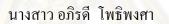
การเปลี่ยนแปลงปริมาณพอลิเอมีนภายใต้ภาวะเครียดออสโมติกและรังสีอัลตราไวโอเลต ในไซยาโนแบคทีเรีย Synechocystis sp. PCC 6803



ศูนย์วิทยทรัพยากร จุฬาลงกรณ์มหาวิทยาลัย

วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรปริญญาวิทยาศาสตรมหาบัณฑิต สาขาวิชาชีวเคมี กณะวิทยาศาสตร์ จุฬาลงกรณ์มหาวิทยาลัย ปีการศึกษา 2552 ลิขสิทธิ์ของจุฬาลงกรณ์มหาวิทยาลัย CHANGES OF POLYAMINES CONTENT UNDER OSMOTIC AND UV-RADIATION STRESSES IN CYANOBACTERIUM Synechocystis sp. PCC 6803

Miss Apiradee Pothipongsa

ศูนย์วิทยทรัพยากร จุฬาลงกรณ์มหาวิทยาลัย

A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree of Master of Science Program in Biochemistry Department of Biochemistry Faculty of Science Chulalongkorn University Academic Year 2009 Copyright of Chulalongkorn University

Thesis Title	CHANGES OF POLYAMINES CONTENT UNDER
	OSMOTIC AND UV-RADIATION STRESSES IN
	CYANOBACTERIUM Synechocystis sp. PCC 6803
Ву	Miss Apiradee Pothipongsa
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Thesis Advisor	Saowarath Jantaro, Ph.D.
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อภิรคี โพธิพงศา : การเปลี่ยนแปลงปริมาณพอลิเอมีนภายใด้ภาวะเครียดออสโมติกและรังสี อัลตราไวโอเลตในไซยาโนแบคทีเรีย *Synechocystis* sp. PCC 6803. (Changes of polyamines content under osmotic and UV-radiation stresses in cyanobacterium *Synechocystis* sp. PCC 6803) อ.ที่ปรึกษา วิทยานิพนธ์หลัก : อ.คร. เสาวรัตน์ จันทะโร, อ.ที่ปรึกษาวิทยานิพนธ์ร่วม : ศ.คร. อรัญ อินเจริญศักดิ์, 133 หน้า.

จากการศึกษาถึงผลกระทบของเกลือ โซเดียมคลอไรด์และซอร์บิทอลในอาหารเลี้ยงเชื้อ (BG-11) ร่วมกับ รังสีอัลตราไวโอเลต ชนิดรังสียูวี-เอ (365 นาโนเมตร, 11-13 วัตต์/ตารางเมตร), รังสียูวี-บี (302 นาโนเมตร, 1.2-1.3 วัตต์/ตารางเมตร) และ รังสียูวี-ซี (25<mark>4 นาโนเมตร, 1.0-1.3 วัตต์/ตารา</mark>งเมตร) เป็นเวลา 3 ชั่วโมง ต่อการเจริญเดิบโต ของเซลล์ ปริมาณรงควัตถุภายในเซลล์ (คลอโรฟิลล์-เอ และแคโรทีนอยค์) และปริมาณพอลิเอมีนในไซยาโน แบกที่เรียแบบเซลล์เดี่ยว Synechocystis sp. PCC 6803 พบว่าภายใต้แสงปกติ อาหารเลี้ยงเชื้อที่มีเกลือโซเดียม คลอไรค์เข้มข้น 650 มิลลิโมลาร์ และซอร์บิทอลเข้มข้น 500 มิลลิโมลาร์ นั้นไม่มีผลต่อการเจริญเติบโต และการ เปลี่ยนแปลงปริมาณคลอ โรฟิลล์และปริมาณแค โรทีนอยด์ของเซลล์ อย่างไรก็ตามเซลล์ที่ถูกกคคันเนื่องจากเกลือและ ซอร์บิทอลมีปริมาณคลอโรฟิลล์ และแคโรทีนอยค์สูงกว่าในอาหารเลี้ยงเชื้อปกติ สำหรับการเจริญเติบโตของเซลล์ ภายใต้ความเครียดเนื่องจากรังสียุวี นั้นมีการตอบสนองที่แตกต่างกัน การเจริญเติบโตของเซลล์ลดลงเล็กน้อยเมื่อ ใด้รับรังสียูวี-เอ แต่จะลดลง<mark>มากขึ้นภายใด้ภาวะเครียดร่วมของเกลือหรือ</mark>ซอร์บิทอลที่ความเข้มข้นสูงร่วมกับรังสี ี่ยูวี-เอ และรังสียูวี-บี นอกจากนี้<mark>พบว่ารังสียูวี-ซี ร่วมกับซอร์บิทอลมีผลต่อ</mark>การเจริญเดิบโตของเซลล์เช่นกัน สำหรับ ภาวะเครียดของยูวี-ไอออนิก และยู<mark>วี-ออส โมติก ไม่ส่งผลต่อก</mark>ารเปลี่ยนแปลงปริมาณคลอ โรฟิลล์ ในขณะที่ปริมาณ แคโรทีนอยค์มีแนวโน้มเพิ่มขึ้นภายใด้ภาวะเครียดจากรังสียูวี-เอ, รังสียูวี-เอและไอออนิก, และรังสียูวี-บีและ ออสโมติก ภายในเวลา 3 ชั่วโมง สำหรับพอลิเอมีนมีการสะสมมากในรูปแบบอิสระ โดยเฉพาะพอลิเอมีนชนิด สเปอร์มีดีน จากการศึกษาพบว่าปริมาณพอลิเอมีนเพิ่มขึ้นอย่างมีนัยสำคัญภายหลังได้รับรังสียูวี-บี หรือรังสียูวี-ซี เป็นเวลา 1 ชั่วโมง ขณะที่ปริมาณพอลิเอมีนลดลงหลังได้รับรังสียูวี-ออสโมติกเป็นเวลานาน 3 ชั่วโมง

นอกจากนี้งานวิจัยได้ทำการศึกษาขึ้นอาร์จีนีน ดีการ์บอกซิเลส (adcl และ adc2) สำหรับการสังเคราะห์ พิวเทรสซีน ในระดับขึ้นและโปรดีน ด้วยเทคนิค RT-PCR และ Western blot พบว่ามีปริมาณ adcl mRNA สูงกว่า adc2 mRNA ภายใต้ความเครียดจากเกลือ ส่วนความเครียดจากออสโมติกนั้นไม่มีผลต่อปริมาณ adcl และ adc2 mRNA สำหรับการแสดงออกระดับโปรตีนนั้น โปรตีน ADC1 มีปริมาณเพิ่มขึ้นเล็กน้อย ภายใต้ความเครียดจาก ใอออนิก, ชูวี-เอและไอออนิก, ชูวี-บีและไอออนิก แต่ในทางกลับกัน ภาวะออสโมติก, ออสโมติก-ชูวี ไม่มีผลต่อ ระดับขึ้นและระดับโปรตีนอย่างมีนัยสำคัญ สำหรับความสัมพันธ์ในระดับขึ้นและโปรตีน พบว่า ภายในระยะเวลา 1 ชั่วโมงของภาวะเครียดเนื่องจากเกลือ, ออสโมติก, ชูวี-ซี, เกลือและชูวี-เอ, เกลือและชูวี-บี, เกลือและชูวี-ซี, ออสโมติกและชวี-ซี มีความสอดกล้องกันทั้งระดับขึ้นและโปรตีน ADC ในเซลล์ Synechocystis

ภาควิชาชีวเคมี	ลายมือชื่อนิสิตนิโรจี	โพอิพอศา
สาขาวิชา ชีวเคมี	ลายมือชื่อ อ.ที่ปรึกษาวิทยานิพนธ์	ร์หลักเ
ปีการสึกษา 2552	ลายมือชื่อ อ.ที่ปรึกษาวิทยานิพนธ์	is'au and
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KEYWORDS: POLYAMINES / INTRACELLUAR PIGMENTS/ UV RADIATION / Synechocystis sp. PCC 6803

APIRADEE POTHIPONGSA : CHANGES OF POLYAMINES CONTENT UNDER OSMOTIC AND UV-RADIATION STRESSES IN CYANOBACTERIUM Synechocystis sp. PCC 6803. THESIS ADVISOR : SAOWARATH JANTARO, Ph.D., THESIS CO-ADVISOR : PROF. ARAN INCHAROENSAKDI, Ph.D., 133 pp.

Effect of salt and sorbitol at various concentrations and combined with UV radiations, including UV-A (365 nm; 11-13 w/m²), UV-B (302 nm; 1.2-1.3 w/m²) and UV-C (254 nm; 1.0-1.3 w/m²), for 3 hours on cell growth, intracellular pigments (chlorophyll a and carotenoids) and polyamine contents were investigated in a unicellular cyanobacterium Synechocystis sp. PCC 6803. Long-term stress (6-7 days) of Synechocystis cells grown in media up to 650 mM NaCl or 500 mM sorbitol did not severely affect growth, chlorophyll-a and carotenoids content of cells under normal growth light. Salt and sorbitol stresses stimulated the chlorophyll a and carotenoids accumulation. However, the response of cell growths showed different patterns after exposing to UV radiations. Under UV-A alone, growth was slightly decreased but was greatly decreased after combining with high concentration of salt or sorbitol. UV-B affected growth after co-treating with NaCl or sorbitol and UV-C showed the effect only when co-stress with sorbitol. The levels of chlorophyll a were constant under the combined stresses of both UV-ionic and UV-osmotic whereas those levels of carotenoids were slightly increased during the last 3 hours under UV-A both alone and in combination with salt stress and UV-B plus sorbitol treatments when compared to untreated cells. PCA-soluble polyamines were found as major forms and spermidine was present dominantly in all conditions. Short-term stress (1 hour) of UV radiations significantly increased their polyamine contents, especially salt stress combined with either UV-B or UV-C while long-time stress (3 hours) of UV radiations decreased polyamines content, especially under osmotic treatments.

Two different genes (*adc*1 and *adc*2) encoding ADC, the first enzyme for putrescine synthesis. The transcription and protein levels of ADC were analyzed by RT-PCR and Western blot, respectively. The results showed that *adc*1 mRNA level was up-regulated higher than *adc*2 mRNA level under salt stress while osmotic stress seemed to have no effect on *adc*1 and *adc*2 mRNA levels. For the protein levels, ADC1 was slightly increased under high concentrations of salt, salt combined with UV-A or UV-B. However, osmotic stress did not have much effect on both transcription and protein levels. In addition, osmotic stress seemed to abolish a tight correlation of both levels when combined osmotic stress with UV radiation. Both transcription and protein levels of ADC were connected by salt and osmotic, as well as salt treatment combined with UV-A and UV-B. On the other hand, UV-C alone or combined with salt or sorbitol had influence on the transcription and protein levels in *Synechocystis* cells under short-term stress (1 hour).

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LIST OF ABBREVIATIONS

ADC	Arginine decarboxylase
bp	Base pair
BSA	Bovine serum albumin
°C	Degree Celsius
DTT	Dithiothreitol
EDTA	Ethylenediamine tetraacetic acid
g	Gram
HEPES	Hydroxyethyl piperazineethanesulfonic acid
kb	Kilo base
kDa	Kilo Dalton
_h คุนยวิ	hour
เหาลงก	Liter
mM	Millimolar
min	Minute
μg	Microgram
μ1	Microliter

ml	Milliliter
mM	Millimolar
М	Molar
nm	nanometer
OD	Optical density
PCR	Polymerase Chain Reaction
Put	Putrescine
PMSF	Phenylmethylsulfonyl fluoride
RT-PCR	Reverse transcription- Polymerase Chain Reaction
rpm	Revolution per minute
SDS	Sodium dodecyl sulphate
Spd	Spermidine
Spm	Spermine
TAE	Tris-acetate electrophoresis
TEMED	Tetramethylethylenediamine
TES	Tris(hydroxymethyl)methyl]-2-
	aminoethanesulfonic acid
UV	Ultraviolet

CHAPTER I

INTRODUCTION

1.1 Environment stresses

1.1.1 Ultraviolet radiation

An essential factor of environment stresses contributing to organism is ultraviolet (UV) radiation. Due to depletion of the stratospheric ozone layer results in increased levels of incident solar UV radiation at the Earth's surface (Lubin and Jensen, 1995; Madronich *et al.*, 1998). The stratospheric ozone layer efficiently which filters out most of the detrimental, shortwave UV radiation, shorter than 280 nm was destroyed (Robberecht, 1989). A small decrease of ozone layers may cause a large relative increase in biologically effective UV radiation (Madronich, 1992, 1993). In general, each 1% reduction in ozone causes an increase of 1.3-1.8% in UV-B radiation reaching the biosphere (McFarland and Kaye, 1992).

Ultraviolet radiation is a part of the non-ionizing region of the electromagnetic spectrum (Figure 1.1) which comprises approximately 8-9% of the total solar radiation (Frederick, 1993). UV is traditionally divided into three wavelength ranges (Figure 1.2) including UV-C (200-280 nm) is extremely harmful to organisms, but not relevant under natural conditions of solar irradiation; high energy, UV-B (280-320 nm) is of particular interest because this wavelength represents only approximately 1.5% of the total spectrum, but can induce a variety of damaging effects in plants; lower energy and UV-A (320-400 nm) represents approximately 6.3% of the incoming solar radiation and is the less hazardous part of UV radiation (Hollósy, 2002; Barta *et al.*, 2004).

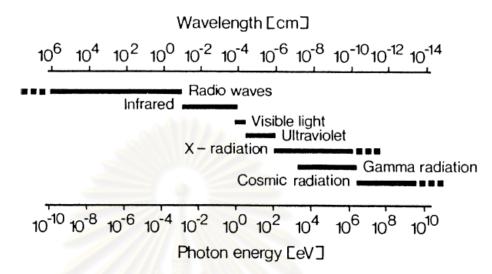


Figure 1.1 The electromagnetic spectrum. (Kovács and Keresztes, 2002)

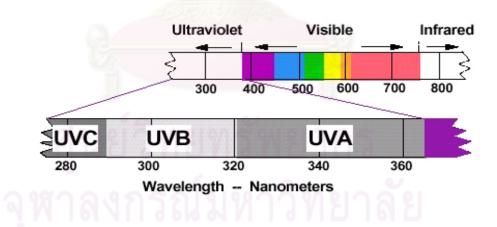


Figure 1.2 The three wavelength range of ultraviolet radiation, namely, UV-C (200-280 nm), UV-B (280-320 nm) and UV-A (320-400 nm), respectively. (Source: http://www.vcharkarn.com/uploads/63/63591.jpg).

UV radiation can induce deleterious and specific effects on living organisms (Worrest, 1982; Caldwell et al., 2003). UV radiation can affect principally many biological processes (Fiscus and Booker, 1995) because it is readily absorbed by important biomolecules (nucleic acids, proteins and lipids) that are essential for genetic, biochemical and physiological functions within cells (Melis et al., 1992; Frohnmeyer and Staiger, 2003). For non-photosynthetic organisms, DNA absorbs \sim 50% of the incident UV-B radiation and is the primary target of photodamage. However, in oxygenic photosynthetic organisms, such as plants, algae, and cyanobacteria, chlorophyll and other pigments may contribute significantly to shield DNA from ultraviolet radiation (He and Häder, 2002). It has been calculated that the light-harvesting proteins (phycobiliproteins and chlorophyll proteins) account for >99% of the UV-B absorption (Lao and Glazer, 1996). The negative effects of UV radiation were shown to impair various physiological and biochemical processes including growth, photosynthesis (Kumar et al., 2003; Wu et al., 2005; Rinalducci et al., 2006; Gao and Ma, 2008), pigmentation (Cakirlar et al., 2008), nitrogen metabolism (Sinha et al., 1996). However, the various organism response of UV action spectra are limited by a given dose of radiation (Barta et al., 2004). Also, under biotic and abiotic stimuli including UV radiation, generation of reactive oxygen species (ROS) including superoxide (O_2^-) , hydroxyl radicals (OH), hydrogen peroxide (H_2O_2), and singlet oxygen (1O_2), enhances and can overcome the enzymatic and nonenzymatic detoxification mechanisms, giving rise to oxidative stress (He and Häder, 2002; Obermüller et al., 2005) which react very rapidly with DNA, lipids and proteins causing cellular damage (Zacchini and Agazio, 2004). As well as, UV radiation increased the levels of lipid peroxidation in Physcia semipinnata (Unal et

al., 2008), Capsicum annuum (Mahdavian et al., 2008) and Pisum sativum (Agrawal and Mishra, 2009). Also, adaptation strategies of some cyanobacteria and eukaryotic algae try to avoid toxicity of UV radiation by evolving a variety mechanisms (Fedina et al., 2005) including production of UV-absorbing substances, such as scytonemin (Garcia-Pichel and Castenholz, 1991) and mycosporine-like amino acids (MAAs) (Obermüller et al., 2005; Zhang and Wu, 2007). To escape from UV radiation was a migration into habitats with reduced light exposure such as sinking and floating behaviour by a combination of gas vacuoles and ballast (Rajagopal et al., 2005), a production of quenching agents such as carotenoids (Obermüller et al., 2005; Gao and Ma, 2008) a production of antioxidant enzymes such as superoxide dismutase (SOD, EC 1.15.1.1), and glutathione reductase (GR, EC 1.6.4.2) (Gao and Zhang, 2008). Furthermore, specific role of polyamines in preventing photooxidative damages is reported (Løvaas, 1997). The antioxidative effect of polyamines was due to a combination of their anion- and cation-binding properties involving a radical scavenging function (Bors et al., 1989), and a capability to inhibit both lipid peroxidation (Kramer et al., 1991; Unal et al., 2008) and metal-catalysed oxidative reactions (Tadolini, 1988). Moreover, polyamine catabolism produces hydrogen peroxide that could enter the stress signal transduction chain promoting an activation of an antioxidative defence response (Agazio and Zacchini, 2001).

1.1.2 Salinity

One of the major environmental factors limiting the worldwide productivity and distribution of cereal crops is water stress resulting from drought and salinity (Lee *et al.*, 2001) which found major in arid and semi-arid regions of soil or water (Ashraf and Harris, 2004). High salinity causes both hyperionic and hyperosmotic effects and the consequence of these can be plant demise (Niu *et al.*, 1995; Leshem *et al.*, 2007). The deleterious effects of salinity are associated with the induction of water stress induced by the increase of osmotic potential, the increase of ions or other plant toxins in the soil, the increase of ions in the plant tissues (Howard and Mendelssohn, 1999) and a combination of these factors (Ashraf, 1994). All of these cause adverse pleiotropic effects on plant growth and development at physiological, biochemical and molecular levels (Munns, 2002; Mansour, 2000; Jantaro *et al.*, 2003; Demetriou *et al.*, 2007; He *et al.*, 2008).

Salt stress can also trigger various interacting events including the reduction of initial growth, inhibition of cell division and expansion, acceleration of cells death (Yeo, 1998), the inhibition of enzyme activities in metabolic pathways and the decomposition of protein and membrane structures (Tsugane *et al.* 1999). Moreover, salt stress generated the active oxygen species (ROS) are thought to play an important role in inhibiting plant growth, photosynthetic pigments (Thompson, 1987; Lee *et al.*, 2001; Mahdavian *et al.*, 2008).

However, stress adaptation effectors are categorized as those that mediate ion homeostasis, osmolyte biosynthesis, toxic radical scavenging, water transport, and transducers of long-distance response coordination (Asada, 1999; Morgan and Drew, 1997; Niu *et al.*, 1995; Leung and Giraudat, 1998). One response of cells against salt stress, to changes in the external osmotic potential is the accumulation of metabolites that act as "compatible" solutes which do not inhibit normal metabolic reactions (Ford, 1984; Yancey *et al.*, 1982). With protection of structures and osmotic balance supporting continued water influx (or reduced efflux) accepted functions of low molecular weight osmolytes such as glycine betaine (Incharoensakdi and Wutipraditkul, 1999), proline (He *et al.*, 2008; Mahdavian *et al.*, 2008), ectoine (Louis and Galinski, 1997) and plant growth regulator polyamines (Das *et al.*, 1995; Bouchereau *et al.*, 1999; Jantaro *et al.*, 2003; Sanchez *et al.*, 2005; Demetriou *et al.*, 2007). Furthermore, many research found polyamines act as scavenging of reactive oxygen species (Drolet *et al.*, 1986; Bors *et al.*, 1989; Løvaas and Carlin, 1991; Li and Wang, 2004; He *et al.*, 2008). However, polyamine accumulation is a non-specific response to salt stress (Ashraf and Harris, 2004).

1.2 Polyamine

1.2.1 Physiology

Polyamines (PAs) are small aliphatic polycations that are widely present in living organisms (Wang and Liu, 2009). The most common ones are the diamine putrescine (Put; 1,4-diaminobutane), triamine spermidine (Spd; 1,8-diamino-4-azaoctane) and tetraamine spermine (Spm; 1,12-diamino-4,9-diazododecane) shown in Figure 1.3.

