Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. APS

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Almost all aphid species (Homoptera, Insecta) have 60–80 huge cells called bacteriocytes, within which are round-shaped bacteria that are designated *Buchnera*[1]. These bacteria are maternally transmitted to eggs and embryos through host generations, and the mutualism between the host and the bacteria is so obligate that neither can reproduce independently[2]. *Buchnera* is a close relative of *Escherichia coli*[3], but it contains more than 100 genomic copies per cell[4], and its genome size is only a seventh of that of *E. coli*[5]. Here we report the complete genome sequence of *Buchnera* sp. strain APS, which is composed of one 640,681-base-pair chromosome and two small plasmids. There are genes for the biosyntheses of amino acids essential for the hosts in the genome, but those for non-essential amino acids are missing, indicating complementarity and syntrophy between the host and the symbiont. In addition, *Buchnera* lacks genes for the biosynthesis of cell-surface components, including lipopolysaccharides and phospholipids, regulator genes and genes involved in defence of the cell. These results indicate that *Buchnera* is completely symbiotic and viable only in its limited niche, the bacteriocyte.

One of the principal ecological niches of microbes is the inside of eukaryotic cells[6]. Although the majority of associations between microbe and eukaryote is either commensal or, quite often, mutually beneficial, most studies of animal-associated microbes have dealt with those rare bacterial species that cause diseases. Our major interest focuses on endocellular mutualistic bacteria, which, unlike pathogenic parasites, have been transmitted through host generations for an evolutionary length of time. The endocellular mutualistic associations must have evolved repeatedly and have had major consequences for the diversification of both bacteria and hosts. One typical mutualism is observed in the symbiosis between *Buchnera* and aphids. A phylogenetic analysis has indicated that the symbiotic relationship was established 200–250 Myr ago and led to co-speciation of the hosts and their symbionts[7].

Buchnera sp. APS is harboured by the pea aphid, *Acyrthosiphon pisum* (Harris). We sequenced the *Buchnera* genome by the whole genome random sequencing method. The genome comprises one circular chromosome and two circular plasmids, pLeu and pTrp. The chromosome is 640,681 base pairs (bp), the smallest of the completely sequenced genomes, except for that of *Mycoplasma genitalium* (580,070 bp) which is regarded as a genome of the minimal gene set[8]. The pLeu plasmid is 7,786 bp and has 7 open reading frames (ORFs) including a *leuABCD* operon, and the pTrp plasmid has at least two tandem repeats of the *trpEG* operon[3,9,10]. The average G+C content of the *Buchnera* genome is 26.3%. This AT richness is a feature of many endocellular bacteria, including both endosymbiotic and parasitic bacteria[11].

As *E. coli* and *Haemophilus influenzae* are closely related to *Buchnera* phylogenetically (see below), we assumed the DnaA box upstream of the *gidA* gene is the replication origin, and designated the start of the DnaA box as base pair one. *Buchnera* has only one

DnaA box, and slight shifts in the GC skew values are observed at the third codon position and in the non-coding region around *rho*, which is located 13 kilobases (kb) upstream of *gidA* (data not shown). We did not find an insertion sequence (IS) or a phage-related sequence by database homology search. Neither are there any significant repetitive elements. *Buchnera* has a single copy of each of the three types of ribosomal RNA and 32 transfer RNA genes.

We identified 583 ORFs in the genome with an average size of 988 bp, covering 88% of the whole genome (Fig. 1). It is intriguing that the predicted isoelectric points (pIs) of the products of the ORFs are on average much more basic than those of polypeptides of other bacteria. The average pI of *Buchnera* polypeptides is 9.6, whereas that of *E. coli* and *H. influenzae* polypeptides is 7.2 and 7.3,

Table 1 Gene repertoire of the *Buchnera* genome by functional category

Small-molecule metabolism	
Degradation of small molecules	3
Energy metabolism	51
Glycolysis	9
Pyruvate dehydrogenase	3
Tricarboxylic acid cycle	2
Pentose phosphate pathway	6
Entner–Doudoroff pathway	0
Respiration	23
Fermentation	0
ATP-proton motive force	8
Central intermediary metabolism	13
Amino-acid biosynthesis	55
Glutamate family	8
Aspartate family	11
Serine family	4
Aromatic amino acid family	16
Histidine	8
Pyruvate family	0
Branched-chain family	8
Polyamine biosynthesis	2
Purines, pyrimidines, nucleosides and nucleotides	34
Biosynthesis of cofactors, prosthetic groups and carriers	26
Fatty acid biosynthesis	6
Broad regulatory functions	
Broad regulatory functions	7
Macromolecule metabolism	
Synthesis and modification of macromolecules	187
rRNA and stable RNAs	4
Ribosomal protein synthesis and modification	54
Ribosome maturation and modification	0
tRNA	32
Aminoacyl tRNA synthetases and their modification	34
Nucleoproteins	2
DNA replication, restriction/modification and recombination	32
Protein translation and modification	18
RNA synthesis, RNA modification and DNA transcription	9
Polysaccharides (cytoplasmic)	0
Phospholipids	2
Degradation of macromolecules	22
Cell envelope	46
Membranes, lipoproteins and porins	4
Surface polysaccharides, lipopolysaccharides, and antigens	2
Surface structures	25
Murein sacculus and peptidoglycan	15
Cell processes	
Transport/binding proteins	18
Chaperones	11
Cell division	12
Chaemotaxis and mobility	0
Protein and peptide secretion	7
Osmotic adaptation	0
Detoxification	3
Other	
Colicin-related functions	1
Drug/analogue sensitivity	2
Adaptations and atypical conditions	2
Other unclassified	111
Other categories	28
Conserved hypothetical	79
Unknown (unique to Buchnera)	4

