MvaT proteins in *Pseudomonas* spp.: a novel class of H-NS-like proteins

The H-NS protein was isolated for the first time from *Escherichia coli* as a contaminant in RNA polymerase preparations (Jacquet *et al.*, 1971). A few years later, on the basis of nucleotide sequence homology, H-NS proteins were identified by different groups in other enteric or related bacteria such as *Proteus mirabilis*, *Serratia marcescens*, *Salmonella typhimurium* and *Erwina chrysanthemi* (Ussery *et al.*, 1994). Moreover, by *in silico* analysis of the first completely sequenced bacterial genome, an additional H-NS-related protein was detected in *Haemophilus influenzae* (Fleischmann *et al.*, 1995). Finally, a paralogous protein named StpA was found in both *Escherichia coli* and *Salmonella typhimurium* (Dorman *et al.*, 1999). All these proteins display more than 70%
amino acid sequence identity, indicating that they belong to the same protein family.

Initially, H-NS proteins were thought to be restricted to members of the Enterobacteriaceae and related bacteria (Atlung & Ingerm, 1997), until the discovery of the first H-NS-like protein outside this group. Indeed, by biochemical methods, the so-called BphH3 protein was isolated from Bordetella pertussis, a non-enteric Gram-negative bacterium belonging to the β-Proteobacteria. The protein sequence shows only 40% identity with the E. coli H-NS protein but is able to reverse H-NS deficiency in an E. coli mutant strain (Goyard & Bertin, 1997). Consequently, these data raised new perspectives concerning the existence of such proteins in phylogenetically distant bacterial species. Taking advantage of the serine susceptibility on minimal medium of an E. coli hns mutant strain, we recently isolated several H-NS-related proteins from various bacteria, for example, Vibrio cholerae, the pathogen of cholera disease (Tendeng et al., 2000), Yersinia enterocolitica, responsible for gastroenteritis in humans (Bertin et al., 2001), Photobacterium luminescens, an entomopathogenic bacterium (Tendeng, 2002), and Psychrobacter TAD1, a psychrophilic micro-organism isolated in Antarctica (Tendeng et al., 2003).

Except for enterobacteria, where H-NS has been shown to control the expression of many genes, for example, in E. coli (Hommaias et al., 2001), the role in bacterial physiology of most H-NS-related proteins remains unknown. However, they constitute a family of proteins displaying an evolutionarily conserved structural and functional organization in two modules (Dorman et al., 1999; Bertin et al., 1999). The N-terminal oligomerization domain displays strong amino acid sequence divergence but is predicted to adopt an α-helix structure in all H-NS proteins (Bertin et al., 1999, 2001), consistent with the recent three-dimensional structure of this domain in H-NS of E. coli (Renzoni et al., 2001; Bloch et al., 2003). Unlike the N-terminal part, the C-terminal DNA-binding domain displays a strong consensus motif in the proteins characterized so far, with six strictly conserved residues Y-x(6)-[GS]-[ED]-x(0,2)-T-W-[TS]-G-[QR]-G-[RK]-x-P-x(4,5)-A-x(3,4)-G (Bertin et al., 2001). These observations suggest that all H-NS-related proteins have the capacity to bind DNA via their C-terminal part and the propensity to form oligomers by their N-terminal domain. Both properties may explain why the proteins examined so far can restore the wild-type phenotype in an E. coli hns mutant strain (Bertin et al., 1999, 2001).

To date, no H-NS protein has been characterized in Gram-positive bacteria or in archaea. Surprisingly, within Gram-negative bacteria, no H-NS-related protein has been identified in Pseudomonas strains, which, along with the enteric bacteria, belong to the γ-Proteobacteria. Pseudomonas spp. are known for their ability to use a-glucoside as a sole carbon and energy source, as observed previously with other H-NS-like proteins (Goyard & Bertin, 1997; Bertin et al., 1999, 2001; Tendeng et al., 2000). This strongly suggests that the protein we characterized belongs to the H-NS family and shares the same structural and functional organization as members of this family despite the unusually low amino acid conservation.

The comparison of the Pseudomonas strain Y1000 revealed the presence of a complete coding sequence (CDS) of 366 bp, in the opposite orientation with respect to the resident lac promoter. A putative ribosome-binding site was identified 5 bp upstream from the ATG start codon. Minus 35 and –10 hexamers showing 67% similarity with the σ70 consensus of E. coli separated by an 18 bp spacer were identified 49 bp upstream from this translational initiation codon. A motif reminiscent to the Y box recognized by nucleic-acid-binding protein, i.e. CAAAT, was identified 16 bp upstream from the ATG start codon. Interestingly, such a motif has also been identified as a putative cold-box upstream of the coding sequence of H-NS in E. coli (La Teana et al., 1991), as well as in V. cholerae (Tendeng et al., 2000) and Y. enterocolitica (Bertin et al., 2001). The CDS encodes a putative protein of 121 aa with a predicted molecular mass of 13 614 kDa and a pI of 10 62 (EMBL accession no. AJ567347).

