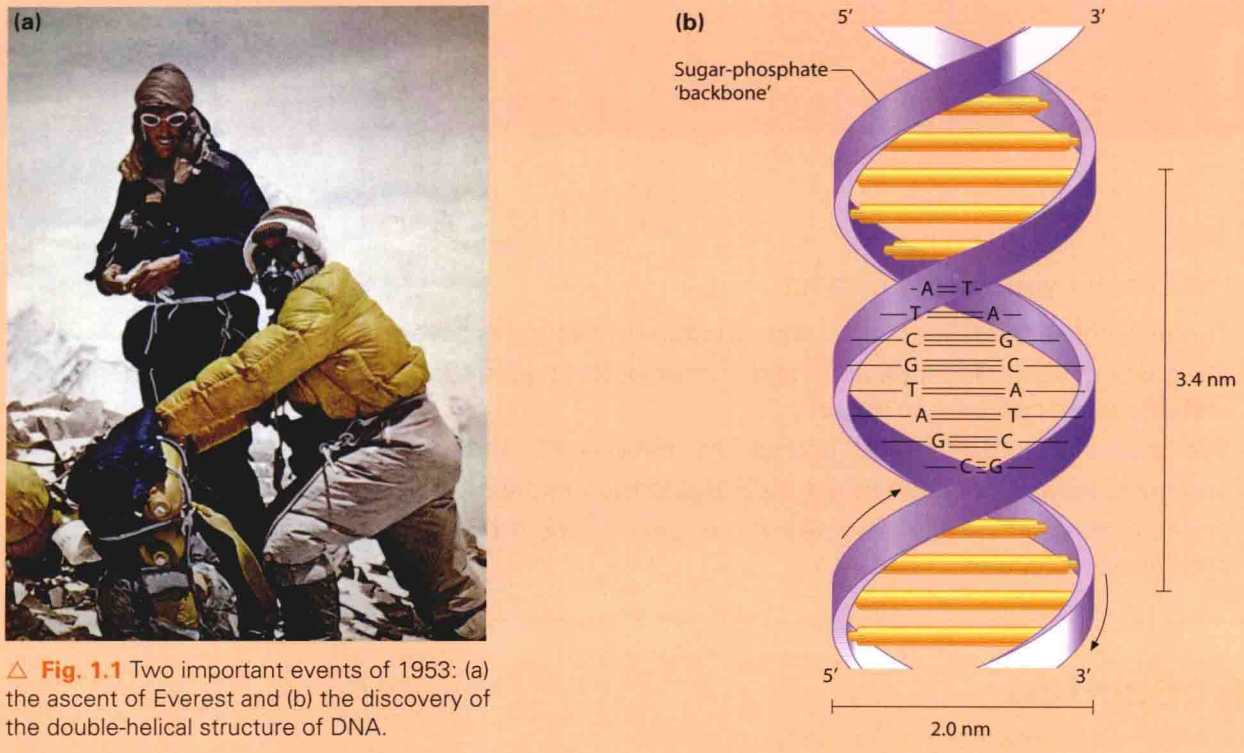
Exercise scientists joke (although there is a hint of truth in everything we say) that to succeed in sport you are well advised to choose your parents carefully. Each individual is significantly influenced by their own genetic make-up (genotype), as well as by environmental factors such as living conditions during growth and development – genotype plus environmental factors produces our phenotype.

In this chapter we will first consider where sciences such as human anatomy and physiology of exercise fit in the bigger picture of life, the universe and everything. The biology of exercise resides in the domain of the life sciences, which encompasses a diverse range of scientific fields such as psychology, medicine, marine biology and environmental biology. How might our pursuit of an increasing knowledge and practice base in human anatomy and the physiology of exercise relate to other branches of the life sciences?

We can celebrate two important events at the forefront of endeavour in sport and exercise, and in science that occurred around 60 years ago. These were the feats of reaching the highest point on earth (Everest) for the first time and the discovery of the double helical structure of DNA (Figure 1.1) and, thus, the first precisely defined amino acid sequence of a protein.