All genes were classified according to Riley's classification[30]. The number of genes for each category are listed. The complete list of genes is available on our website (http://buchnera.gsc.riken.go.jp/).

respectively. Comparison of amino-acid composition between *E. coli* and *Buchnera* shows that lysine usage of *Buchnera* is twice that of *E. coli*, causing the increased pI (data not shown). The 583 predicted ORFs were compared against a non-redundant protein database and their biological roles were assigned (Table 1). Similarity searching permitted the functional assignment of 500 ORFs, and another 79 ORFs are similar to hypothetical proteins deposited for other bacteria. Only four ORFs are unique to *Buchnera*. Generally, the most similar counterparts of *Buchnera* proteins are those of *E. coli*, and the gene order in *E. coli* operons is well conserved in *Buchnera*. Considering these observations, we conclude the *Buchnera* genome is a subset of the *E. coli* genome.

The biosynthesis capabilities of *Buchnera* characterize it as a symbiont. Endocellular and epicellular parasites that have dramatically reduced their genome size, like *Buchnera*, depend on their hosts for most nutrients, and the reduction of their genome size is, at least partly, due to the loss of biosynthetic genes for nutrients. However, nutritional and physiological studies show that *Buchnera* is a provider, rather than a recipient, of biosynthetic products including essential amino acids and vitamins, to its host[3,10,12–14]. We found 54 genes involved in amino-acid biosynthesis in the *Buchnera* genome. One of the most characteristic features of *Buchnera*, unveiled by our genome analysis, is that the genes for biosyntheses of the amino acids essential for the aphid hosts[3,15] are present, but those for the non-essential amino acids are almost completely missing (Fig. 2). This complementarity of the gene repertoire shows how successfully the symbiosis is operating, in that *Buchnera* provides the host with what the host cannot synthesize, and conversely, the host provides the symbiont with what *Buchnera* cannot synthesize. Moreover, as the precursors of some essential amino acids are non-essential amino acids, glutamate and aspartate (Fig. 2a), the biosynthetic pathways of both the host and the symbiont are not only complementary, but also mutually dependent. This analysis is consistent with experimental evidence that aphids do not usually excrete a nitrogenous waste product, but recycle the amino groups as glutamine, which *Buchnera* uses as a substrate for the synthesis of essential amino acids[10,13,16].
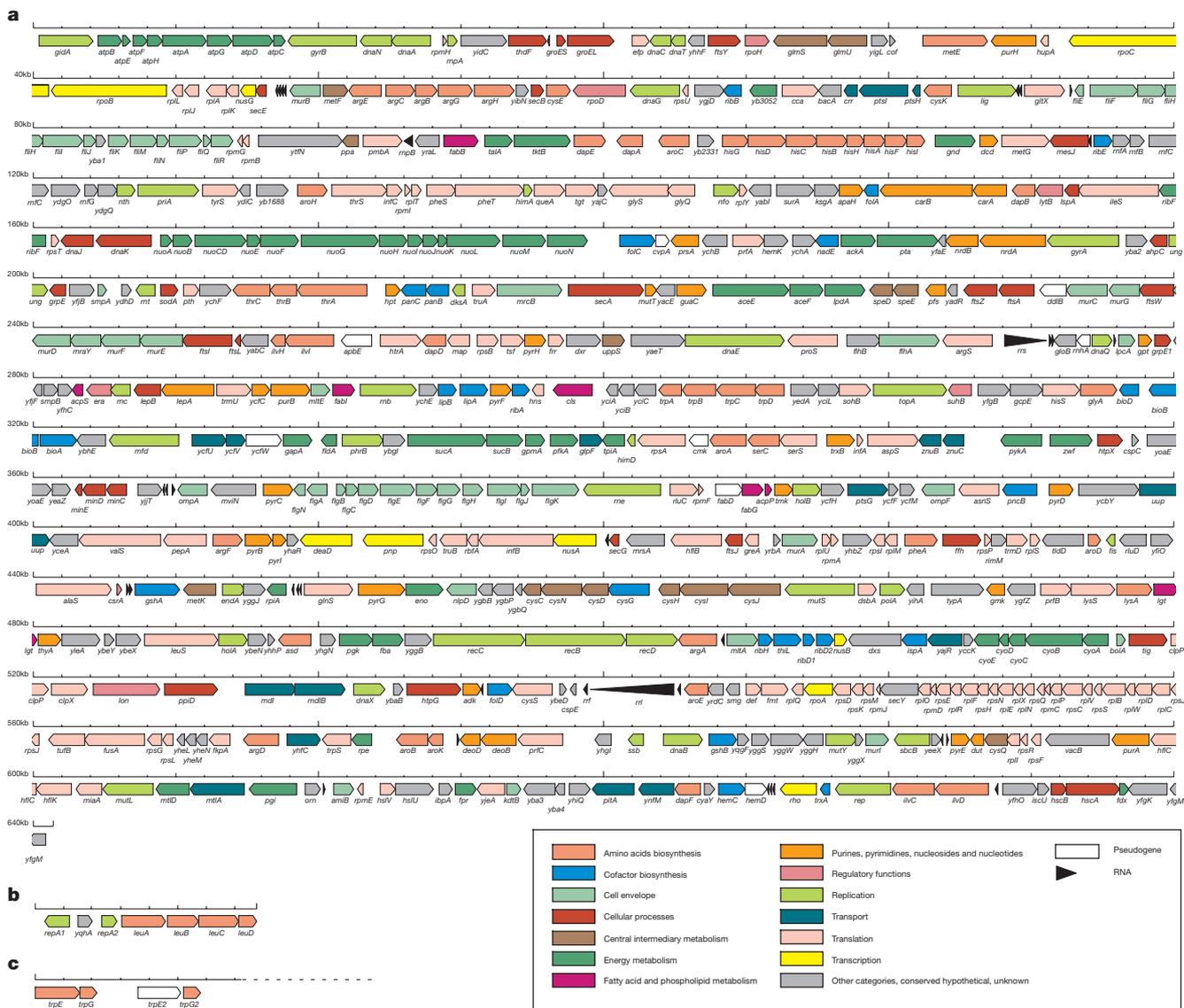
Figure 1 Linear representation of the *Buchnera* sp. APS genome illustrating the location of each predicted protein-coding region and RNA genes. All of these are essentially circular. **a**, Chromosome. **b**, pLeu plasmid. **c**, pTrp plasmid. The *trpEG* plasmid is composed of tandem repeats of the *trpEG* operon. As the repeats are highly similar, the assembled sequence converged at 7,258 bp, which is equivalent to two units of the repeat. The pTrp plasmid of *Buchnera* of *A. pisum* may contain five, six or ten repeats of this operon[3].

