I

Cambridge University Press 978-0-521-71230-9 - Bacterial Physiology and Metabolism Byung Hong Kim and Geoffrey Michael Gadd Excerpt More information

Introduction to bacterial physiology and metabolism

The biosphere has been shaped both by physical events and by interactions with the organisms that occupy it. Among living organisms, prokaryotes are much more metabolically diverse than eukaryotes and can also thrive under a variety of extreme conditions where eukaryotes cannot. This is possible because of the wealth of genes, metabolic pathways and molecular processes that are unique to prokaryotic cells. For this reason, prokaryotes are very important in the cycling of elements, including carbon, nitrogen, sulfur and phosphorus, as well as metals and metalloids such as copper, mercury, selenium, arsenic and chromium. A full understanding of the complex biological phenomena that occur in the biosphere therefore requires a deep knowledge of the unique biological processes that occur in this vast prokaryotic world.

After publication in 1995 of the first full DNA sequence of a freeliving bacterium, Haemophilus influenzae, whole genome sequences of hundreds of prokaryotes have now been determined and many others are currently being sequenced (www.genomesonline.org/). Our knowledge of the whole genome profoundly influences all aspects of microbiology. Determination of entire genome sequences, however, is only a first step in fully understanding the properties of an organism and the environment in which the organism lives. The functions encoded by these sequences need to be elucidated to give biochemical, physiological and ecological meaning to the information. Furthermore, sequence analysis indicates that the biological functions of substantial portions of complete genomes are so far unknown. Defining the role of each gene in the complex cellular metabolic network is a formidable task. In addition, genomes contain hundreds to thousands of genes, many of which encode multiple proteins that interact and function together as multicomponent systems for accomplishing specific cellular processes. The products of many genes are often co-regulated in complex signal transduction networks, and understanding how the genome functions as a whole presents an even greater challenge. It is also known that for a significant proportion of metabolic activities, no representative genes have been identified across all organisms, such activities being

Cambridge University Press 978-0-521-71230-9 - Bacterial Physiology and Metabolism Byung Hong Kim and Geoffrey Michael Gadd Excerpt More information

2 INTRODUCTION TO BACTERIAL PHYSIOLOGY AND METABOLISM

termed 'orphan' to indicate they are not currently assigned to any gene. This also represents a major future challenge and will require both computational and experimental approaches.

It is widely accepted that less than 1% of prokaryotes have been cultivated in pure culture under laboratory conditions. Development of new sequencing techniques has allowed us to obtain genomic information from the multitudes of unculturable prokaryotic species and complex microbial populations that exist in nature. Such information might provide a basis for the development of new cultivation techniques. Elucidation of the function of unknown genes through a better understanding of biochemistry and physiology could ultimately result in a fuller understanding of the complex biological phenomena occurring in the biosphere.

Unlike multicellular eukaryotes, individual cells of unicellular prokaryotes are more exposed to the continuously changing environment, and have evolved unique structures to survive under such conditions. Chapter 2 describes the main aspects of the composition and structure of prokaryotic cells.

Life can be defined as a reproduction process using materials available from the environment according to the genetic information possessed by the organism. Utilization of the materials available in the environment necessitates transport into cells that are separated from the environment by a membrane. Chapter 3 outlines transport mechanisms, not only for intracellular entry of nutrients, but also for excretion of materials including extracellular enzymes and materials that form cell surface structures.

Many prokaryotes, including Escherichia coli, can grow in a simple mineral salts medium containing glucose as the sole organic compound. Glucose is metabolized through glycolytic pathways and the tricarboxylic acid (TCA) cycle, supplying all carbon skeletons, energy in the form of ATP and reducing equivalents in the form of NADPH for growth and reproduction. Glycolysis is described in Chapter 4 with emphasis on the reverse reactions of the EMP pathway and on prokaryote-specific metabolic pathways. When substrates other than glucose are used, parts of the metabolic pathways are employed in either forward or reverse directions. Chapter 5 describes the TCA cycle and related metabolic pathways, and energy transduction mechanisms. Chapter 6 describes the biosynthetic metabolic processes that utilize carbon skeletons, ATP and NADPH, the production of which is discussed in the previous chapters. These chapters summarize the biochemistry of central metabolism that is employed by prokaryotes to enable growth on a glucose-mineral salts medium.