Reaching the top of Sagarmartha (the Nepalese name for Mount Everest) cannot be achieved without considerable physiological, psychological and biomechanical endurance. Whilst not being technically difficult to climb, it requires the support of a highly skilled team, including members trained in the life sciences. Multi-tasking and multidisciplinarity are fundamental for any expeditionary and scientific team. The environment is extreme, and respect for this and for the people, flora and fauna and the health economy of the Himalaya are important factors. The support of the indigenous people is also essential. They are genetically adapted, both physiologically and psychologically, to survival at higher altitudes. This is exemplified by the new record set in 2004 by the 26-year-old Sherpa, Pemba Dorjee, who reached the summit of Everest, from base camp, in just over eight hours, a journey that is normally scheduled over four days, with overnight recovery periods.

Modern day teams of Western climbers need to include medical, paramedical, physiological, nutritional and psychological support in order to achieve success. The physiologist on the 1953 Everest Expedition was Griffith Pugh, who had accompanied Eric Shipton to the Himalaya in 1952 and wrote a report from which a number of useful lessons could be learnt. In his account of the ascent, Hunt (1953) notes 'This climbing party was further enlarged by the attachment of two others . . . . The first was Griffith Pugh, a physiologist employed in the Division of Human Physiology of the M.R.C., who had a long experience of what may be termed mountain physiology.' There was considerable discussion about including 'members whose objectives are different from those of the rest of the team. But there was no denying the contribution made by a study of physiology to the problem of Everest in the past'. One of Pugh's roles was to look after food and diet for the expedition. The sport and exercise scientist can



△ **Fig. 1.1** Two important events of 1953: (a) the ascent of Everest and (b) the discovery of the double-helical structure of DNA.

perform a key role in such a team and must be able to participate fully and understand where everyone 'is coming from'. The ultimate team is greater than the sum of its component parts and the team effect is to add value, to provide a platform for individuals to excel. At the same time it must be remembered that such individuals are impotent without the support of the other team members.

The ascent of Everest can be compared with other sport and exercise pinnacles, such as becoming the fastest person in the world on the track or in the pool, or in a dinghy, kayak or rowing boat. Again, nearly 60 years ago (in 1954), the mile was run by Roger Bannister in less than 4 minutes for the first time. In 2012 the record stands at around 3 minutes 43 seconds (Hicham El Guerrouj, in 1999). In 1952, the world record for the marathon of 2 hours and 25 minutes (Yun Bok Suh, Korea, in the 1947 Boston Marathon, having been knocked to the ground by a dog, suffering a serious gash and broken shoelace) was broken by James Peters in 2 hours and 20 minutes, despite him being hit by a car 8 miles into the race! Women were not even 'allowed' to run such a distance competitively. Now the marathon has been run in less than 2 hours and 4 minutes (Kenyan, Patrick Macau Musyoki in Berlin, 2011) at an average speed just over 20 km/hour, and Paula Radcliffe holds the women's world record time of 2:15:25 set in 2003. An interesting account of the fight to establish the women's Olympic marathon race can be found in Lovett (1997). People now speculate *when*, not *if*, the marathon will be run in less than 2 hours – requiring an average speed of just over 21 km/hour. A current estimate is that this will be achieved by 2028.

These are achievements and challenges of a sporting nature, but equally important challenges and other dimensions for exercise biology in the twenty-first century can be found in the field of medicine. The epidemics of modern diseases, such as cardiovascular disease, diabetes, obesity and cancer, are a threat. Knowledge of these medical conditions, prevalent in industrialized countries are an opportunity for exercise biologists to shape the future of human morbidity and mortality through a greater dependence on primary prevention. The relative importance of this was described as the need to wage war on modern chronic diseases (Booth *et al.*, 2000).

Previous U.K. government health policies called National Service Frameworks (see the section 'Health' in Chapter 6) set out targets for the prevention and control of such diseases. Related to this is the opportunity to relate and apply functional exercise biology to the genomic potential (and susceptibility) of an individual through newfound knowledge of the human genome.

