การตอบสนองที่แตกต่างกันของเคนไครติกเซลล์ต่อแมนแนนในผนังเซลล์ของเชื้อรา



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บทคัดย่อและแฟ้มข้อมูลฉบับเต็มของวิทยานิพนธ์ตั้งแต่ปีการศึกษา 2554 ที่ให้บริการในคลังปัญญาจุฬาฯ (CUIR) เป็นแฟ้มข้อมูลของนิสิตเจ้าของวิทยานิพนธ์ ที่ส่งผ่านทางบัณฑิตวิทยาลัย

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DIFFERENTIAL DENDRITIC CELL RESPONSE TO FUNGAL CELL WALL MANNANS

Mr. Sirawit Jirawannaporn



Chulalongkorn University

A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree of Master of Science Program in Medical Microbiology (Interdisciplinary Program) Graduate School Chulalongkorn University Academic Year 2014 Copyright of Chulalongkorn University

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สิรวิชญ์ จิรวรรณาภรณ์ : การตอบสนองที่แตกต่างกันของเคนไครติกเซลล์ต่อแมนแนนใน ผนังเซลล์ของเชื้อรา (DIFFERENTIAL DENDRITIC CELL RESPONSE TO FUNGAL CELL WALL MANNANS) อ.ที่ปรึกษาวิทยานิพนธ์หลัก: พัชรี ฤทธิ์ประจักษ์, อ.ที่ปรึกษา วิทยานิพนธ์ร่วม: อรนาฏ มาตังกสมบัติ{, หน้า.

แมนแนนในผนังเซลล์ของเชื้อรามีบทบาทสำคัญในการกระตุ้นภูมิกุ้มกันโดยกำเนิด อย่างไรก็ตามขัง ไม่มีการศึกษาเกี่ยวกับผลของโครงสร้างแมนแนนที่แตกต่างกันต่อการตอบสนองของภูมิกุ้มกันโดยกำเนิด ดังนั้น งานวิจัยนี้จึงมีวัตถุประสงค์เพื่อศึกษาบทบาทของโครงสร้างแมนแนนที่แตกต่างกันในผนังเซลล์ของเชื้อราแซคคา โรไมซิส เซเรวิซีอี ต่อการตอบสนองของเดนดริติกเซลล์ โดยทำการกระตุ้นเดนดริติกเซลล์ที่พัฒนามาจากไข กระดูกด้วยยีสต์สายพันธุ์ปกติ และยีสต์ที่ไม่มียืนส์ที่เกี่ยวข้องกับการเติมแมนแมนโครงสร้างต่าง ๆ ในผนังเซลล์ ซึ่งยีสต์ดังกล่าวจะถูกทำให้ตายด้วยความร้อนและนำมากระตุ้นเดนดริติกเซลล์ที่พัฒนามาจากไข การะดูกด้วยยีสต์สายพันธุ์ปกติ และยีสต์ที่ไม่มียืนส์ที่เกี่ยวข้องกับการเติมแมนแมนโครงสร้างต่าง ๆ ในผนังเซลล์ ซึ่งยีสต์ดังกล่าวจะถูกทำให้ตายด้วยความร้อนและนำมากระตุ้นเดนดริติกเซลล์ที่พัฒนามาจากไขกระดูก จากนั้น ทำศึกษาระดับการแสดงออกของไซโตไลน์ยืนส์ที่เกี่ยวข้องกับการเหนี่ยวเฮลเปอร์ทีลิมโฟไซต์ชนิดต่างๆ ด้วยการ วิเคราะห์การแสดงออกของสารพันธุกรรมเชิงปริมาณ โดยใช้เทคนิกปฏิกิริยาลูกโซ่โพลีเมอเรสในสภาพจริง

จากผลการวิจัยพบว่ายีสต์ที่ไม่มียืนส์เอ็มเอ็นเอ็น 1 ซึ่งทำให้ขาดโครงสร้างแมนแนนแอลฟา 1,3 สามารถเพิ่มการแสดงออกของยืนส์อินเตอร์ลิวคิน-12 แอลฟา และอินเตอร์เฟียรอนแกมมาอย่างมีนัยสำคัญใน เดนไดรติกเซลล์เมื่อเทียบกับยีสต์สายพันธ์ปกติ และยีสต์ไม่มียืนส์เอ็มเอ็นเอ็น 2 ซึ่งทำให้ขาดโครงสร้างแมน แนนแอลฟา 1,2 และ 1,3 สามารถเพิ่มการแสดงออกของยืนส์อินเตอร์เฟียรอนแกมอย่างมีนัยสำคัญในเดนไดรติก เซลล์ โดยอินเตอร์ลิวกิน-12 และอินเตอร์เฟียรอนแกมมาเป็นไซโตไกน์สำคัญต่อการแปรสภาพของทีเฮลเปอร์ 1 นอกจากนี้ยังพบว่าการกระตุ้นเดนไดรติกเซลล์ด้วยยีสต์ที่ไม่มียืนส์โอซีเฮช 1 ซึ่งทำให้ขาดโครงสร้างเอ็นลิงค์ แมนแนน มีผลทำให้มีการแสดงออกที่เพิ่มขึ้นอย่างมีนัยสำคัญของไซโตไกน์ยืนส์ชนิดอินเตอร์ลิวกิน 1 ซึ่งมี ความสำคัญในการแปรสภาพของทีเฮลเปอร์ 17 และอินเตอร์ลิวกิน 23 ซึ่งทำหน้าที่ช่วยเพิ่มจำนวนและควบคุม การทำงานของทีเฮลเปอร์ 17 จากผลการศึกษาดังกล่าวแสดงว่าโครงสร้างแมนแนนที่แตกต่างกันในผนังเซลล์ ของเชื้อราแซกกาโรไมซิส เซเรวิซีอีมีผลต่อการกำหนดทิศทางการตอบสนองของเดนไดรติกเซลล์ ซึ่งอาจมี อิทธิพลต่อการแปรสภาพของทีเซลล์ได้ ผลงานวิจัยนี้จะสามารถนำไปต่อยอดเพื่อการพัฒนาสารเสริมฤทธิ์ชนิด การโบไฮเดรตได้ในอนาคต

