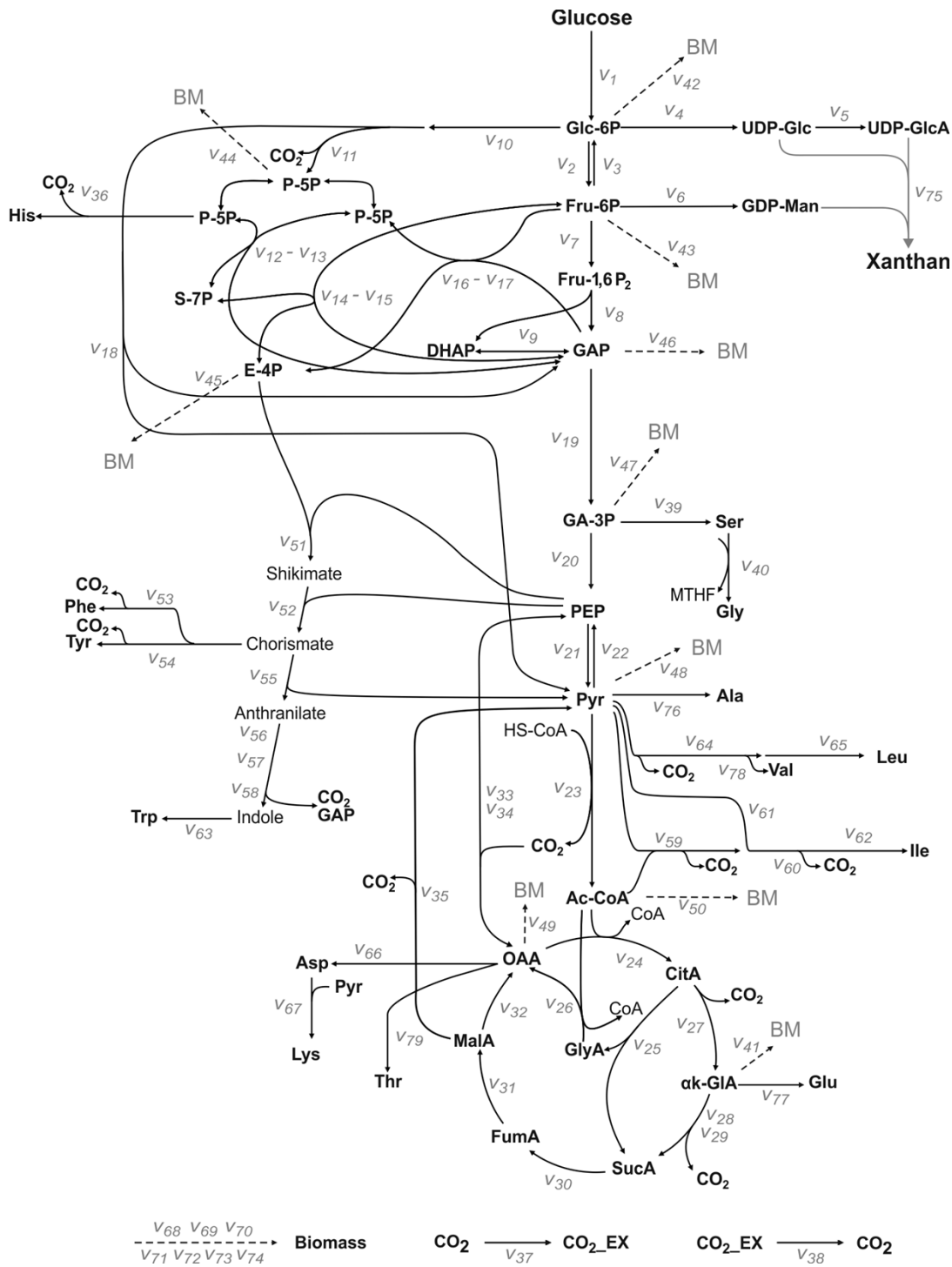


**Metabolic flux pattern of glucose utilization by the phytopathogen and xanthan-producer
Xanthomonas campestris pv. *campestris*: prevalent role of the Entner-Doudoroff pathway and
minor fluxes through the pentose phosphate pathway and through glycolysis**