A similar example is observed in the pantothenate–coenzyme A (CoA) biosynthetic pathway. Although pantothenate seems to be synthesized from pyruvate in *Buchnera*, no genes for the pathway from pantothenate to CoA are found. On the other hand, animals generally have the ability to produce CoA from pantothenate, whereas they are not able to synthesize pantothenate itself. That *Buchnera* possesses complete gene sets for the sulphur reduction pathway and biosynthesis of cysteine is interesting, because insects cannot reduce sulphate to sulphide. Also experimental evidence shows that the *Buchnera*–bacteriocyte system is responsible for sulphate assimilation[17]. In contrast to obligatory parasitic bacteria, *Buchnera* has almost complete nucleotide biosynthetic pathways (Fig. 3). It is not known whether they are for the host or for its own use.

Such an obligatory mutualistic association as that between *Buchnera* and aphids should be maintained through exchange of various substances between the symbiont and the cytoplasm of the host cell. However, only a few transporter genes are present in the *Buchnera* genome (Table 1). Although the ABC transport system is a major class of cellular translocation machinery and many paralogueous genes involved in this system are found in all bacterial species sequenced to date[18], *Buchnera* has only a few ABC transporter genes.

Phosphoenolpyruvate–carbohydrate phosphotransferase systems (PTSs) seem to function in the *Buchnera* cell to import glucose and mannitol. Apart from these transporters, we found no other substrate-specific transporter genes. Hypothetical proteins YnfM and YajR are probably low-affinity transporters such as multidrug-efflux proteins. GlpF and OmpF-like porin may be involved in passive diffusion. The genes responsible for the *sec* protein secretion system are conserved in the *Buchnera* genome. Possibly, the flagellum of *Buchnera* serves as a transporter structure rather than a motor apparatus, as in *Salmonella typhimurium* and *Yersinia enterocolitica*[19,20]. In general, the flagellum is composed of three components: a basal body, a hook and a filament. In the *Buchnera* genome, however, there is no evidence for a gene for filament (*fliC*), which confers motility on the cell. In addition, *Buchnera* lacks genes involved in chemotaxis. Indeed, neither flagellum nor motility has been observed with *Buchnera*.