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SIRAWIT JIRAWANNAPORN: DIFFERENTIAL DENDRITIC CELL RESPONSE TO FUNGAL CELL WALL MANNANS. ADVISOR: PATCHAREE RITPRAJAK, D.D.S.,Ph.D., CO-ADVISOR: ASSOC. PROF. ORANART MATANGKASOMBUT, D.D.S.,Ph.D.{, pp.

Mannan in fungal cell wall plays a crucial role in the activation of innate immunity, however it has not been studied how different mannan structure involves in innate immune responses. Thus, this study aims to investigate the effects of *Saccharomyces cerevisiae* possessing different cell wall mannan structures on dendritic cells (DCs) responses. Bone marrow-derived dendritic cells (BM-DCs) were stimulated with heat-killed *S. cerevisiae Wt* and mutants that lack of the single gene involving in each step of mannosylation. Then, mRNA expression of T helper lymphocyte (Th)-inducing cytokines was determined by quantitative real-time PCR.

The results demonstrated that *S. cerevisiae* $mnn1\Delta$, lacking of α -1,3 mannan, notably enhanced the expression of Th-1 inducing cytokines, *Il12a* and *Ifng*, while $mnn2\Delta$, lacking of α -1,3 and α -1,2 mannan, significantly increased *Ifng* expression in BM-DCs when compared to *Wt*. Furthermore, BM-DCs stimulated with $och1\Delta$, which N-linked mannan was absence, showed the significant increase in Il1a, Il1b, and Il23a, the cytokines involving in Th17 induction and amplification respectively. The data suggested that the different mannan structures affected DC responses, which may consequently influence Th differentiation. This knowledge will be beneficial for the development of carbohydrate adjuvants in the future.

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CHAPTER I INTRODUCTION

Adjuvants are immunological substances used to improve vaccine efficacy by several ways, such as recruiting immune cells to the injection site, boosting the adaptive immune responses, and directing the immunity to protect against infectious diseases. The major mechanism of adjuvant is to act as pathogen-associated molecular patterns (PAMPs), which bind to pathogen recognition receptors (PRRs) on antigen presenting cells (APCs), especially dendritic cells (DCs). The interaction between PAMPs and PRRs results in the maturation, migration and cytokine production of DCs, which consequently directing the immune response (1, 2). Nowadays, there are only five licensed adjuvants, alum, MF59, AS093, virosomes, and AS04. However, these adjuvants still lack the ability to induce adequate cell-mediated immunity (1, 3-7). Thus, it is important to develop new formulations of adjuvants and vaccines simultaneously.

Carbohydrate is a natural compound that can bind with various PRRs, such as C-type lectin receptors (CLRs) and Tollliked receptors (TLRs), resulting in the induction of immunity (8). There are 4 major types of carbohydrate adjuvants; glucans, fructans, chitins and mannans, and each type possesses distinct ability to interact with PRRs (9). Saccharomyces cerevisiae is a non-pathogenic yeast which has been used for vaccine delivery. The cell wall of S. cerevisiae comprises mannans, glucans and chitins (10, 11). Mannan is a polymer of mannose that can be recognized by its specific PRRs e.g. TLR-2, TLR-4, dectin, DC-SIGN, mannose recptor, mincle, $Fc\gamma R$, and langerin, depending on the sugar structures (12).

By taking the advantage of the availability of single-gene deletion mutants of various genes involved in the synthesis of mannan structures of *S. cerevisiae*, this study tested the effects of different mannan structures on DCs and immune responses.

Our findings will be beneficial for the development of carbohydrate adjuvants in the future.



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CHAPTER II OBJECTIVES

To study the responses of bone marrow-derived dendritic cells to different mannan structures of *Saccharomyces cerevisiae in vitro*.



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CHAPTER III LITERATURE REVIEW

1. Vaccine

Vaccines are the most cost-efficient tools to promote individual and public health by particularly preventing serious infections. The aim of vaccine is to stimulate a specific or an acquired immunity, which possesses a memory ability that responds more vigorously when repeatedly exposes to the same pathogen (13). Vaccination induces specific immunity via the potent antigen-presenting cell, a dendritic cell (DC). When DC is activated, it maturates and migrates into peripheral lymphoid organs. Antigen presentation to T cells by DC leads to T cell activation, proliferation and differentiation (13, 14). Vaccines are classified as the follow;

1) Live attenuated pathogen is the weakened pathogen that cannot cause the diseases. It can be made by growth under abnormal culture conditions or genetic engineering. The advantages are long live immune memory, single immunization, and induction of strong immune responses. However, this kind of vaccine can be a double-edged sword because it can revert into the pathogenic form in some condition and it induces the complex immune response due to many PAMPs (5).