The next five chapters describe metabolism in some of the various trophic variations found in prokaryotes. These are the use of organic compounds other than glucose as carbon and energy sources (Chapter 7), anaerobic fermentation (Chapter 8), anaerobic respiratory processes (Chapter 9), chemolithotrophy (Chapter 10) and photosynthesis (Chapter 11). Some of these metabolic processes are

CAMBRIDGE

Cambridge University Press 978-0-521-71230-9 - Bacterial Physiology and Metabolism Byung Hong Kim and Geoffrey Michael Gadd Excerpt More information

INTRODUCTION TO BACTERIAL PHYSIOLOGY AND METABOLISM

prokaryote specific, while others are found in both prokaryotes and eukaryotes.

Prokaryotes only express a proportion of their genes at any given time, just like eukaryotes. This enables them to grow in the most efficient way under any given conditions. Metabolism is regulated not only through control of gene expression but also by controlling the activity of enzymes. These regulatory mechanisms are discussed in Chapter 12. Finally, the survival of prokaryotic organisms under starvation conditions is discussed in terms of storage materials and resting cell structures in Chapter 13.

This book has been written as a text for senior students at undergraduate level and postgraduates in microbiology and related subjects. A major proportion of the book has been based on review papers published in various scientific journals including those listed below:

Annual Review of Microbiology Annual Review of Biochemistry Current Opinion in Microbiology FEMS Microbiology Reviews Journal of Bacteriology Microbiology and Molecular Biology Reviews (formerly Microbiology Reviews) Nature Reviews Microbiology Trends in Microbiology.

The authors would also like to acknowledge the authors of the books listed below that have been consulted during the preparation of this book.

- Caldwell, D. R. (2000). *Microbial Physiology and Metabolism*, 2nd edn. Belm, CA: Star Publishing Co.
- Dawes, D. A. (1986). Microbial Energetics. Glasgow: Blackie.
- Dawes, I.W. & Sutherland, I.W. (1992). *Microbial Physiology*, 2nd edn. Basic Microbiology Series, 4. Oxford: Blackwell.
- Gottschalk, G. (1986). Bacterial Metabolism, 2nd edn. New York: Springer-Verlag.
- Ingraham, J. L., Maaloe, O. & Neidhardt, F. C. (1983). *Growth of the Bacterial Cell.* Sunderland, MA: Sinauer Associates Inc.
- Mandelstam, J., McQuillin, K. & Dawes, I. (1982). *Biochemistry of Bacterial Growth*, 3rd edn. Oxford: Blackwell.
- Moat, A. G., Foster, J. W. & Spector, M. P. (2002). *Microbial Physiology*, 4th edn. New York: Wiley.
- Neidhardt, F. C. & Curtiss, R. (eds.) (1996). Escherichia coli and Salmonella: Cellular and Molecular Biology, 2nd edn. Washington, DC: ASM Press.
- Neidhardt, F.C., Ingraham, J.L. & Schaechter, M. (1990). Physiology of the Bacterial Cell: A Molecular Approach. Sunderland, MA: Sinauer Associates Inc.
- Stanier, R. J., Ingraham, J. L., Wheelis, M. K. & Painter, P. R. (1986). *The Microbial World*, 5th edn. Upper Saddle River, NJ: Prentice-Hall.
- White, D. (2000). *The Physiology and Biochemistry of Prokaryotes*, 2nd edn. Oxford: Oxford University Press.

3

4 INTRODUCTION TO BACTERIAL PHYSIOLOGY AND METABOLISM

FURTHER READING

General

- Downs, D. M. (2006). Understanding microbial metabolism. Annual Review of Microbiology 60, 533–559.
- Galperin, M.Y. (2004). All bugs, big and small. *Environmental Microbiology* 6, 435–437.
- Klamt, S. & Stelling, J. (2003). Two approaches for metabolic pathway analysis? Trends in Biotechnology 21, 64–69.
- Papin, J.A., Price, N.D., Wiback, S.J., Fell, D.A. & Palsson, B.O. (2003). Metabolic pathways in the post-genome era. *Trends in Biochemical Sciences* 28, 250–258.
- Park, S., Lee, S., Cho, J., Kim, T., Lee, J., Park, J. & Han, M.J. (2005). Global physiological understanding and metabolic engineering of microorganisms based on omics studies. *Applied Microbiology and Biotechnology* 68, 567–579.
- Postgate, J. R. (1992). *Microbes and Man*, 3rd edn. Cambridge: Cambridge University Press.