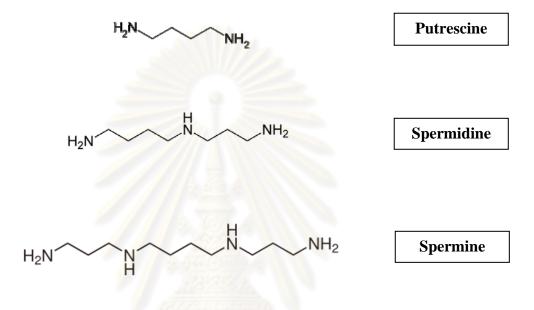


Figure 1.3 The most common polyamines are putrescine (Put; NH₂(CH₂)₄NH₂), spermidine (Spd; NH₂(CH₂)₃NH(CH₂)₄NH₂) and spermine (Spm; NH₂ (CH₂)₃ NH (CH₂)₄NH(CH₂)₃NH₂) (Source: http://en.wikipedia.org/wiki).

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Many other di- and polyamines are usually present in plants and microorganisms, such as the diamines 1,3-diaminopropane and cadaverine (1,5-diaminopentane). Strikingly, unusual polyamines have also been found in bacteria, algae, fungi, animals and higher plants (Niitsu and Samejima, 1993). In the extreme thermophilic bacteria *Thermus thermophilus* at least 14 polyamines, among which some linear and branched pentamines, hexamines and heptamines, have been isolated (Table 1). Caldopentamine was accumulated in detectable content especially in bacterial cells grown at extremely high temperatures (80°C or more) (Oshima, 1989). These unusual polyamines, typical and abundant in thermophilic bacteria, can be found widespread. They were detected previously in some Leguminoseae, such as *Canavalia gladiata* and *Vicia radiata* (Matsuzaki *et al.*, 1990; Hamana *et al.*, 1991), leading to hypothesize a putative role of these molecules in growth and differentiation processes (Bagni and Tassoni, 2001). Moreover, many polyamine analogs were discovered in the algae (Hamana and Matsuzaki, 1982; Maiss *et al.*, 1982).

Polyamines, low molecular weight compounds, are positively charged at physiological pH and ubiquitous in nature. By their the positive charge, polyamines are known to bind to negatively charged molecules, e.g. nucleic acids, acidic phospholipids and various types of proteins (Cohen, 1998). In higher plants, polyamines were occurred dominantly in free form, bound electrostatically to negatively charged molecules, and conjugated to small molecules and proteins (Martin-Tanguy, 1997). Polyamines are required for normal development of prokaryotes and eukaryotes (Tabor and Tabor, 1984). For biotic stresses, polyamine levels were changed in plant responding to pathogen infection (Walters, 2000). Moreover, many reports suggest that polyamines play a critical role in a range of

Trivial name	Systematic name	Chemical structure
1,3-Diaminopropane	1,3-Diaminopropane	NH ₂ (CH ₂) ₃ NH ₂
Putrescine	1,4-Diaminobutane	NH ₂ (CH ₂) ₄ NH ₂
Cadaverine	1,5-diaminopentane	NH ₂ (CH ₂) ₅ NH ₂
Norspermidine (caldine)	1,7-Diamino-4-azaheptane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH ₂
Spermidine	1,8-Diamino-4-azaoctane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₄ NH ₂
sym-Homospermidine	1,9-Diamino-5-azanonane	NH ₂ (CH ₂) ₄ NH(CH ₂) ₄ NH ₂
Thermine	1,11-Diamino-4,8-diazaundecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH ₂) ₃ NH ₂
Spermine	1,12-Diamino-4,9-diazadodecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₄ NH(CH ₂) ₃ NH ₂
Thermospermine	1,12-Diamino-4,8-diazadodecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH ₂) ₄ NH ₂
Homospermine	1,13-Diamino-4,9-diazatridecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₄ NH(CH ₂) ₄ N H ₂
Caldopentamine	1,15-Diamino-4,8,12-	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH2) ₃
	triazapentadecane	NH(CH ₂) ₃ NH ₂
Homocaldopentamine	1,16-Diamino-4,8,12-triazahexadecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH ₂) ₃
Homopentamine	1,19-Diamino-5,10,15-	NH(CH ₂) ₄ NH ₂
	triazanonadecane	NH ₂ (CH ₂) ₄ NH(CH ₂) ₄ NH(CH ₂) ₄
Caldohexamine	1,19-Diamino-4,8,12,16-	NH(CH ₂) ₄ NH ₂
	tetraazanonadecane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH ₂) ₃
Homocaldohexamine	1,20-Diamino-4,8,12,16-	NH(CH ₂) ₃ NH(CH ₂) ₃ NH ₂
	tetraazaeicosane	NH ₂ (CH ₂) ₃ NH(CH ₂) ₃ NH(CH ₂) ₃
		NH(CH ₂) ₃ NH(CH ₂) ₄ NH ₂
N ⁴ -Aminopropyl-		[NH ₂ (CH ₂) ₃] ₃ N
norspermidine		
N ⁴ -Aminopropyl-		[NH ₂ (CH ₂) ₃] ₂ N[NH ₂ (CH ₂) ₄]
spermidine		

 Table 1.1 Common and uncommon natural occurring aliphatic polyamines*

*Bagni and Tassoni, 2001

developmental processes including root growth, somatic embryogenesis, floral initiation, and the development of flowers and fruits (Evans and Malmberg, 1989; Takahashi et al., 2003; Ziosi et al., 2006). These compounds were related to plant growth regulator or hormonal second messengers, avoiding senescence (Galston, 1983) and stabilization of nucleic acids and membranes (Thomas and Thomas, 2001). Polyamines have also been implicated in plant responses to abiotic stress such as potassium deficiency, osmotic shock, drought, salt stress (Watson and Malmberg, 1996; Evans and Malmberg, 1989; Tassoni et al., 2008). Moreover, enhanced UV-B radiation may cause the accumulation of polyamines in plants (Kramer and Mirecke, 1992; An et al., 2004). It was also revealed that polyamines might play an important role in the protection mechanisms of plants during exposure to UV-B radiation in cucumber (Kramer et al., 1991; An et al., 2004) which increase under enhanced UV-B radiation (Predieri et al., 1993). On the other hand, the reduction of free polyamines was found in *Phaseolus vulgaris* under UV-B radiation (Smith et al., 2001). Thus, polyamines might act as scavengers of active oxygen species and stabilize membranes under different environmental stress conditions (Bouchereau et al., 1999) and UV-A radiation (Unal et al., 2008). The amount of the various polyamines, was reported that, depends on environmental and stress conditions. This variation in the amount of polyamines under different conditions has suggested an adaptive and protective role for these compounds (Smith, 1985). Furthermore, the control of polyamine levels is regulated in a very fast, sensitive and precise manner. This control can be achieved at four different strategies; de novo biosynthesis, degradation (oxidative deamination), conjugation and transport (Bouchereau et al.,

1999; Urdiales *et al.*, 2001). However, the polyamine contents under combination stresses of UV and salt or sorbitol have never been reported.

1.2.2 Polyamine biosynthesis

In higher plants and bacteria, the first step in polyamine biosynthesis (Figure 1.4) is the formation of putrescine. Putrescine is synthesized directly from ornithine by ornithine decarboxylase (ODC; EC 4.1.1.17) and indirectly from arginine by arginine decarboxylase (ADC; EC 4.1.1.19) via two important intermediates are involved; agmatine and N-carbamoylputrescine, respectively, which is subsequently converted to putrescine. In mammalian cells and fungi, only the ODC reaction leads to putrescine formation (Walters, 2000). According to *Arabidopsis* has not only no ODC activity but also no ODC gene (Hanfrey *et al.*, 2001). Moreover, the two different genes coding for ADC (*adc1* and *adc2*) in *Arabidopsis thaliana* have been identified under potassium deficiency stress. The several reports showed that *adc2* is induced upon osmotic stress (Soyka and Heyer, 1999) and salt stress (Bagni *et al.*, 2006). In animals and plants have been reported that ODC is located in both the cytoplasm and nucleus (Voigt *et al.*, 2000). As the ADC protein which widely appears in plants is localized in chloroplasts associated with the thylakoid membrane of oat (Borrell *et al.*, 1995) that shown in Figure 1.5.

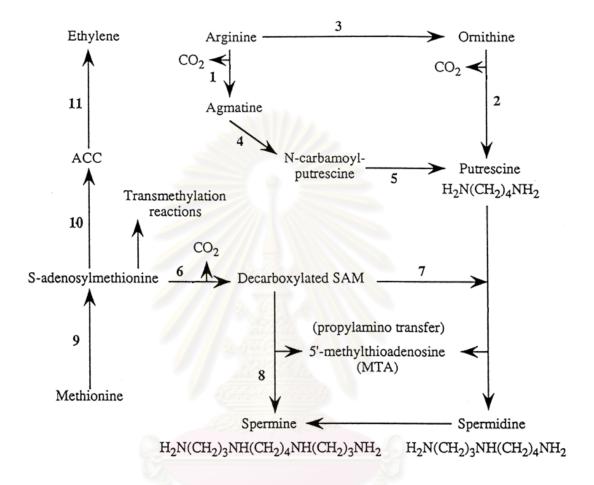


Figure 1.4 Pathways of biosynthesis of the major plant polyamines (Putrescine, Spermidine and Spermine), relationships with ethylene biosynthesis. 1, Arginine decarboxylase (ADC); 2, Ornithine decarboxylase (ODC); 3, Arginase; 4, Agmatine iminohydrolase; 5, *N*-carbamoyl putrescine amidohydrolase; 6, SAM decarboxylase (SAM DC); 7, Spermidine synthase; 8, Spermine synthase; 9, SAM synthase; 10, ACC synthase; 11, ACC oxydase. (modified from Bouchereau *et al.*, 1999).

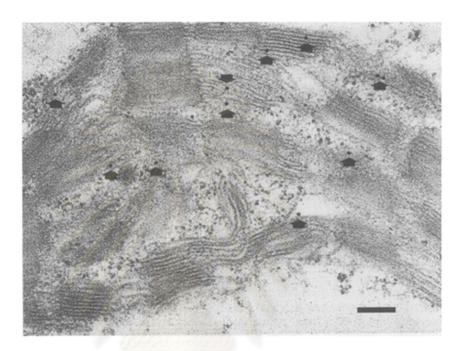


Figure 1.5 Electron micrograph of arginine decarboxylase protein localization. The osmotically stressed oat leaves were investigated by immunogold labelling. Gold particles localizing ADC antigen are indicated by arrows. Scale bar represents 200 nm. (Borrell *et al.*, 1995)

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The polyamines spermidine and spermine are formed by the subsequent addition of an aminopropyl moiety to putrescine and spermidine, respectively. These reactions are catalysed by the aminopropyltransferase enzymes, spermidine synthase (EC 2.5.1.16) and spermine synthase (EC 2.5.1.22), respectively. The aminopropyl moiety is formed by the decarboxylation of S-adenosylmethionine (AdoMet or SAM) in a reaction catalysed by the enzyme AdoMet decarboxylase (AdoMetDC or SAMDC; EC 4.1.1.50) (Walters, 2003).

1.2.3 Polyamine degradation

The polyamines are oxidatively deaminated by the action of amine oxidases. These enzymes include the copper containing diamine oxidases (DAO; EC 1.4.3.6), which preferentially oxidize diamines, and the polyamine oxidases (PAO; EC 1.5.3.3.) which contain flavoprotein. Then, PAOs oxidize their substrates, spermidine and spermine (Cohen, 1998). The action of DAO on putrescine yields pyrroline, hydrogen peroxide and ammonia while PAO action on spermidine and spermine yields pyrroline and 1,5-diabicylcononane, respectively, as well as diaminopropane (DAP) and hydrogen peroxide (Figure 1.6). Diaminopropane can be metabolised to β -alanine, while pyrroline can be converted to γ -aminobutyric acid (GABA) by pyrroline dehydrogenase (PDH). GABA can then be transaminated and oxidized to form succinic acid, following by entering the Krebs cycle (Flores and Filner, 1985). Also, this pathway ensures that the carbon and nitrogen resulting from putrescine is recycled (Walters, 2000). For degradation of spermidine by PAO yields Δ 1-pyrroline and 1,3-diaminopropane and hydrogen peroxide (Bagni and Tassoni, 2001).

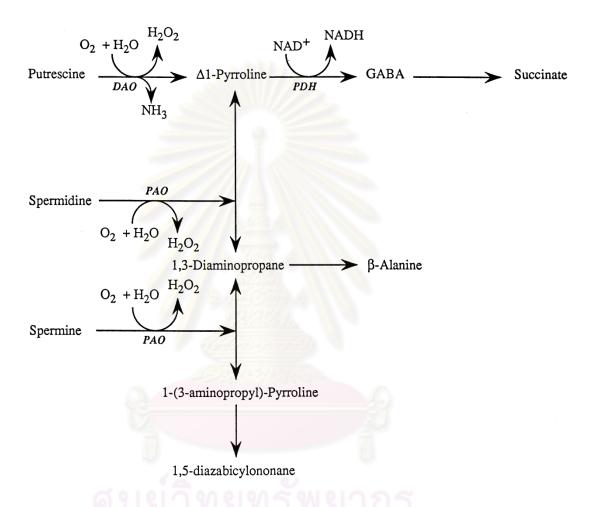


Figure 1.6. Schematic representation of polyamine degradation. Amine oxidases. DAO, diamine oxidase; GABA, 7-aminobutyric acid; PAO, polyamine oxidase; PDH, pyrroline dehydrogenase. (Bouchereau *et al.*, 1999).

1.2.4 Polyamine conjugation

In nature, polyamines often occur as free molecular bases, but they can also be associated with small molecules like phenolic acids (conjugated forms) and also to various macromolecules like proteins (bound forms). The most common amine conjugated, i.e. polyamines and aromatic amines conjugates, covalently linked to hydroxycinnamic acids have also been shown to occur at high levels in plants and are thought to be correlated with developmental phenomena (Martin-Tanguy, 1985).

This conjugation occurs as water-soluble or water-insoluble forms. In the former, the single amine group of an aliphatic amine is linked with a phenolic cinnamic acid. The water-insoluble forms can be divided into two classes. In the first, each terminal amine group of an aliphatic amine is bound to cinnanic acid, while in the second class the amine group of aromatic amine is linked to cinnamic acid. These amine conjugates are found in roots but do not normally in shoots. In the roots of tobacco, increases in water-soluble and water-insoluble conjugates have been shown before flowering (Martin-Tanguy et al., 1990) and occur in shoot apices upon floral initiation (Havelange et al., 1996). The synthesis of polyamine conjugates has been elucidated in tobacco callus (Negrel, 1989). They are conjugated by the formation of an amide linkage, using esters of Co-A for provision of the activated carboxyl groups such as cinnamoylputrescine (Martin-Tanguy et al., 1985), which are formed by non-specific putrescine caffeoyl-CoA transferase. Therefore, the synthesis of the water-insoluble polyamine such as di-p-coumaroylputrescine, di-pcoumaroylspermidine, di-feruloylputrescine and di-feruloylspermidine has not been elucidated (Martin-Tanguy, 1997). Furthermore, posttranslational covalent linkage of polyamines to protein is catalyzed by a class of enzymes known as transglutaminases (EC; 2.3.2.13) (Margosiak *et al.*, 1990).

1.2.5 Polyamine transport

The transport of polyamines across the plasmalema of plant cells is energydependent and it is now clear that calcium is involved in the uptake mechanism. Indeed, calcium-activated putrescine uptake can be markedly reduced by treatments which reduce calmodulin action or the activities of protein kinases or phosphatase (Antognoni *et al.*, 1995). Polyamine-specific carriers are widely distributed in prokaryotes and eukaryotes and can replenish polyamine pools upon inhibition of the biosynthetic enzymes (Seiler *et al.*, 1996). The transport of polyamines classified as ABC (ATP binding cassette)-type transporters (Higgins, 1992) have been well characterized in bacteria, yeast, parasite, animal (Igarashi and Kashiwagi, 1999; Tassoni *et al.*, 2002; Rinehart and Chen, 1984) and cyanobacterium *Synechocystis* sp. PCC 6803 (Raksajit *et al.*, 2006). For the putrescine and spermidine transport into *Synechocystis* cells found that pH dependent with highest activity at pH 7.0 and 8.0, respectively. Moreover, the transport of putrescine and spermidine are energydependent (Raksajit *et al.*, 2006; 2009).

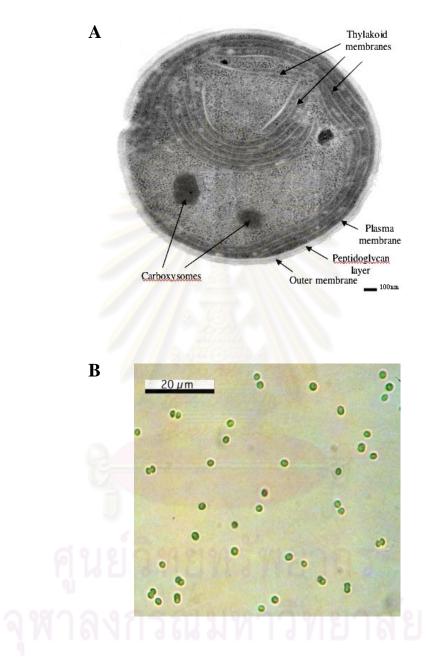
1.3 Synechocystis sp. PCC 6803

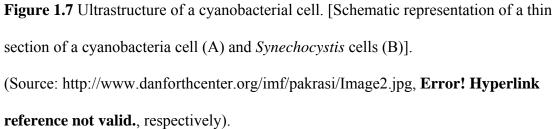
Living organisms have the capability to adapt to sudden changes in their environment. Since most of these stimuli (temperature up- and downshift, UV-B light, etc.) have detrimental effects on cells, they had to develop adequate protective systems (Glatz et al., 1999). Among prokaryotes, cyanobacteria are the only organisms to engage in oxygenic photosynthesis, and there is evidence to suggest that they are the progenitor(s) of plant plastids. Their phylogenetic position in the bacterial kingdom is still obscure, although recent analysis of ancient genes has indicated a genetic relationship with Gram-positive bacteria (Xiong et al. 2000). Cyanobacteria can be classified as the Procaryota, Division of cyanophyta and Cyanophyseae class. The bacteria and cyanobacteria lack mitochondria, chloroplast, true vacuoles, endoplasmic reticular. There is no membrane bounded chloroplast; in cyanobacteria the photosynthetic lamellae are usually distributed in the peripheral cytoplasm. Cells of cyanobacteria are surrounded by the cytoplasmic membrane, the cell wall which contains an outer membrane and a peptidoglycan layer, and in many case a glycocalyx layer (Figure 1.7). The outer membrane functions more as a passive molecular sieve, whereas the cytoplasmic membrane serves as a true selective permeability barrier (Gantt, 1994).

Synechocystis sp. PCC 6803 is an unicellular, non-nitrogen (N_2)-fixing cyanobacterium and a ubiquitous inhabitant of fresh water. They divide by binary fission at two or three successive planes. Based on their GC contents, many cultured strains of *Synechocystis* can be classified into three groups; the marine group, the low GC group and the high GC group (Holt *et al.*, 1998). Strain PCC 6803 belongs to the latter group, whose members, including PCC 6714, have been mostly isolated from

freshwater. They also have the propensity to utilize glucose (Rippka *et al.*,1979). A phylogenetic tree based on 16S rRNA sequences suggests that high GC content species are more closely related to *Microcystis aeruginosa*, which is a unicellular spherical cyanobacterium with gas vesicles, than to other *Synechocystis* groups (Honda *et al.*, 1999). There are four culture substrains of *Synechocystis* ('PCC', 'ATCC', 'GT' (glucose-tolerant) and 'Kazusa'), all of which were derived from the Berkeley strain 6803, which was isolated from freshwater in California by R. Kunisawa (Stanier *et al.* 1971) shown in Figure 1.8.

The complete nucleotide sequence of Synechocystis sp. PCC 6803 was determined in 1996. This was the first photoautotrophic organism to be fully sequenced. Sequencing was carried out using a clone-by-clone strategy based on the physical map of the genome, resulting in a highly accurate sequence. The circular genome was originally deduced to be 3,573,470 bp long (Figure 1.9). The average GC content is 47.7% (Kaneko et al. 1996). Consequently, Synechocystis has been one of the most popular organisms for genetic and physiological studies of photosynthesis for two major reasons; it is naturally transformable by exogenous DNA (Grigorieva and Shestakov, 1982) and grows heterotrophically at the expense of glucose (Rippka et al., 1979). Moreover, Synechocystis cells has several features that make this strain particularly suitable for studying stress response at the molecular level (Glatz et al., 1999). There is unequivocal evidence that in higher plant cells exposed to heat stress, the photosynthetic apparatus is irreversibly damaged prior to impairment of other cellular functions (Berry and Bjorkman, 1980). The general assembly of photosynthetic membranes in cyanobacteria is similar to that of higher plant, therefore





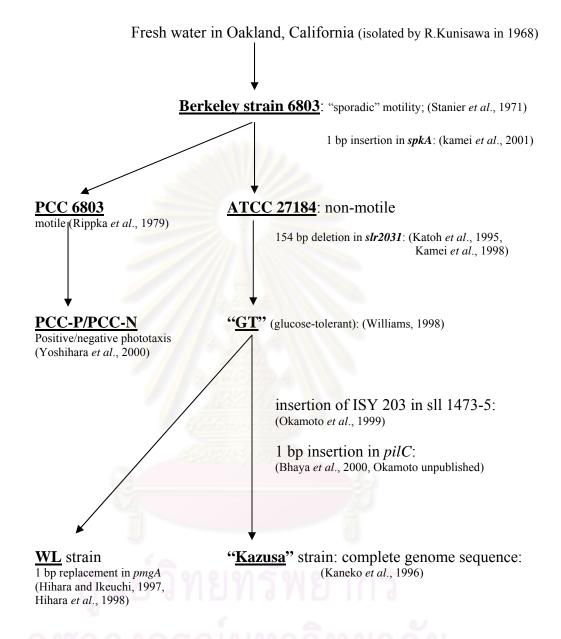


Figure 1.8 Strain history of Synechocystis sp. PCC 6803 (Ikeuchi and Tabata, 2001).