2) Inactivated pathogen vaccine is made by using physical or chemical agents to kill the pathogen to prevent the ability to cause the disease. The advantage of this vaccine is that it could be safer than the live attenuated vaccine. However, the immunogenicity is also decreased, so multiple doses is required. Furthermore, it is difficult to choose the method of inactivation due to the risk of important antigen denaturation (5).

3) Subunit vaccine is the vaccine that contain purified antigens from pathogen instead of using the whole organism. Therefore, the advantages include safety and less complex immune response due to the use of a single antigen. However, the disadvantages are that the immunogenicity is very poor, and the antigens may not retain their native conformation due to extraction protocol which could mislead the immune responses (15).

4) Synthetic antigen vaccine is a vaccine containing mainly synthetic peptides, carbohydrates, or antigens. The advantages are similar to subunit vaccine. However, since synthetic antigen vaccine has no native structure, it may not bind to PRRs on antigen presenting cells, such as DCs, which promote pathogen uptake and direct the adaptive immune response (16).

5. DNA vaccine uses genes that encode important pathogen antigens inserted into a vector, usually a virus that has a very low virulence. It provides a safe way of vaccination and could induce prolonged immune memory. However, there is a risk of interfering with host genes that control important functions, such as cell growth, and that it may induce immunological tolerance of the antigen (17).

The ideal vaccine is the vaccine that has high level of safety and efficacy. Thus, to develop the ideal vaccine we may

need the helper called "adjuvant". Among the types of vaccines listed above, almost all vaccines need adjuvant except the live attenuated vaccine and some inactivated vaccine.

2. Adjuvants

2.1 Adjuvant classification

2.1.1 Particulate adjuvant is the adjuvant that forms particles for better induction of the immune responses (1, 18).

2.1.2 Aluminium salts is the adjuvant that compose of aluminium hydroxide or alum with the size between 100-1000nm (4, 18).

2.1.3 Water-in-oil emulsion is the adjuvant that composed of water in mineral oil phase, such as Freund incomplete adjuvant (FIA) (18)

2.1.4 Oil-in-water emulsion is the adjuvant that composed of mineral oil in water phase (18).

2.1.5 Immune stimulating complex (ISCOM) is the adjuvant that looks like the open-cage with the size around 40

nm and composed of cholesterol, lipid, immunogen, and some mineral salts, such as saponins (18).

2.1.6 Liposome is the adjuvant that composed of lipid bilayer with the size around 20nm to 3μ m (18).

2.1.7 Nano and microparticles is the adjuvant with very small size $1-100\mu m$ for microparticles and 10-100nm for nanoparticles (18).

2.2 Adjuvant mechanisms of action

2.2.1 **Immunomodulation Adjuvant** can regulate the direction of adaptive immune response by binding to the PRRs in antigen presenting cell and inducing different T-cell differentiation cytokines secretion. For example, flagellin purified from microbes can bind to Toll-like receptor 5 (TLR-5), resulting in secretion of IL-12p70 cytokine, a T-helper 1 differentiation cytokine, from antigen presenting cells (1, 3, 18).

2.2.2 **Presentation** Some adjuvants can enhance antigen presentation by MHC molecules, which can be the result

of many mechanisms such as the interaction between adjuvant and PRRs (1, 3, 18).

2.2.3 **Enhanced antigen uptake** by antigen presenting cells by regulating the danger signal and inflammation (1, 3, 18).

2.2.4 **Immune cell recruitment** by inducing inflammation or danger signal (1, 3, 18).

2.3 Currently licensed adjuvants

There are several classes of adjuvants e.g. mineral salts, emulsion, microbial derivatives, cytokines, immune stimulating complexes (ISCOM), particulate compounds, and carbohydrate (19, 20), which possesses the different immune induction properties. Thus, the mixture of vaccine with appropriate adjuvant is crucial for the efficient immune induction. At present, there are five licensed adjuvants used in human vaccines (Table 1). 2.3.1 Alum, which is composed of aluminium salts, can induce good antibody response and T helper 2 response, but poor T helper 1 response (3, 5, 21).

2.3.2 MF59, which is composed of squalene, polysorbate 80, sorbitan trioleate with oil-in-water form, can induce good antibody response and balanced T helper 1 and T helper 2 response. (3, 5, 21).

2.3.3 AS03, which is composed of squalene, Tween 80, and α -tocopherol with oil-in-water form, can induce good antibody response and T helper 1 response (3, 5, 21).

2.3.4 AS04 is composed of Aluminium hydroxide and monophosphoryl lipid A. It is an Alum-absorbed TLR-4 agonistic adjuvant that induces good antibody response and increase immune memory (3, 5, 21).

2.3.5 Virosome, which is composed of lipids and hemagglutinin with liposome form, induces antibody response and cytotoxic T lymphocyte (3, 5, 21).

Adjuvant	Classification	Immune induction	Reference
Alum	Mineral salts	Ab Th 2 poor Th1	(3, 5, 21)
MF59	Oil-in-water emulsion	Ab Balanced Th1 and Th2 response	(3, 5, 21)
AS03	Oil-in-water emulsion	Ab Th1	(3, 5, 21)
AS04	Alum-absorbed TLR-4 agonists	Ab Increase immune memory	(3, 5, 21)
Virosome	Liposomes	Ab CTL	(3, 5, 21)

Table 1 Currently licensed adjuvants

2.4 Current problems of adjuvants

Most of the currently licensed adjuvants stimulate humeral-mediated immune response, but not satisfactory cellmediated immune responses which are required in many infectious diseases. For example, the protective immunity against Tuberculosis requires the T-helper 1 responses, and the protective immunity against HIV infection required responses from CTL (1, 3-7).

