RAMA UNIVERSITY

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FACULTY OF ENGINEERING &TECHNOLOGY
DEPARTMENT OF BIOTECHNOLOGY

Detailed mechanism

The glucose PTS system in *E. coli* and *B. subtilis*. The mannose PTS in *E. coli* has the same overall structure as the *B. subtilis* glucose PTS, i.e. the IIABC domains are fused into one protein.

In the process of glucose **PTS** transport specific of enteric bacteria, **PEP** transfers its phosphoryl to a histidine residue on **EI**. **EI** in turn transfers the phosphate to **HPr**.

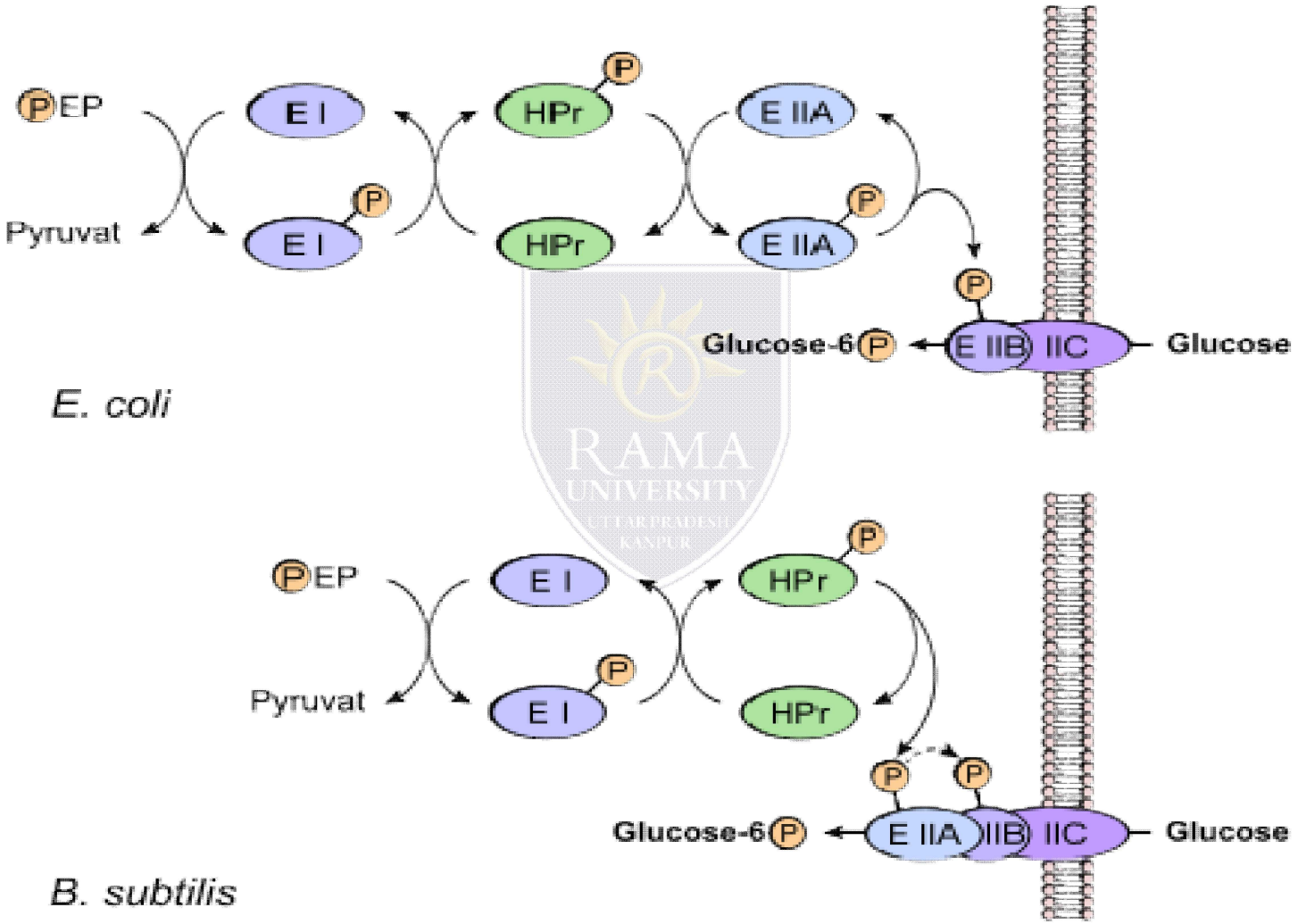
From **HPr** the phosphoryl is transferred to **EIIA**. **EIIA** is specific for glucose and it further transfers the phosphoryl group to a juxtamembrane **EIIB**.

Finally, **EIIB** phosphorylates glucose as it crosses the plasma membrane through the transmembrane Enzyme II C (**EIIC**), forming glucose-6-phosphate.

The benefit of transforming glucose into glucose-6-phosphate is that it will not leak out of the cell, therefore providing a one-way concentration gradient of glucose. The **HPr** is common to the phosphotransferase systems of the other substrates mentioned earlier, as is the upstream **EI**.

Proteins downstream of **HPr** tend to vary between the different sugars.

The transfer of a phosphate group to the substrate once it has been imported through the membrane transporter prevents the transporter from recognizing the substrate again, thus maintaining a concentration gradient that favours further import of the substrate through the transporter.


PEP
Pyruvat
E I
E I
HPr
HPr
E IIA
E IIA
Glucose-6
E IIB
IIC
Glucose
E. coli
PEP
Pyruvat
E I
E I
HPr
HPr
Glucose-6
E IIA
IIB
IIC
Glucose
B. subtilis

Tat pathway:

The twin-arginine translocation pathway (Tat pathway) is a protein export or secretion pathway found in plants, bacteria, and archaea.