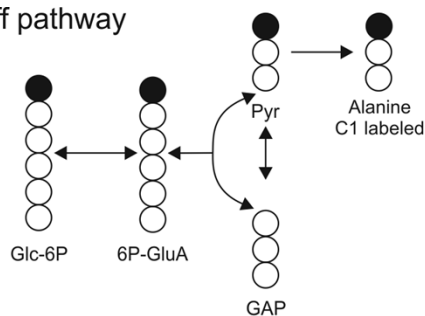
Sarah Schatschneider, Claudia Huber, Heiko Neuweiger, Tony Francis Watt, Alfred Pühler, Wolfgang Eisenreich,
Christoph Wittmann, Karsten Niehaus, Frank-Jörg Vorhölter

Supplementary Data

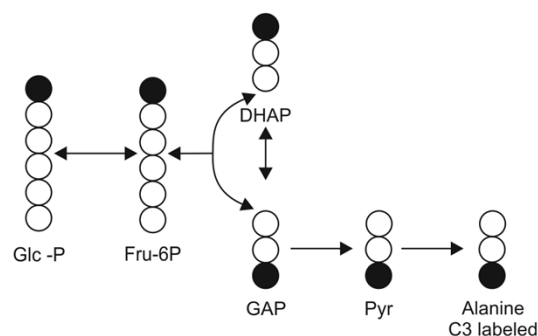


Supplementary Figure 1. Graphical display of the *X. campestris* pv. *campestris* B100 metabolic network employed to establish a model for ^{13}C metabolic flux analysis. The metabolic network underlying the model includes the Embden-Meyerhof-Parnas pathway, the pentose phosphate pathway, the Entner-Doudoroff pathway, gluconeogenesis, the tricarboxylic acid cycle, biosynthesis of xanthan precursors, and lumped reactions for the amino acids biosyntheses of alanine (Ala), valine (Val), aspartate (Asp), glutamate (Glu), serine (Ser), phenylalanine (Phe), glycine (Gly), tyrosine (Tyr), threonine (Thr), tryptophan (Trp), isoleucine (Ile), histidine (His), lysine (Lys) and leucine (Leu). The reactions with ID numbers colored in grey are detailed in Supplementary Table 1. Glc-6P, glucose 6-phosphate; Fru-6P, fructose 6-phosphate; Fru-1,6P₂, fructose 1,6-bisphosphate; P-5P, pentose 5-phosphate; S-7P, sedoheptulose 7-phosphate; E-4P, erythrose 4-phosphate, GAP, glyceraldehyde 3-phosphate; DHAP, dihydroxyacetone phosphate; GA3P, 3-Phosphoglycerate; PEP, phosphoenolpyruvate; Pyr, pyruvate; Ac-CoA, acetyl-CoA; CitA, citrate; αk-GIA, α-ketoglutarate (2-oxoglutarate); SucA, succinate; FumA, fumarate, MalA, malate; OAA, oxaloacetate; CO₂, carbon dioxide.

