



The xylan utilization system of the plant pathogen *Xanthomonas campestris* pv *campestris* controls epiphytic life and reveals common features with oligotrophic bacteria and animal gut symbionts

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Résumé en anglais	Xylan is a major structural component of plant cell wall and the second most abundant plant polysaccharide in nature. Here, by combining genomic and functional analyses, we provide a comprehensive picture of xylan utilization by <i>Xanthomonas campestris</i> pv <i>campestris</i> (Xcc) and highlight its role in the adaptation of this epiphytic phytopathogen to the phyllosphere. The xylanolytic activity of Xcc depends on xylan-deconstruction enzymes but also on transporters, including two TonB-dependent outer membrane transporters (TBDTs) which belong to operons necessary for efficient growth in the presence of xylo-oligosaccharides and for optimal survival on plant leaves. Genes of this xylan utilization system are specifically induced by xylo-oligosaccharides and repressed by a LacI-family regulator named XylR. Part of the xylanolytic machinery of Xcc, including TBDT genes, displays a high degree of conservation with the xylose-regulon of the oligotrophic aquatic bacterium <i>Caulobacter crescentus</i> . Moreover, it shares common features, including the presence of TBDTs, with the xylan utilization systems of <i>Bacteroides ovatus</i> and <i>Prevotella bryantii</i> , two gut symbionts. These similarities and our results support an important role for TBDTs and xylan utilization systems for bacterial adaptation in the phyllosphere, oligotrophic environments and animal guts.
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