Diversity

- Crawford, R. L. (2005). Microbial diversity and its relationship to planetary protection. *Applied and Environmental Microbiology* **71**, 4163–4168.
- DeLong, E.F. (2001). Microbial seascapes revisited. *Current Opinion in Microbiology* **4**, 290–295.
- Fernandez, L. A. (2005). Exploring prokaryotic diversity: there are other molecular worlds. *Molecular Microbiology* **55**, 5–15.
- Fredrickson, J. & Balkwill, D. (2006). Geomicrobial processes and biodiversity in the deep terrestrial subsurface. *Geomicrobiology Journal* **23**, 345–356.
- Pedros-Alio, C. (2006). Marine microbial diversity: can it be determined? *Trends in Microbiology* **14**, 257–263.
- Rappe, M. S. & Giovannoni, S. J. (2003). The uncultured microbial majority. Annual Review of Microbiology 57, 369–394.

Ecology

- Gadd, G. M., Semple, K. T. & Lappin-Scott, H. M. (2005). Micro-organisms and Earth Systems: Advances in Geomicrobiology. Cambridge: Cambridge University Press.
- Galperin, M.Y. (2004). Metagenomics: from acid mine to shining sea. *Environmental Microbiology* **6**, 543–545.
- Geesey, G.G. (2001). Bacterial behavior at surfaces. *Current Opinion in Microbiology* **4**, 296–300.
- Ivanov, M. V. & Karavaiko, G. I. (2004). Geological microbiology. *Microbiology-Moscow* 73, 493–508.
- Johnston, A. W. B., Li, Y. & Ogilvie, L. (2005). Metagenomic marine nitrogen fixation feast or famine? *Trends in Microbiology* **13**, 416–420.
- Karl, D. (2002). Nutrient dynamics in the deep blue sea. *Trends in Microbiology* **10**, 410–418.
- Riesenfeld, C. S., Schloss, P. D. & Handelsman, J. (2004). Metagenomics: genomic analysis of microbial communities. *Annual Review of Genetics* **38**, 525–552.

Cambridge University Press 978-0-521-71230-9 - Bacterial Physiology and Metabolism Byung Hong Kim and Geoffrey Michael Gadd Excerpt More information

FURTHER READING 5

- Shively, J. M., English, R. S., Baker, S. H. & Cannon, G. C. (2001). Carbon cycling: the prokaryotic contribution. *Current Opinion in Microbiology* **4**, 301–306.
- Tyson, G. W. & Banfield, J. F. (2005). Cultivating the uncultivated: a community genomics perspective. *Trends in Microbiology* **13**, 411–415.

Evolution

- Altermann, W. & Kazmierczak, J. (2003). Archean microfossils: a reappraisal of early life on Earth. *Research in Microbiology* **154**, 611–617.
- Arber, W. (2000). Genetic variation: molecular mechanisms and impact on microbial evolution. *FEMS Microbiology Reviews* **24**, 1–7.
- Boucher, Y., Douady, C. J., Papke, R. T., Walsh, D. A., Boudreau, M. E., Nesbo, C. L., Case, R. J. & Doolittle, W. F. (2003). Lateral gene transfer and the origins of prokaryotic groups. *Annual Review of Genetics* 37, 283–328.
- Groisman, E.A. & Casadesus, J. (2005). The origin and evolution of human pathogens. *Molecular Microbiology* **56**, 1–7.
- Koch, A. L. (2003). Were Gram-positive rods the first bacteria? Trends in Microbiology 11, 166–170.
- Koch, A. L. & Silver, S. (2005). The first cell. Advances in Microbial Physiology 50, 227–259.
- Moran, N. (2003). Tracing the evolution of gene loss in obligate bacterial symbionts. *Current Opinion in Microbiology* **6**, 512–518.
- Orgel, L. E. (1998). The origin of life a review of facts and speculations. *Trends in Biochemical Sciences* **23**, 491–495.
- Ouzounis, C. A., Kunin, V., Darzentas, N. & Goldovsky, L. (2006). A minimal estimate for the gene content of the last universal common ancestor exobiology from a terrestrial perspective. *Research in Microbiology* **157**, 57–68.
- Rainey, P.B. & Cooper, T.F. (2004). Evolution of bacterial diversity and the origins of modularity. *Research in Microbiology* 155, 370–375.
- Sallstrom, B. & Andersson, S.G.E. (2005). Genome reduction in the α -proteobacteria. *Current Opinion in Microbiology* **8**, 579–585.
- Trevors, J.T. (1997). Bacterial evolution and metabolism. *Antonie van Leeuwenhoek* **71**, 257–263.
- Trevors, J.T. (2003). Origin of the first cells on Earth: a possible scenario. *Geomicrobiology Journal* **20**, 175–183.
- van der Meer, J. R. & Sentchilo, V. (2003). Genomic islands and the evolution of catabolic pathways in bacteria. *Current Opinion in Biotechnology* **14**, 248–254.
- Weinbauer, M. G. & Rassoulzadegan, F. (2004). Are viruses driving microbial diversification and diversity? *Environmental Microbiology* **6**, 1–11.