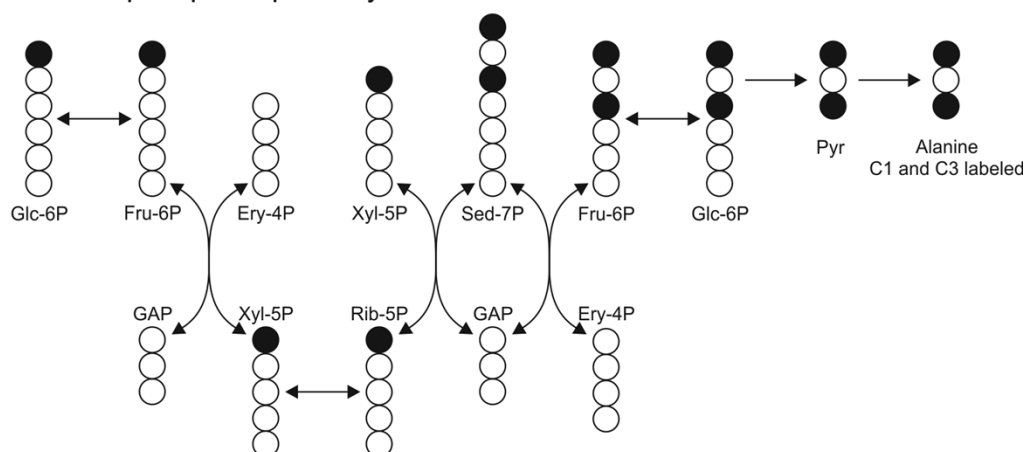
A Entner-Doudoroff pathway



B Embden-Meyerhof-Parnas pathway



C Pentose phosphate pathway: reversible reactions of the non-oxidative branch



Supplementary Figure 2. Distribution of ^{13}C labeling pattern derived from 1- ^{13}C glucose through the three main pathways of the *X. campestris* pv. *campestris* carbohydrate catabolism leading to labeling of the amino acid alanine. Carbon atoms are symbolized by open circles. Shaded circles indicate ^{13}C labeling of the respective C atom. **(A)** The ED pathway generates alanine precursors with labeled C1. **(B)** Activity of the EMP pathway leads to labeling of the alanine C3. **(C)** In the reversible reactions of the non-oxidative branch of the PP pathway, reactions of isomerization, transketolation and epimerization can result in labeling of the C1 and the C3 of alanine. Gluconeogenesis reactions that might add further complexity to the labeling pattern were not considered in this overview as we observed no indications for gluconeogenesis activity for the cultivation conditions underlying this study. Abbreviations: DHAP, dihydroxyacetone phosphate; Ery-4P, erythrose 4-phosphate; Fru-6P, fructose 6-phosphate; Glc-6P, glucose 6-phosphate; 6P-GluA, 6-Phosphogluconic acid; GAP, glyceraldehyde 3-phosphate; Pyr, pyruvate; Rib-5P, ribose 5-phosphate; Sed-7P, sedoheptulose 7-phosphate, Xyl-5P, xylulose 5-phosphate.

Supplementary Table 1

OpenFLUX model of *Xanthomonas campestris* pv. *campestris* B100

rxnID	rxnEQ	cTrans	rates	type	basis	deviation
R01	GLC_EX + ATP = GLC6P	abcdef + X = abcdef		F	100	0
R02	GLC6P = F6P	abcdef = abcdef		FR		
R03	F6P = GLC6P	abcdef = abcdef		R	X	
R04	GLC6P = UDPG	abcdef = abcdef		F		
R05	UDPG = UDPGA	abcdef = abcdef		F		
R06	F6P = GDPM	abcdef = abcdef		F		
R07	F6P + PPi = F16BP	abcdef + X = abcdef		F		
R08	F16BP = DHAP + G3P	abcdef = abc + def		F		
R09	DHAP = G3P	abc = cba		F		
R10	GLC6P = 6PG + NADH	abcdef = abcdef + X		F		
R11	6PG = P5P + CO2 + NADH	abcdef = bcdef + a + X		F	X	
R12	P5P + P5P = S7P + G3P	abcde + fghij = fgabcde + hij		FR		
R13	S7P + G3P = P5P + P5P	fgabcde + hij = abcde + fghij		R	X	
R14	S7P + G3P = E4P + F6P	abcdefg + hij = defg + abchij		FR		
R15	E4P + F6P = S7P + G3P	defg + abchij = abcdefg + hij		R	X	
R16	E4P + P5P = F6P + G3P	abcd + efghi = efabcd + ghi		FR		
R17	F6P + G3P = E4P + P5P	efabcd + ghi = abcd + efghi		R	X	
R18	6PG = G3P + PYR	abcdef = def + abc		F	X	
R19	G3P = 3PG + ATP + NADH	abc = abc + X + X		F		
R20	3PG = PEP	abc = abc		F		
R21	PEP = PYR + ATP	abc = abc + X		FR		
R22	PYR + ATP = PEP	abc + X = abc		R	X	
R23	PYR = ACCOA + CO2 + NADH	abc = bc + a + X		F		
R24	ACCOA + OAA = CIT	ab + cdef = fedbac		F		
R25	CIT = GLYOXY + 0.5 SUC + 0.5 SUC	abcdef = ab + 0.5 cdef + 0.5 fedc		F	X	
R26	ACCOA + GLYOXY = OAA	ab + cd = cdab		F		
R27	CIT = AKG + CO2 + NADH	abcdef = abcde + f + X		F		
R28	AKG = SUCCOA + CO2 + NADH	abcde = bcde + a + X		F		
R29	SUCCOA = 0.5 SUC + 0.5 SUC + ATP	abcd = 0.5 abcd + 0.5 dcba + X		F		
R30	SUC = FUM + FADH2	abcd = dcba + X		F		
R31	FUM = MAL	abcd = bcad		F		
R32	MAL = OAA + NADH	abcd = acbd + X		F		
R33	OAA = PEP + CO2	abcd = abc + d		FR		
R34	PEP + CO2 = OAA	abc + d = abcd		R	X	
R35	MAL = PYR + CO2 + NADH	abcd = abc + d + X		F	X	
R36	P5P + CO2 + ATP + ATP + ATP + ATP +	abcde + f + X + X + X + X + X = edcbaf		F		
R37	CO2 = CO2_EX	a = a		FR		
R38	CO2_EX = CO2	a = a		R	X	
R39	3PG = SER + NADH	abc = abc + X		F		
R40	SER = GLY + MTHF	abc = ab + c		F		
R41	AKG = AKG_B			B	4.172	0.6827
R42	GLC6P + ATP = GLC6P_B			B	1.1825	0.1935
R43	F6P = F6P_B			B	0.4081	0.0688
R44	P5P = P5P_B	abcde = abcde		F	4.1565	0.68015