This is the context for this chapter, briefly introducing the key features of molecular biology and the chemistry of life that sport and exercise scientists might contemplate in order to take a holistic approach to the subject as it sits in the life sciences. So let us begin with the exciting human genome revelations of our time.

Plunging into the gene pool

Sixty years ago the first protein amino acid sequence was defined and the double helical structure of DNA was explained; both were exciting landmarks in science. In 1996 the first ever DNA sequence of a eukaryotic organism (a yeast) was completed, and in 1990 an international project – the Human Genome Project (HGP) – began to map and sequence the whole of the **human genome**. The working draft sequence of the human genome was published in 2001 and in the subsequent years final touches were made to the sequences and map of the human genome. This is quite simply what it is – a map. Maps are of little use unless they can be interpreted and used to their maximum potential. Enter the navigator – the physiologist!

The cost of DNA sequencing has fallen dramatically, such that whilst the HGP took 13 years and cost $3 billion, now the human genome can be sequenced in a day for £4,000. Brandler (2011) cites the view of a Chief Executive of a biotech firm suggesting that all babies born from around 2020 will have their genetic code mapped at birth. Such knowledge is a double-edged sword – knowing that you carry variants that put you at an increased risk of developing type 2 diabetes could make you rush out, hire a personal trainer, start exercising more often, and get your BMI the right side of 25. Making appropriate lifestyle choices to minimise the risks of disease is one benefit of knowing the risks, but not everyone will make such choices, and lifestyle habits are notoriously resistant to change (discussed more in Chapter 6), and difficult to sustain. For other medical conditions, there might be little one can do to prevent or delay onset, thereby causing undue stress. Furthermore, genetic risk assessment could lead to genetic hypochondria (Pääbo, 2001) causing many to spend their lives waiting for a disease that may never arrive.

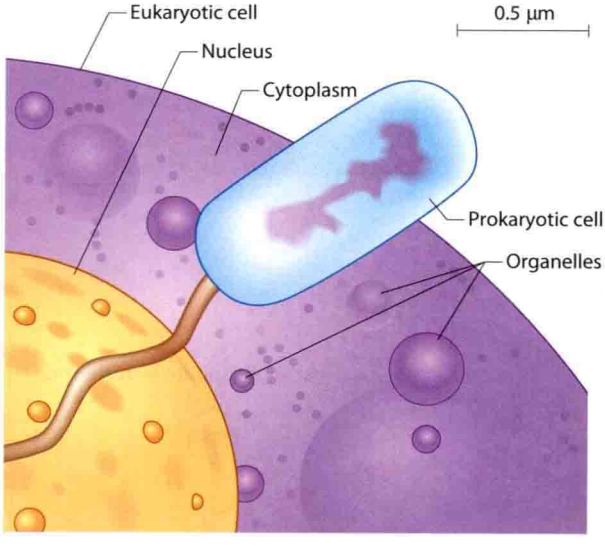
So what is the human genome? It is the complete genetic make-up (total of all the genes in the cell) of an individual. In humans, the genome consists of 23 pairs of **chromosomes** contained in the nucleus of the somatic cell (i.e. any cells other than an ovum or sperm). These chromosomes are made up of 22 autosomes and one sex chromosome. The 22 autosomes are present as homologous pairs, having, for example, the same length and centromere position. The sex chromosomes of the female are also homologous – there are two XX chromosomes. Males, however, have one X and one Y chromosome and only small parts of the X and Y chromosomes are homologous.

Each chromosome contains the double-helical **deoxyribonucleic acid (DNA)** molecule, as shown in Figure 1.1(b). The human genome contains 30 000 different genes, a gene being a sequence of DNA that codes for one polypeptide. Peptides are sequences of amino acids – the building blocks of proteins – and will be discussed in a little more detail under the heading 'Molecules and macromolecules', on page 15.

