Table 1. Sequence identity in percent for the individual genes located on the photosynthesis operon of KT71 with the BAC clones EBAC65D09, EBAC29C02, and EBAC69B03

			% identity		
Gene	**E.C.**	**Match**	**EBAC29C02**	**EBAC65D09**	**EBAC69B03**
BLUF	--	BLUF (Sensor of blue-light using FAD) domain protein	46	--	--
AcsF	1.14.13.81	Magnesium-protoporphyrin IX monomethyl ester aerobic oxidative cyclase	63	--	--
orf KT71_19333	--	Membrane protein	no similarity	--	--
bchP	--	Geranylgeranyl hydrogenase, bacteriochlorophyll biosynthesis	58	62	62
pucC-like orf KT71_19343	--	Transcription regulator, membrane protein	51	54	63
bchG	2.5.1.62	Geranylgeranyl bacteriochlorophyll synthase, bacteriochlorophyll biosynthesis	63	58	65
CrtJ	--	Transcription regulator	42	42	42
bchF	4.2.1.-	2-Vinyl bacteriochlorophyll hydratase, bacteriochlorophyll biosynthesis	51	61	70
bchN	1.18.-.-	light-independent protochlorophyllide reductase, N subunit, bacteriochlorophyll biosynthesis	61	63	63
bchB	1.18.-.-	light-independent protochlorophyllide reductase, B subunit, bacteriochlorophyll biosynthesis	69	66	66
BchH	6.6.1.1	Magnesium-chelatase subunit H, bacteriochlorophyll biosynthesis	56	58	59
bchL	1.18.-.-	light-independent protochlorophyllide reductase, L subunit, bacteriochlorophyll biosynthesis	74	75	83
bchM	2.1.1.11	Mg-protoprophyrin IX methyl transferase, bacteriochlorophyll biosynthesis	60	54	58
pucC-like orf KT71_19388	--	Transcription regulator, membrane protein	49	53	60
PuhA	--	reaction center protein H chain	53	55	55
orf KT71_19398	--	hypothetical 23.7 kDa protein in puhA 5'region	39	45	--
orf KT71_19403	--	hypothetical 17.4 kDa protein in puhA 5'region	36	44	--
orf KT71_19408	--	hypothetical 30.4 kDa protein in puhA 5'region	42	41	--
HemN	1.3.99.22	oxygen-independent coproporphyrinogen III oxidase	37	35	--
Idi	5.3.3.2	isopentenyl-diphosphate delta-isomerase	48	54	--

PufA	--	Light-harvesting protein B-880, alpha chain	64	40	--
PufB	--	Light-harvesting protein B-880, beta chain	40	56	--
PufC	--	photosynthetic reaction center cytochrome c subunit	61	64	--
PufM	--	photosynthetic reaction center protein M chain	68	66	--
PufL	--	photosynthetic reaction center protein L chain	71	81	--
orf KT71_19443	--	conserved hypothetical protein	37	52	--
BchZ	1.18.-.-	chlorophyllide reductase subunit Z	72	73	--
BchY	1.18.-.-	chlorophyllide reductase subunit Y	66	68	--
BchX	1.18.-.-	chlorophyllide reductase subunit X	69	72	--
bchC	1.-.-.-	2-Desacetyl-2-hydroxyethyl bacteriochlorophyllide a dehydrogenase, bacteriochlorophyll biosynthesis	47	55	--
CrtF	2.1.1.-	hydroxyneurosporene methyltransferase, steroid biosynthesis	43	45	--
CrtE	2.5.1.29	geranylgeranyl pyrophosphate synthetase, steroid biosynthesis	57	51	--
CrtC	1.-.-.-	hydroxyneurosporene dehydrogenase, steroid biosynthesis	--	43	--
CrtB	2.5.1.-	phytoene synthase, steroid biosynthesis	--	42	--
CrtI	1.14.99.-	phytoene dehydrogenase, steroid biosynthesis	--	62	--
BchO	6.6.1.1	magnesium-protoporphyrin IX chelatase, O subunit, bacteriochlorophyll biosynthesis	--	--	--
bchD	6.6.1.1	magnesium-protoporphyrin IX chelatase, D subunit, bacteriochlorophyll biosynthesis	--	--	--
bchI	6.6.1.1	magnesium-protoporphyrin IX chelatase, I subunit, bacteriochlorophyll biosynthesis	--	--	--
orf KT71_19508	--	Conserved hypothetical protein	--	--	--
bchE	1.14.13.-	magnesium-protoprophyrin IX monomethyl ester anaerobic oxidative cyclase, bacteriochlorophyll biosynthesis	--	--	--
bchJ	--	4-vinyl reductase, bacteriochlorophyll biosynthesis	--	--	--
orf KT71_ 19523	--	Rhodanese-domain protein	--	--	--
Average identity			**55**	**56**	**62**