Synechocystis 6803 might serve as a powerful model for studying the molecular mechanisms of stress response and long-term adaptation (Lehel *et al.*, 1993; Jantaro *et al.*, 2003).

Cyanobacteria owe the ubiquitous distribution to remarkable capacities to adapt to varying environmental conditions. A few data are available regarding adaptation of natural populations, most studies having been performed on a few model strains selected for specific adaptive capacities to a chosen environmental or stress factors as well as for solving agricultural problems (Ikeuchi and Tabata, 2001). Therefore, *Synechocystis* is a useful tool in the study of the biochemistry and genetics of cyanobacteria (Joset *et al.*, 1996).

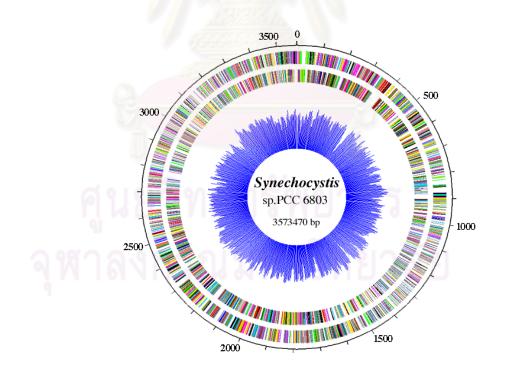


Figure 1.9 The cellular genome of *Synechocystis* sp. PCC 6803 according to Cyanobase (Source: www.kazusa.or.jp/cyano/Synechocystis).

1.4 OBJECTIVE OF THIS RESEARCH

- To determine the effects of salinity and UV radiation on cell growth, intracellular pigments and polyamines content in *Synechocystis* sp. PCC 6803.
- 2. To study the transcription of arginine decarboxylase (*adc1* and *adc2*) genes and the translation of ADC protein under salinity and UV radiation in *Synechocystis* sp. PCC 6803.



CHAPTER II

MATERIALS AND METHODS

Materials

2.1 Equipments

Balances	METTLER PJ360 DeltaRange [®] GWB, USA
Centrifuge	HERMLE Z233 MK, USA
C-18 column	4.6 x 150 mm inertsil [®] ODS-3 5 μm i.d.,
Electrophoresis Unit	BIO-RAD PROTEIN [®] II xi Cell, USA
Gel documentation	Syngene [®] Gel Documentation
HPLC	Hewlett Packard series 1050, Japan
Laminar flow	BVT-124 International Scientific Supply, Thailand
Light source unit	Prekeo S250 Zeiss IKON, Japan
PCR apparatus	PERKIN ELMER DNA Thermal Cycler, Japan
pH meter	ORION model 420A, USA
Power supply	BIO-RAD POWER PAC 1000, USA
Spectrophotometer	Jenway UV/VIS 6400, USA
Vortex	Model K-550-GE, Scientific Industries, USA
Water bath	THERMOMIX [®] B B.BRAUN, USA

2.2 Chemicals

Acetic acid	Lab Scan, Poland
Acrylamide	Scharlau Chemie S.A., Spain

Agarose
Ammonium ferric citrate
Ammonium persulfate (APS)
Benzoyl chloride
Calcium chloride
Citric acid
Chloroform
Coomassie blue R-250
Diethyl ether
Dimethylformamide
Dipotassium phosphate
Dithiothreitol (DTT)
EDTA
Ethanol
Ethidium bromide
Glycerol
Glycine
Hexanediamine
HEPES
Isoamylalcohol
Isopropanol
Magnesium chloride
Magnesium sulfate
Mercaptoethanol

Invitrogen, USA Ajax Finechem, Australia Merck, Germany Sigma, USA Ajax Finechem, Australia Ajax Finechem, Australia Merck, Germany Sigma, USA Lab Scan, Poland Lab Scan, Poland Ajax Finechem, Australia Sigma, USA Merck, Germany Merck, Germany Sigma, USA Ajax Finechem, Australia Ajax Finechem, Australia Sigma, USA USB Corporation, USA Sigma, USA Sigma, USA Ajax Finechem, Australia Ajax Finechem, Australia Sigma, USA

Methanol	Lab Scan, Poland
Methylene-bis-acrylamide	Amersham Bioscience, Sweden
Perchloric acid	Merck, Germany
Pyridoxal-5-phosphate	Sigma, USA
Phenol	Merck, Germany
PMSF	Sigma, USA
Putrescine	Sigma, USA
Sodium acetate	Ajax Finechem, Australia
Sodium bicarbonate	Ajax Finechem, Australia
Sodium chloride	Ajax Finechem, Australia
Sodium dithiosulfate	Ajax Finechem, Australia
Sodium dodecyl sulfate	Ajax Finechem, Australia
Sodium hydroxide	Ajax Finechem, Australia
Sodium nitrate	Ajax Finechem, Australia
Sodium phosphate	Ajax Finechem, Australia
Sodium thiosulfate	Ajax Finechem, Australia
Sorbitol	Ajax Finechem, Australia
Spermidine	Sigma, USA
Spermine	Fluka, USA
Sucrose	Ajax Finechem, Australia
TEMED	BIO-RAD, USA
TES	Sigma, USA
Tris (hydroxymethyl)-aminomethane	USB Corporation, USA
Triton X-100	Packard, USA

Tween-20

Urea

BIO-RAD, USA

Ajax Finechem, Australia

2.3 Kits and supplies

Nylon membrane filter	0.45 µm, Sartorius, Germany
Immobilon-P membrane	Millipore Coorperation, USA
1 kb DNA Ladder	Invitrogen, USA
PCR amplification kit	Invitrogen, USA
SuperScript TM III First-Strand Synthesis Synthesis	stem Invitrogen, USA
Prestained Protein Marker	Fermentas, Canada
RNase-Free DNase	Invitrogen, USA

2.4 Primers

Table 2.1 Sequences of the primers for RT-PCR

Target gene	Name	Primers	Length in pairs
16s rRNA	forward-16s	5'-AGTTCTGACGGTACCTGATGA-3'	521
	reverse-16s	5'-GTCAAGCCTTGGTAAGGTTCT-3'	
adc1	forward-adc1	5'-ATATTACCTGCGACAGTGATGG-3	315
	reverse-adc1	5'-GATCAAGGCTAACTCCGTATGAC	-3'
adc2	forward-adc2	5'-ATATTACCTGCGACAGTGATGG-3	457
	reverse-adc2	5'-TTAGCTGGTGTGGATGCCT-3'	

2.5 Organism

Synechocystis sp. PCC 6803 wild type strain was obtained from the Laboratoty of Plant Physiology and Molecular Biology, Department of Biology, University of Turku, Finland.

Methods

2.6 Culture conditions

Axenic cells of *Synechocystis* sp. PCC 6803 were grown in BG-11 medium (Appendix A) with continuously bubbling by filtered air, under normal growth light (40-50 μ mol photon/m² s⁻¹) at 32°C. Cell growth of the culture was measured for the optical density at 730 nm with Spectronic spectrometer. For ionic stress conditions, NaCl was added in various concentrations of 25, 125, 350 and 650 mM in BG-11 media, respectively, whereas BG-11 media containing 50, 250 and 500 mM sorbitol, respectively, were used as osmotic stress conditions. The culture with mid-logarithmic stage was diluted to the optical density at 730 nm of 0.5 and exposed under UV radiations; UV-A (365 nm; 11-13 w/m²), UV-B (302 nm; 1.2-1.3 w/m²) and UV-C (254 nm; 1.0-1.3 w/m²), respectively. The UV-stressed cells were harvested for further analysis. The radiation intensity was measured by a UVX radiometer (UVP, Inc., Upland, CA).

2.7 Determination of intracellular pigments

The UV-stressed cells were collected in order to determine for the intracellular pigments at intervals of 0, 30, 60, 90, 120, 150 and 180 min. One ml of

cell culture was extracted by *N*,*N*-dimethylformamide with vortexing vigorously. After centrifugation at 8,000 rpm for 5 min to remove debris, the optical density of supernatant was measured at 461, 625 and 664 nm, respectively. The contents of chlorophyll a and carotenoids were calculated according to following equations (Jantaro, *et al.*, 2006) :

chlorophyll a content (µg/cell) = $[(12.1 \times OD_{664}) - (0.17 \times OD_{625})] / \text{total cells}^*$ (Moran, 1982) carotenoid content (µg/cell) = $[(OD_{461} - (0.046 \times OD_{664})) \times 4] / \text{total cells}^*$ (Chamovitz *et al*, 1993) total cells* (cell/ml) = $(OD_{730} / 0.25) \times 10^8$

2.8 Polyamine biosynthesis analysis

2.8.1 Extraction and determination of polyamines

Synechocystis cells under UV radiation at 1 and 3 hours were harvested and extracted by 5% cold HClO₄. After the extraction by 5% perchloric acid for 1 hour on an ice bath, the samples were centrifuged at 8,000 rpm for 10 min. The supernatant and pellet fractions (represented as free and bound forms of polyamines, respectively) were derivatized by benzoylation reaction. The derivatized-polyamines were then analyzed by high performance liquid chromatography (HPLC) (Flores and Galston, 1982), using 1,6-hexanediamine as an internal standard. One ml of 2 M NaOH was added into 500 μ l of 5% HClO₄ extract firstly following by mixing with 10 μ l of benzoyl chloride. The mixture was vigorously vortexed and incubated for 20 min at room temperature. To stop the reaction, 2 ml of saturated NaCl was added. The benzoyl-polyamines were then separated by solvent fractionation with 2 ml of cold diethyl ether. Two ml of the ether phase with benzoyl-polyamines was taken to a new tube and evaporated to dryness, followed by redissolving in 1 ml of methanol. Samples were filtered through a 0.45 μ m cellulose acetate membrane filter. Authentic polyamine standards were prepared similarly as the stressed cells. Derivatized polyamines were analyzed by high performance liquid chromatography (HPLC) with inertsil®ODS-3 C-18 reverse phase column (5 μ m; 4.6 x 150 mm) using UV-Vis detector at 254 nm. The mobile phase was a gradient of 60 – 100% methanol : water. The flow rate was 0.5 ml/min. Chromatogram and standard curve of polyamines shown in the Appendix B

2.8.2 Extraction of total RNA

One hundred ml of *Synechocystis* cells grown at the mid-logarithmic phase were harvested by centrifugation at 5000 rpm, 4°C for 15 min. The pellet was immediately frozen in liquid nitrogen. The total RNA was extracted by the hot phenol method (Mohamed and Jansson, 1989). Cells were resuspended in 1 ml resuspension buffer (Appendix C) on ice.and centrifugated at 12,000 rpm, 4°C for 5 min. Pellet was resuspened in 250 μ l resuspension buffer and added 75 μ l of 250 mM EDTA, pH 8.0 before incubating on ice for 5 min. The 375 μ l lysis buffer (Appendix C) was added and incubated at 65°C for 3 min. After that, hot phenol (65°C) was added into the reaction mixture and incubated at 65°C for 3 min. Then, the mixture was cooling down on a freeze aluminium block for 1 min. Centrifugation at 12,000 rpm for 5 min was done at room temperature. Repeatedly, the upper phase was reextracted with the hot phenol. Subsequently, the mixture was extracted once with an equal volume of phenol/chloroform/isoamyl alcohol (25:24:1). The extracted mixture was gentle mixed and centrifuged at 12,000 rpm for 5 min at room temperature. After that, the RNA was precipitated by adding 1/10 volume of 3 M sodium acetate buffer, pH 6.0 and 2.5 volume of cold ethanol (-20°C). After incubation at -20°C for 30 min, the tube was centrifuged at 12,000 rpm (4°C) for 10 min. The resulting pellet was washed with 70% ethanol and centrifuged at 12,000 rpm for 5 min. Then, the dried pellet was resuspened in 50 μ l of RNA storage buffer (Appendex C). The total RNA was kept at freezer (-80°C) until used. To determine concentration and purity of RNA, sample was diluted with RNA storage buffer and checked by measuring the optical density at 260 nm and ran 0.8% agarose gel in 1x TAE buffer (Appendex E).

2.8.3 Preparation of total RNA

Firstly, RNA samples from 2.9.2 were treated with RNase-free DNase. The reaction mixture was contained 50 μ g of RNA, 5 μ l of 10x buffer, 5 μ l of RNase-free DNase and adjusted the final volume to 50 μ l with Milli-Q water. After that, the samples were added 5 μ l more of RNase-free DNase and incubated at 37°C for 2 hours. Then, the mixture was added 200 μ l of 40 mM Tris-HCl, pH 8.0 and extracted once with 250 μ l of phenol/chloroform/isoamyl alcohol (25:24:1) mixture. After centrifugation at 12,000 rpm (room temperature) for 5 min, the upper phase was added 1/10 volume of 3 M sodium acetate buffer, pH 5.2 and 0.6 volume of isopropanol and incubated at -20°C for 30 min. The extract was then centrifuged at 12,000 rpm, 4°C for 10 min to separate supernatant and pellet. The resulting pellet was washed with 70% ethanol and mixed gently by inversion and centrifuged at 12,000 rpm, 4°C for 2 min. Finally, the dried pellet was resuspened with 25 μ l of RNA-storage buffer. The solution was checked for RNA concentration by measuring at 260 nm and ran 0.8% agarose gel in 1x TAE buffer.

2.8.4 Reverse Transcription-Polymerase Chain Reaction (RT-PCR)

Total RNA of Synechocystis cells obtained from 2.8.3 was used as template to generate cDNA by SuperScriptTM III First-Strand Synthesis System. Each reaction was added 5 µg of total RNA which treated with RNase-free DNase, 0.8 µl of 25 µM of 3'-primer, namely, *adc1*, *adc2* and 16s rRNA genes which designed from the Cyanobase sequence (Figure 2.1) and dissolved with Milli-Q water to 10 µl. After incubation the reaction at 65° C for 5 min, the 10 µl of cDNA Synthesis Mix (containing 2 µl of 10X RT buffer, 4 µl of 25 mM MgCl₂, 2 µl of 0.1 M DTT, 1 µl of RNaseOUTTM and 1µl of SuperScriptTM III Reverse transcriptase) was added to the mixture and incubated the tube at 50°C for 50 min. Terminate the reactions of cDNA synthesis at 85°C for 5 min. The one microlitter of RNaseH was added and incubated again at 37°C for 20 min to remove RNA. The cDNA synthesis reaction can be used for PCR amplification. PCRs were performed, the initial denaturation at 95°C for 5 min was done, followed by 29 cycles of denaturation at 95°C for 1 min, annealing step of adc1, adc2, 16s rRNA genes were performed at 50.7°C, 64°C and 56°C, respectively, for 1 min and extention at 72°C for 1 min, followed by final extention at 72°C for 5 min. The PCR products were analyzed by electrophoresis of 0.8% agarose gel in 1x TAE buffer. Quantification was carried out using Syngene® Gel Documentation.