DNA is the genetic building block of what we are, and the stuff of life that can be boiled down to a sticky residue in the bottom of a test tube and played around with to modify organisms, including humans. There are two major plans of cellular organization – prokaryotic (microorganisms such as bacteria and archaea) and more complex eukaryotic. The simpler prokaryotes have DNA that is not separated from the rest of the cell in a nucleus, neither do they have the typical organelles in the cell, like those of a eukaryote.

The **prokaryotic** world is characterized by its ubiquitous distribution, its rapid growth and short generation time, its tremendous biochemical versatility and genetic flexibility, and its consequent usefulness to experimental biologists, who in recent years have exploited these properties to great advantage (in the science of molecular biology).

The **eukaryotes** are plants, animals, fungi and protozoa and have cells with distinct membrane-enclosed compartments (organelles, e.g. mitochondria), including a nucleus that contains DNA. An exception to this rule is the red blood cell (erythrocyte), which lacks a nucleus and mitochondria. Plant and animal cells are differentiated into numerous forms, each specialized for the different functions that they perform in the organism. In the mammalian body, we find many different cell types; for example, the striated muscle cell, which is multinucleate and full of mitochondria to produce the energy necessary for contraction, and the motor neuron, which has long extensions of cytoplasm that conduct electrical potential (Figure 1.2).



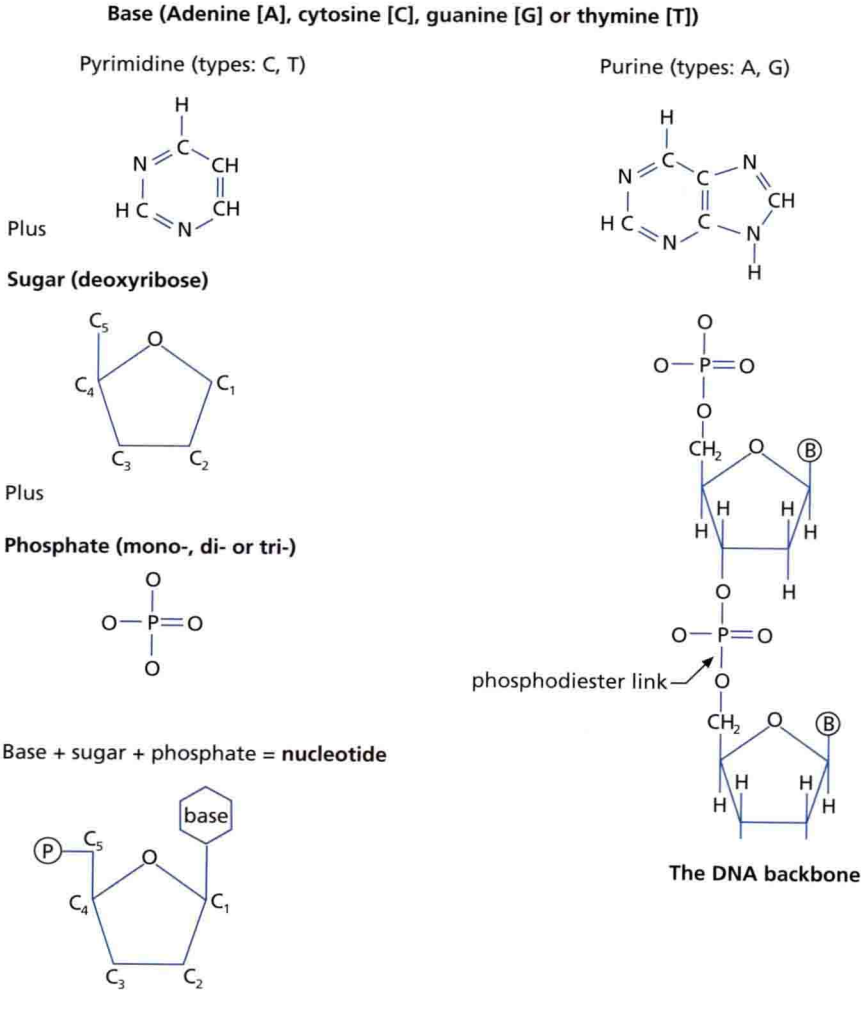
△ **Fig 1.2** Typical organization of eukaryotic and prokaryotic cells. This illustration shows a bacteria (prokaryotic) invading a human (eukaryotic) cell. The bacterial cell is much simpler and lacks the organelles found in the eukaryotic cell. From Campbell & Reece (2002).