The genome data indicates that *Buchnera* respires aerobically. This seems reasonable as this bacterium inhabits the bacteriocyte, which receives an ample supply of oxygen through the trachea and contains many mitochondria in the cytoplasm. *Buchnera* has complete gene sets responsible for glycolysis, the pentose phosphate cycle and aerobic respiration; however, it does not have a gene set for
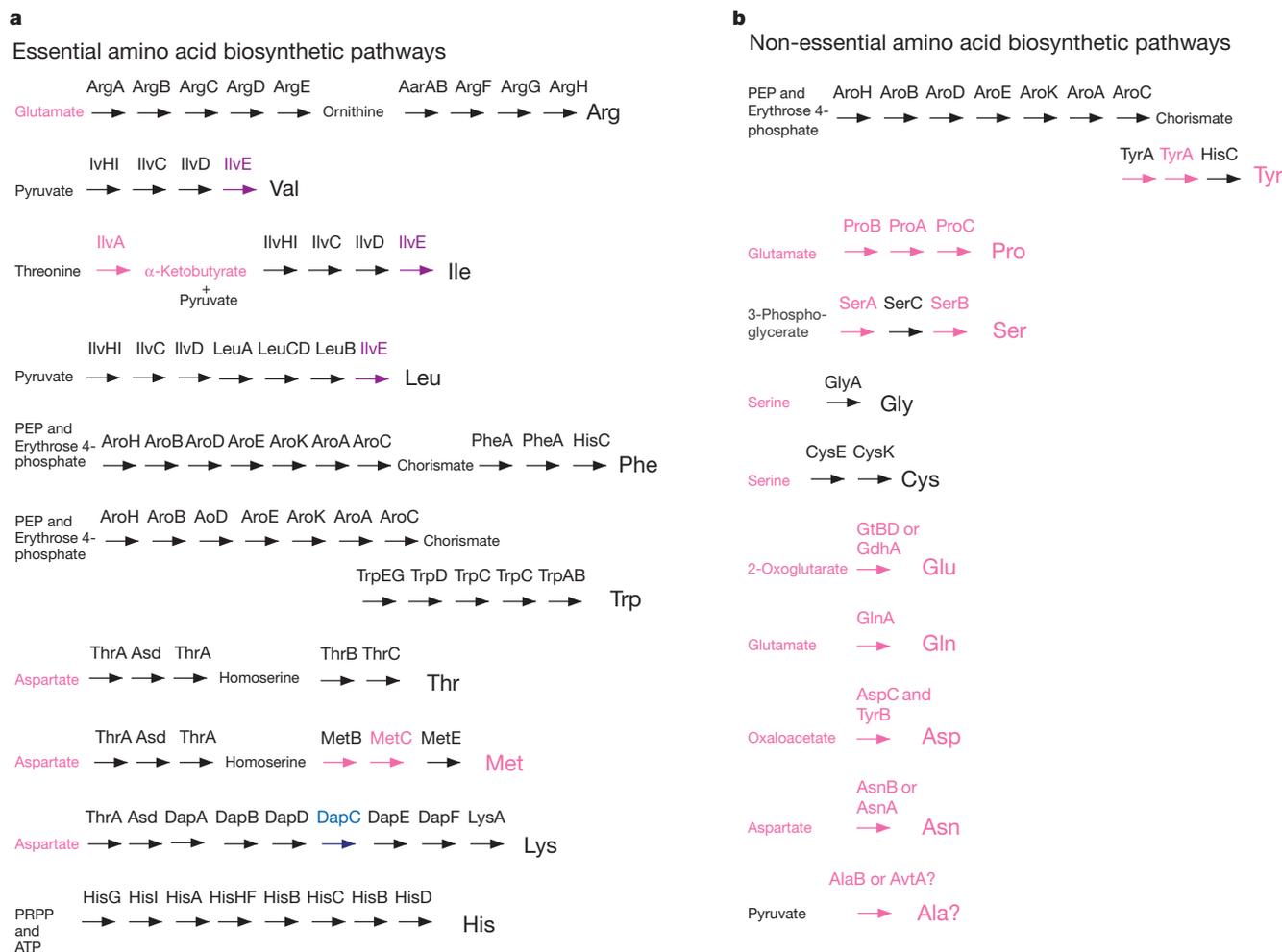
Figure 2 Amino-acid biosynthetic pathways in *Buchnera* deduced from the gene set. The sequential pathways are represented by arrows, each of which indicates one step catalysed by the named enzyme. The steps for which no genes were found in the *Buchnera* genome are pink, as are precursors for which *de novo* synthetic pathways were not identified. **a**, Essential amino acids of animals. In the valine, isoleucine and leucine biosynthetic pathways, the gene for common enzyme *ilvE* is absent (purple). IlvE is a branched-chain amino-acid aminotransferase and typically the final enzyme in the pathway, so the reaction may take place by some other aminotransferase enzyme. In the lysine biosynthetic pathway, the *dapC* gene (blue) has never been identified in any organisms. The terminal step of the phenylalanine biosynthesis is catalysed by TyrB in *E. coli*, but HisC may substitute for TyrB in *Buchnera*. **b**, Non-essential amino acids of animals. The alanine biosynthetic pathway has not been elucidated, even in *E. coli*.