Genomics

- Boucher, Y., Nesbo, C. L. & Doolittle, W. F. (2001). Microbial genomes: dealing with diversity. *Current Opinion in Microbiology* **4**, 285–289.
- Clayton, R.A., White, O. & Fraser, C.M. (1998). Findings emerging from complete microbial genome sequences. *Current Opinion in Microbiology* **1**, 562–566.
- Conway, T. & Schoolnik, G. K. (2003). Microarray expression profiling: capturing a genome-wide portrait of the transcriptome. *Molecular Microbiology* **47**, 879–889.

6 INTRODUCTION TO BACTERIAL PHYSIOLOGY AND METABOLISM

Doolittle, R. F. (2005). Evolutionary aspects of whole-genome biology. *Current Opinion in Structural Biology* **15**, 248–253.

- Francke, C., Siezen, R.J. & Teusink, B. (2005). Reconstructing the metabolic network of a bacterium from its genome. *Trends in Microbiology* 13, 550–558.
- Glaser, P. & Boone, C. (2004). Beyond the genome: from genomics to systems biology. *Current Opinion in Microbiology* **7**, 489–491.
- Groisman, E. A. & Ehrlich, S. D. (2003). Genomics: a global view of gene gain, loss, regulation and function. *Current Opinion in Microbiology* **6**, 479–481.
- Koonin, E. V. (2004). Comparative genomics, minimal gene-sets and the last universal common ancestor. *Nature Reviews Microbiology* **1**, 127–136.
- Nelson, K.E. (2003). The future of microbial genomics. *Environmental Microbiology* **5**, 1223–1225.
- Puhler, A. & Selbitschka, W. (2003). Genome research on bacteria relevant for agriculture, environment and biotechnology. *Journal of Biotechnology* **106**, 119–120.
- Ward, N. & Fraser, C. M. (2005). How genomics has affected the concept of microbiology. *Current Opinion in Microbiology* 8, 564–571.

Extreme environments

- Cowan, D. A. (2004). The upper temperature for life where do we draw the line? *Trends in Microbiology* **12**, 58–60.
- Deming, J. (2002). Psychrophiles and polar regions. Current Opinion in Microbiology 5, 301–309.
- Javaux, E. J. (2006). Extreme life on Earth: past, present and possibly beyond. *Research in Microbiology* **157**, 37-48.
- Mock, T. & Thomas, D.N. (2005). Recent advances in sea-ice microbiology. Environmental Microbiology **7**, 605–619.
- Simonato, F., Campanaro, S., Lauro, F. M., Vezzi, A., D'Angelo, M., Vitulo, N., Valle, G. & Bartlett, D. H. (2006). Piezophilic adaptation: a genomic point of view. *Journal of Biotechnology* **126**, 11–25.
- Steven, B., Leveille, R., Pollard, W. H. & Whyte, L. G. (2006). Microbial ecology and biodiversity in permafrost. *Extremophiles* **10**, 259–267.

New areas

- Anderson, N. L., Matheson, A. D. & Steiner, S. (2000). Proteomics: applications in basic and applied biology. *Current Opinion in Biotechnology* 11, 408–412.
- Chen, L. & Vitkup, D. (2007). Distribution of orphan metabolic activities. *Trends in Biotechnology* **25**, 343–348.
- Dufrene, Y. F. (2002). Atomic force microscopy, a powerful tool in microbiology. *Journal of Bacteriology* **184**, 5205–5213.
- Whitfield, E.J., Pruess, M. & Apweiler, R. (2006). Bioinformatics database infrastructure for biotechnology research. *Journal of Biotechnology* **124**, 629–639.