adc1													C 0
adc2	AIGGA	AGGGC	AGTCA	ATCGA	ACTAG	AACTA	AGTGT	CATGG	CAATG	CCGGA	GIIAA	TCGAC	60
adc1	- ATGG	GGGAA	GAACC	TGTGC	CGGCG	GATAA	AGCAT	TAGGC	AAGAA	ATTCA	AGAAA	Δ	55
adc2		TGAAG											
	*	* *	* *		** **		* *		*		* *		
adc1	-AAAA	TGCCT	CCTGG	AGCAT	TGAAG	AAAGC	GAAGC	TCTGT	ACCGG	GTTGA	GGCCT	GGGGG	114
adc2	CAAGA												180
	** *		* * *	* ***	*** *	* ***	* * *	** *	* * * *	*	* *	* * * * *	
					-				mamam				1 1 1
adc1 adc2		TTATT TTACT											
aucz		*** *											240
adc1	GGCGG	TTCGT	TAGAT	TTGTT	GGAAC	TGGTG	GAAGC	CCTGC	GGCAA	AGAAA	GCTCG	GCTTA	234
adc2		AGCGT											
	** **	* * *	* ***	****	****	****	* *	* *	* * * * *	* * * * *	* *	* * * *	
adc1		ATTAA											
adc2		ACTGT										CGGCC	360
	** *	* *	* **	*****	****	** **	** **	***	* *	** *	***		
adc1	ጥጥጥርሶ	CAAGG	CGATC	GCCCC	TTACA	ATTAC	CCCAA	CACCT	ATCAC	GCCCT	ጥጥልጥጦ	CGGTC	354
adc1 adc2		CCGGG											
uucz		* **											120
adc1	AAATG	TAACC	AGCAA	CGACA	TCTGG	TGGAA	GCCCT	GGTTC	GCTTT	GGGCA	AACTT	CCCAG	414
adc2		CAACC										ATAAT	480
	** **	****	****	** **	* *	****	****	*** *	* * *	* *	* *	*	
adc1		ATTGG											
adc2		CTTGG ****											540
adc1	CCCTT	AGACC	GT	CAGGA	CAAGC	ATACC	AAGCC	CCTAA	TCATT	TGTAA	TGGCT	ACAAA	531
-													
adc2	CAGGA	GAACC	CAGAG	CCGGA	TCAAC	AAAAT	CAGCC	TTTAC	TAATT	TGTAA	TGGTT	ATAAA	600
adc2	CAGGA *	GAACC ***		CCGGA * ***									600
adc2													600
adc1	* GACCA	*** GGATT	ATCTA	* *** GAAAC	* * AGCTC	* * TGTTA	**** GCCAA	** ACGCT	* *** TAGGC	***** CATCG	*** * TCCCA	* *** TCATC	591
	* GACCA GACCG	*** GGATT GGAAT	ATCTA ATATT	* *** GAAAC GAAAC	* * AGCTC CGCCT	* * TGTTA TGCTA	**** GCCAA GCCCG	** ACGCT TCGTC	* *** TAGGC TGGGG	***** CATCG CATCG	*** * TCCCA GCCGA	* *** TCATC TTATT	591
adc1	* GACCA GACCG	*** GGATT	ATCTA ATATT	* *** GAAAC GAAAC	* * AGCTC CGCCT	* * TGTTA	**** GCCAA GCCCG	** ACGCT TCGTC	* *** TAGGC TGGGG	***** CATCG	*** * TCCCA GCCGA	* *** TCATC TTATT	591
adc1 adc2	* GACCA GACCG ****	*** GGATT GGAAT *** *	ATCTA ATATT ** *	* *** GAAAC GAAAC ****	* * AGCTC CGCCT **	* * TGTTA TGCTA ** **	**** GCCAA GCCCG ***	** ACGCT TCGTC **	* *** TAGGC TGGGG * **	***** CATCG CATCG ****	*** * TCCCA GCCGA ** *	* *** TCATC TTATT * **	591 660
adc1 adc2 adc1	* GACCA GACCG	*** GGATT GGAAT *** * TGAAC	ATCTA ATATT ** * AACTA	* *** GAAAC GAAAC ***** CGGGA	* * AGCTC CGCCT ** ACTGG	* * TGTTA TGCTA ** ** AATGG	**** GCCAA GCCCG *** GTACT	** ACGCT TCGTC ** ACACA	* *** TAGGC TGGGG * ** TCTCT	***** CATCG CATCG ***** CAGCA	*** * TCCCA GCCGA ** * GT-TA	* *** TCATC TTATT * ** AACAT	591 660 650
adc1 adc2	* GACCA GACCG **** ATCAT	*** GGATT GGAAT *** * TGAAC	ATCTA ATATT ** * AACTA AGGTA	* *** GAAAC GAAAC ***** CGGGA	* * AGCTC CGCCT ** ACTGG GGTGG	* * TGTTA TGCTA ** ** AATGG	**** GCCAA GCCCG *** GTACT GCCAT	** ACGCT TCGTC ** ACACA CGAAA	* *** TAGGC TGGGG * ** TCTCT TTTC-	***** CATCG CATCG ***** CAGCA	*** * TCCCA GCCGA ** * GT-TA ATCTG	* *** TCATC TTATT * ** AACAT	591 660 650
adc1 adc2 adc1	* GACCA GACCG **** ATCAT	*** GGATT GGAAT *** * TGAAC GGAGC	ATCTA ATATT ** * AACTA AGGTA	* *** GAAAC GAAAC ***** CGGGA GCGGA	* * AGCTC CGCCT ** ACTGG GGTGG	* * TGTTA TGCTA ** ** AATGG CCTTG	**** GCCAA GCCCG *** GTACT GCCAT	** ACGCT TCGTC ** ACACA CGAAA	* *** TAGGC TGGGG * ** TCTCT TTTC-	CATCG CATCG ***** CAGCA CAGCA	*** * TCCCA GCCGA ** * GT-TA ATCTG	* *** TCATC TTATT * ** AACAT GGCAT	591 660 650
adc1 adc2 adc1	* GACCA GACCG **** ATCAT GTGGT * * TAAAC	*** GGATT GGAAT TGAAC GGAGC **** CCATG	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG	* *** GAAAC GAAAC **** CGGGA GCGGA *** GGTAC	* * AGCTC CGCCT ** ACTGG GGTGG *** GGGCC	* * TGTTA TGCTA ** ** AATGG CCTTG * * CGGTT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT	** ACGCT TCGTC ** ACACA CGAAA * * GTCAG	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT	***** CATCG CATCG ***** CAGCA CAGCA ***** CAAAT	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT	591 660 650 719 710
adc1 adc2 adc1 adc2	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC	*** GGATT GGAAT *** * TGAAC GGAGC ** * CCATG CAATT	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG	* *** GAAAC GAAAC ***** CGGGA GCGGA *** GGTAC GGTAC	* * AGCTC CGCCT ** ACTGG GGTGG *** GGGCC GGGCC	* * TGTTA TGCTA ** ** AATGG CCTTG * * CGGTT AAACT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA	** ACGCT TCGTC ** ACACA CGAAA * * GTCAG CCCAG	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT GGCAT	***** CATCG CATCG ***** CAGCA CAGCA ***** CAAAT	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG GTTGG	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT GGCAT	591 660 650 719 710
adc1 adc2 adc1 adc2 adc2	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC	*** GGATT GGAAT TGAAC GGAGC **** CCATG	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG	* *** GAAAC GAAAC ***** CGGGA GCGGA *** GGTAC GGTAC	* * AGCTC CGCCT ** ACTGG GGTGG *** GGGCC GGGCC	* * TGTTA TGCTA ** ** AATGG CCTTG * * CGGTT AAACT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT	** ACGCT TCGTC ** ACACA CGAAA * * GTCAG CCCAG	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT	***** CATCG CATCG ***** CAGCA CAGCA ***** CAAAT	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG GTTGG	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT	591 660 650 719 710
adc1 adc2 adc1 adc2 adc1 adc2	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC TAAGC *** *	*** GGATT GGAAT *** * TGAAC GGAAC ** * CCATG CAATT * **	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG *****	* **** GAAAC GAAAC ***** CGGGA CGGA GCGGA **** GGTAC GGTAC	* * AGCTC CGCCT ** ACTGG GGTGG GGTGG GGGCC GGGCC *****	* * TGTTA TGCTA ** ** AATGG CCTTG * * CCGTT AAACT *	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA ***	** ACGCT TCGTC ** ACACA CGAAA * * GTCAG CCCAG CCCAG ***	* *** TAGGC TGGGG * ** TCTCT * ** TCCCT GCCT GCCAT *	***** CATCG CATCG ***** CAGCA CAGCA ***** CAAAT GGGCC	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG GTTCG GTTCG * *	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT GGCAT * **	591 660 650 719 710 779
adc1 adc2 adc1 adc2 adc1 adc2 adc1	* GACCA GACCA TCAT GTGGT * * TAAAC TAAAC *** *	*** GGATT GGAAT GGAAC GGAGC ** * CCATG CAATT ****	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG TTGGG ***** AACGG	* **** GAAAC GAAAC ***** CGGGA GGGAC GGTAC CGATC	* * AGCTC CGCCT ** ACTGG GGTGG GGGCG GGGCC GGGCC C***** GGGCC	* * TGTTA TGCTA ** ** AATGG CCTG * * AAACT * AAACT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA *** TGGTC	** ACGCT TCGTC ** ACACA CGAAA * * GTCAG CCCAG CCCAG *** TGACC	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT GCAT * ATGCC	***** CATCG CATCG ***** CAGCA CAGCA ***** CAAAT GGGCC GGACA	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG GTTGG GTTGG * *	* *** TCATC TTATT * ** AACAT GGCAT * ** ACCGT	591 660 650 719 710 779 770
adc1 adc2 adc1 adc2 adc1 adc2	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC *** * TTCCT TTCCA	*** GGATT GGAAT *** * TGAAC GGAAC ** * CCATG CAATT * **	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG ***** AACGG	* **** GAAAC GAAAC ***** CGGGA GGGAC GGTAC CGATC	* * AGCTC CGCCT ** ACTGG GGTGG *** GGGCC GGGCC GGGCT GGGCT	* * TGTTA TGCTA ** * AATGG CCTTG * * CGGTT AAACT * AAGCT AAATT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA *** TGGTC TGGTT	** ACGCT ** ACACA CGAAA * * GTCAG CCAG *** TGACC	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT GGCAT * ATGCC	CATCG CATCG CATCG CAGCA CAGCA CAGCA CAGCA CAAAT GGGCC GGACA GGAAA	*** * TCCCA GCCGA *** * GT-TA ATCTG * * CCTCG GTTGG * * TGTGG TGTTG	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT GGCAT * ** ACCGT	591 660 650 719 710 779 770
adc1 adc2 adc1 adc2 adc1 adc2 adc1	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC *** * TTCCT TTCCA	*** GGATT GGAAT GGAAC GGAAC GGAAC ** * CCATG CAATT *** CTGGC CTGGC	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG ***** AACGG	* **** GAAAC GAAAC ****** CGGGA GCGGA CGGAC GGTAC CGATC -GATC	* * AGCTC CGCCT ** ACTGG GGTGG *** GGGCC GGGCC GGGCT GGGCT	* * TGTTA TGCTA ** * AATGG CCTTG * * CGGTT AAACT * AAGCT AAATT	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA *** TGGTC TGGTT	** ACGCT ** ACACA CGAAA * * GTCAG CCAG *** TGACC	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** TCGCT GGCAT * ATGCC	CATCG CATCG CATCG CAGCA CAGCA CAGCA CAGCA CAAAT GGGCC GGACA GGAAA	*** * TCCCA GCCGA *** * GT-TA ATCTG * * CCTCG GTTGG * * TGTGG TGTTG	* *** TCATC TTATT * ** AACAT GGCAT *** GAAAT GGCAT * ** ACCGT	591 660 650 719 710 779 770
adc1 adc2 adc1 adc2 adc1 adc2 adc1	* GACCA GACCG **** ATCAT GTGGT * * TAAAC TAAAC *** * TTCCT TTCCA ****	*** GGATT GGAAT GGAAC GGAAC GGAAC ** * CCATG CAATT *** CTGGC CTGGC	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG ***** AACGG	* **** GAAAC GAAAC ***** CGGGA GCGGA GGTAC GGTAC -GATC -GATC *****	* * AGCTC CGCCT ** ACTGG GGTGG GGGCG GGGCC GGGCC GGGCT GGGCT ****	* * TGTTA TGCTA ** ** AATGG CCTTG * CGGTT AAACT * AAGCT AAATT ** *	**** GCCAA GCCCG *** GTACT GCCAT * * AAGTT GAGTA *** TGGTC TGGTT ****	** ACGCT ** ACACA CGAAA * * GTCAG CCCAG *** TGACC TAACC ***	* *** TAGGC TGGGG * ** TCTCT TTTC- * ** GGCAT * ATGCC ATCCC ** **	***** CATCG CATCG ***** CAGCA CAGCA CAGCA GGGCC GGACA GGAAA **** *	*** * TCCCA GCCGA ** * GT-TA ATCTG * * CCTCG GTTGG GTTGG TGTGG TGTTG * *	* *** TCATC TTATT * ** AACAT GGCAT **** ACCGT ACGGC ** *	591 660 719 710 779 770 833
adc1 adc2 adc1 adc2 adc1 adc2 adc1 adc1 adc2	* GACCA GACCG **** GTGGT * * TAAAC TAAAC TAAAC *** * TTCCT TCCT **** *	*** GGATT GGAAC GGAGC ** * CCATG CAATT * ** CTGGC CTGGC **** ATCGT AGCAA	ATCTA ATATT ** * AACTA AGGTA * ** TTGGG TTGGG TTGGG AACGG CTAGA CTGCG	* **** GAAAC GAAAC ***** CGGGA GCGGA **** GGTAC GGTAC CGATC -CATC ***** CGAAA CCGAG	* * AGCTC CGCCT ** ACTGG GGTGG **** GGGCC GGGCC GGGCC GGGCC GGGCC ***** ATAAT CTGAT	* * TGTTA TGCTA ** ** AATGG CCTTG * * CGGTT AAACT * AAGCT AAATT ** *	**** GCCAA GCCCG *** GCCAT * * AAGTT GAGTA **** TGGTC TGGTT ****	** ACGCT CGAAA ** GTCAG CCCAG CCCAG *** TGACC TAACC * *** GCCTG GCCTG	* *** TAGGC TGGCG TTTC- * ** TCCCT TTTC- * ** ATGCC ATCCC * ** AAAAT CAATT	***** CATCG CATCG ***** CAGCA CAGCA CAGAAT GGGCC GGACA GGACA CGAAA *** * GCTTC GCTCC	*** * TCCCA GCCGA ** * ATCTG GTTGG GTTGG GTTGG GTTGG GTTGG TGTTG * * ATTTT	* *** TCATC TTATT * ** AACAT GGCAT *** ACCGT ACCGC * ** ACCGT ACCGC CATCT CACAT	591 660 719 710 779 770 833 830
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Figure 2.1 Alignment of arginine decarboxylase nucleotide sequences (*adc1* and *adc2* genes) of *Synechocystis* sp. PCC 6803 from Cyanobase (Source: http://bacteria.kazusa.or.jp/cyanobase/). Star symbols represented the homology area (65% similarity). The area designing for the forward (red font) and reverse primers of *adc1* (pink font) and *adc2* (blue font), respectively.

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2.8.5 Protein extraction

Synechocystis cells, grown 7-8 days with $OD_{730} \sim 0.6$, were harvested (about 100 ml of culture) by centrifugation at 5000 rpm, 4°C for 15 min. The pellet was diluted with extraction buffer (Appendix D) in ratio of 1:2 (cells:buffer, w/v) (Primikirios and Roubelakis-Angelakis, 1999). After pre-cooled glass beads, the glass beads were added into the tube in ratio of 1:1 (glass beads:solution, w/v) and vortexed the mixture for 20 sec per time, about 7-8 times (after vortexing kept on ice). After centrifugation, the solutions of crude protein were transferred to new tube. The 5 ml of extraction buffer was added into the tube and repeated the vortexing step for 3 times and centrifugation at 5,000 rpm, 4°C for 30 min. The supernatant was collected in new tube and kept in -20°C until used.

2.8.6 Sodium Dodecyl Sulphate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Total proteins from *Synechocystis* cells were extracted following in 2.8.5. To analyse the extracted proteins, 10 µg of total proteins in sample buffer (Appendix .F) with the ratio of 4:1 of total proteins: sample buffer were denatured by boiling for 5 min. SDS-polyacrylamide gel with 12% separating gel and 5% stacking gel (Appendix F) was prepared. After that, the polymerized SDS-polyacrylamide gel was placed into electrophoresis chamber and samples were loaded into each well of SDSgel electrophoresis was performed at a constant current of 20 mA per gel for 40 min and stained the gel with staining solution containing coomassie blue (Appendix F).

2.8.7 Western blot analysis

The 7 x 9 cm SDS-polyacrylamide gels following in 2.9.6 were transferred to immobilonTM PVDF transfer membrane by blotting solution (Appendix G). After activation the polyvinylidene fluoride (PVDF) membrane with 100% methanol for 30 min, blotting was done at 100 mA for 4 hours. After that membrane were washed with 1XTBS (Appendix G) and blocked with blocking solution (Appendix G) for 1 hour at room temperature. The membranes were washed with TBS-T (Appendix G) and follow with incubated with first antibody (diluted 1:3000) in PBS containing 3% skim milk (w/v) and 0.05% Tween-20 for 4 h at room temperature and later with second antibodies with anti-Horseradish peroxidase – Goat antimouse, HRP-GAM (diluted 1:3000) at 4°C, overnight in PBS containing 3% skim milk (w/v) and 0.05% Tween-20. Peroxidase activity was visualized by staining with the substrate mixture, consisting of 0.025% DAB, 0.01% H₂O₂ and 0.001% CoCl₂ in PBS. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation.

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CHAPTER III

RESULTS

3.1 Effect of salinity stress on growth of Synechocystis sp. PCC 6803

3.1.1 Effect of ionic stress

3.1.1.1 The growth of Synechocystis cells

Axenic cells of *Synechocystis* grown in BG-11 media adding various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl, respectively, for 20 days were determined for the cell growth. The results show that the mid-logarithmic stage of cell growth ($OD_{730} \sim 0.7$) in NaCl-containing medium, represented as an ionic condition, was found at 6-7 days. The growth of cells under ionic stress (Figure 3.1a) was increased with the concentration of NaCl up to 650 mM. However, cell growth at 650 mM NaCl condition was lower than that of the control and those of low NaCl concentrations (25, 125 and 350 mM NaCl, respectively).

3.1.1.2 The content of intracellular pigments

Synechocystis cells grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl, respectively, were determined for the intracellular pigments of chlorophyll a and carotenoids content under normal growth light for 20 days. The results are shown in Figure 3.1b that the chlorophyll a content of cells grown in those concentrations started about 0.68 μ g/10⁸ cells. After 6- day of cell cultures, they tended to increase. However, cells grown in normal BG-11 and BG-11 plus moderate salt concentrations of 25, 125 and 350 mM gave higher chlorophyll a content than cells grown in the high salt concentration of 650 mM. On the other hand, the carotenoids content (Figure 3.1c) showed the pattern which was as similar as that of chlorophyll a. The carotenoids content of day 0-cultivation was about 0.20 μ g/10⁸ cell/ml which was 3.4-fold lower than chlorophyll a content. However, cells grown in various salt concentrations for 20 days showed an increase in carotenoids content. Only the conditions of 350 and 650 mM NaCl affected the carotenoids content when compared to those of lower concentrations of 0, 25 and 125 mM NaCl.

3.1.2 Effect of osmotic stress

3.1.2.1 The growth of Synechocystis cells

Axenic cells of *Synechocystis* grown in BG-11 media adding various sorbitol concentrations for 20 days were determined for the cell growth. The results show that the mid-logarithmic stage of cell growth ($OD_{730} \sim 0.7$) in sorbitol-containing media (0, 50, 250 and 500 mM sorbitol, respectively), represented as osmotic condition, was found at 6-7 days. For osmotic stress, cell growth showed similar pattern as that in ionic stress condition. However, *Synechocystis* cells which were grown under the 500 mM sorbitol-containing medium showed the slowest growth rate when compared to those under low sorbitol concentrations of 0, 50 and 250 mM (Figure 3.2a).

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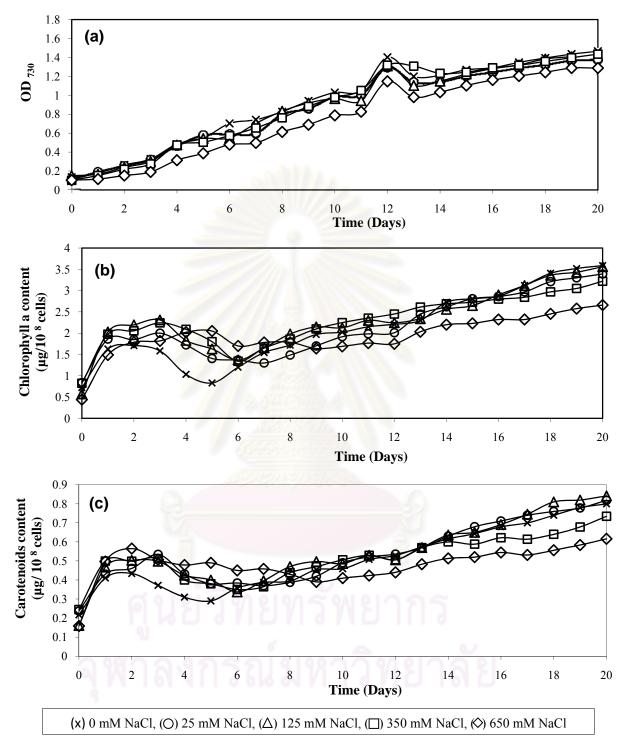


Figure 3.1 Effect of NaCl concentrations on *Synechocystis* cells grown under normal growth light for 20 days. Cells were grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl. Growth curve (a), chlorophyll a (b) and carotenoids content (c).

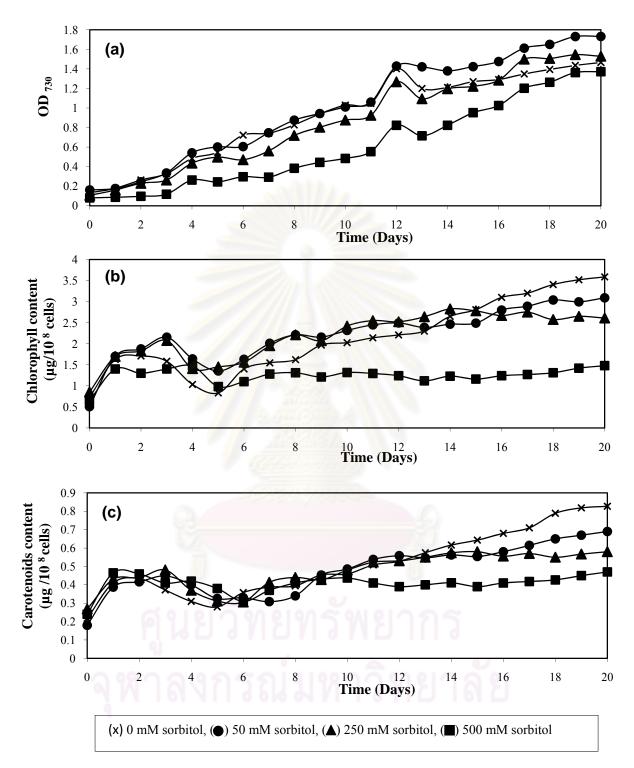


Figure 3.2 Effect of sorbitol concentrations on *Synechocystis* cells grown under normal growth light for 20 days. Cells were grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol. Growth curve (a), chlorophyll a (b) and carotenoids content (c)

3.1.2.2 The content of intracellular pigments

Synechocystis cells grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol, respectively, were determined for the intracellular pigments of chlorophyll a and carotenoids content under normal growth light for 20 days. The results showed that the chlorophyll a content (Figure 3.2b) started about 0.68 μ g/10⁸ cells at day 1. After 6 day-cultivation, the chlorophyll a content tended to increase. Cells grown in normal BG-11 and BG-11 plus sorbitol concentrations of 50 and 250 and 250 mM sorbitol gave higher pigment contents higher than cells grown in 500 mM sorbitol condition. For the carotenoids content of cells (Figure 3.2c) showed similar trend as that of chlorophyll a. On the other hand, carotenoids content was about 0.23 μ g/10⁸ cells at starting culture. The high sorbitol concentration (500 mM) had influenced on carotenoids content at day 20-culture, which showed the stable/decreasing tendency whereas the others showed increasing-pattern.

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3.2 Combined effects of salinity and UV-radiation on growth and intracellular pigments of *Synechocystis* cells

3.2.1. Salt stress under normal growth light

3.2.1.1 The growth of Synechocystis cells

The mid-logarithmic stage of *Synechocystis* cells grown in BG-11 media plus various NaCl concentrations were diluted to the optical density at 730 nm of 0.5 and followed by determining cell growth within 3 hours. The growth of cells grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl under normal growth light for 3 hours tended to increase (F igure 3.3a). Under normal growth light conditions were used as their control when compared with those exposed to UV radiation. However, cells grown in BG-11 without salt showed higher growth rate than these of cells grown in the media plus NaCl.

3.2.1.2 The content of intracellular pigments

One ml of cultures was collected and extracted for the intracellular pigments. It was clear that the chlorophyll a content (Figure 3.3b) of cells grown in BG-11 plus various NaCl concentrations gave higher levels than that of cells grown in normal BG-11 under normal growth light. These contents showed no apparent change within 3 hours of treatment. For carotenoids content (Figure 3.3c), they were somewhat less changed except the 125 mM NaCl-treated cells which showed gradually decreased. All salt stresses (650, 350, 125, 25 mM NaCl, respectively) stimulated the accumulation of intracellular pigments which was higher than that of cells grown in medium without salt.

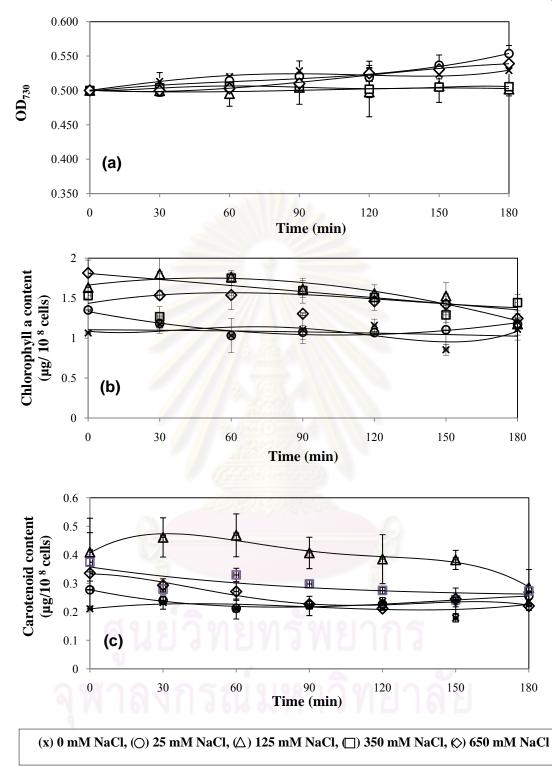


Figure 3.3 Effect of NaCl concentrations on *Synechocystis* cells grown under normal growth light for 3 hours. Cells were grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.2 Salt and UV-A stresses

3.2.2.1 The growth of Synechocystis cells

The *Synechocystis* cells grown in BG-11 media plus 0, 25, 125, 350 and 650 mM NaCl concentrations were determined for the growth of cells within 3 hours under UV-A treatment. The results show that the growth of cells (Figure 3.4a) was not changed significantly. However, at 650 mM NaCl, growth was obviously decreased when compared to control without salt addition. Moreover, the result indicates that the growth of UV-A treated cells alone (Figure 3.4a) was slightly decreased when compared to the control under normal growth light condition.