Each chain of the DNA molecule is made up of four types of chemical building blocks called **nucleotides**. A nucleotide is formed from the combination of a molecule type called a base with a sugar (to form a nucleoside) and the addition of a phosphate. Deoxyribose sugars linked by phosphodiester bonds form the backbone of DNA (Figure 1.3).

In the DNA helix, the backbone on the outside consists of alternating sugar and phosphate molecules. The **base molecules** (attached to the sugars) form the 'rungs' of the helix 'ladder', and adenine (A) forms a link only with thymine (T), and guanine (G) only with cytosine (C). The bases A and T pair via two hydrogen bonds whereas G and C have three (Figure 1.1 (b)). The pairing of the bases AT/GC explains one of the principal findings on the road to the discovery of the structure of DNA – that the amount of A in DNA always equals the amount of T, while there are always the same amounts of G and C. James Watson and Francis Crick (1953) reported their molecular model of the double helical structure of DNA, its structure suggesting the basic mechanism for DNA replication, and in 1962 were awarded a Nobel Prize (along with Maurice Wilkins).

In the molecular biology laboratory, a method that amplifies DNA in the test tube – the **polymerase chain reaction** (PCR) – has been developed. This technique now underpins much of modern biology and medicine. It is the basis of genetic testing, of obtaining DNA 'fingerprints' from crime scenes, or extracting DNA from fossils. The standard PCR method involves a number of cycles of heating and cooling but this may be improved by a helicase method that uncoils double-stranded DNA in cells and allows all of the amplification process to be done at a single, lower temperature.

A very small amount of DNA is found in mitochondria (the 'mitochondrial genome'). Although the vast majority

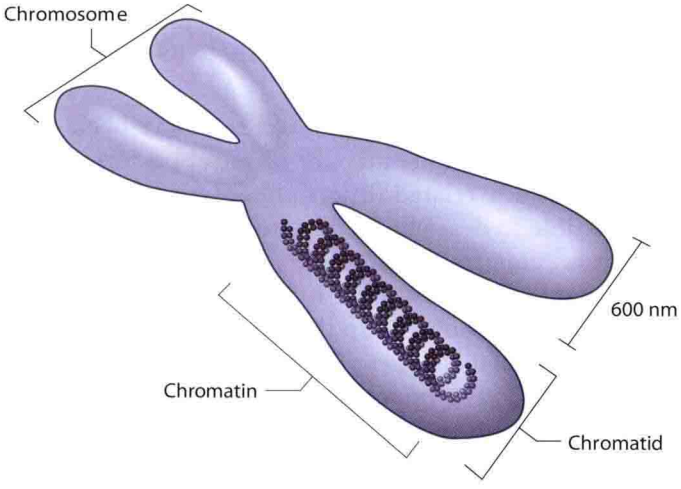


△ **Fig 1.3** DNA is made up of four bases – adenine (A), cytosine (C), guanine (G) and thymine (T) – linked to sugar and phosphate molecules in the form of a chain.

of proteins are encoded by nuclear genes, mitochondrial DNA codes for a small number of proteins (about 13).

Sequences of DNA are described by writing the sequence of bases in one strand. The strands of DNA in a human cell are estimated to be around 2 m in length, so how is it all packed into a small nucleus? Basically, DNA is packaged into a nucleosome that consists of proteins known as **histones**. Coiling of DNA around histone proteins enables the long strands to be tightly packed into a nucleoprotein complex known as **chromatin**.

When a cell divides, chromatin becomes more condensed and can be seen as chromosomes under light microscopy. Chromosomes have been numbered and genes that are responsible for (encode) particular proteins can be identified as being localized to the regions, bands and sub-bands of an arm of that chromosome (Figure 1.4).



△ **Fig 1.4** The chromosome.