Cambridge University Press 978-0-521-71230-9 - Bacterial Physiology and Metabolism Byung Hong Kim and Geoffrey Michael Gadd Excerpt More information

2

Composition and structure of prokaryotic cells

Like all organisms, microorganisms grow, metabolize and replicate utilizing materials available from the environment. Such materials include those chemical elements required for structural aspects of cellular composition and metabolic activities such as enzyme regulation and redox processes. To understand bacterial metabolism, it is therefore helpful to know the chemical composition of the cell and component structures. This chapter describes the elemental composition and structure of prokaryotic cells, and the kinds of nutrients needed for biosynthesis and energy-yielding metabolism.

2.1 | Elemental composition

From over 100 natural elements, microbial cells generally only contain 12 in significant quantities. These are known as major elements, and are listed in Table 2.1 together with some of their major functions and predominant chemical forms used by microorganisms.

They include elements such as carbon (C), oxygen (O) and hydrogen (H) constituting organic compounds like carbohydrates. Nitrogen (N) is found in microbial cells in proteins, nucleic acids and coenzymes. Sulfur (S) is needed for S-containing amino acids such as methionine and cysteine and for various coenzymes. Phosphorus (P) is present in nucleic acids, phospholipids, teichoic acid and nucleotides including NAD(P) and ATP. Potassium is the major inorganic cation (K^+) , while chloride (Cl^-) is the major inorganic anion. K⁺ is required as a cofactor for certain enzymes, e.g. pyruvate kinase. Chloride is involved in the energy conservation process operated by halophilic archaea (Section 11.6). Sodium (Na⁺) participates in several transport and energy transduction processes, and plays a crucial role in microbial growth under alkaline conditions (Section 5.7.4). Magnesium (Mg²⁺) forms complexes with phosphate groups including those found in nucleic acids, ATP, phospholipids and lipopolysaccharides. Several microbial intracellular enzymes, e.g. monomeric alkaline phosphatase, are calcium dependent. Ferrous and ferric ions play a

8 | COMPOSITION AND STRUCTURE OF PROKARYOTIC CELLS

Table 2.1. Major elements found in microbial cells with their functions and predominant chemical forms used by microorganisms

_			
Element	Atomic number	Chemical forms used by microbes	Function
С	6	organic compounds, CO, CO ₂	major constituents of cell material in proteins, nucleic acids, lipids, carbohydrates and others
0	8	organic compounds, CO ₂ , H ₂ O, O ₂	,
Н	I	organic compounds, H_2O , H_2	
Ν	6	organic compounds, NH_4^+ , NO_3^- , N_2	
S	16	organic sulfur compounds, SO4 ^{2–} , HS [–] , S ⁰ , S ₂ O3 ^{2–}	proteins, coenzymes
Р	15	HPO4 ²⁻	nucleic acids, phospholipids, teichoic acid, coenzymes
К	19	K+	major inorganic cation, compatible solute, enzyme cofactor
Mg	12	Mg ²⁺	enzyme cofactor, bound to cell wall, membrane and phosphate esters including nucleic acids and ATP
Ca	20	Ca ²⁺ Fe ²⁺ , Fe ³⁺	enzyme cofactor, bound to cell wall
Fe	26	Fe^{2+} , Fe^{3+}	cytochromes, ferredoxin, Fe-S proteins, enzyme cofactor
Na		Na ⁺	involved in transport and energy transduction
Cl	17	CI ⁻	major inorganic anion

crucial role in oxidation-reduction reactions as components of electron carriers such as Fe-S proteins and cytochromes.

In addition to these 12 major elements, others are also found in microbial cells as minor elements (Table 2.2). All the metals listed in Table 2.2 are required for specific enzymes. It is interesting to note that the atomic number of tungsten is far higher than that of the other elements and that this element is only required in rare cases.

2.2 | Importance of chemical form

2.2.1 Five major elements

The elements listed in Tables 2.1 and 2.2 need to be supplied or be present in the chemical forms that the organisms can use. Carbon is the most abundant element in all living organisms. Prokaryotes are broadly classified according to the carbon sources they use: organotrophs (heterotrophs) use organic compounds as their carbon source while CO_2 is used by lithotrophs (autotrophs). These groups