2.5 Current new adjuvant development

The current new adjuvant development begins to use part of the pathogens or non-pathogens, such as Flagellin (TLR-5 ligand), Pam3Cys (TLR-2 ligand), or CpG (TLR-9 ligand) (5).

3. Carbohydrate adjuvant

Carbohydrate is one type of adjuvant that has the ability to bind with many PRRs and results in various direction of immune responses.(8) There are four major types of carbohydrate adjuvants.

3.1 Glucans are composed of repeating units of D-glucose binding together by glycosidic bonds in various conformations. Alpha-glucans (α -glucans), such as Dextran from *Streptococcus bovis*, can induce protective antibody. β -glucans, such as Zymosan from yeast cell wall, induces nonspecific resistance against some bacteria and fungi (8, 9).

3.2 Fructans are composed of repeating units of Fructose binding together by glycosidic bonds, such as Y-Inulin, which induces both humoral and cellular immunity (8, 9).

3.3 Mannans are composed of repeating units of Mannose binding together by glycosidic bonds, such as N-linked mannan that induces various immune responses (8, 9).

3.4 Chitin is linear β -1–4-linked polymer of D-glucosamine and *N*-acetyl-D-glucosamine. It can induce inflammatory cytokines including IL-12, IL-18, TNF- α and IFN- γ and enhanced antibody production (8, 9).

4. Carbohydrate constituents of yeast cell wall and immune responses

4.1 Fungal cell wall

Fungal cell wall is mostly composed of polysaccharides, which are mannan, glucan, and chitin. The differences in structures and proportion of cell wall polysaccharides have been shown to influence the type of immune responses (10, 22).

4.2 Immune induction by carbohydrate constituents in fungal cell wall

The innate recognition of fungal cell wall can be recognized by various groups of PRRs (Table 2). For example, C-type lectin receptors (CLR) can recognize N-linked mannan, α -Glucan, β -Glucan and chitin, while toll-like receptors (TLRs) can recognize O-linked mannan, RNA and DNA.

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PRRs	Family	Ligands	References
DC-SIGN	C-type lectin	N-linked mannan,	(2, 22, 23)
		α -Glucan, β -Glucan	
		and chitin	
Dectin-1	C-type lectin	N-linked mannan,	(2, 22, 23)
		α -Glucan, β -Glucan	
		and chitin	
Dectin-2	C-type lectin	N-linked mannan,	(2, 22, 23)
		α -Glucan, β -Glucan	
		and chitin	
Mincle	C-type lectin	N-linked mannan,	(2, 22, 23)
		α -Glucan, β -Glucan	
		and chitin	
Galactin-3	C-type lectin	B-mannosides	(2, 22, 23)

 Table 2: Innate recognition receptors for fungal cell wall components

CR3	Complement	C3b or C3d	(2, 22, 23)
	receptor		
CD36	Class B	B-glucan	(2, 22, 23)
	scavenger		
	receptor		
TLR-2	Toll-like	O-linked mannan,	(2, 22, 23)
	receptor	RNA and DNA.	
TLR-3	Toll-like	O-linked mannan,	(2, 22, 23)
	receptor	RNA and DNA.	
TLR-4	Toll-like	O-linked mannan,	(2, 22, 23)
	receptor	RNA and DNA.	
TLR-6	Toll-like	O-linked mannan,	(2, 22, 23)
	receptor	RNA and DNA.	
TLR-9	Toll-like	O-linked mannan,	(2, 22, 23)
	receptor	RNA and DNA.	

4.3 The role of mannan in immune responses

Mannan is an outer cell wall component that initially interacts with immune cells(10, 22). Previous report showed that ablation of *OCH1* gene, which leads to defect in N-linked mannan elongation, shifted specific immune response from Th1 to Th17 (24). In addition, deletion of β -1,2 mannan in *C*. *albicans* cell wall obviously enhanced TNF- α , IL-6 and IL-12 production in DC (25). Hence, the structure of cell wall mannan may play a crucial role in the differential DC responses and T cell differentiation.

4.4 *Saccharomyces cerevisiae* single gene deletion and its benefit

4.4.1. Saccharomyces cerevisiae

Saccharomyces cerevisiae is a fungal species with cell wall containing mannans, glucans, and chitins (10, 11). It is a candidate for development of new adjuvant because S. cerevisiae is non-pathogenic. Furthermore, genes involved in mannan glycosylation are well characterized, and strains with deletions of these genes are readily available in a deletion library.(11, 26, 27) In addition, previous studies showed that whole heat-killed recombinant S. cerevisiae expressing HIVAX-Gag markedly enhanced DC maturation and IL-12 production, and subsequently augmented antigen-specific CTL responses (28). Furthermore, recombinant S. cerevisiae containing E.G7 protein notably increased CTL numbers resulting in the reduction of lymphoma progression (29).

The glycosylation process of N-linked mannan is regulated by many genes (30). It has been shown that *OCH1* gene plays a role in the initiation of the first α -1,6 mannosylation, and *MNN9* and *VAN1* genes are involved in the elongation of α -1,6 mannose backbone (31). *MNN2*, *MNN5* and *MNN1* genes have been revealed to control the glycosylation of the first, the second α -1,2 mannose, and the terminal α -1,3 mannose residues, respectively (26, 30). In addition, previous reports have shown that *MNN4* and *MNN6* genes encode enzymes transferring mannosylphosphate to both O-linked and N-linked mannan (Fig. 1)(30, 32).