operation of the TCA cycle apart from genes for the 2-oxoglutarate dehydrogenase complex. In the *Buchnera* genome, the NADH dehydrogenase (*nuo*) operon and the cytochrome *o* (*cyo*) operon are conserved with the same gene arrangements as *E. coli*, but the ubiquinone biosynthetic pathway is not even found. *Buchnera* has an F_0F_1 type ATP synthase operon, indicating that this bacterium is able to produce ATP using the proton electrochemical gradient generated by the electron transport system. *Buchnera* lacks genes responsible for fermentation and anaerobic respiration.

Buchnera seems to have a limited capacity for DNA repair and recombination, and exhibits an unusual repertoire of genes in this category. It is striking that the *recA* gene is missing from the *Buchnera* genome, as RecA is the most crucial component for the homologous recombination reaction. *Buchnera* is the first organism found to have *recBCD* without *recA*, though some mollicutes species have truncated *recA*[21]. Similarly, in the *uvr* excision repair system, *Buchnera* lacks *uvrABC*, but retains *mfd*. The *recA* and *uvrABC* are retained in all sequenced eubacterial genomes[22], except for *Buchnera*. This unique inventory of repair genes implies that the repair system and the recombination mechanism of this symbiotic bacterium are severely impaired. Alternatively, *Buchnera* uses these

residual components differently from other organisms to provide the minimum requirement for its survival. The absence of a series of genes responsible for the SOS system, *recA, lexA, umuCD* and *uvrABC*, indicates that the *Buchnera* genome is vulnerable to DNA damage. Genes for DNA methylation and restriction are also missing, further evidence that *Buchnera* has limited defences.

Buchnera has only a few genes for cell-surface components. Our genome analysis indicates that *Buchnera* is not able to make lipopolysaccharides (LPSs). The genes for the biosynthesis of the LPS components, except for *lpcA* and *kdtB*, are missing from the *Buchnera* genome. We found only a few genes encoding lipoproteins and outer membrane proteins. Scarcity of genes for these components indicates that the cell surface of *Buchnera* is structurally vulnerable. This is in contrast to other bacteria, including pathogenic and free-living ones, which have complex and flexible surface structures to evade attack by the host immune system or to survive harsh environments. This structural fragility of *Buchnera* may be caused by its prolonged intracellular life, sheltered from attack by the host and foreign enemies.

Surprisingly, genes responsible for phospholipid biosynthesis are completely missing from the *Buchnera* genome, except that for
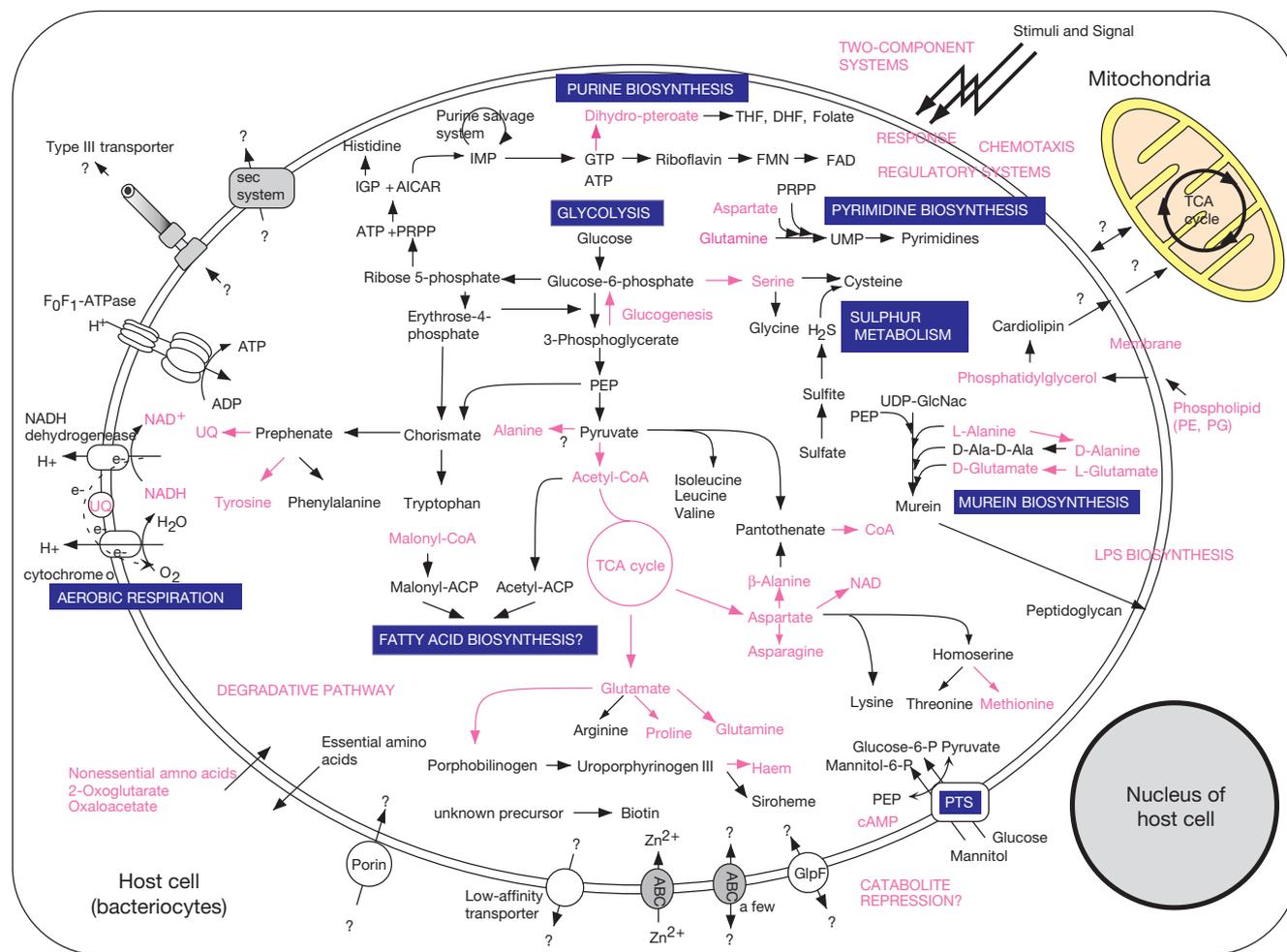