In contrast to the Sec pathway which transports proteins in an unfolded manner, the Tat pathway serves to actively translocate folded proteins across a lipid membrane bilayer.

In bacteria, the Tat translocase is found in the cytoplasmic membrane and serves to export proteins to the cell envelope or to the extracellular space.

In Gram-negative bacteria the Tat translocase is composed of three essential membrane proteins: TatA, TatB, and TatC. In Gram-negative bacterium *Escherichia coli,* these three proteins are expressed from an operon with a fourth Tat protein, TatD, which is not required for Tat function.

A fifth Tat protein TatE that is homologous to the TatA protein is present at a much lower level in the cell than TatA. It is not believed to play any significant role in Tat function.

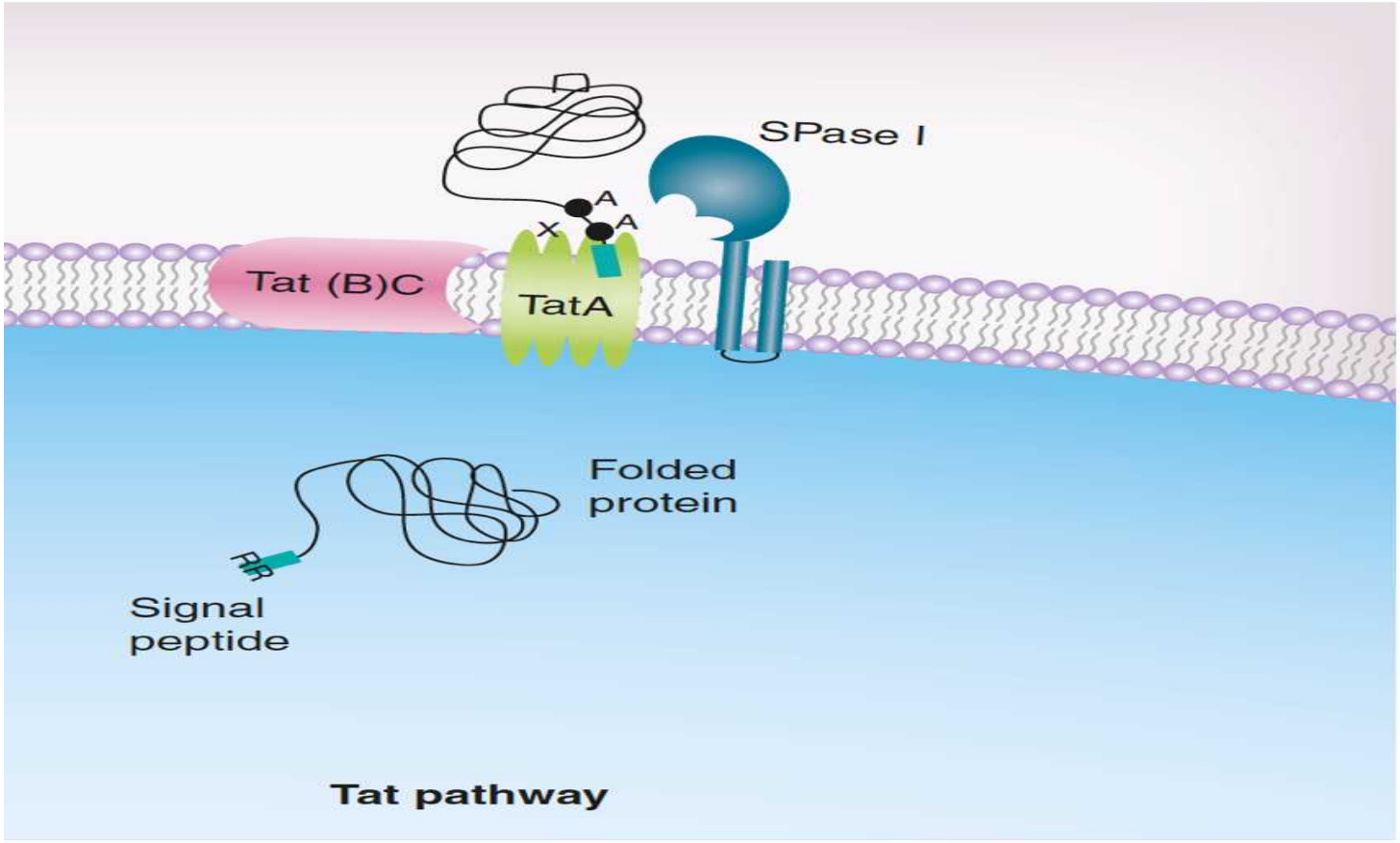
The Tat pathways of Gram-positive bacteria differ in that they do not have a TatB component.

In these bacteria the Tat system is made up from a single TatA and TatC component, with the TatA protein being bifunctional and fulfilling the roles of both E. coli TatA and TatB.

Not all bacteria carry the tatABC genes in their genome.
However, of those that do, there seems to be no discrimination between pathogens and nonpathogens.

Despite that fact, some pathogenic bacteria such as *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Yersinia pseudotuberculosis*, *and E. coli O157:H7* rely on a functioning Tat pathway for full virulence in infection models.
In addition, a number of exported virulence factors have been shown to rely on the Tat pathway.

One such category of virulence factors are the phospholipase C enzymes, which have been shown to be Tat-exported in *Pseudomonas aeruginosa* and thought to be Tat-exported in *Mycobacterium tuberculosis*.


SPase I
A
X
A
Tat (B)C
TatA
Folded
protein
RR
Signal
peptide
Tat pathway