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Figure 1 Glycosylation of N-linked mannan infungal cell wall (30).

If we select the single gene deletion from the library in each step we assumed that the structure of the mutant would be like in (**Fig. 2**)



Figure 2 N-linked mannan cell wall structure of single gene deletion mutants.

We hypothesize that single deletions of *S. cerevisiae* genes controlling the production of N-linked mannans in the cell wall will affect their structures, and lead to differential responses of DCs. Our result will provide crucial information for the development of natural carbohydrate adjuvants, and will be able to apply for the public health prevention and clinical therapeutic treatment.

CHAPTER IV MATERIALS AND METHODS

PART I Yeast culture and preparation

1. Saccharomyces cerevisiae strains

Saccharomyces cerevisiae BY4741 WT(wild type), $och1\Delta$, mnn1 Δ , mnn2 Δ , mnn4 Δ , mnn5 Δ , and van1 Δ mutants were obtained from the Mata haploid yeast deletion library (Invitrogen, USA), and stored in 15% glycerol at -80°C.

2. Yeast culture

Yeast strains were cultured in Yeast Peptone Dextrose (YPD) media, containing yeast extract (HiMedia), peptone (HiMedia), and glucose (Univar), at 30°C with 200 rpm shaking for 15 hours. Then, the yeast suspension was diluted to OD_{600} of 0.1 and was continued incubating until OD_{600} reach 0.6 (24).

3. Growth curve determination

Yeasts were cultured from OD_{600} of 0.1 for 24 hours, and the growth curve were determined by measuring OD_{600} at 2, 4, 6, 8, 16 and 24 hours.

4. Heat-killed yeast preparation

Yeast cells were collected from the culture, washed 3 times in sterile PBS, and resuspended in PBS at the concentration of 1×10^8 cells/ml. The cells were incubated at 65° C for 2 hours in the preliminary experiments and 100° C for 10 minutes in all subsequent experiments.

PART II Bone marrow-derived dendritic cell culture and stimulation

1. Balb/c mice

The 5-week old female Balb/c mice were purchased from The National Laboratory Animal Center, Mahidol University (NLAC-MU). All procedures were reviewed and approved by the Animal Care and Use Committee of Faculty of Medicine, Chulalongkorn University (Ethics certificate number 7/58).

2. Generation of BM-DCs

Bone marrow cells were collected from femurs of mice and cultured in RPMI medium (GIBCO[®], Invitrogen) supplemented with 10% fetal bovine serum (GIBCO[®], Invitrogen), 100 U/ml Penicillin and 0.1 mg/ml Streptomycin (GIBCO[®], Invitrogen), 10 ng/ml GM-CSF (PeproTech) and 10 ng/ml IL-4 (PeproTech). The cells were seeded in 24-well plate at the concentration of 1×10^6 cells/ ml. BM cells were cultured at 37°C in 5% CO₂ for 7 days, and the culture media were changed every 2 days.

3. BM-DC stimulation

In preliminary experiment, BM-DCs were stimulated with heat-killed WT and mutants at various DC:Yeast ratios for 2 and 4 hours for gene expression analysis, and 24 hours for flow cytometric analysis.

In all subsequent experiments, BM-DCs were stimulated with heat-killed WT and mutants at DC:Yeast ratio of 1:5 for 2 and 4 hours for gene expression analysis and 24 hours for flow cytometric analysis.

PART III Genes expression analysis

1. RNA extraction

The stimulated BM-DCs were harvested and total RNA was extracted by using TRIzol[®] Reagent (Invitrogen, USA) and chloroform, and precipitated by isopropanol and ethanol. RNA was dissolved in DEPC water, and the concentration was measured by Nanodrop (Thermo Scientific, USA) and stored at -80°C.

2. cDNA synthesis

The mRNA was converted to cDNA by SuperScript® III First-Strand Synthesis reverse transcriptase kits (Invitrogen) according to manufacturer's instruction, and stored at -80°C.

3. Quantitative PCR analysis

The mRNA levels were examined by Real-Time PCR (Light cycler 480, Roche). The PCR mixture contained 2 μ l of water, 0.5 μ l of 10 pmol/ μ l primers, 5 μ l of Master mix (Roche, USA), and 2 μ l of cDNA. The PCR was amplified for 40 cycles

with the conditions shown in Table 3. The sequences of the primers are as previously described (33) and shown in Table 4.

Step	Temperature	Time
Pre-incubation	95°C	5 minutes
Denature	95°C	10 seconds
Annealing	60°C	10 seconds
Extension	72°C	30 seconds

Table 3 Real-time PCR Cycle

 Table 4 Real-time PCR primer sequences (33).