Surprisingly, this putative protein showed no significant homology with any known H-NS-related protein (e.g. 18% identity with the E. coli H-NS protein), even in the C-terminal domain that did not display the H-NS consensus sequence. Nevertheless, like the other members of the H-NS family, the N-terminal domain of the Pseudomonas strain Y1000 protein is predicted to be mainly α-helical and to adopt a coiled-coil conformation, while the C-terminal domain is a mixed α/β structure (data not shown). Moreover, using FROST, a fold-recognition method (http://www-mig.jouy.inra.fr), this domain was predicted to share the same three-dimensional structure as the E. coli H-NS C-domain resolved previously by NMR (Shindo et al., 1995). Finally, the expression of the strain Y1000 protein structural gene in an E. coli mutant fully reversed additional hns-related phenotypes, for example, the loss of motility on semi-solid medium and the ability to use β-glucoside as a sole carbon source, as observed previously with other H-NS-like proteins (Goyard & Bertin, 1997; Bertin et al., 1999, 2001; Tendeng et al., 2000).
Y1000 H-NS-like protein amino acid sequence with all sequences present in databases revealed approximately 50% identity with MvaT, a transcriptional activator that participates in the control of mevalonate metabolism in *Pseudomonas mevalonii* (Rosenthal et al., 1998). By scanning complete and unfinished bacterial genome sequences, we identified at least one homologous protein in each *Pseudomonas* species. Indeed, two putative proteins are present in *Pseudomonas aeruginosa*, three in *Pseudomonas fluorescens*, four in *Pseudomonas syringae* and five in *Pseudomonas putida*. In addition, an orthologous protein was identified in *Azotobacter vinelandii*, a bacterium belonging to the family *Pseudomonadaceae* (Fig. 1). All these proteins display at least 47% amino acid identity. Except for the MvaT proteins of *P. mevalonii* and *P. aeruginosa*, which possess a regulatory role in mevalonate metabolism and in virulence gene expression, respectively (Rosenthal et al., 1998; Diggle et al., 2002), the function of the *Pseudomonas* H-NS-related proteins remains unknown and some have been annotated as hypothetical proteins. Overexpression of the *hns*-like gene of *Pseudomonas* strain Y1000 in the same strain from the low-copy-number vector pDIA584, i.e. a pBBR1MCS derivative (Kovach et al., 1994) carrying this gene, resulted in a significant reduction in motility on semi-solid medium (12 mm of swarming ring at 25°C as compared to 20 mm for the control with pBBR1MCS alone). This suggests that, like H-NS in *E. coli* (Bertin et al., 1999; Soutourina et al., 1999, 2001), the protein described here may play a role in the control of bacterial motility, at least in *Pseudomonas* strain Y1000. This is in accordance with the recently reported altered swarming ability of an *mvaT* mutant strain of *P. aeruginosa* (Diggle et al., 2002).

Taken together, these observations suggest that, despite a low amino acid conservation, proteins structurally and functionally related to H-NS in *E. coli* are even more widespread than thought previously. The comparison of these proteins in terms of structure and function may help in the future to understand the properties of H-NS itself, in particular with respect to protein–protein interactions and DNA-binding specificity. More generally,

![Fig. 1. MvaT proteins of *Pseudomonas* spp. and the H-NS family. Unfinished bacterial genome sequences were obtained from the Genomes OnLine Database (http://igweb.integratedgenomics.com/GOLD). H-NS-related sequences are from bacteria of the α-Proteobacteria (*Rhodobacter sphaeroides* and *Rhodobacter capsulatus*), β-Proteobacteria (*Bordetella pertussis*) and γ-Proteobacteria (*Escherichia coli*, *Yersinia enterocolitica*, *Vibrio cholerae*, *Psychrobacter TAD1*, *Xanthomonas axonopodis*, *Xylella fastidiosa*, *Pseudomonas* strain Y1000, *P. fluorescens*, *P. syringae*, *P. putida*, *P. aeruginosa* and *P. mevalonii*). (a) Structurally based alignment of H-NS-related proteins. The alignments were achieved using the program CLUSTAL W and refined manually as described previously (Bertin et al., 1999, 2001; Tendeng et al., 2003). Identical residues are in black boxes and similar residues are in grey boxes, with a threshold of 70%. (b) Phylogenetic tree constructed by using a cluster algorithm from the GeneBee – Molecular Biology Server (http://www.genebee.msu.su).
such studies may lead to a better understanding of chromosome organization and the regulation of gene expression in bacterial cells.

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