Figure 3 An integrated view of metabolism in *Buchnera* deduced from the genes identified. Pathways or steps for which no enzymes were identified are pink, as are the compounds for which *de novo* synthetic pathways were not identified. Question marks indicate that particular uncertainties exist or that the pathway has not been completely elucidated, even in *E. coli*. AICAR, 5′-phosphoribosyl-4-carboxamide-5-aminoimidazole;

cAMP, cyclic AMP; DHF, dihydrofolate; GlcNac, *N*-acetylglucosamine; IGP, imidazoleglycerol phosphate; IMP, inosine monophosphate; PE, phosphatidyl ethanolamine; PEP, phosphoenolpyruvate; PG, phosphotidyl glycerol; PRPP, phosphoribosyl-pyrophosphate; PTS, phosphoenolpyruvate:carbohydrate phosphotransferase system; TCA, tricarboxylic acid; THF, tetrahydrofolate; UQ, ubiquinone.

cardiolipin synthetase (*cls*), although phospholipid is an indispensable component in the formation of the membrane lipid bilayer. Possibly, *Buchnera* either imports phospholipid from the host or synthesizes it, employing relevant enzymes transferred from the host cell, like mitochondria do.

Another prominent feature of the *Buchnera* genome is that genes for various regulatory systems are almost completely missing. Among these are two-component regulatory systems, which generally control gene expression in response to environmental changes. In addition, all the other types of transcriptional regulators, except *dnaA*, are missing. Indeed, no transcriptional regulator of amino-acid biosynthesis is present despite the conservation of many genes for amino-acid biosynthesis. Comparison of operon structure between *E. coli* and *Buchnera* indicates that genes of *Buchnera* do not have leader sequences, and that *Buchnera* is not equipped with a transcriptional attenuation system. Although *Buchnera* has PTSs, which are involved in catabolite repression through cyclic AMP in many bacteria, the genes for adenylate cyclase (*cyaA*) and cAMP receptor protein (*crp*) are absent, indicating the lack of transcriptional regulation for the response to carbon-source change. Instead, a carbon storage regulator CsrA might be involved in global post-trancriptional regulation of the carbohydrate metabolism[23] in *Buchnera*. The *Buchnera* genome contains only two predicted sigma factors, *rpoD* and *rpoH*. Other parasitic bacteria with small genomes, such as *M. genitalium* and *Rickettsia prowazekii*, have also lost large parts of their regulatory systems. However these organisms have also lost the genes that are normally under the control of the regulators. *Buchnera* is unique in lacking regulatory genes, but having their regulatees. It is possible that the loss of regulatory genes is a consequence of the homeostatic environment in which *Buchnera* has been housed for so long.

