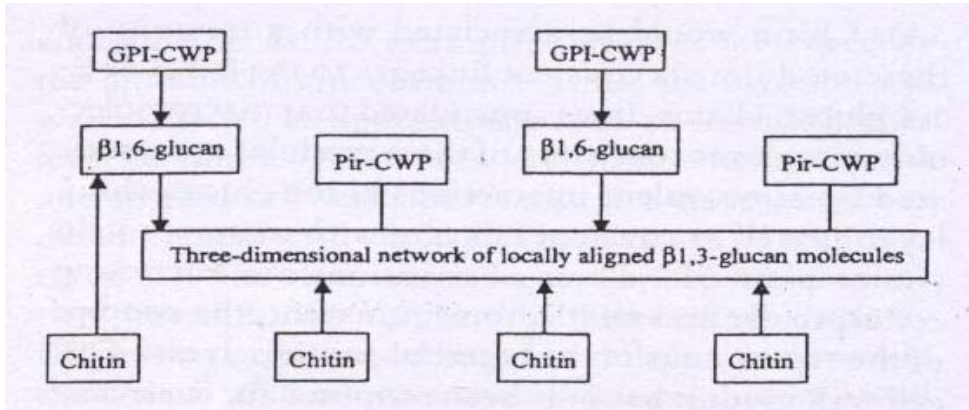


# 附錄

<A>



<B>



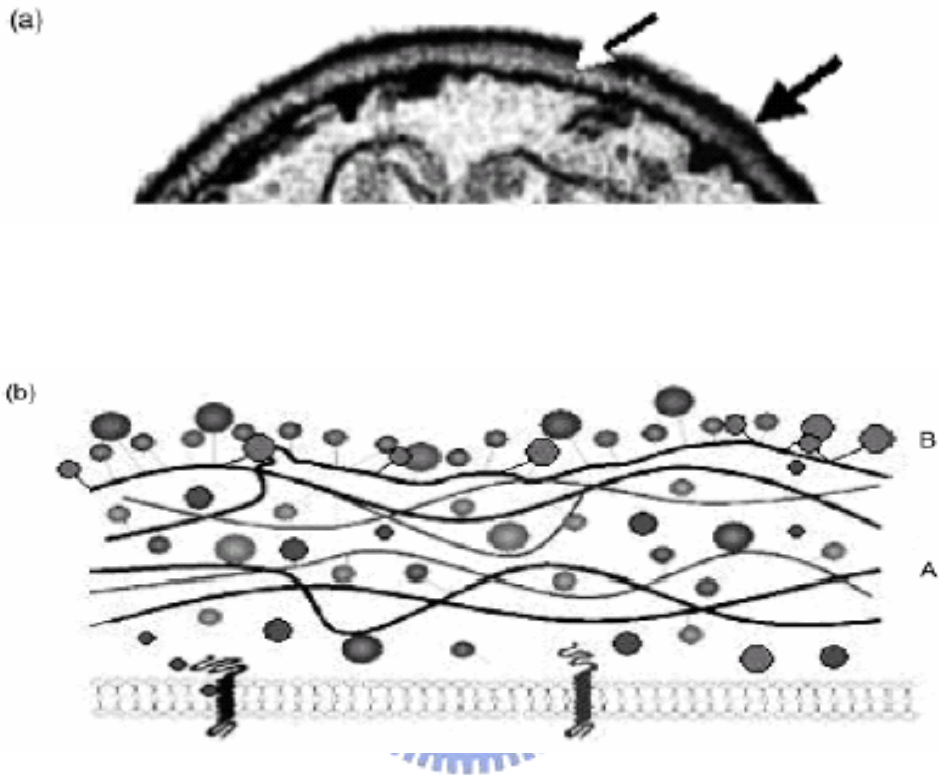
Table 1. Components of *Candida albicans* cell wall