Primers	Sequences	
1. Il1a	5'- TCCAGGGCAGAGAGGGAGT -3'	
	5'- GGAACTTTGGCCATCTTGATTT-3'	
2. Il1b	5'- GTGGCTGTGGAGAAGCTGTG -3'	
	5'- GAAGGTCCACGGGAAAGACAC -3'	
3. <i>Il14</i>	5'- GCAACGAAGAACACCACAGA -3'	
	5'- AAATATGCGAAGCACCTTGG -3'	
4. <i>Il16</i>	5'- CCAGAAACCGCTATGAAGTTCC -3'	
	5'- TTGTCACCAGCATCAGTCCC -3'	
5. 11110	5'- GAAGCTGAAGACCCTCAGGA -3'	
	5'- TTTTCACAGGGGAGAAATCG -3'	
6. Il12a	5'- CAGAAACCTCCTGTGGGAGA -3'	
	5'- GGAGCTCAGATAGCCCATCA -3'	
7. Il12b	5'- ATCCAGCGCAAGAAAGAAAA -3'	
	5'- GGAACGCACCTTTCTGGTTA -3'	
8. Il123a	5'- GCACCTGCTTGACTCTGACA -3'	
	5'- CATGGGGCTATCAGGGAGTA -3'	

9. Ifng	5'- ATCTGGAGGAACTGGCAAAA -3'	
	5'- TCTGGCTCTGCAGGATTTTC -3'	
10. <i>Tgfb1</i>	5'- CCTGAGTGGCTGTCTTTTGACG -3'	
	5'- AGTGAGCGCTGAATCGAAAGC -3'	
11. Gapdh	5'- ATCACTGCCACCCAGAAGAC -3'	
	5'- ATGAGGTCCACCACCTGTT -3'	

4. mRNA expression calculation

The relative mRNA expression was calculated by the formula: $2^{-(\Delta CPtarget gene - \Delta CPgapdh)}$, and the fold changes were calculated by comparing the relative mRNA expression of stimulated BM-DCs with those of negative controls.

PART V. Flow cytometric analysis.

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1. Cell staining

BM-DCs were stimulated with yeasts for 24 hours. The cells were harvested and stained for the maturation markers using specific antibodies as follow: APC-conjugated anti-mouse CD11c (eBiscience), FITC-conjugated anti-mouse CD80 (eBioscience), PE-conjugated anti-mouse CD86 (eBioscience),

and PerCP Cy5.5-conjugated anti-mouse I-A/I-E mAbs (Biolegend).

2. Flow cytometric analysis

The stained samples were analyzed by flow cytometry (BD FACSCaliburTM system) and BD CellQuestTM software.

PART VI. Statistical analysis

The number of samples was five per group. Statistical analysis was performed using Mann-Whitney U Test, and p value of ≤ 0.05 was considered statistically significant.

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CHAPTER V RESULTS

PART I. Saccharomyces cerevisiae growth curve

The yeasts WT and mutants were cultured overnight and the OD₆₀₀ was measured at 2, 4, 6, 8, 16 and 24 hours (Fig. 3). The log phase of all yeasts started at 4 hours and ended at 16 hour, and the mid log phase was 10-12 hours. The growth rate of *och1* Δ mutant was slowest, however, its log phase was still in the same period as the others.



Figure 3 Growth curve of S. cerevisiae WT and mutants.

PART II. Selection of the condition for BM-DC stimulation

To investigate the effect of yeast cell wall to DC responses, yeast must be inactivated to eliminate the undesired signal from secreted products. High temperature was applied to but the heat inactivate yeasts, may also affect their immunogenicity. In addition, the ratio of DC:yeasts may affect DC activation. To determine the suitable temperature for yeast inactivation and proper DC:yeasts ratio, BM-DCs were stimulated with 65°C (24) and 100°C (34) heated-killed WT and $och1\Delta$, at the ratio of DC: yeasts of 1:2, 1:4 and 1:8. Then, the levels of DC maturation marker CD86 were determined by flow cytometry (Fig 4). The different temperatures used to kill yeast cells did not influence BM-DC maturation. The results showed that BM-DC maturation was induced in a dose-dependent manner. From the result, thus, heat-killed condition of 100°C for



various ratios of heat-killed yeast. S. cerevisiae WT and $och1\Delta$ were incubated at 65°C for 2 hours or 100°C for 10 minutes, and then were added to BM-DC culture at DC:Yeast ratios of 1:2, 1:4 and 1:8. BM-DCs were stimulated for 24 hours, and CD86 expression was analyzed by flow cytometry. The indicated numbers are mean fluorescence intensity of CD86 surface molecules. Neg : Negative control or unstimulated BM-DCs.

Although, the DC:Yeast ratio of 1:8 (Fig. 4) showed Characterization in the properties of the highest CD86 expression on BM-DCs, it was still necessary to find the proper amount of yeasts for mRNA analysis of BM-DC stimulation. Therefore, in the next experiment, we aimed to find the suitable ratio and stimulation time by observing the mRNA expression of *Il12a*, encoding IL-12 subunit p35; *Ifng*, encoding IFN- γ ; and *Il23a*, encoding IL-23 subunit p19, following the previous report that WT *S. cerevisiae* enhanced IL-12 and IFN- γ production in monocyte-derived DCs and $och1\Delta$ mutant drove Th17 differentiation (24). BM-DCs were stimulated with 100°C heat-killed WT S. cerevisiae at the ratio of 1:5, 1:10 and 1: 20 for 2, 4 and 8 hours, and mRNA expression levels of *Il12a*, *Ifng* and *Il23a* were determined (Fig. 5). There was no difference in mRNA expression of *Il12a*, *Ifng* and *Il23a* genes when BM-DCs were stimulated with heat-killed yeasts at all ratios. However, the viability of BM-DCs in the cultures was decreased when stimulated with 1:10 and 1:20 (data not shown). The *Ill2a* expression in BM-DCs was increased with the stimulation time (Fig. 5A), while Ifng and Il23a expressions were highest at 4 hours and 2 hours, respectively (Fig. 5B and 5C). Thus, the DC: Yeast ratio of 1:5 and the stimulation time of 2 and 4 hours were selected for BM-DC stimulation in the analysis of mRNA expression.