3.2.2.2 The content of intracellular pigments

Under UV-A radiation, the chlorophyll a content (Figure 3.4b) of cells grown in BG-11 plus various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl, respectively, showed the constant levels within 3 hours-treatment. For carotenoids content under either UV-A radiation alone or combination with salt stress (Figure 3.4c) showed the constantly levels and tended to increase slightly at last 3 hours.

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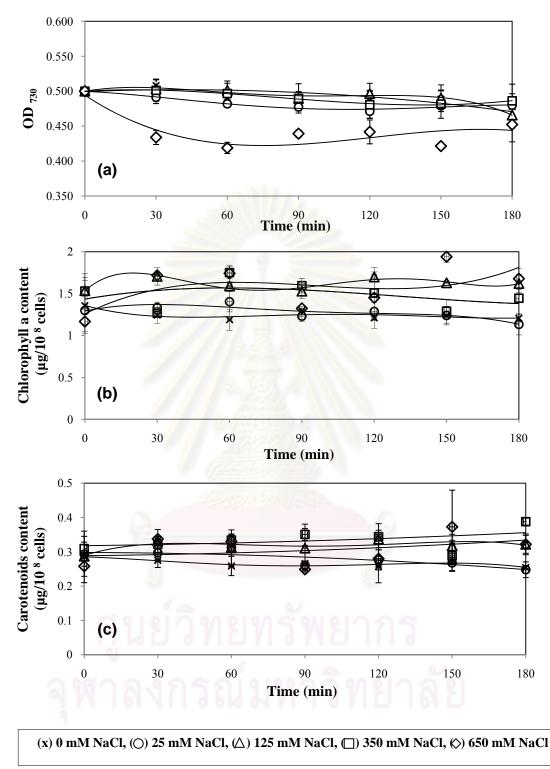


Figure 3.4 Effect of NaCl concentrations on *Synechocystis* cells grown under UV-A radiation for 3 hours. Cells were grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.3 Salt and UV-B stresses

3.2.3.1 The growth of Synechocystis cells

The *Synechocystis* cells grown in BG-11 media plus 0, 25, 125, 350 and 650 mM NaCl, respectively, were determined for the growth of cells within 3 hours under UV-B radiation. The results show that the growth of cells (Figure 3.5a) tended to decrease obviously in media plus 0, 350 and 650 mM NaCl conditions, respectively, whereas growth of cells grown in media containing 25 and 125 mM NaCl, respectively, were slightly increased. However, they showed the increase within 3 hours under control of normal growth light condition (Figure 3.3a).

3.2.3.2 The content of intracellular pigments

Under UV-B radiation, the chlorophyll a content (Figure 3.5b) of cells grown in BG-11 plus various NaCl concentrations showed the constant levels. However, cells in high salt conditions of 650 and 350 mM NaCl, respectively, exposed under UV-B for 3 hours showed the chlorophyll a content higher than those in control (without NaCl addition). For carotenoids content under UV-B radiation (Figure 3.5c) also gave constant levels. *Synechocystis* cells grown in 350 and 650 mM NaCl conditions showed the carotenoids content higher than those in the medium without NaCl addition.

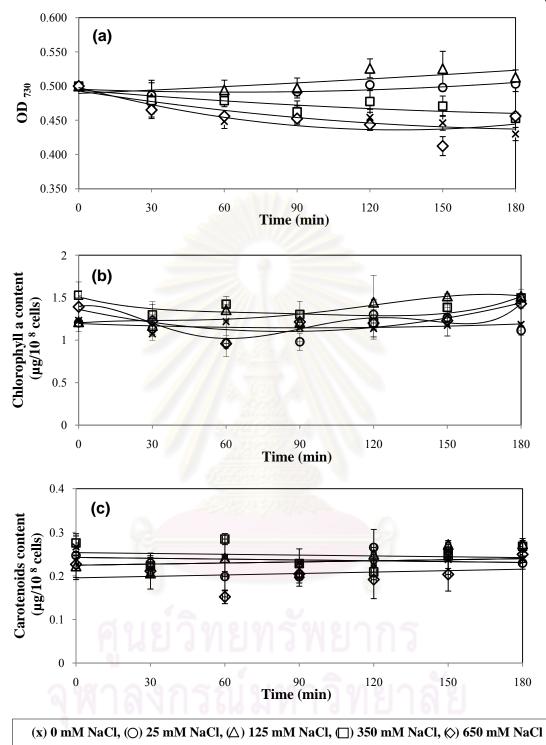


Figure 3.5 Effect of NaCl concentrations on *Synechocystis* cells grown under UV-B radiation for 3 hours. Cells were grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.4 Salt and UV-C stresses

3.2.4.1 The growth of *Synechocystis* cells

The *Synechocystis* cells grown in BG-11 media plus 0, 25, 125, 350 and 650 mM NaCl, respectively, were determined for the growth of cells within 3 hours under UV-C radiation. The results show that their cells growth were not different significantly in various media containing 0, 25, 125, 350 and 650 mM NaCl, respectively (Figure 3.6a). Interestingly, these results demonstrated differently from those pattern of cells grown under normal growth light (Figure 3.3a).

3.2.4.2 The content of intracellular pigments

Under UV-C radiation, the chlorophyll a content (Figure 3.6b) of cells were decreased under the condition of 125, 350 and 650 mM NaCl stressed media, respectively whereas these contents in low NaCl concentration (25 mM) and medium without salt showed no apparent changes on their levels within 3 hours under UV-C exposure. For the carotenoids content under UV-C radiation (Figure 3.6c) were slightly decreased. *Synechocystis* cells grown in media plus 125, 350 and 650 mM NaCl, respectively, gave the carotenoids content higher than those cells grown in the medium without NaCl addition.

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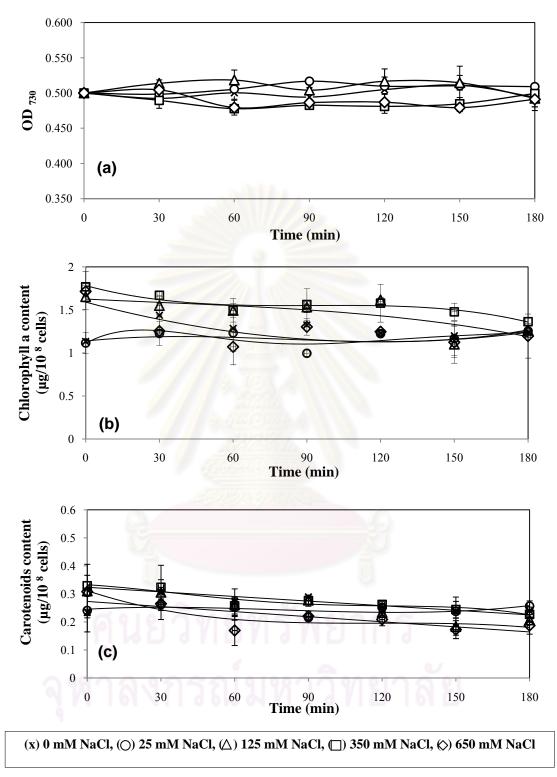


Figure 3.6 Effect of NaCl concentrations on *Synechocystis* cells grown under UV-C radiation for 3 hours. Cells were grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.5 Sorbitol stress under normal growth light

3.2.5.1 The growth of Synechocystis cells

The mid-logarithmic stage of *Synechocystis* cells grown in BG-11 media plus various sorbitol concentrations were diluted to the optical density at 730 nm of 0.5 and followed by determining the growth of cells within 3 hours. The cells grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol, respectively, tended to increase their growth under normal growth light for 3 hours (Figure 3.7a). These normal growth light conditions were used as controls when compared with those exposed to UV-radiation. However, cells grown in BG-11 without sorbitol showed no significant changes to cells grown under sorbitol condition.

3.2.5.2 The content of intracellular pigments

The content of intracellular pigments, namely chlorophyll a and carotenoids, were determined. For the chlorophyll a content of cells which grown in BG-11 media plus 50, 250 and 500 mM sorbitol, respectively, under normal growth light (Figure 3.7b) shown chlorophyll a content higher mM sorbitol (normal BG-11) significantly. However, these contents were constant within 3 hours of treatment. For carotenoids content (Figure 3.7c), they were as similar result as those patterns of chlorophyll a content under the same condition. However, content of carotenoids were 5-fold lower than chlorophyll a content. Although cells in media plus various sorbitol concentrations gave higher contents than that grown in medium without sorbitol, all these cells still possessed the constant levels of pigments within 3 hours under normal growth light.

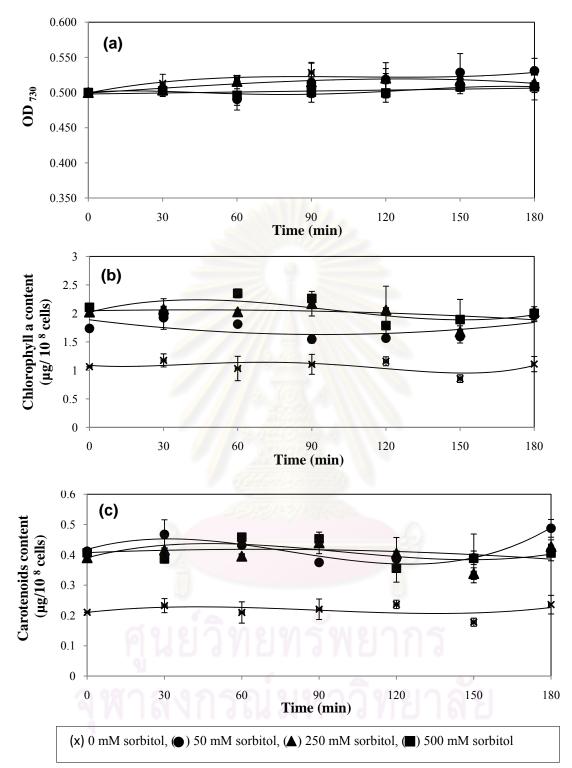


Figure 3.7 Effect of sorbitol concentrations on *Synechocystis* cells grown under normal growth light for 3 hours. Cells were grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.6 Sorbitol and UV-A stresses

3.2.6.1 The growth of Synechocystis cells

The *Synechocystis* cells grown in BG-11 media plus 0, 50, 250 and 500 mM sorbitol, respectively, were determined for the growths of cells under UV-A radiation for 3 hours. From the results, the growth of cells grown in BG-11 media containing various sorbitol concentrations combined with UV-A radiation were decreased, especially the cells grown in 500 mM sorbitol condition within 3 hours-treatment (Figure 3.8a). These conditions showed the decrease on their growth rate of cells when compared with control (under normal growth light; Figure 3.7a).

3.2.6.2 The content of intracellular pigments

The pigments of *Synechocystis* cells under UV-A radiation gave the chlorophyll a content in constant levels (Figure 3.8b) under the condition of cells grown in BG-11 plus various sorbitol concentrations, namely 0, 50, 250 and 500 mM sorbitol, respectively. Interestingly, under combination stresses of sorbitol and UV-A were observed that the increase of chlorophyll a content depended on the increase of sorbitol concentration in media obviously when compared to cells in medium without sorbitol. In addition, the carotenoids content of cells showed that they were similar to the pattern of chlorophyll a content. The cell cultures grown in media adding sorbitol gave contents higher than those cells grown in normal BG-11 without sorbitol (Figure 3.8c) within 3 hours of UV-A exposure.

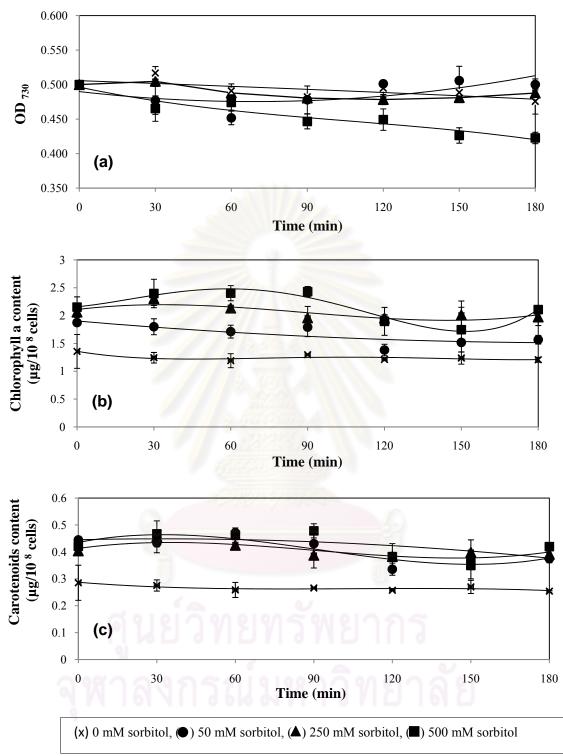


Figure 3.8 Effect of sorbitol concentrations on *Synechocystis* cells grown under UV-A radiation for 3 hours. Cells were grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.7 Sorbitol and UV-B stresses

3.2.7.1 The growths of Synechocystis cells

The *Synechocystis* cells grown in BG-11 media plus 0, 50, 250 and 500 mM sorbitol, respectively were determined for the growths of cells under UV-B radiation for 3 hours. As the results, UV-B radiation had affected on the growths of cells grown in BG-11 media containing various sorbitol concentrations. The tendency of cell growth was decreased after exposing under UV-B for 3 hours (Figure 3.9a). These combined conditions tended to decrease the growth of cells when compared to control (under normal growth light; Figure 3.7a).

3.2.7.2 The content of intracellular pigments

The intracellular pigments of *Synechocystis* cells under UV-B radiation showed that the chlorophyll a content (Figure 3.9b) of cells grown in BG-11 plus various sorbitol concentrations, namely 0, 50, 250 and 500 mM sorbitol, respectively, gave constant levels. However, after UV-B exposure for 3 hours, the chlorophyll a levels of cells grown in normal BG-11 (without sorbitol) were lower than these grown in BG-11 plus various sorbitol concentrations. In addition, the carotenoids content of cells were accumulated in the similar tendency as chlorophyll a content in the same condition. Their contents gave higher than those pigments from cells grown in normal BG-11 without sorbitol (Figure 3.9c) within 3 hours of UV-B radiation.

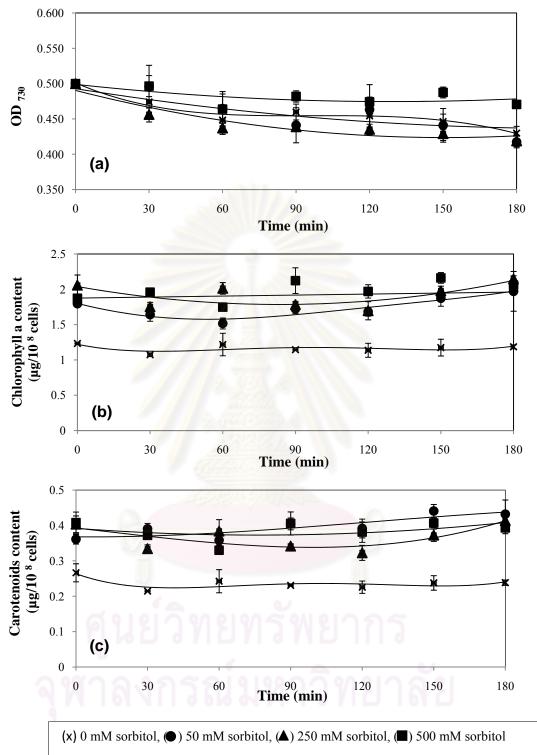


Figure 3.9 Effect of sorbitol concentrations on *Synechocystis* cells grown under UV-B radiation for 3 hours. Cells were grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.2.8 Sorbitol and UV-C stresses

3.2.8.1 The growths of Synechocystis cells

The *Synechocystis* cells grown in BG-11 media plus 0, 50, 250 and 500 mM sorbitol, respectively, were determined for the growths of cells under UV-C radiation for 3 hours. The growth of cells grown in BG-11 media containing various sorbitol concentrations combined with UV-C radiation were decreased, especially cells grown in 500 mM sorbitol condition within 3 hours of stresses (Figure 3.10a). On the other hand, cells grown in normal BG-11 medium without sorbitol were not affected by UV-C radiation due to the growth rate still showed the constant amount.

3.2.8.2 The content of intracellular pigments

The intracellular pigments of *Synechocystis* cells under UV-C radiation of chlorophyll a content (Figure 3.10b) gave the constant levels in cells grown in BG-11 plus various sorbitol concentrations, namely 0, 50, 250 and 500 mM sorbitol, respectively. However after UV-C exposure for 3 hours, the chlorophyll a levels of cells grown in normal BG-11 (without sorbitol) showed lower amount than those in cells from BG-11 plus various sorbitol conditions. Additionally, the carotenoids content of cells were similar to the tendency of chlorophyll a content namely, all cultures grown in media containing sorbitol gave chlorophyll a content higher than those cells grown in normal BG-11 without sorbitol (Figure 3.10c) within 3 hourstreatment. Both chlorophyll a and carotenoids content under UV-C radiation demonstrated their contents higher than those under normal growth light in significance.

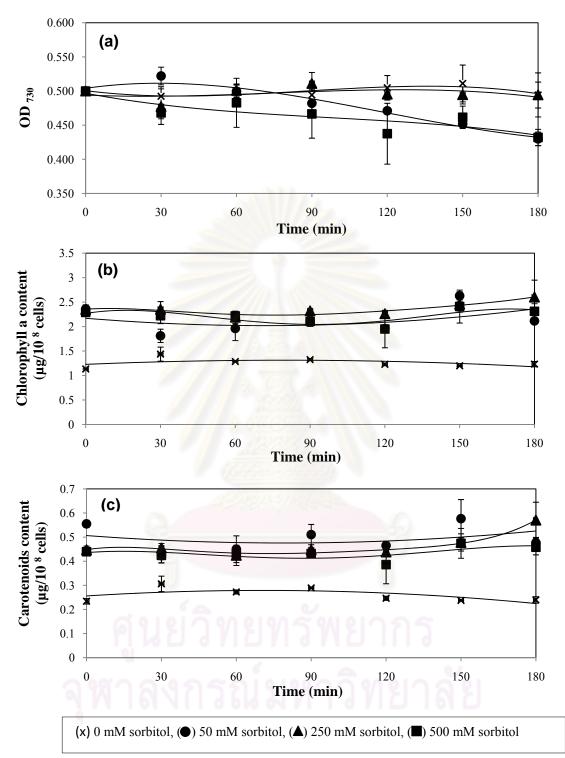


Figure 3.10 Effect of sorbitol concentrations on *Synechocystis* cells grown under UV-C radiation for 3 hours. Cells were grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol. Growth curve (a), chlorophyll a (b) and carotenoids content (c). The data represent means \pm SD., n = 3.

3.3 Polyamine biosynthesis of *Synechocystis* cells under salinity and UV radiations

3.3.1 Polyamines content under salt and normal growth light

Polyamines content of *Synechocystis* cells at mid-logarithmic stage in BG-11 containing various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl exposed under normal growth light (shown in Figure 3.11). The polyamines content at short-term stress (Figure 3.11a) were higher in PCA-soluble fraction (the major form of free form) than in PCA-insoluble fraction (minor form). For PCA-soluble polyamines, the results show that the highest level among three kinds of them was spermidine, especially from the cells grown in BG-11 plus 650 and 350 mM NaCl, respectively, whereas putrescine and spermine contents showed very small amounts. On the other hand, PCA-insoluble polyamines were not changed significantly. The total polyamines including PCA-soluble and PCA-insoluble polyamines were increased upon the increase of NaCl concentrations. However, results from long term stress of 3 hours (Figure 3.11b) show the decrease of the polyamines content when compared with short term stress (1 hour).