	Percentage of cell wall (dry weight)		Chemical units	Linkages	Physical state	Chemical solubilization	Biological degradation
	Blastospore	Mycelium					
Chitin	2	6	<i>N</i> -acetylglucosamine	$\beta$ -1,4	Crystalline antiparallel associated chains	-	Chitinase
Glucan	58-60	54-56	Glucose	$\beta$ -1,3/1,6	Amorphous with microcrystalline segments	Partial degradation with acid	$\beta$ -glucanase
Mannoproteins	38-40	38-40	Amino acids, <i>N</i> -acetylglucosamine, Mannose phosphorous	Peptide <i>N</i> -glycosidic mainly a mannose pyrophosphate	Amorphous	Detergents, reducing agents, HF-pyridine Degradation with alkali and acids	Proteases

附圖一、*Candida albicans*細胞壁之組成成份

<A> *Candida albicans*細胞壁之組成結構

<B> *Candida albicans*細胞壁成分

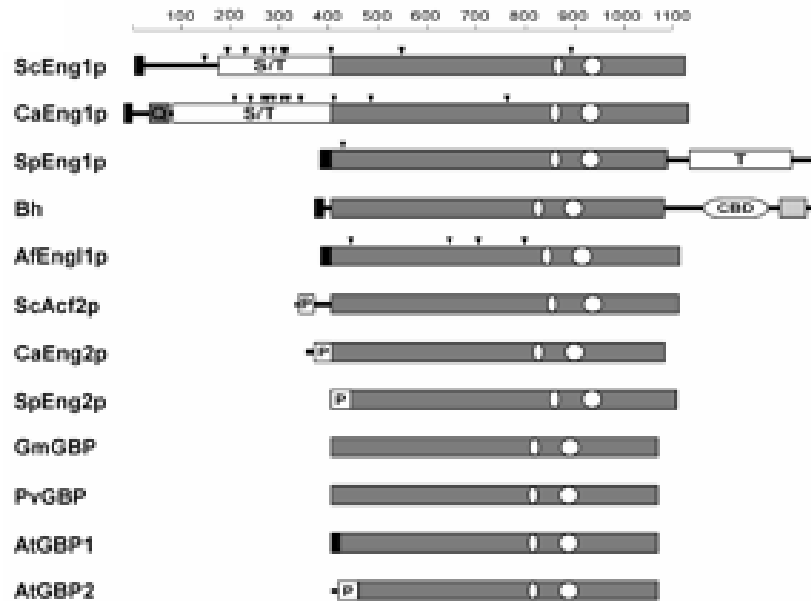


### Structure and schematic representation of the architecture of *Candida albicans* cell wall.

(a) Electron micrograph of a median cell section. The electron transparent inner layer of the wall (thin black and white arrow) is made mainly of polysaccharides ( $\beta$ -glucans and chitin) and small amounts of proteins. The electron-dense outer layer (thick black arrow) is built mostly of different types of mannoproteins.

(b) Scheme of the cell wall.  $\beta$ -1,3/1,6- Glucan chains are linked by covalent bonds to chitin microfibrils and, together with some proteins, give rise to a basic composite (A). The outer surface of this composite (B) is enriched in different types of proteins which are anchored by either noncovalent bonds or by an assortment of covalent linkages.

附圖二、白色念珠菌之細胞壁結構



### Schematic representation of endo-1,3--glucanases and plant -glucan elicitor binding proteins.

The structure of each protein is shown at the same scale (indicated at the top as number of amino acids), with a gray rectangle indicating the region conserved among all the proteins. A black box in the N-terminal region indicates the predicted secretory signal sequence, while triangles mark the positions of putative N-glycosylation sites. White boxes represent Ser/Thr-rich regions (indicated by S/T), the Thr-rich domain (marked with a T), Pro-rich regions (P), or a cellulose-binding domain (CBD). A gray box in the sequence of *C. albicans* Eng1p indicates the presence of a poly-Gln stretch (Q) and a region common to other bacterial xylanases in the sequence of Bh.

附圖三、*ENGI* 在各物種之蛋白質序列比對結果

1. 倍增時間(double time ; D.T.):

$$D.T. = (t-t_0)\log 2 / \log N - \log N_0$$

其中 $t$ 、 $t_0$ 為計算細胞數目的時間， $N_0$ 為 $t_0$ 時的細胞數目， $N$ 為 $t$ 時的細胞數目。



$$2.1 \text{ OD}_{600} = 8 \times 10^8 \text{ cell / ml}$$

附圖四、倍增時間計算公式