To evaluate the evolution of the characteristic gene set in *Buchnera*, we tried to reconstruct the history of *Buchnera*. First, we determined the evolutionary position of *Buchnera* among prokaryotes. We made orthologue groups of all ORFs in 23 complete prokaryotic genomes. For each group, we constructed a molecular phylogenetic tree and inferred the most plausible phylogeny of *Buchnera* and its relatives by searching for the most frequent sub-tree of the same topology that included one or more *Buchnera* genes or domains. The results indicate that after the speciation of *R. prowazekii*, *Buchnera* then diverged from the lineage to *E. coli* and *H. influenzae*, although a certain number of trees support the topology in which the closest relative of *E. coli* is *Buchnera*. To see whether the *Buchnera* genome is small because the genome of the last common ancestor (LCA) of *Buchnera*, *E. coli* and *H. influenzae* was as small as that of *Buchnera*, or because of gene loss in *Buchnera* after speciation, we inferred the gene set of the LCA. The gene set of *Buchnera*, excluding a few genes, is a small subset of that of the LCA, and many genes of the LCA were missing in *Buchnera*, such as those for non-essential amino-acid metabolism. In addition, no *Buchnera*-specific duplicated gene was found. These results strongly indicate that the small *Buchnera* genome is the result of reductive evolution.

The gene repertoire of the *Buchnera* genome is so specialized to intracellular life that it cannot survive outside the eukaryotic cell. Although the features of genome size reduction and heavy reliance on the host are shared between obligatory parasites and *Buchnera*, the gene sets show a marked difference in the manner of dependency between these two types of organisms. Whereas parasites depend upon nutrients from the host commensally, *Buchnera* provides nutrients to the host, using host-derived precursors. Moreover, *Buchnera* even seems to owe its membrane bilayer to the host and requires the host's protective environment. In this view, *Buchnera* is similar to organelles, which also require the endocellular environment of the host cells and make a contribution to the host, for example, in energy production.

This study is the first case where genomic evolution of a mutualistic organism is revealed at the genomic level. Although this kind of organism has been difficult to study experimentally because of its absolute mutualism, this genomic data should promote experimental approaches to symbiosis, and further experimental data may give us an even deeper insight into the evolutionary significance of tight interspecies associations. □

Methods

Whole genome random shotgun sequencing

We prepared genomic DNA from the APS strain of *Buchnera* sp. harboured by the pea aphid, *Acyrthosiphon pisum* (Harris). *A. pisum* is a long-established parthenogenetic clone maintained on young broad bean plants, *Vicia faba* (L.), at 15 °C under a long-day regime of 18 h light and 6 h dark. We collected the bacteriocytes by dissecting 2,000 pea aphids in buffer A (35 mM Tris-HCl (pH 7.5), 25 mM KCl, 10 mM MgCl₂, 250 mM sucrose). The bacteriocytes were crushed by pipetting and subjected to filtration through a 5-μm filter to obtain *Buchnera*.

We prepared genomic DNA from *Buchnera* cells by a standard phenol/chloroform protocol. The shotgun sequence libraries were prepared as described[24], except that we used vectors with cohesive ends (one with a T-overhang and one partially filled) to avoid chimaera formation. Briefly, the genomic DNA fragments were hydrodynamically sheared using HydroShear (GeneMachines), blunt-ended and subjected to A-tailing. The A-tailed fragments were ligated with pGEM-T Easy vector (Promega). The method of using partially filled-in restriction endonuclease fragments has been described[25]. The sequences were assembled using PHRED (P. Green and B. Ewing, University of Washington) and PHRAP (P. Green, University of Washington) and the consensus sequence was checked and edited using CONSED (D. Gordon, University of Washington). The gaps between the contigs were closed by primer walking. About 7-fold genome coverage was achieved by 9,747 sequencing reactions. According to CONSED, the overall error probability was estimated at less than 0.01%. The sizes of the predicted restriction endonuclease fragments coincided with the physical map[5].

Informatics

We used two strategies for identifying ORFs. An initial set of ORFs likely to encode proteins was identified by the GeneHacker program, a system for gene structure prediction using a hidden Markov model (HMM)[26]. Both predicted ORFs and the intergenic regions were compared against a non-redundant protein database using the BLAST (D. Altschul, *et al.*, NCBI) programs. Combining these results, we identified and annotated the ORFs. Frameshifts were detected and corrected where appropriate as described[27]. The isoelectric point for each protein was predicted using the ISOELECTRIC program in the GCG analysis suite (Genetics Computer Group). Possible metabolic pathways were examined using the online service KEGG[28].

Comparative genomic analysis was performed, using 23 complete prokaryotic genomes: *Haemophilus influenzae* (NC_000907), *Mycoplasma genitalium* (NC_000908), *Methanococcus jannaschii* (NC_000909), *Synechocystis* sp. (NC_000911), *Mycoplasma pneumoniae* (NC_000912), *Helicobacter pylori* 26695 (NC_000915), *Helicobacter pylori* J99 (NC_000921), *Escherichia coli* (NC_000913), *Methanobacterium thermoautotrophicum* (NC_000916), *Bacillus subtilis* (NC_000964), *Archaeoglobus fulgidus* (NC_000917), *Borrelia burgdorferi* (NC_001318), *Aquifex aeolicus* (NC_000918), *Pyrococcus horikoshii* (NC_000961), *Pyrococcus abyssi* (NC_000868), *Mycobacterium tuberculosis* (NC_000962), *Treponema pallidum* (NC_000919), *Chlamydia trachomatis* (NC_000117), *Rickettsia prowazekii* (NC_000963), *Chlamydia pneumoniae* (NC_000922), *Aeropyrum pernix* (NC_000854), *Thermotoga maritima* (NC_000853) and *Buchnera* sp. APS. See Supplementary Information. These sequence data, except the *Buchnera* genome, were obtained from Entrez Genomes at NCBI website (http://ww.ncbi.nlm.nih.gov/entrez/query.fcgi?db = Genome).