2.2 IMPORTANCE OF CHEMICAL FORM

9

Table 2.2.Minor elements found in microbial cells with their functions and predominant chemical formused by microorganisms					
Element	Atomic number	Chemical form used by microbes	Function		
Mn	23	Mn ²⁺	superoxide dismutase, photosystem II		
Со	27	Co ²⁺	coenzyme B ₁₂		
Ni	28	Ni ⁺	hydrogenase, urease		
Cu	29	Cu ²⁺	cytochrome oxidase, oxygenase		
Zn	30	Zn^{2+}	alcohol dehydrogenase, aldolase, alkaline phosphatase, RNA and DNA polymerase, arsenate reductase		
Se	34	SeO_3^{2-}	formate dehydrogenase, glycine reductase		
Mo	42	MoO_4^{2-}	nitrogenase, nitrate reductase, formate dehydrogenase, arsenate reductase		
\sim	74	WO_{4}^{2-}	formate dehydrogenase, aldehyde oxidoreductase		

are divided further according to the form of energy they use: chemotrophs (chemoorganotrophs and chemolithotrophs) depend on chemical forms for energy while phototrophs (photoorganotrophs and photolithotrophs) utilize light energy ('organo' refers to an organic substance while 'litho' refers to an inorganic substance).

Nitrogen sources commonly used by microbes include organic nitrogenous compounds such as amino acids, and inorganic forms such as ammonium and nitrate. Gaseous N_2 can serve as a nitrogen source for a limited number of nitrogen-fixing prokaryotes. Nitrogen fixation is not known in eukaryotes. Some chemolithotrophs can use ammonium as their energy source (electron donor, Section 10.2) while nitrate can be used as an electron acceptor by denitrifiers (Section 9.1).

Sulfate is the most commonly used sulfur source, while other sulfur sources used include organic sulfur compounds, sulfide, elemental sulfur and thiosulfate. Sulfide and sulfur can serve as electron donors in certain chemolithotrophs (Section 10.3), and sulfate and elemental sulfur are used as electron acceptors and reduced to sulfide by sulfidogens (Section 9.3).

2.2.2 Oxygen

Oxygen in cells originates mainly from organic compounds, water or CO_2 . Molecular oxygen (O_2) is seldom used in biosynthetic processes. Some prokaryotes use O_2 as the electron acceptor, but some cannot grow in its presence. Thus, organisms can be grouped according to their reaction with O_2 into aerobes that require O_2 , facultative anaerobes that use O_2 when it is available but can also grow in its absence, and obligate anaerobes that do not use O_2 . Some obligate anaerobes cannot grow and/or lose their viability in the presence of O_2 while others can tolerate it. The former are termed strict anaerobes and the latter aerotolerant anaerobes.

10 COMPOSITION AND STRUCTURE OF PROKARYOTIC CELLS

Table 2.3. Common growth factors required by prokaryotes and their major function				
Growth factor	Function			
p-aminobenzoate Biotin Coenzyme M Folate Hemin Lipoate Nicotinate Pantothenate Pyridoxine Riboflavin Thiamine Vitamin B ₁₂ Vitamin K	part of tetrahydrofolate, a one-carbon unit carrier prosthetic group of carboxylase and mutase methyl carrier in methanogenic archaea part of tetrahydrofolate precursor of cytochromes and hemoproteins prosthetic group of 2-keto acid decarboxylase precursor of pyridine nucleotides (NAD ⁺ , NADP ⁺) precursor of coenzyme A and acyl carrier protein precursor of pyridoxal phosphate precursor of flavins (FAD, FMN) precursor of thiamine pyrophosphate precursor of coenzyme B ₁₂ precursor of menaquinone			

2.2.3 Growth factors

Some organotrophs such as *Escherichia coli* can grow in simple media containing glucose and mineral salts, while others, like lactic acid bacteria, require complex media containing various vitamins, amino acids and nucleic acid bases. This is because the latter organisms cannot synthesize certain essential cellular materials from only glucose and mineral salts. These required compounds should therefore be supplied in the growth media: such compounds are known as growth factors. Growth factor requirements differ between organisms with vitamins being the most commonly required growth factors (Table 2.3).

2.3 Structure of microbial cells

Microorganisms are grouped into either prokaryotes or eukaryotes according to their cellular structure. With only a few exceptions, prokaryotic cells do not have subcellular organelles separated from the cytoplasm by phospholipid membranes such as the nuclear and mitochondrial membranes. Organelles like the nucleus, mitochondria and endoplasmic reticulum are only found in eukaryotic cells. The detailed structure of prokaryotic cells is described below.

2.3.1 Flagella and pili

Motile prokaryotic cells have an appendage called a flagellum (plural, flagella) involved in motility, and a similar but smaller structure, the fimbria (plural, fimbriae). Fimbriae are not involved in motility and are composed of proteins.

The bacterial flagellum consists of three parts. These are a basal body, a hook and a filament (Figure 2.1). The basal body is embedded in the cytoplasmic membrane and cell surface structure and