Supplementary Table 1

OpenFLUX model of *Xanthomonas campestris* pv. *campestris* B100

R45	E4P = E4P_B	abcd = abcd	F	1.9457	0.3184
R46	G3P = G3P_B		B	1.1825	0.1935
R47	3PG = 3PG_B	abc = abc	F	7.461	0.1935
R48	PYR = PYR_B	abc = abc	F	8.3069	1.22
R49	OAA = OAA_B	abcd = abcd	F	7.245	1.19
R50	ACCOA = ACCOA_B	ab = ab	F	19.717	1.185
R51	E4P_B + PEP = SHKM	abcd + efg = efgabcd	F		
R52	SHKM + PEP = CHRM	abcdefg + hij = abcdefghij	F		
R53	CHRM + ATP + NADH = PHEX + CO2	abcdefghij + X + X = hijbcdefg + a	F		
R54	CHRM + NADH + ATP = TYRX + CO2 +	abcdefghij + X + X = hijbcdefg + a + X	F		
R55	CHRM = ANTHR + PYR	abcdefghij = abcdefg + hij	F		
R56	ANTHR + P5P_B = CPADR5P	abcdefg + hijkl = abcdefghijkl	F		
R57	CPADR5P = INDG + CO2	abcdefghijkl = abcdghijkl + e	F		
R58	INDG = IND + G3P	abcdefghijk = abcdefgh + ijk	F		
R59	PYR_B + ACCOA_B = 2OBUT + CO2	abc + de = abdc + e	F		
R60	2OBUT + PYR_B = 2AHBUT + CO2	abcd + efg = abcdg + e	F		
R61	2AHBUT = 23DHMP	abcdef = abedcf	F		
R62	23DHMP + NADH = ILEX	abcdef + X = abcdef	F		
R63	IND + 3PG_B + ATP + ATP + ATP +	abcdefgh + ijk + X + X + X + X =	F		
R64	PYR_B + PYR_B = ISV + CO2	abc + def = abefc + d	F		
R65	ISV + ACCOA_B + NADH = LEUX +	abcde + fg + X = fgbcde + a + X	F		
R66	OAA_B = ASPX	abcd = abcd	F		
R67	ASPX + PYR_B + ATP + NADH + NADH	abcd + efg + X + X + X = abcdgf + e	F		
R68	P5P_B = P5P_BT		B		
R69	E4P_B = E4P_BT		B		
R70	PYR_B = PYR_BT		B		
R71	OAA_B = OAA_BT		B		
R72	ACCOA_B = ACCOA_BT		B		
R73	3PG_B = 3PG_BT		B		
R74	0.12 HIS + 0.376 GLY + 0.34 LEUX + 0.166 ILEX + 0.149 PHEX + 0.017 TRPX + 0.187		B	5.5	0.9
R75	0.4 GDPM + 0.4 UDPG + 0.2 UDPGA = XANTHAN				B 7.99 1.3
R76	PYR_B = ALAX	abc = abc			S
R77	AKG + NADH = GLUX	abcde + X = abcde			S
R78	PYR_B + PYR_B + NADH = VALX + CO2	abc + def + X = abefc + d			S
R79	OAA_B + ATP + ATP + NADH + NADH = THR	abcd + X + X + X + X = abcd			S
##	excludedMetabolites				
#	ATP				
#	NADH				
#	FADH2				
#	PPi				
#	MTHF				
#	GLC_EX				
#	THR_B				
#	ASP_B				
#	GLY_B				
#	AKG_B				