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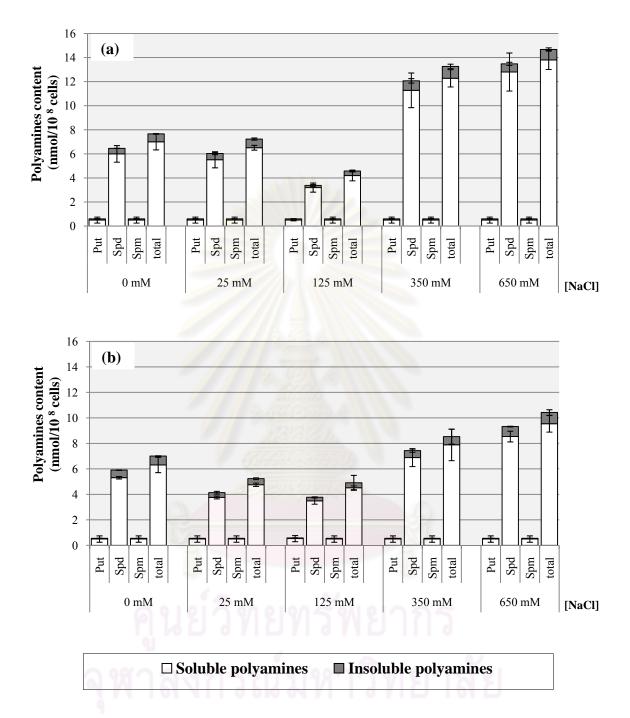


Figure 3.11 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl, respectively, under normal growth light for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.2 Polyamines content under salt and UV-A stresses

Polyamines content of Synechocystis cells at mid-logarithmic stage in BG-11 containing various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl exposed under UV-A for 3 hours (shown in Figure 3.12). The polyamines content at short-term (Figure 3.12a) were found higher in PCA-soluble fraction than in PCAinsoluble fraction. For PCA-soluble polyamines, the results show that the highest level among three kinds of them was spermidine, especially from the cells in BG-11 plus 350 mM NaCl whereas putrescine and spermine contents showed very small amounts. On the other hand, for PCA-insoluble polyamines, spermidine showed the highest content of polyamines from cells grown in all media condition, especially BG-11 plus 650 mM NaCl. Moreover, the total polyamines including PCA-soluble and PCA-insoluble polyamines were increased under UV-A, especially cells grown in BG-11 plus 350 mM NaCl (for 1 hour). However, at long term stress (Figure 3.12b), the major form was PCA-soluble polyamines whereas the PCA-insoluble polyamines occurred as minor forms. Spermidine was found in higher level than putrescine and spermine. Interestingly, polyamines of cells exposed to long term stress (3 hours) of UV-A were increased, higher than those of cells at 1-hour stress, especially in BG-11 plus 350 and 650 mM NaCl. Furthermore, the contents of PCA-insoluble polyamines at 3-hours treament were increased significantly when compared to cells grown under normal growth light (Figure 3.11), especially in BG-11 plus 350 and 650 mM NaCl.

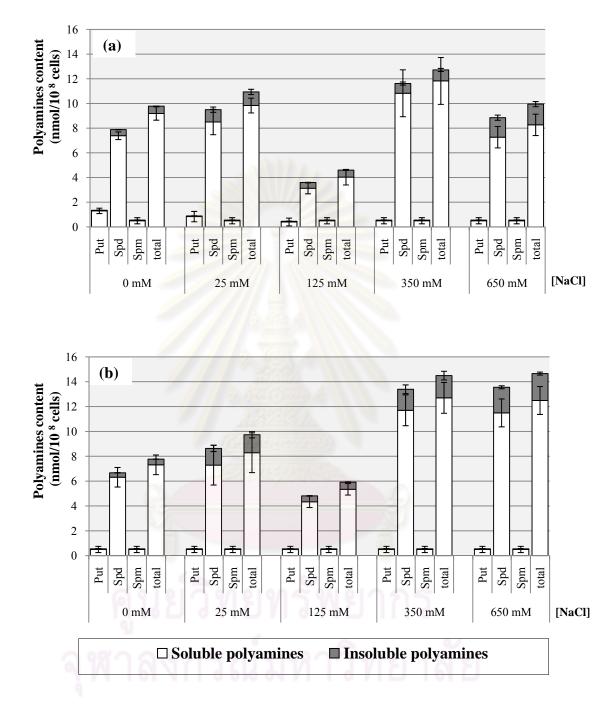


Figure 3.12 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl, respectively, under UV-A radiation for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.3 Polyamines content under salt and UV-B stresses

Polyamines content of Synechocystis cells at mid-logarithmic stage in BG-11 containing various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl exposed under UV-B for 3 hours (shown in Figure 3.13). The polyamines content at short-term stress (Figure 3.13a) were higher in PCA-soluble fraction than in PCAinsoluble polyamines. For PCA-soluble polyamines, the results show that the highest level among three kinds of them was spermidine whereas putrescine and spermine contents showed very small amounts. The polyamines content were increased obviously from cells grown in all conditions under UV-B stress, especially in BG-11 plus 350 mM NaCl. It was 5.58 fold higher than control group (under normal growth Moreover, the results from long-term stress under UV-B (Figure 3.13b) light). showed that cells grown in BG-11 plus 350 mM NaCl showed the induction of soluble-polyamine content of 1.53 and 8.8 fold of those from cells after exposing to UV-B for short-term stress and to normal growth light, respectively. However, UV-B stress induced the contents of PCA-insoluble spermidine slightly when compared to short-term exposure of UV-B. On the other hand, putrescine and spermine contents were accumulated in small amounts. Also, the total polyamines including PCAsoluble and PCA-insoluble fractions were increased under UV-B exposure, especially from cells grown in BG-11 plus 350 mM NaCl both for 1 and 3 hours-treatments.

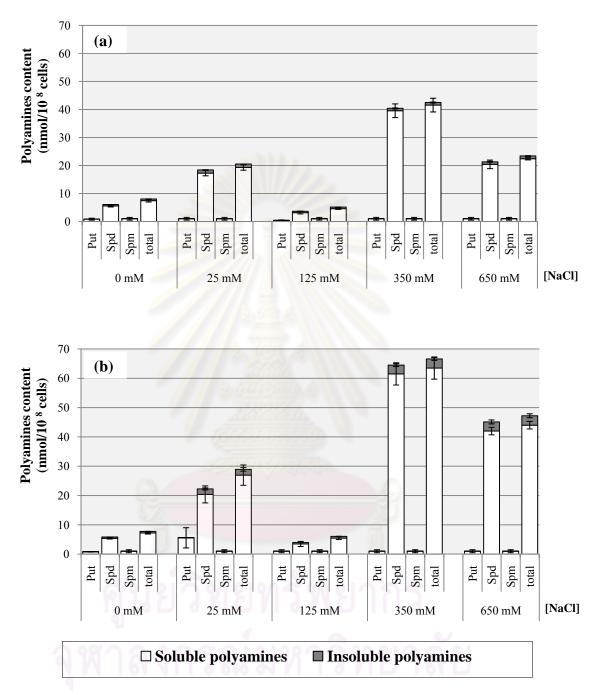
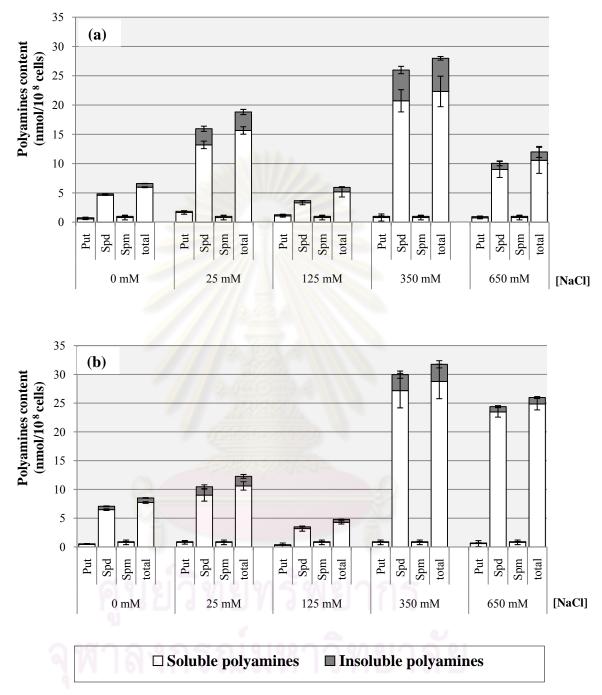
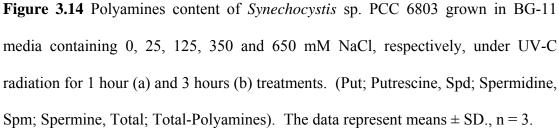


Figure 3.13 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 25, 125, 350 and 650 mM NaCl, respectively, under UV-B radiation for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.4 Polyamines content under salt and UV-C stresses

Polyamines content of Synechocystis cells at mid-logarithmic stage in BG-11 containing various NaCl concentrations of 0, 25, 125, 350 and 650 mM NaCl exposed under UV-C for 3 hours (shown in Figure 3.14). The polyamines content at short-term stress (Figure 3.14a) were found in PCA-soluble fraction (the major form of free form) higher than minor form of PCA-insoluble fraction. For PCA-soluble polyamines, the results show that the highest level among three kinds of them was spermidine whereas putrescine and spermine contents showed very small amounts. The polyamines content of cells grown in BG-11 plus 350 mM NaCl were increased obviously at 3.74 fold of control group (under normal growth light). While PCAinsoluble fraction, only spermidine was increased at cells grown in BG-11 plus 350 mM NaCl. Moreover, the results from long-term stress under UV-C radiation (Figure 3.14b) show that PCA-soluble spermidine was higher than putrescine and spermine. Cells grown in BG-11 plus 350 mM NaCl accumulated the soluble polyamine content of 1.29- and 3.73-fold of those from cells after exposing to UV-C for short-term stress and to normal growth light, respectively. However, PCA-insoluble polyamines in BG-11 plus 350 mM NaCl and UV-C conditions with for 3 hours-treatment were increased on spermidine content slightly when compared to those of cells in other media conditions whereas putrescine and spermine contents showed in small amounts. Also, the total polyamines including PCA-soluble and PCA-insoluble polyamines were increased under UV-C radiation, especially in BG-11 plus 350 mM NaCl-treated cells for 1 and 3 hours-treatments.





3.3.5 Polyamines content under sorbitol and normal growth light

Polyamines content of *Synechocystis* cells grown in BG-11 various sorbitol concentrations, namely 0, 50, 250 and 500 mM sorbitol, respectively, under normal growth light shown in Figure 3.15. The polyamines content at short-term stress (Figure 3.15a) were found in PCA-soluble fraction which was the major form whereas their minor form was occurred in PCA-insoluble fraction. For PCA-soluble polyamines, the results show that the highest levels of polyamines, especially from the cells grown in BG-11 plus 250 mM sorbitol were spermidine and putrescine whereas spermine gave very small amounts. For PCA-insoluble polyamines, they were not changed significantly. Obviously, the total polyamines including both soluble and insoluble fractions were increased under 250 mM sorbitol condition within 3 hours of treatment. Surprisingly, putrescine in soluble form was stimulated obviously at 3 hours-treatment under 250 mM NaCl condition. The results under this normal growth light were used as the control when compared to cells after exposed to UV-radiation.

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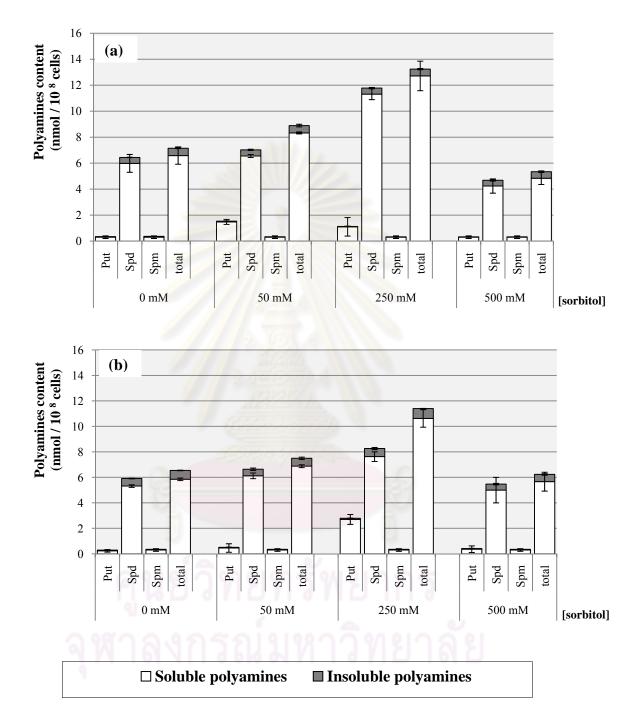


Figure 3.15 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol, respectively, under normal growth light for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.6 Polyamines content under sorbitol and UV-A stresses

Polyamines content of Synechocystis cells grown in BG-11 various sorbitol concentrations, namely, 0, 50, 250 and 500 mM sorbitol, respectively, under UV-A radiation for 3 hours shown in Figure 3.16. The polyamines content at shortterm stress of one hour under UV-A and sorbitol stresses (Figure 3.16a) were found in PCA-soluble fraction as the major form whereas their minor form was in insoluble fractions. For PCA-soluble polyamines, spermidine was up-regulated dominantly whereas putrescine and spermine were found in trace amounts. On the other hand, only PCA-insoluble spermidine gave induced contents in all conditions, though somewhat less than PCA-soluble fractions. The total polyamines including PCAsoluble and PCA-insoluble fractions were slightly increased under sorbitol stress of 250 mM. However, these amounts were less than those of control without sorbitol. Results in Figure 3.16b show that PCA-soluble polyamines of cells grown under BG-11 plus 250 and 500 mM sorbitol for long term stress (3 hours) of UV-A were decreased when compared to cells grown in normal BG-11 without sorbitol. Furthermore, the contents of PCA-insoluble polyamines were unchanged significantly in all media conditions.

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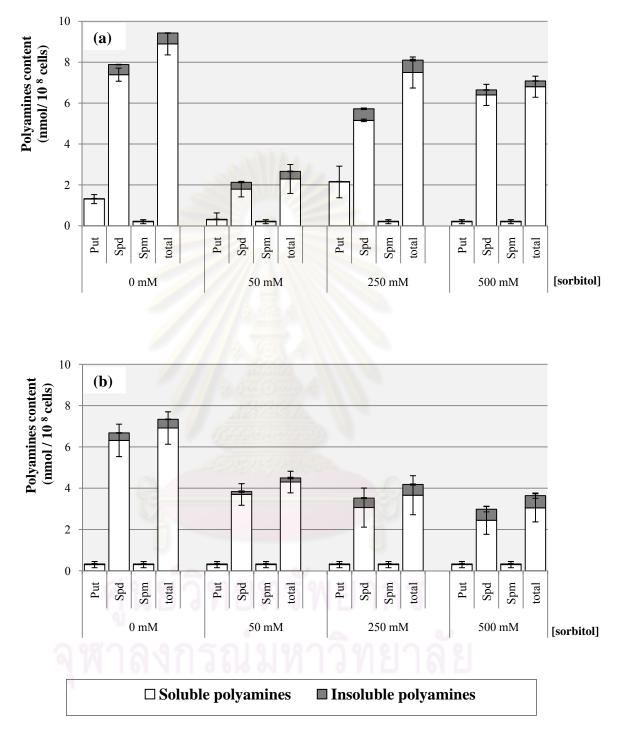


Figure 3.16 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol, respectively, under UV-A radiation for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.7 Polyamines content under sorbitol and UV-B stresses

Polyamines content of *Synechocystis* cells grown in BG-11 various sorbitol concentrations, namely, 0, 50, 250 and 500 mM sorbitol, respectively, under UV-B radiation within 3 hours shown in Figure 3.17. The polyamines content at short-term of one hour under UV-B combined with sorbitol stresses (Figure 3.17a) were found in PCA-soluble as the major form whereas minor form was found in PCA-insoluble fractions. For PCA-soluble polyamines, high level of spermidine was observed whereas putrescine and spermine were accumulated in small levels. The PCA-insoluble polyamines had the similar pattern to PCA-soluble polyamines. Although the total polyamines including PCA-soluble and PCA-insoluble fractions were up-regulated at 500 mM sorbitol condition when compared to these cells grown in normal BG-11 without sorbitol under UV-B stress for 1 hour. For longer term stress of 3 hours (Figure 3.17b), soluble polyamines under 250 and 500 mM sorbitol conditions were decreased significantly when compared to cells grown in normal BG-11 without sorbitol. Furthermore, cells grown in BG-11 plus 250 mM sorbitol were slightly increased the PCA-insoluble polyamines under UV-B radiation for 3 hours.

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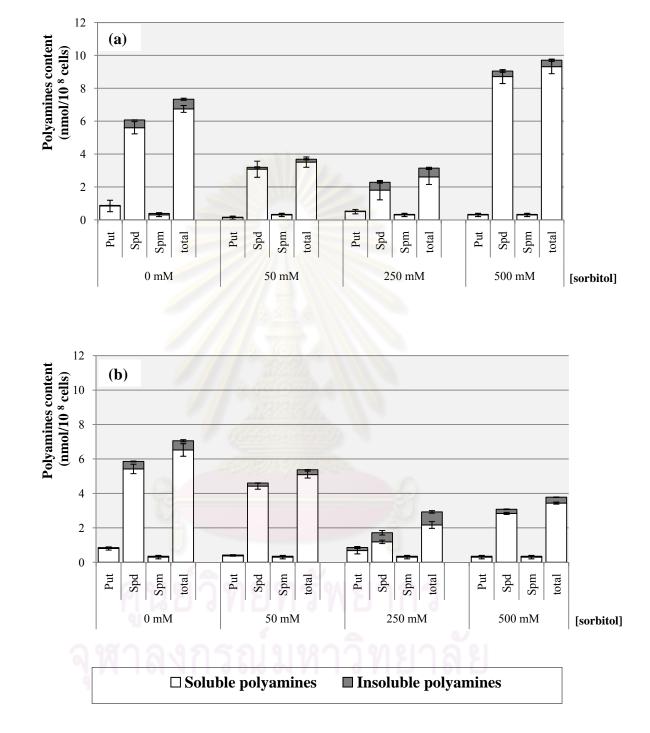
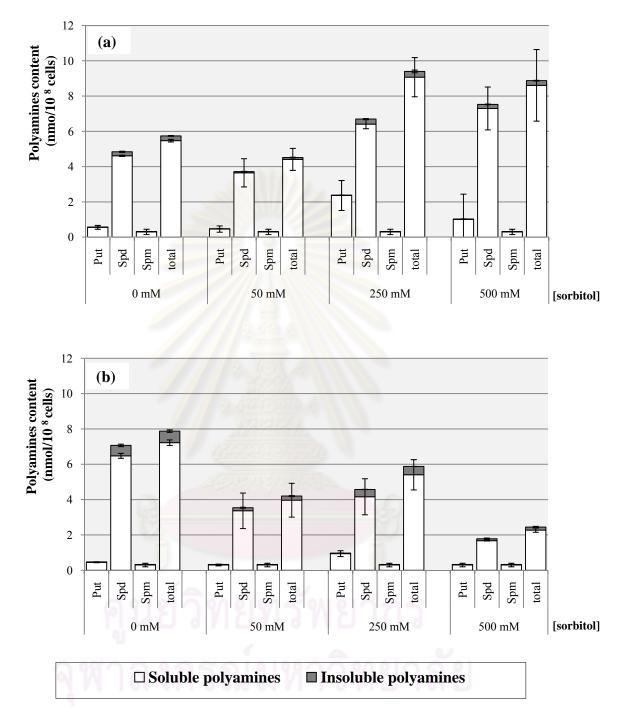


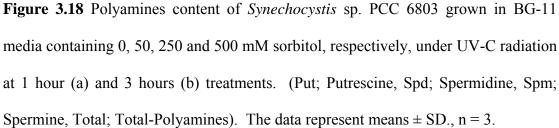
Figure 3.17 Polyamines content of *Synechocystis* sp. PCC 6803 grown in BG-11 media containing 0, 50, 250 and 500 mM sorbitol, respectively, under UV-B radiation for 1 hour (a) and 3 hours (b) treatments. (Put; Putrescine, Spd; Spermidine, Spm; Spermine, Total; Total-Polyamines). The data represent means \pm SD., n = 3.

3.3.8 Polyamines content under sorbitol and UV-C stresses

Polyamines content of Synechocystis cells grown in the conditions which were varied sorbitol concentrations, namely, 0, 50, 250 and 500 mM sorbitol, respectively, into BG-11 medium under UV-C radiation for 3 hours (Figure 3.18). The polyamines content at short-term stress of one hour under UV-C and sorbitol stresses (Figure 3.18a) were found in PCA-soluble fraction in majority whereas PCAinsoluble polyamines were found in minority. For PCA-soluble polyamines, spermidine and putrescine were up-regulated whereas spermine was accumulated in small amounts under BG-11 plus 250 mM sorbitol condition. On the other hand, PCA-insoluble polyamines were induces in trace level in all conditions. Total polyamines including PCA-soluble and PCA-insoluble fractions of cells grown in BG-11 plus 250 mM sorbitol were increased significantly when compared to cells grown in normal BG-11 without sorbitol under UV-B stress for 1 hour. At 3 hours of long term stress (Figure 3.18b) total polyamines were down-regulated under BG-11 plus 250 and 500 mM sorbitol conditions. The PCA-soluble polyamines of cells under 50, 250 and 500 mM sorbitol conditions were significantly decreased when compared to cells grown in normal BG-11 without sorbitol.

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3.4 Combination effects of salinity and UV-radiation on *adc* mRNA levels

3.4.1 Effects of salinity under normal growth light

Total RNAs of *Synechocystis* cells grown in normal BG-11, BG-11 plus 350 mM NaCl and 500 mM sorbitol, respectively were used as a template for RT-PCR amplification. The relative amount of arginine decarboxylase (*adc*) mRNA was shown in Figure 3.19. From the results, *adc1* mRNA level of 350 mM NaCl-treated cells was higher than that of cells grown in normal BG-11. Whereas *adc2* mRNA level of cells under same salt-treatment showed a slight increase when compared to control (Figure 3.19). From the results of cells under salt stress, *adc1* mRNA was increased under high salt concentration. For sorbitol stress, *adc1* and *adc2* mRNA levels were constant when compared to the control. However, both salt and sorbitol treatments showed the levels of *adc2* mRNA higher than *adc1* mRNA. The results for *16s* rRNA in samples derived from the same amount of total RNA was also included which represented as an internal standard.