Figure 5 The mRNA expression of *Il12a*, *Ifng* and *Il23a* **genes in BM-DCs stimulated with heat-killed WT at various ratios.** *S. cerevisiae* was inactivated by 100°C heat and incubated with BM-DCs at DC: Yeast ratio of 1:5, 1:10 and 1:20 for 2, 4, and 8 hours. The relative mRNA expression of (A) *Il12a* (B) *Ifng* and (C) *Il23a* was shown as fold induction over unstimulated controls.

PART III. Determination of mRNA expression of the target genes involving in Th induction

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The generation of CD4 T cell subsets is mainly dependent

on the type of cytokines in the microenvironment during T cell

activation (Fig. 6).

(C)



Figure 6 T helper differentiation. When naïve CD4 T cells are activated in the presence of different groups of Th-inducing cytokines, CD4 T cells are induced to differentiate into distinct subsets. IL-12 and IFN- γ direct Th1 differentiation, while IL-4 is essential for Th2 differentiation. In addition, TGF- β , IL-6 and IL-21 are crucial for Th17 differentiation, and TGF- β or IL-10 plays a role in regulatory T cells (Treg) induction.

To investigate mRNA expression of the genes involving in Th1 induction (Fig. 7), BM-DCs were stimulated with heatkilled WT and mutant yeasts for 2 and 4 hours. BM-DCs stimulated with $mnn1\Delta$ mutant showed a notable increase in *Il12a* (Fig. 7A), encoding IL-12p35, which is the subunit of IL-12, and *Ifng* expression at 4 hours (Fig. 7B) when compared to

BM-DCs stimulated with WT. However, $mnn1\Delta$ stimulation did not alter *II12b*, which encodes IL-12p40, the subunit of IL-12 and IL-23. BM-DCs stimulated with $mnn2\Delta$ mutant also significantly enhanced *Ifng* expression at 4 hours (Fig. 7C). The data suggested that the lack of terminal α -1,3 mannan (in $mnn1\Delta$) and the second branch of α -1,2 mannan (in $mnn2\Delta$) in *S. cerevisiae* led to the augment of Th1-inducing cykines in DCs.







(C)

Figure 7 The mRNA expression of Th1-inducing cytokine genes. BM-DCs were stimulated with heat-killed WT and mutants at DC: Yeast ratio of 1:5 for 2 (gray bar) and 4 (black bar) hours. The relative mRNA expression of (A) *Il12a* (B) *Il12b* and (C) *Ifng* was shown as the fold induction. * P value \leq 0.05 compared to WT at 4 hours; n = 5.

In general IL-6, IL-21, and small amount of TGF- β , are the key cytokines for Th17 induction (35). It has been reported that IL-1 and IL-23 play crucial roles in finalizing Th17 differentiation program and maintaining Th17 functions (35). BM-DCs can produce TGF- β , IL-1, IL-6 and IL-23 upon stimulation, however, we could not detect IL-21 (data not shown). Thus, IL-1, IL-6, and IL-23 were selected as Th17 inducing cytokines to be examined in this work (Fig. 8). The data demonstrated that $och1\Delta$ mutant did not affect the level of *Il6* mRNA (Fig. 8A), while it enhanced the induction of *Il23a* (Fig. 8B) encoding IL-23p19 subunit, *Il1a* (Fig. 8C) and *Il1b* (Fig. 8D) at 2 and 4 hours. The results suggested that N-linked mannan may play a role in the control of Th17 induction by DCs.





Figure 8 The mRNA expression of Th17-inducing cytokine genes. BM-DCs were stimulated with heat-killed WT and mutnats at DC: Yeast ratio of 1:5 for 2 (gray bar) and 4 (black bar) hours. The relative mRNA expression of (A) *Il16* (B) *Il23a* (C) *Il1a* and (D) *Il1b* was shown as the fold induction. ⁺ P value ≤ 0.05 compared to WT at 2 hours; * P value ≤ 0.05 compared to WT at 4 hours; n = 5.

Next, we investigated whether the different mannan structures affect the expression of *Il4*, a Th2-inducing cytokine, in BM-DCs (Fig. 9). BM-DCs stimulated with *och1* Δ , *mnn1* Δ , and *mnn2* Δ displayed significant reduction in *Il4* expression when compared to WT-stimulated BM-DCs. According to the above data, *mnn1* Δ and *mnn2* Δ stimulated the gene expression of Th1-inducing cytokines (Fig. 7), and *och1* Δ stimulated Th17-inducing cytokines (Fig. 8), in BM-DCs.



Figure 9 The mRNA expression of Th2-inducing cytokine genes. BM-DCs were stimulated with heat-killed WT and mutnats at DC: Yeast ratio of 1:5 for 2 (gray bar) and 4 (black bar) hours. The relative mRNA expression of *Il4* was shown as the fold induction. * P value ≤ 0.05 compared to WT at 4 hours; n = 5.

Finally, we determined the capability of *S. cerevisiae* WT and mutants in the mRNA expression of Treg-inducing cytokines (Fig. 10). There was no difference in *Il10* (Fig 10A) and *Tgf* β (Fig. 10B) among all *S. cerevisiae* strains. From the results, it is possible that mannan may not be involved in Treg induction.