Supplementary Table 1OpenFLUX model of *Xanthomonas campestris* pv. *campestris* B100

#	ACETAL_B
#	GLC6P_B
#	F6P_B
#	P5P_BT
#	E4P_BT
#	G3P_B
#	3PG_BT
#	PYR_BT
#	OAA_BT
#	ACCOA_BT
#	BIOMASS
#	XANTHAN
#	CO2_EX
##	simulatedMDVs
#	ALAX#111
#	VALX#11111
#	ASPX#1111
#	GLUX#11111
#	SER#111
#	PHEX#111111111
#	GLY#11
#	TYRX#111111111
#	LEUX#011111
#	THR#1111
#	ALAX#011
#	VALX#01111
#	ASPX#1100
#	HIS#111111
#	SER#011
#	PHEX#110000000
#	GLY#01
#	TYRX#110000000
#	THR#0111
##	inputSubstrates
#	CO2_EX
#	GLC_EX

Supplementary Table 2 Confidence intervals for individual reaction rates using a nonlinear approach: calculated optimum of free fluxes and the associated 95% confidence interval

Reaction equation	fluxPar	opVal	low	high
GLC6P = F6P/F6P = GLC6P	v(2)-v(3)	3.6	2.3	4.4
F6P + PPi = F16BP	v(7)	2.4	1.7	2.8
GLC6P = 6PG + NADH	v(10)	90.4	89.6	91.8
6PG = P5P + CO2 + NADH	v(11)	9.4	7.9	11.4
P5P + P5P = S7P + G3P/S7P + G3P = P5P + P5P	v(12)-v(13)	2.2	2.0	2.7
S7P + G3P = E4P + F6P/E4P + F6P = S7P + G3P	v(14)-v(15)	2.2	2.0	2.7
E4P + P5P = F6P + G3P/F6P + G3P = E4P + P5P	v(16)-v(17)	0.2	0.0	0.7
GLC6P = G3P + PYR	v(18)	81.0	80.5	81.8
G3P = 3PG + ATP + NADH	v(19)	84.9	84.2	85.3
3PG = PEP	v(20)	75.4	74.7	75.8
PEP = PYR + ATP	v(21)	61.6	38.1	63.2
PYR + ATP = PEP	v(22)	0.2	0.0	1.0
PYR = ACCOA + CO2 + NADH	v(23)	134.2	132.5	136.6
ACCOA + OAA = CIT	v(24)	113.2	112.7	113.4
CIT = GLYOXY + 0.5 SUC + 0.5 SUC	v(25)	1.3	0.0	3.3
ACCOA + GLYOXY = MAL	v(26)	1.3	0.0	3.3
CIT = AKG + CO2 + NADH	v(27)	111.9	110.3	113.0
AKG = SUCCOA + CO2 + NADH	v (28)	107.7	106.1	108.9
SUCCOA = 0.5 SUC + 0.5 SUC + ATP	v(29)	107.7	106.1	108.9
SUC = FUM + FADH2	v(30)	109.0	108.5	109.2
FUM = MAL	v(31)	109.0	108.5	109.2
MAL = OAA + NADH	v(32)	109.0	87.0	109.2
PEP + CO2 = OAA/ OAA = PEP + CO2	v(34)- v(33)	10.1	8.2	33.5
MAL = PYR + CO2 + NADH	v(35)	0.0	0.0	27.4