Paralogue and orthologue analyses were performed on the amino-acid sequences of all the predicted genes based on the BLAST bit scores. Species-specific duplicated genes were defined as paralogues of the same species that were more similar to each other than to any genes of other species. Orthologue groups were determined using an orthologue identification method[29], by taking into account gene duplications after speciation and multi-domain structures. For each orthologue group, the following analyses were carried out with our original script package, Whole genome Analysis Tools (WAT), for automated phylogenetic analyses: multiple alignment construction with CLUSTALW (J. Thompson *et al.*. NCBI), extraction of conserved regions, using a program, xcons (H. W., unpublished), calculation of the distances between the group members with the PROTDIST program of the PHYLIP program package (J. Felsenstein, University of Washington), and construction of a neighbour-joining tree. Conserved regions were defined as the common segments in the CLUSTALW alignment, all possible pairs of which should show positive alignment scores using a local alignment scoring method.

The gene set in the LCA was inferred by a simple cladistical methodology. For a given tree topology, the gene set in the LCA of a clade is inferred from the assumption that the LCA had an ancestral gene for each orthologue group identified between the sister groups of the LCA or between descendant of the LCA and outgroup of the clade radiating from the LCA. This is a reasonable assumption as orthologous genes are defined as descendants of a single ancestral gene in the LCA inherited by different species, and an ancestral species should have had an ancestral orthologue corresponding to an orthologue pair identified between the descendant and the ancestor/outgroup. The actual gene set of the LCA may be larger than the one inferred as some genes could have been lost or evolved rapidly in either or both of the sister groups. The gene list of the LCA of *Buchnera*, *E.coli*, and *H. influenzae*, and the information on the WAT scripts used for this LCA analysis is available on request.

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Cloned pigs produced by nuclear transfer from adult somatic cells

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Since the first report of live mammals produced by nuclear transfer from a cultured differentiated cell population in 1995 (ref. 1), successful development has been obtained in sheep[2,3], cattle[4], mice[5] and goats[6] using a variety of somatic cell types as nuclear donors. The methodology used for embryo reconstruction in each of these species is essentially similar: diploid donor nuclei have been transplanted into enucleated MII oocytes that are activated on, or after transfer. In sheep[2] and goat[6] preactivated oocytes have also proved successful as cytoplast recipients. The reconstructed embryos are then cultured and selected embryos transferred to surrogate recipients for development to term. In pigs, nuclear transfer has been significantly less successful; a single piglet was reported after transfer of a blastomere nucleus from a four-cell embryo to an enucleated oocyte[7]; however, no live offspring were obtained in studies using somatic cells such as diploid or mitotic fetal fibroblasts as nuclear donors[8,9]. The development of embryos reconstructed by nuclear transfer is dependent upon a range of factors. Here we investigate some of these factors and report the successful production of cloned piglets from a cultured adult somatic cell population using a new nuclear transfer procedure.

To date, the efficiency of somatic cell nuclear transfer, when measured as development to term as a proportion of oocytes used, has been very low (1–2%)[10]. A variety of factors probably contribute to this inefficiency. These include laboratory to laboratory variation, oocyte source and quality, methods of embryo culture (which are more advanced in some species (such as cows) than others (such as pigs)), donor cell type, possible loss of somatic imprinting in the nuclei of the reconstructed embryo, failure to reprogram the transplanted nucleus adequately, and finally, the failure of artificial methods of activation to emulate reproducibly those crucial membrane-mediated events that accompany fertilization.

In the pig, there is the additional difficulty that several (> 4) good quality embryos are required to induce and maintain a pregnancy[11]. As fully developmentally competent embryos are rare in nuclear transfer procedures, there is every chance of squandering those good embryos unless very large numbers of reconstructed embryos are transferred back into recipients. Even if it were possible in the pig to select good quality blastocysts for transfer (after, for example, the use of a temporary recipient), most blastocysts formed from reconstructed embryos in other species are not competent to proceed to term[10]. The co-transfer of reconstructed embryos with 'helper', unmanipulated embryos, parthenotes or tetraploid embryos has been suggested as an aid to inducing and maintaining pregnancy. However, studies in mice after zygote pronuclear injection have suggested that the manipulated embryos are 'compromised' and selected against[12]. An alternative to the use of 'helper' embryos is the hormonal treatment of recipient sows to maintain pregnancy with low embryo numbers[13].

We cannot currently address all of the methodological problems, and, to improve our chances of success in pig nuclear

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