The structure of DNA enables a process of nucleic acid replication to occur and produce the information required to build proteins. During DNA replication the two chains break away from each other and each becomes a template for the formation of two complementary DNA strands. The flow of genetic information (**expression**) continues when information is retrieved from one of the available strands (the template strand). The segment of DNA containing a gene is used to produce a single strand of messenger ribonucleic acid (mRNA) in a process called **transcription**.

RNA is required to read the DNA code and translate it into proteins. RNA is structurally different from DNA in a number of ways: it is usually single stranded, its sugar is ribose instead of deoxyribose, and uracil replaces thymine as one of its bases. The mRNA strand formed in transcription diffuses out of the nucleus into the cytoplasm where the genetic message is read by ribosomes to produce a polypeptide. The process of **translation** – the formation of a polypeptide under the control of mRNA in the cytoplasm – has three stages: initiation, elongation and termination. This requires a further type of RNA found in cytoplasm, transfer RNA (tRNA). In fact, RNA exists in three forms – mRNA, rRNA and tRNA (see **Box 1.1**), and there are also microRNAs.

Box 1.1

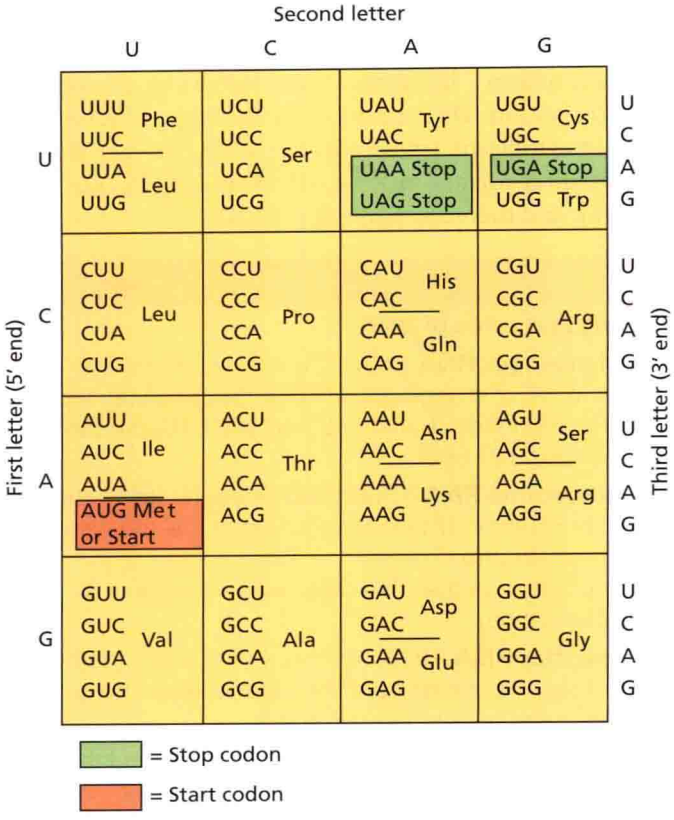
Forms and roles of RNA

- **Messenger RNA** (mRNA) is formed in the transcription of a segment of DNA that encodes a protein sequence. Transcription is the DNA-directed synthesis of RNA.
- **Ribosomal RNA** (rRNA) facilitates the interaction of mRNA and tRNA. This results in the translation of mRNA into protein.
  Translation is the RNA-directed synthesis of a polypeptide.
- **Transfer RNA** (tRNA) carries amino acids to ribosomes. Ribosomes are the organelles in the cell that carry out protein synthesis.
- **microRNAs** (miRNA) are small RNA molecules, typically 20–25 nucleotides in length, that do not encode proteins but instead regulate gene expression.

