H

	All			Active		
	flux [$\frac{nmol}{g\ FW\ s}$ C atoms]			**flux** [$\frac{nmol}{g\ FW\ s}$ C atoms]		
reaction	optimum	lower	upper	optimum	lower	upper
Starch synthesis	6.32	5.57	6.62	3.19	2.23	3.26
Sucrose synthesis	2.45	2.25	2.57	7.11	6.70	7.73
Carbon atoms lost via photorespiration	1.86	1.67	2.10	2.60	2.28	2.83
myo-inositol synthesis	0.057	0.056	0.064	0.050	0.049	0.051
Trehalose synthesis	0.00053	0.00055	0.00064	0.00050	0.00049	0.00052
Gross carbon fixation (RuBP carboxylation)	10.70	10.04	10.98	12.95	11.94	13.27
Net carbon fixation	8.83	8.05	9,11	10.35	9.40	10.67
RuBP oxygenation [$\frac{nmol}{g\ FW\ s}$ molecules]	3.72	3.34	4.20	5.20	4.56	5.66

(H) Selected fluxes and rates for the two scenarios included that were used for benchmarking. The rates of Rubisco carboxylation and oxygenation are given as RuBP consumption (i.e., use of CO_2 or O_2, respectively). Fluxes were estimated for two scenarios (1) All, using unadjusted ^{12}C isotopomer decay and metabolite content data sets. (2) Active, using the pool of each metabolite that is actively involved in photosynthetic fluxes. The inactive pool was nominally defined as the proportion that remains as ^{12}C isotopomer at 60 min. It was subtracted from the ^{12}C isotope kinetic (i.e., the 60-min value is set as zero). The absolute pool (Table 1) was also decreased in the same proportion. For each scenario, flux estimates are denoted by the optimal value obtained with the fit “optimum” and the “lower” and “upper” 95% confidence limits obtained from the Monte-Carlo simulation.