(B)



Figure 10 The mRNA expression of Treg-inducing cytokine genes. BM-DCs were stimulated with heat-killed WT and mutnats at DC: Yeast ratio of 1:5 for 2 (gray bar) and 4 (black bar) hours. The relative mRNA expression of *Il4* was shown as the fold induction. n = 5.

CHAPTER VI DISCUSSIONS

In this study, we investigated the influence of various fungal cell wall mannan structures on BM-DC responses. Our results demonstrated that the absence of terminal α -1,3 mannan in *mnn1* Δ (Fig. 1 and 2) markedly induced the expression of *Il12a* (Fig. 7A) and *Ifng* (Fig. 7C). In contrast, the lack of α -1,2, and terminal α -1,3 mannan in *mnn2* Δ (Fig. 1 and 2) specifically induced the expression of *Ifng* (Fig. 7C). It is possible that α -1,2 mannan binds to a receptor transducing the signal to target *Il12a*. The interaction of mannan and dectin-2 receptor has been shown to target *Il12b* (36), however, there is no evidence of the specific receptor for *Il12a* induction.

In contrast to the increased expression of *Ifng*, BM-DCs stimulated with *och1* Δ , *mnn1* Δ , and *mnn2* Δ displayed significant reduction in *Il*4 expression comparing to WT. It has been demonstrated that the suppression of *Il*4 expression in T cells was epigenetically controlled by *Ifng* (37). Therefore, it is

possible that the reduced *Il4* expression in $och1\Delta$, $mnn1\Delta$, or $mnn2\Delta$ stimulated BM-DCs possibly resulted from epigenetic control.

Deletion of *OCH1* gene in *S. cerecisiae* has been shown to involve in the shift of Th1 to Th17 in vitro (24). Consistently, BM-DCs stimulated with *och1* Δ showed a significant increase in *Il23a* (Fig. 8B), *Il1a* (Fig. 8C) and *Il1b* (Fig. 8D) expression. Ample evidences demonstrated that signal transductions via the engagement of β -glucan and dectin-1 receptor led to Th17 induction (38-41). Mannan is located in the outermost layer of the yeast cell wall and it covers the glucan layer. Thus, it is possible that lack of N-linked mannan in *och1* Δ mutant led to exposure of glucan, which then binds to dectin-1 on BM-DCs, and consequently enhanced Th17-inducing cytokines.

Similar to *OCH1*, *VAN1* involves in the first step of mannan synthesis. However, mRNA expression of cytokine profile in BM-DCs stimulated with $van1\Delta$ mutant and $och1\Delta$ mutant differed. *VAN1* is a gene in *MNN9* family (42). It

encodes Van1p, a component of mannan polymerase I, which form a complex with Mnn9p that encoded by *MNN9*. *VAN1* and *MNN9* elongate α -1,6-mannosyl linkage on the backbone, and there is no further α -1,6-linked residues added in *van1* Δ and *mnn9* Δ mutant (42, 43). However, it was found that instead of α -1,6-linked residues, some α -1,2-linked residues were added in *van1* Δ and *mnn9* Δ mutant (43, 44). Thus, the differed responses of BM-DCs to *van1* Δ may be possible from the recognition of α -1,2-mannosyl residues that are absent in *och1* Δ .

A previous study in *C. albicans* showed that the O-linked and phosphomannan in the cell wall did not influence the production of proinflammatory cytokines in DCs (45). Consistently, our data demonstrated that the phosphomannan structure in *S. cerevisiae* cell wall was not involved in BM-DC stimulation. *MNN5* encodes α -1,2-mannosyltransferase that is responsible for the addition of second alpha-1,2-linked mannose of the branches on the mannan backbone of oligosaccharides (46). Our results demonstrated that lack of second alpha-1,2linked residues in *mnn5* Δ did not affect BM-DC responses, whereas lack of first α -1,2-linked residues in *mnn2* Δ leaded to the induction of IFN- γ mRNA expression. Although there is no enough supporting evidence, it is possible that terminal α -1,3linked mannose may be transferred to the first α -1,2-linked residues directly. Therefore, *mnn5* Δ stimulated BM-DCs showed the similar gene expression profile to BM-DCs stimulated with *Wt S. cerevisiae*.

Our data demonstrated the responses of DCs *in vitro* in mRNA level, however, the production of cytokines should be further observed. In addition, *in vitro* BM-DCs responses to purified mannan from *Wt* and *mutant* cell wall must be evaluated, and *in vivo* immunization experiment will be necessary to determine the direction and magnitude of actual adaptive immune responses.

CHAPTER VII CONCLUSIONS

In the past decades, several lines of evidence suggested that the lack of some α - or β -mannan structures caused a deviation of immune responses (24, 45, 47). It is possible that DCs recognize various mannan structures via different PRRs, resulting in distinct signal transduction pathways, and consequently leading to differences in immune responses. According to our data, genetic engineering of mannan structure in *S. cerevisiae* influenced DC responses, which possibly affect T cell differentiation. This work will be advantage for the further development of carbohydrate vaccine adjuvants.

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จุฬาลงกรณ์มหาวิทยาลัย Chulalongkorn University

APPENDIX



จุฬาลงกรณ์มหาวิทยาลัย Chulalongkorn University



จุฬาลงกรณ์มหาวิทยาลัย Chulalongkorn University

VITA



จุฬาลงกรณ์มหาวิทยาลัย Chulalongkorn University