Genes carry the code for a sequence of amino acids to be formed (amino acids are the building blocks of proteins and will be discussed later in the chapter) and translation results in amino acids being linked together to form an amino acid chain or polypeptide. The genetic code for the 20 amino acids is the same in all organisms, and each is encoded by a triplet of nucleotide bases. 'Codes' of three bases specify a particular amino acid, and as there are 64 possible combinations of three bases, there are plenty to specify all 20 amino acids. The codon AUG, for example, codes for the amino acid methionine and also acts as a 'start' signal for ribosomes to begin translating the mRNA at that point. There are three codons that function as 'stop' signals (UAA, UAG and UGA; Figure 1.5).

In the genetic code there is redundancy; for example codons CAC and CAU both specify histidine, but there is no ambiguity (neither codon specifies another amino acid). Some amino acids have four or more codons. This genetic code was deciphered during the 1960s and Marshall Nirenberg received the Nobel Prize for Medicine in 1968 for his contribution to the work.

The proteins synthesized through this process create what is termed the **proteome** – the complete protein make-up of an individual – and the analysis by measurement of proteins in terms of their presence and relative



△ **Fig 1.5** The genetic code and codons. Sixty-one of the 64 possible codons specify amino acids. There are also start and stop codons that signal the ribosome to start or stop translation.

abundance is termed **proteomics**. There are around 50 000 proteins in the human body. The emerging field of proteomics allows us to better understand protein expression and formation.

A recent exciting scientific development in molecular biology has been the discovery of microRNAs. These are small RNA molecules that do not encode proteins but instead regulate gene expression. MicroRNAs (also written as μRNAs and miRNAs) are non-protein coding small RNAs, approximately 20–25 nucleotides in length that regulate gene expression at the post-transcriptional level. They act by negatively regulating gene expression, interacting with target mRNAs to inhibit translation or induce cleavage of the message. The cellular functions of human miRNAs are little known, however, since the discovery of the first miRNA gene in *C. elegans* the roles of these molecules in biological processes are surfacing. It is conceivable that the dysregulation of microRNAs may participate in the pathogenesis of prevalent human diseases such as cancer and diabetes and in ageing. It has been suggested that microRNA genes (estimated to be about 1 per cent of all human genes) regulate protein production for 10 per cent or more of all human genes. Micro-RNAs feed into the same pathway as short-interfering RNAs (siRNAs), double-stranded RNAs (dsRNAs) that mediate gene silencing by RNA interference (RNAi). The biogenesis of microRNAs are derived from two major processing events, driven by sequential cleavages by the RNAse-III enzymes Drosha and Dicer (for reviews see He and Hannon, 2004; Kim 2005). MicroRNAs are transcribed, producing primary-microRNAs (pri-miRNAs) which are then subjected to processing, resulting in the excision of a pre-micro-RNA. These pre-microRNAs are then recognized and transported from the nucleus to the cytoplasm and further processed to ultimately be incorporated into the RNA-induced silencing complex (RISC) where they act. There are emerging methodologies for the expression profiling of microRNAs, and the implication of roles and involvement in developmental and disease processes emphasises the importance of developing such methodologies to obtain detailed expression profiles in human tissues.

Since the year 2000, a group of workers have been building a human gene map for physical performance and health-related fitness phenotypes. In 2001, it was possible to describe 73 chromosomal loci where there was evidence of association or linkage with a performance or fitness phenotype in sedentary or active people, in adaptation to acute exercise or for training-induced changes. The 2002 map included 90 gene entries and quantitative trait loci (QTL), plus two on the X chromosome (Perusse *et al.*, 2003). The work is concentrating on physical performance phenotypes that include cardiorespiratory endurance, elite endurance athlete status, muscle strength and exercise intolerance, and with health-related fitness phenotypes such as exercise heart rate, blood pressure, heart size and shape, body composition, and metabolic factors.

By reviewing papers published up to the end of 2007, the latest human gene map for physical performance and health-related phenotypes includes 214 autosomal gene entries and QTL, and seven X chromosome gene entries. Moreover there are 18 mitochondrial genes in which sequence variants have been shown to influence fitness and performance phenotypes (Bray *et al.*, 2009).

Evolution, diversity and classification

Form reflects function at different structural levels within and between species – the existence of a backbone, for example, represents the evolutionary transition from a relatively sedentary lifestyle to a more active