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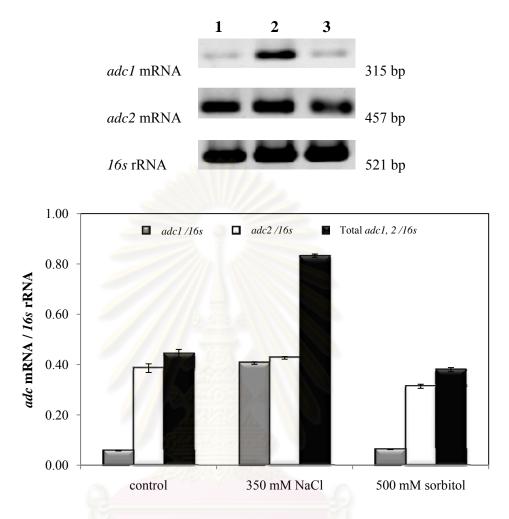


Figure 3.19 RT-PCR expression analysis of arginine decarboxylase (*adc1* and *adc2*) mRNA levels in *Synechocystis* sp. PCC 6803 exposed under normal growth light for 1 hour. Cells were grown in salinity treatment, namely, normal BG-11 media, control (lane 1), BG-11 containing 350 mM NaCl (lane 2) and 500 mM sorbitol (lane 3) respectively. The relative abundance of *16s* rRNA is also shown in lower row. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation.

3.4.2 Effects of salinity and UV-A stresses

Total RNAs of *Synechocystis* cells which grown in normal BG-11, BG-11 plus 350 mM NaCl and 500 mM sorbitol, respectively, under UV-A exposure for 1 hour were used as a template for RT-PCR amplification. The relative amount of arginine decarboxylase (adc) mRNA was shown in Figure 3.20. The transcription levels of adc1 mRNA under salt stress were increased upon increasing of salt concentration. However, UV-A radiation induced adc1 mRNA levels when compared to both controls under UV-A exposure and under normal growth light (Figure 3.19). Moreover, combined stresses of salt and UV-A to cells grown in 350 mM NaClcondition affected the level of *adc1* mRNA decreasingly when compared to that of cells grown under normal growth light. While adc1 mRNA level of 500 mM sorbitoltreated cells under short-term of UV-A exposure was higher constant when compared to control, but cells grown under normal growth light. For adc2 mRNA level of cells under UV-A exposure was increased at high concentration of salt and sorbitol when compared with control. Interestingly, both cells grown in salt- and sorbitol-treatments showed the levels of *adc2* gene higher than *adc1*, as well as those of cells grown in normal growth light. The results for 16s rRNA in samples derived from the same amount of total RNA was also included which represented as an internal standard.

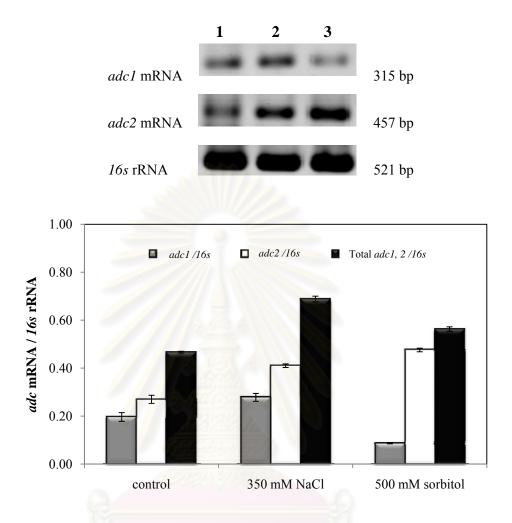


Figure 3.20 RT-PCR expression analysis of arginine decarboxylase (*adc1* and *adc2*) mRNA levels in *Synechocystis* sp. PCC 6803 exposed under UV-A exposure for 1 hour. Cells were grown in salinity treatment, namely, normal BG-11 media, control (lane 1), BG-11 containing 350 mM NaCl (lane 2) and 500 mM sorbitol (lane 3) respectively. The relative abundance of *16s* rRNA is also shown in lower row. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation.

3.4.3 Effects of salinity and UV-B stresses

Total RNAs of *Synechocystis* cells under UV-B exposure for 1 hour which cells grown in normal BG-11, BG-11 plus 350 mM NaCl and 500 mM sorbitol, respectively, were reverse-transcribed. The relative amount of arginine decarboxylase (*adc*) mRNA was shown in Figure 3.21. The amount of *adc1* mRNA under salt stress was increased apparently at high salt concentration of 350 mM NaCl whereas it was slightly increased under 500 mM-sorbitol treatment. Expression level of *adc2* mRNA was increased under both salt (350 mM NaCl) and sorbitol (500 mM) stresses when compared to those of cells grown in BG-11 media without salt and sorbitol addition (control). Interestingly, the levels of *adc2* mRNA were higher than *adc1* mRNA levels under normal BG-11 (control) and BG-11 plus 500 mM sorbitol condition. Moreover, cells treated with 350 mM NaCl and UV-B radiation showed no difference on expressions of *adc1* and *adc2* mRNA levels. Moreover, they were higher than that of control. For *16s* rRNA of cells were represented as an internal standard.

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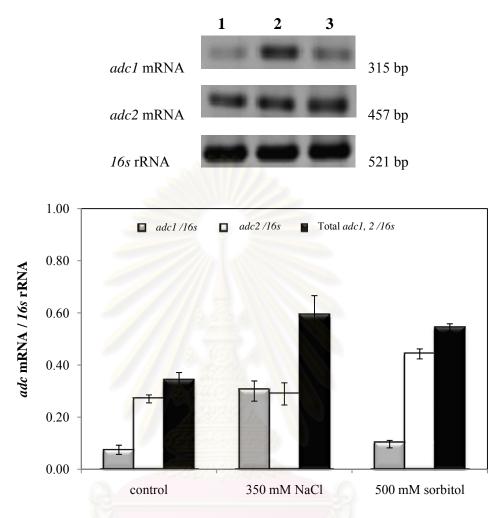


Figure 3.21 RT-PCR expression analysis of arginine decarboxylase (*adc1* and *adc2*) mRNA levels in *Synechocystis* sp. PCC 6803 exposed under UV-B exposure for 1 hour. Cells were grown in salinity treatment, namely, normal BG-11 media, control (lane 1), BG-11 containing 350 mM NaCl (lane 2) and 500 mM sorbitol (lane 3) respectively. The relative abundance of *16s* rRNA is also shown in lower row. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation.

3.4.4 Effects of salinity and UV-C stresses

Total RNAs of *Synechocystis* cells which grown in normal BG-11, BG-11 plus 350 mM NaCl and 500 mM sorbitol, respectively, under UV-C exposure for 1 hour were reverse transcribed. The relative amount of arginine decarboxylase (*adc*) mRNA was shown in Figure 3.22. The amount of *adc1* mRNA was apparently increased after treating with 350 mM NaCl and UV-C radiation. However, cell grown in BG-11 plus 500 mM sorbitol treatment was not different from the *adc1* mRNA level of control. On the other hand, *adc2* mRNA amount was lower than *adc1* mRNA level under 350 mM NaCl condition combined with UV-C. The results for *16s* rRNA in samples derived from the same amount of total RNA was also included which represented an internal standard.

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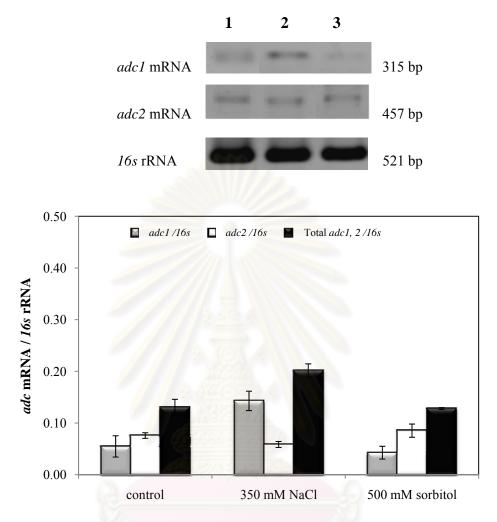


Figure 3.22 RT-PCR expression analysis of arginine decarboxylase (*adc1* and *adc2*) mRNA levels in *Synechocystis* sp. PCC 6803 exposed under UV-C exposure for 1 hour. Cells were grown in salinity treatment, namely, normal BG-11 media, control (lane 1), BG-11 containing 350 mM NaCl (lane 2) and 500 mM sorbitol (lane 3) respectively. The relative abundance of *16s* rRNA is also shown in lower row. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation.

3.5 Combination effects of salinity and UV-radiation on ADC protein

3.5.1 Effects of salinity under normal growth light

Total protein of *Synechocystis* cells under salinity treatment were extracted and observed by SDS-PAGE analysis (Figure 3.23A). The arginine decarboxylase (ADC) protein was analyzed by Western blot (Figure 3.23B). After western blot incubation with the antibody, it was immunodetected and found a single protein band with an apparent molecular mass of about 55 kDa. However, ADC proteins of cells were moderately increased under salt stress whereas highly increased under sorbitol stress, namely, BG-11 plus 500 mM sorbitol (Figure 3.23C).

3.5.2 Effects of salinity and UV-A stresses

Total protein of *Synechocystis* cells under combined stresses of salinity and UV-A radiation were extracted and performed by SDS-PAGE analysis (Figure 3.24A). The arginine decarboxylase (ADC) protein was analyzed by Western blot analysis (Figure 3.24B). After western blot incubation with the antibody, it was immunodetected and found a single protein band with an apparent molecular mass of about 55 kDa. The ADC protein levels of cells were slightly increased under 25 and 350 mM NaCl conditions whereas highly increased under sorbitol stress of 500 mM sorbitol (Figure 3.24C).

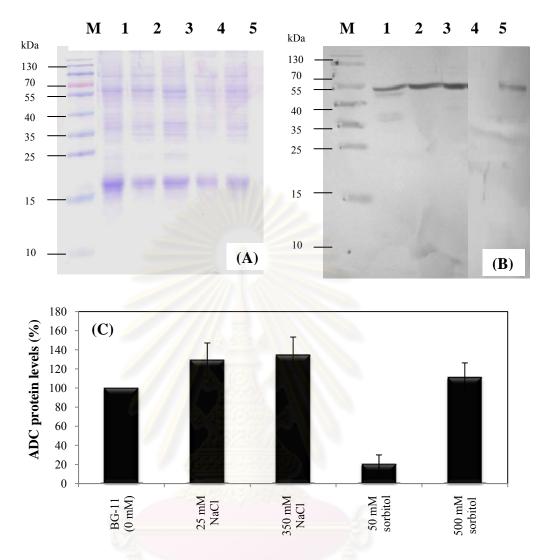


Figure 3.23 Western blot analysis of Arginine decarboxylase (ADC) under salt and sorbitol stresses from *Synechocystis* cells under normal growth light (B). Total protein extract (10 µg) was loaded onto the SDS-gel (A). After SDS-PAGE analysis. The gel was electrophoretically transferred onto PVDF membrane and probe for 4 h at room temperature with a 1:3000 dilution of antiserum against MBP-ADC. Lane M, standard marker ; Lane 1, control ; Lane 2, 25 mM NaCl ; Lane 3, 350 mM NaCl ; Lane 4, 50 mM sorbitol ; Lane 5, 500 mM sorbitol. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation (C). (100% ratio of 13,932)

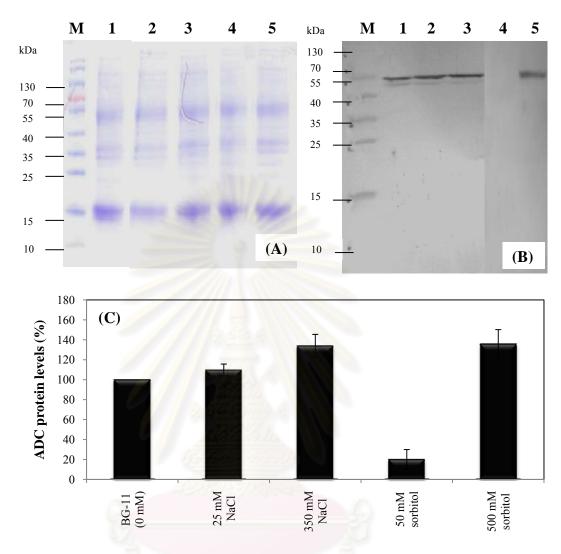


Figure 3.24 Western blot analysis of Arginine decarboxylase (ADC) under salt, sorbitol and UV-A stresses from *Synechocystis* cells (B). Total protein extract (10 μ g) was loaded onto the SDS-gel (A). After SDS-PAGE analysis. The gel was electrophoretically transferred onto PVDF membrane and probe for 4 h at room temperature with a 1:3000 dilution of antiserum against MBP-ADC. Lane M, standard marker ; Lane 1, control ; Lane 2, 25 mM NaCl ; Lane 3, 350 mM NaCl ; Lane 4, 50 mM sorbitol ; Lane 5, 500 mM sorbitol. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation (C). (100% ratio of 15,979).

3.5.3 Effects of salinity and UV-B stresses

Total protein of *Synechocystis* cells under combined stresses of salinity and UV-B radiation were extracted and performed by SDS-PAGE analysis (Figure 3.25A). The arginine decarboxylase (ADC) protein was analyzed by Western blot analysis (Figure 3.25B). After western blot incubation with the antibody, it was immunodetected and found a single protein band with an apparent molecular mass of about 55 kDa. However, ADC protein of cells was significantly increased under 350 mM NaCl stress and 500 mM sorbitol stress. However, ADC protein of 500 mM sorbitol-treated cells was not consistent, it showed in trace amount (Figure 3.25C).

3.5.4 Effects of salinity and UV-C stresses

Total protein of *Synechocystis* cells under combined stresses of salinity and UV-C radiation were extracted and ran by SDS-PAGE analysis (Figure 3.26A). The arginine decarboxylase (ADC) protein was analyzed by Western blot analysis (Figure 3.26B). After incubation of western blot membrane with the antibody, it was found a single protein band with an apparent molecular mass of about 55 kDa. The treatments with 350 mM NaCl and 50 mM sorbitol-treated cells obviously induced the accumulation of ADC proteins when compared with untreated cells (control). However, ADC protein of 500 mM sorbitol-treated cells was not consistent, it showed in less amount. Although, under these stresses were as similar pattern of ADC protein as that under salinity and UV-B treatments, protein levels of salinity and UV-C treatments were higher than those of salinity and UV-B treatments (Figure 3.26C).

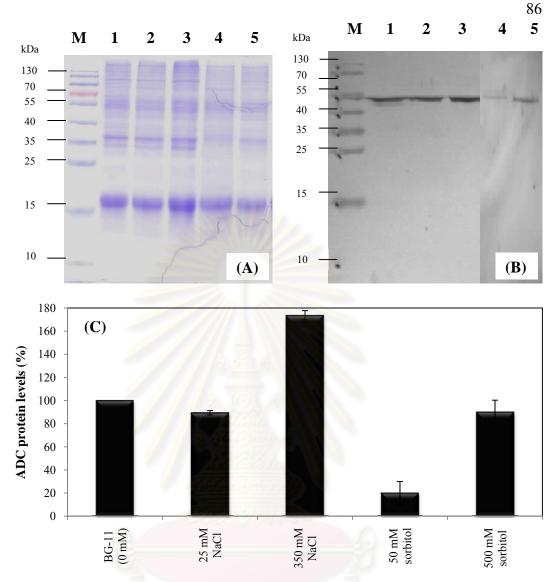


Figure 3.25 Western blot analysis of Arginine decarboxylase (ADC) under salt, sorbitol and UV-B stresses from *Synechocystis* cells (B). Total protein extract (10 μ g) was loaded onto the SDS-gel (A). After SDS-PAGE analysis. The gel was electrophoretically transferred onto PVDF membrane and probe for 4 h at room temperature with a 1:3000 dilution of antiserum against MBP-ADC. Lane M, standard marker ; Lane 1, control ; Lane 2, 25 mM NaCl ; Lane 3, 350 mM NaCl ; Lane 4, 50 mM sorbitol ; Lane 5, 500 mM sorbitol. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation (C). (100% ratio of 16,055)

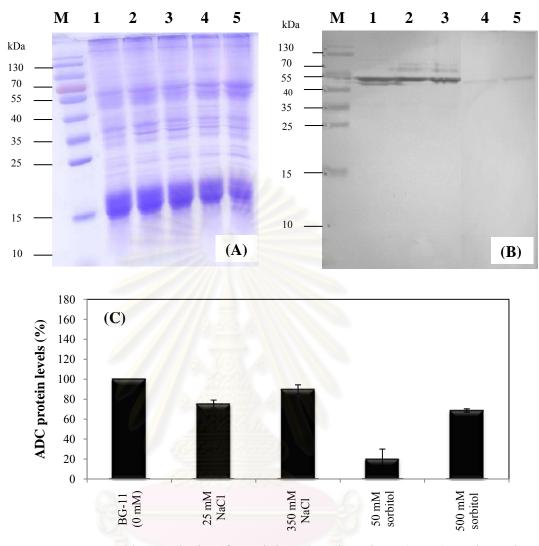


Figure 3.26 Western blot analysis of Arginine decarboxylase (ADC) under salt, sorbitol and UV-C stresses from *Synechocystis* cells (B). Total protein extract (10 μ g) was loaded onto the SDS-gel (A). After SDS-PAGE analysis. The gel was electrophoretically transferred onto PVDF membrane and probe for 4 h at room temperature with a 1:3000 dilution of antiserum against MBP-ADC. Lane M, standard marker ; Lane 1, control ; Lane 2, 25 mM NaCl ; Lane 3, 350 mM NaCl ; Lane 4, 50 mM sorbitol ; Lane 5, 500 mM sorbitol. Quantification was carried out using GeneSnap program from Syngene[®] Gel Documentation (C). (100% ratio of 3,876)

CHAPTER IV

DISCUSSION

4.1 Effects of salinity and UV radiation on growth and content of intracellular pigments

We have demonstrated that 6-7 days culture of Synechocystis sp. PCC 6803 under salinity treatments was at mid-logarithmic phase. These results represented a long term stress of cells on growth and content of intracellular pigments, chlorophyll a and carotenoids under ionic and osmotic stresses (Figure 3.1 and 3.2, respectively). A previous study by Jantaro et al. (2003) showed that Synechocystis cells had increased growth rate up to 550 mM NaCl as well as the growth of cells under untreated condition for long-term stress. While under osmotic stress, the growth of cells grown in sorbitol treatment was decreased upon increasing of sorbitol concentrations. However, no growth was observed at 700 mM sorbitol or higher. In our study, the growth of cells was decreased slightly at high concentration of NaCl and sorbitol, especially 500 mM sorbitol, as well as on their pigment contents. These results suggest that long term stress of *Synechocystis* cells up to 650 mM NaCl or 500 mM sorbitol did not affect severely on growth, chlorophyll a and carotenoid contents of cells under normal growth light. It was reported recently that salt stress led to a decrease in the total chlorophyll content in Hordeum vulgare whereas the carotenoids content were not affected by NaCl treatment (Cakirlar et al., 2008). Moreover, there is an interesting evidence that salt stress could induce the antioxidant enzymes such as superoxide dismutase (SOD), ascorbate peroxidase (APX), and peroxidase in the rice (Oryza sativa L.) (Lee et al., 2001).

We have demonstrated that the UV treatment affected growth and intracellular pigments, compared to those cells under normal growth light (control) (Figures 3.3 and 3.7). Our results showed that the growth of cells under UV-A alone was slightly decreased but was obviously affected after combining with high concentration of salt (Figure 3.4a) or sorbitol (Figure 3.8a). UV-B radiation affected the growth of cells when treated with NaCl (Figure 3.5a) or sorbitol (Figure 3.9a). However, only synergistic effect of sorbitol and UV-C (Figure 3.10a) decreased the growth of cells rather than UV-C plus salt stress. Similar finding was reported by Shinkle *et al.* (2004) that the growth of cells showed different responses to three UV wavebands of short wavelength UV-C, long wavelength UV-B and UV-A. This study it was shown that the content of chlorophyll was no significantly affected by UV radiation (Figures 3.4b-3.6b and 3.8b-3.10b, respectively).

