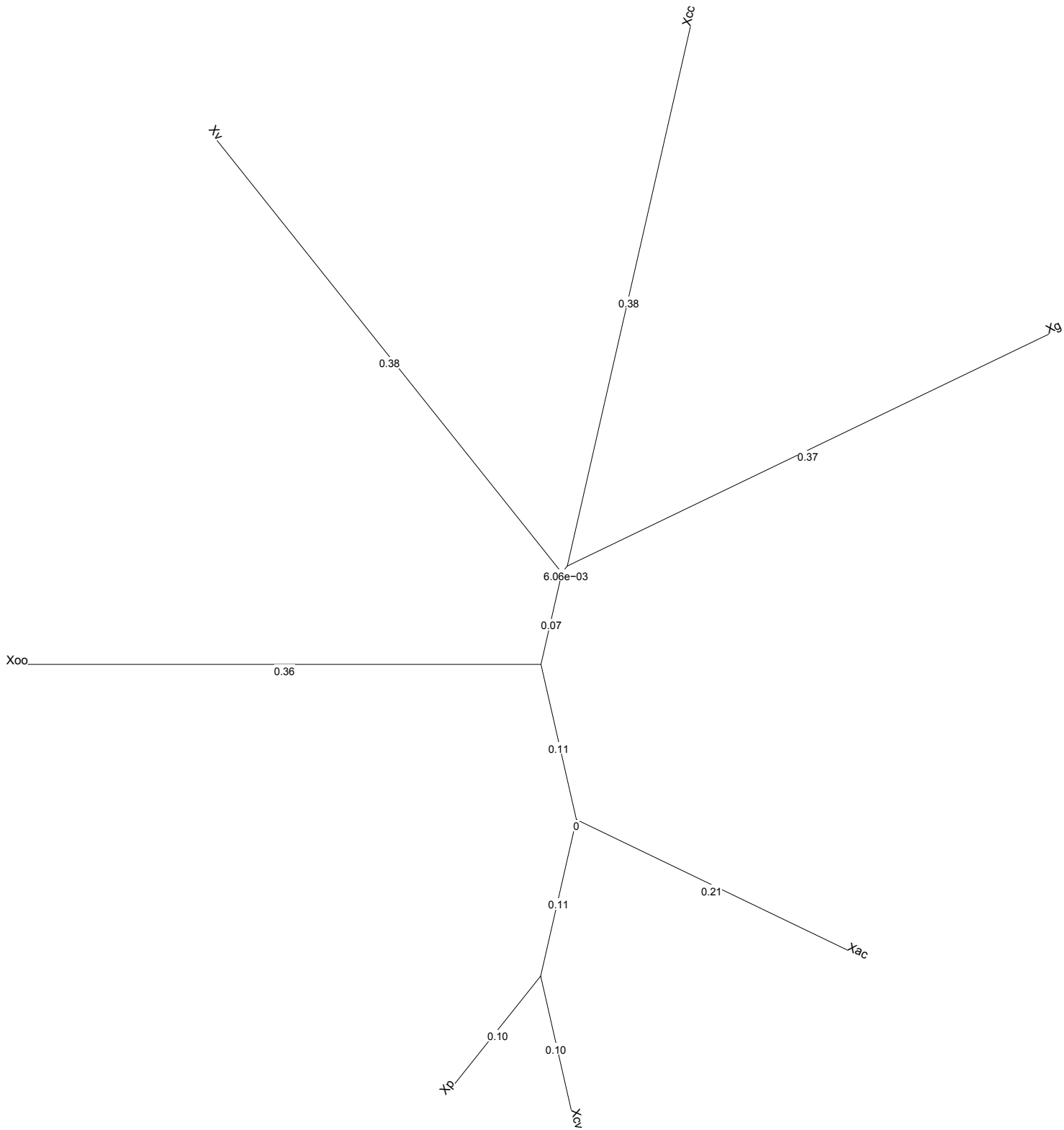


**Additional file 2** – Figure S2: 1a) Phylogenetic tree based on MUMi indices; 1b) Distance matrix based on MUMi indices. MUMi program was used to calculate pairwise distances between draft genomes and reference *Xanthomonas* genomes.



	<b>Xac</b>	<b>Xcc</b>	<b>Xoo</b>	<b>Xcv</b>	<b>Xv</b>	<b>Xp</b>	<b>Xg</b>
<b>Xac</b>	0	0.77	0.67	0.41	0.76	0.41	0.75
<b>Xcc</b>	0.77	0	0.81	0.77	0.77	0.77	0.75
<b>Xoo</b>	0.67	0.81	0	0.67	0.80	0.67	0.79
<b>Xcv</b>	0.41	0.77	0.67	0	0.76	0.19	0.76
<b>Xv</b>	0.76	0.77	0.80	0.76	0	0.76	0.76
<b>Xp</b>	0.41	0.77	0.67	0.19	0.76	0	0.76
<b>Xg</b>	0.75	0.75	0.79	0.76	0.76	0.76	0