Photosynthesis is dependent on the light harvesting properties of the chlorophylls (Gao *et al.*, 2004). Our results showed that salt and sorbitol treatments stimulated chlorophyll a accumulation higher than cells grown in normal BG-11 (Figures 3.3b and 3.7b). However, these contents did not change markedly within 3 hours of treatments under normal growth light. Similarly, UV treatments did not affect the chlorophyll content of *Synechocystis* cells after exposing to UV-A (Figures 3.4b and 3.8b), UV-B (Figure 3.5b and 3.9b) and UV-C (Figure 3.6b and 3.10b), respectively, within 3 hours of treatments. Many studies reported that UV radiation had an effect the content of pigments, such as the reduction of chlorophyll content in *Capsicum annuum* L. under UV-B and UV-C (at 27 min/day for 14 days) but was not significantly decreased under UV-A radiation (Mahdavian *et al.*, 2008). Moreover, salt stress as well as UV-B led to a decrease of the total chlorophyll content in

Lactuca sativa (Caldwell and Britz, 2006), Hordeum vulgare (Cakirlar et al., 2008) and *Pisum sativum* L. (Agrawal and Mishra, 2009). The reduction of chlorophylls by UV-B may be expected to result in lower levels of biomass accumulation and, hence, be a useful indicator of UV-B sensitivity (Smith et al., 2002). Then, we could say that Synechocystis 6803 could maintain its chlorophyll accumulation under 3 hours of UVstresses. On the other hand, many reports showed that the light-harvesting protein pigments in cyanobacteria are readily affected by UV-B as a consequence of reducing their photosynthetic and metabolic activity (Aráoz and Häder, 1997) and also indicated that the photosynthesis of cyanobacterium Spirulina platensis was inhibited by UV-B radiation for at least 4 hours (Wu et al., 2005). The reduction of the chlorophyll content has a negative effect on plant photosynthetic efficiency by UV radiation (Cakirlar et al., 2008; Mahdavian et al., 2008). The high levels of UV-B may reduce phycobilisomes related fluorescence and PSII activity in Arthrospira (Rajagopal *et al.*, 2005). Damage to D1 protein is known to be responsible for the inhibited activity of PSII (Sass et al., 1997). UV-B irradiation alone and with salt significantly decreased the Fv/Fm of four Barley (Hordeum vulgare L.) cultivars studied whereas salt stress alone had no effect (Cakirlar et al., 2008).

Moreover, we determined the carotenoids content of cells for 3 hours. The results showed that the content of carotenoids under salt and osmotic conditions were higher than those of cells grown in normal BG-11 (Figures 3.3c and 3.7c). This is similar to a previous report that carotenoids are not affected by NaCl treatment (Cakirlar *et al.*, 2008). After *Synechocystis* was exposed to UV radiations, the level of carotenoids showed different patterns, under UV-A both alone and combination with salt stress. The carotenoids levels were constant and slightly increased during the last

3 hours (Figure 3.4c). This result is consistent with the previous report by Mahdavian et al. (2008) who found that the carotenoids content of UV-A treated plants was no significant changes when compared to control (under normal growth light). Moreover, carotenoids content in our study showed a slight enhancement under UV-B plus sorbitol treatments (Figure 3.9c). Coincidently, the previous report demonstrated that UV-B irradiation caused an increase by 5-20% of carotenoids content of all cultivars (Cakirlar et al., 2008) and this may be effective in protecting the photosynthetic apparatus against UV-B (Rakhimberdieva et al., 2004). On the other hand, lutein was the major carotenoid in the lettuce samples with less amounts of β carotene and neoxanthin (Caldwell and Britz, 2006). It was reviewed previously in higher plants that photosynthetic pigments such as chlorophylls in plant and phycobilins in cyanobacteria can act as photosensitizers and produce ROS under UV or visible light excess by reaction of chromophore triplet states with molecular oxygen (Rinalducci et al., 2006). The efficacy of carotenoids in protecting the photosystems and acting as scavengers of ROS, thus protecting chlorophylls against photooxidative damage by interaction with triplet form of ROS is likely due to their function as efficient quenchers of high energy short wave radiation (Krinsky, 1979; Mahdavian et al., 2008).

4.2 Effects of salinity and UV radiation on polyamine biosynthesis

In the present study, we found PCA-soluble polyamines as the major form.

Several work showed the evidence that the free molecular bases of polyamines (PAs) were commonly found in nature (Bouchereau *et al.*, 1999; Wang and Liu, 2009). High accumulation of free PAs in callus exposed to stresses can be considered to

directly participate in stress defense via membrane rigidification or free radical scavenging (Shen et al., 2000) and also possible via activation of some antioxidant systems by indirect role (Wang and Liu, 2009). In this study, polyamines were accumulated by salt and osmotic stresses, especially in 650 mM NaCl (Figure 3.11) and 250 mM sorbitol (Figure 3.15) treated-cells, respectively, under normal growth light. The cellular levels of polyamines in *Synechocystis* cells were induced by longterm osmotic stress and to a less extent by salt stress (Jantaro et al., 2003). In our study, it was found that PCA-soluble spermidine was present as the major type of polyamines in all conditions. Many reports recently showed that the free spermidine content was observed among high salinized conditions (Jantaro et al., 2003; Maiale et al., 2004). Free spermidine was the most abundant polyamine levels against salt concentration (Tassoni et al., 2008). Moreover, several reports indicated that high titers of spermidine and/or spermine, but not putrescine, are correlated with the response of plants to long-term salinization (Sanchez et al., 2005; Jiménez-Bremont et al., 2007). For other common polyamines, namely putrescine and spermine, it was hardly detected both in PCA-soluble and insoluble forms of polyamines. The previous report by Jantaro et al. (2003) revealed that putrescine appeared to be unaffected by osmotic stress. Moreover, the PCA-insoluble conjugated polyamines were detected only in trace amounts (Tassoni et al., 2008). Additionally, spermine was found least abundant (Wang and Liu, 2009) and not synthesized in most prokaryotes (Pegg, 1983) and also do not represent a salt tolerance trait under salt stress (Maiale et al., 2004). Several reports have supported a protective role of spermidine and spermine against salinity. From previous study, it has been suggested that the main role of polyamines is to maintain a cation-anion balance in a long term

of salt treatment in tomato leaves (Santa-Cruz *et al.*, 1997). In *Synechocystis* sp. PCC 6803, a similar role of polyamines is also likely in view of the fact that intracellular Na⁺ would be maintained at a low level by the functional Na⁺/H⁺ antiporter under salt stress (Hamada *et al.*, 2001), thereby making anions especially Cl⁻ in excess.

We have demonstrated the cellular polyamines levels in Synechocystis cells after treating with salt or sorbitol treatments and exposed to UV radiation. The report presented by An et al. (2004) showed that polyamine synthesis could be induced by a lower dose of UV-B radiation but such long-time treatment (7 h per day for 25 days). Their results are in agreement with our study that cells after exposing to UV radiation for 1 hour showed significant increased in their polyamine contents, especially under salt stress combined with either UV-B or UV-C (Figures 3.13a and 3.14a), respectively. However, long-time treatment of UV radiation decreased the polyamine accumulation, especially under osmotic treatments (Figures 3.16b, 3.17b and 3.18b). This result was similar to a decrease of these contents at long-time treatment of UV-B radiation in cucumber leaves (An et al., 2004). On the other hand, ionic stress slightly increased polyamines within 1 hour-stress (Figures 3.12b, 3.13b and 3.14b). Coincidently, UV-B radiation treatment caused increases in the contents of putrescine, spermine, and spermidine in cucumber (An et al., 2004). Changes in polyamine contents have also been reported in response to different stresses (Mansour et al., 2000). An interesting report indicates that polyamine accumulation is a non-specific response to salt stress (Ashraf and Harris, 2004).

The polyamines including putrescine, spermidine and spermine were found associating with light harvesting complex (LCH) and the photosystem II (PSII) in higher plants (Kotzabasis *et al.*, 1993). Many results have confirmed that the increase

in intracellular polyamine contents played an important role in growth and developmental processes of plants and in stress resistance (An and Wang, 1995). Polyamines, especially the thylakoid associated polyamines, play a decisive role in protecting photosynthetic apparatus and resist to UV-B treatment (Lütz *et al.*, 2005; Unal *et al.*, 2008).

In this study the transcription level of arginine decarboxylase was also investigated. The results showed that the increase of adc mRNA of Synechocystis sp. PCC 6803 was highest among cells treated with high concentration of NaCl (350 mM) and sorbitol (500 mM). Salt stress caused the increase in adc mRNA more profoundly than osmotic stress (Jantaro et al., 2003). One recent research also mentioned that salt stress efficiently activated ADC expression in Citrus sinensis (Wang and Liu, 2009). The expression of two different genes encoding ADC (adc1 and *adc2*) has not been reported previously in *Synechocystis*. Then, our results demonstrated for the first time the effects of either salt or sorbitol stress combined with UV radiation on adc1 and adc2 mRNA levels in Synechocystis cells by RT-PCR approach. The *adc1* mRNA level was more up-regulated than *adc2* mRNA level under short-term NaCl stress (Figure 3.19). Therefore, the result suggests that adc1 was an inducible gene whereas *adc2* was a constitutive gene, under salt stress (350 mM NaCl). Osmotic stress seemed to have no effect on adc1 and adc2 mRNA levels. On the other hand, many reports showed that the S-adenosylmethionine decarboxylase 1 (samdc1) gene was expressed at higher levels than samdc2 in Arabidopsis. Furthermore, in Arabidopsis, spermidine synthase 2 gene (spds2) was more expressed than spermidine synthase 1 (spds1) (Soyka and Heyer, 1999; Tassoni

et al., 2008). All of these findings indicated that the ADC pathway was tightly connected to the salt stress response (Liu, *et al.*, 2006).

Furthermore, we have investigated the level of ADC1 protein under salt and sorbitol stresses. The ADC1 protein was slightly increased under high concentration of salt and sorbitol (Figure 3.23). The total polyamine contents showed a similar pattern at transcriptional level, as well as translational level under UV-B combined with salt stress. The results indicated that salt stress connected tightly on transcription and translation levels under normal growth light (Figures 3.19 and 3.23). Moreover, salt stress combined with UV-A (Figures 3.20 and 3.24) and combined with UV-B (Figures 3.21 and 3.25) also showed those level correlations. Osmotic stress did not affect highly on both transcription and translation levels under normal growth light whereas it seemed abolish a tight correlation of both levels when combined osmotic stress with UV radiation (Figures 3.19 and 3.23). However, ADC protein of cells treated with UV-C plus salinity was down-regulated when compared to control (without either salt or sorbitol) (Figure 3.26). However, the apparent change in the pattern of *adc1* transcription level was more than ADC1 protein level. These results indicate that UV-C alone or combined with salt or sorbitol had influence on the transcription and translation levels in Synechocystis cells under short-term stress (1 hour). In this research, the size of ADC protein was 55 kDa in Synechocystis. In higher plants such as oat, ADC was originally reported to be cleaved into a 42 kDa Nterminal and a 24 kDa C-terminal part that are held together with a disulfide bond (Malmberg et al. 1992). Similarly, a 42 kDa part of a processed form of A. thaliana ADC has been detected in vivo (Watson and Malmberg, 1996). However, Arabidopsis bears an open reading frame which encodes a 76 kDa of protein, a

monoclonal antibody produced against its product recognized a 42 kDa protein in Western blot (Watson and Malmberg, 1996). On the other hand, ADC enzyme of *Brassica campestris* (a species in the same family as *Arabidopsis*) was found to be homotetramer, with a subunit molecular mass of 60 kDa (Das *et al.*, 1995) and the *adc* of *Brassica juncea* encodes a 76 kDa protein (Mo and Pua, 1998). Jantaro *et al.* (2006) suggested that *Synechocystis* ADCs are post-translationally regulated.



CHAPTER V

CONCLUSION

Based on the results, the following specific conclusion were drawn :

- The long-term stress (6-7 days) of *Synechocystis* cells under up to 650 mM NaCl or 500 mM sorbitol condition did not affect severely on growth, chlorophyll a and carotenoid contents of cells under normal growth light.
- 2. The growth of *Synechocystis* cells showed different responses after exposing to UV radiations for 3 hours.
- 3. For salt and sorbitol stressed-cells, the increase in chlorophyll a and carotenoids level was higher than cells grown in normal BG-11.
- 4. The content of chlorophyll was not significantly affected by UV radiations.
- The content of carotenoids showed slightly increases at last 3 hours under UV-A both alone and combination with salt stress, and UV-B plus sorbitol treatments.
- PCA-soluble polyamines were found as major forms and PCA-soluble spermidine was present dominantly in all conditions, rather than putrescine and spermine.

- Polyamines were up-regulated by salt and osmotic stresses, especially in 650 mM NaCl and 250 mM sorbitol treated-cells, respectively, under normal growth light.
- Short-term stress (1 hour) of UV radiations significantly increased the polyamine contents, especially under salt stress combined with either UV-B or UV-C exposure.
- 9. Long-time stress (3 hours) of UV radiations decreased the intracellular polyamine accumulation, especially under osmotic treatments.
- 10. The *adc1* mRNA level was more up-regulated by salt stress than *adc2* mRNA level. Therefore, *adc1* was an inducible gene whereas *adc2* was a constitutive gene under 350 mM NaCl condition.
- 11. Osmotic stress did un-affect on *adc1* and *adc2* mRNA levels obviously.
- 12. The ADC1 protein was slightly increased under high concentrations of salt and sorbitol.
- 13. The relationship of total polyamine contents was consistent to ADC transcription and protein levels under salt stress combined UV-B.
- 14. Both transcriptional and protein levels were connected by salt and osmotic stresses, salt treatment combined with UV-A and UV-B.

15. UV-C alone or combined with salt or sorbitol stress had influenced on the ADC transcriptional and translational levels in *Synechocystis* cells, at least for short-term stress (1 hour).



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APPENDICES

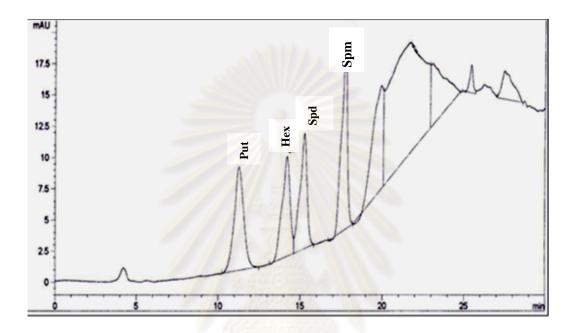
APPENDIX A

BG-11 medium (1,000 ml)

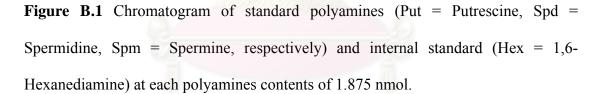
	Solid medium	Liquid medium
H ₂ O	947 ml	967 ml
Bacto-agar	15 g	-
100x BG-FPC*	10 ml	10 ml
189 mM Na ₂ CO ₃	1 ml	1 ml
175 mM K ₂ HPO ₄	1 ml	1 ml
6 mg/ml Ammonium ferric citrate	1 ml	1 ml
1 M TES	10 ml	-
30% Na ₂ S ₂ O ₃ x 5H ₂ O	10 ml	-
1 M Hepes-NaOH, pH 7.5	20 ml	20 ml

100x BG-FPC	*	1,000x Trace metal mix**
(100 ml)		(1,000 ml)
NaNO ₃	14.96 g	H ₃ BO ₃ 2.86 g
MgSO ₄ .7H ₂ O	0.75 g	MnCl ₂ .4H ₂ O 1.81 g
CaCl ₂ .2H ₂ O	0.36 g	ZnSO ₄ .7H ₂ O 0.221 g
Citric acid	0.065 g	Na ₂ MoO ₄ .2H ₂ O 0.390 g
0.5 M Na-EDTA	55.4 µl	CuSO ₄ .5H ₂ O 0.080 g
After autoclaved, ad	d 10 ml of	$Co(NO_3)_2.6H_2O$ 0.049 g
1,000x Trace metal	mix**	Sterile filtrate, store at 4 °C

APPENDIX B



Chromatogram of standard curve of polyamines



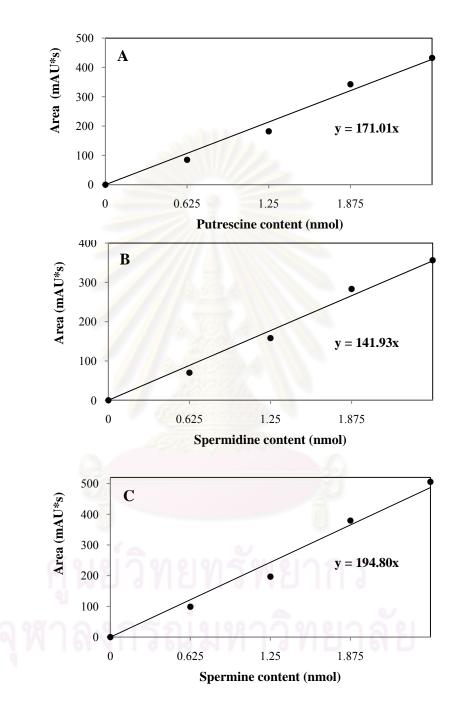


Figure B.2 Standard curve of polyamines (A = Putrescine, B = Spermidine and C = Spermine).

APPENDIX C

RNA extraction buffer

1. Resuspension buffer

0.3 M sucrose

10 mM sodium acetate, pH 4.5

2. Lysis buffer

2% SDS

10 mM sodium acetate, pH 4.5

3. RNA storage buffer

20 mM Na-phosphate buffer, pH 6.5

APPENDIX D

Protein extraction buffer containing:

50 mM Tris-HCl, pH 8.0

1 mM EDTA

50 µM Pyridoxal phosphate

5 mM DTT

0.5 mM PMSF

10 µM Leupeptin

10% (v/v) Glycerol

0.2% Triton X-100

APPENDIX E

TAE buffer

1. Working solution

1X: 0.04 M Tris-acetate

0.01 M EDTA

2. Concentrated stock solution (1 L)

50X : Tris-base 242.0 g

Glacial acetic acid 57.1 ml

0.5 M EDTA, pH 8.0 100.0 ml

Added distilled water to make 1 liter.

APPENDIX F

Preparation for polyacylamide gel electrophoresis

Stock solution

Acylamide	29.2 g
N,N'-methylene-bis-acrylamide	0.8 g

Added distilled water to make 100 ml and stirred until completely dissolved.

2.0 M Tris-HCl, pH 8.8, 100 ml

Tris (hydroxymethyl)-aminomethane 24.2 g

Adjusted pH to 8.8 with concentrated HCl slowly and added distilled water to a total volume of 100 ml.

1.5 M Tris-HCl, pH 8.8, 100 ml

Tris (hydroxymethyl)-aminomethane

18.17 g

Adjusted pH to 8.8 with concentrated HCl slowly and added distilled water to a total volume of 100 ml.

1.0 M Tris-HCl, pH 6.8, 100 ml

Tris (hydroxymethyl)-aminomethane 1 2.10 g

Adjusted pH to 6.8 with concentrated HCl slowly and added distilled water to a total volume of 100 ml.

0.5 M Tris-HCl, pH 6.8, 100 ml

Tris (hydroxymethyl)-aminomethane 6.06 g

Adjusted pH to 6.8 with concentrated HCl slowly and added distilled water to a total volume of 100 ml.

20% Sodium dodecyl sulfate (SDS), 100 ml

Sodium dodecyl sulfate 20.0 g

Added distilled water to make 100 ml and stored at room temperature.

10% Ammonium persulfate (APS), 1 ml

Ammonium persulfate

0.1 g

Added distilled water to a total volume of 1 ml.

22.2% Glycerol, 100 ml

100% Glycerol

22.2 ml

Added distilled water to a total volume of 100 ml.

Working solution

Solution B (for SDS-PAGE), 100 ml

2 M Tris-HCl, pH 8.8 75 ml

10% SDS

4 ml

Added distilled water to a total volume of 100 ml.

Solution C (for SDS-PAGE), 100 ml

1 M Tris-HCl, pH 6.8 50 ml

10% SDS

4 ml

Added distilled water to a total volume of 100 ml

SDS-PAGE

12% Separating gel (for 2 gel)

30% Acrylamide solution	4.17 ml
Solution B	2.50 ml
Distilled water	3.33 ml
10% APS	50.00 µl
TEMED	5.00 µl

5% Stacking gel (for 2 gel)

30% Acrylamide solution	1.67 ml
Solution C	2.50 ml
Distilled water	5.80 ml
10% APS	50.00 µl
TEMED	5.00 µl

Electrophoresis buffer, 1 L (25 mM Tris, 192 mM Glycine, 0.1% SDS)

Tris (hydroxymethyl)-aminomethane 3.0 g

Glycine 14.4 g

SDS

1.0 g

Added the distilled water to a totol volume of 1 liter. (Final pH is approximately 8.3, do not adjust pH with acid or base)



APPENDIX G

Western blotting buffer

10X Blotting solution (Used time = 1X)

100 mM Tris-HCl, pH 9.5

100 mM NaCl

10 mM MgCl₂

10X TBS (Tris-buffer-saline) (Used time = 1X)

200 mM Tris-HCl, pH 7.5

5 M NaCl

T-TBS

1X TBS

0.05% Tween-20

Blocking solution

5% Skim milk in TBS

Antibody buffer

1% Skim milk in T-TBS

Coomassie Gel Stain, 1 L

Coomassie Blue R-250	1.0 g
Methanol	450 ml
Glacial acetic acid	100 ml

Added distilled water to a total volume of 1 liter.

Coomassie Gel Destain, 1 L

Methanol 100 ml

Glacial acetic acid

100 ml

Added distilled water to a total volume of 1 liter.

5X Sample Buffer, 10 ml

1 M Tris-HCl, pH 6.8	0.6 ml
50% glycerol	5.0 ml
10% SDS	2.0 ml
2-mercaptoethanol	0.5 ml
1% bromophenol blue	1.0 ml

Added distilled water to a total volume of 10 ml. Stored at 4 $^{\circ}$ C for weeks or -20 $^{\circ}$ C for months



BIOGRAPHY

Miss Apiradee Pothipongsa was born on February 17, 1985 in Songkhla provience, Thailand. She has graduated with a Bachelor of Science degree in Chemistry, Faculty of Science, Thaksin University in 2006. She has further studied for the Master of Science degree in Biochemistry, Faculty of Science, Chulalongkorn University since 2007.

