The secreted aspartate proteinase of Candida albicans: physiology of secretion and virulence of a proteinase-deficient mutant

IAN K. ROSS, FLAVIA DE BERNARDI,* GEORGE W. EMERSON, ANTONIO CASSONE and PATRICK A. SULLIVAN

1 Department of Biochemistry, University of Otago, PO Box 56, Dunedin, New Zealand
2 Laboratory of Bacteriology and Medical Mycology, Istituto Superiore di Sanita, Viale Regina Elena, Rome, Italy

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It was established that Candida albicans grew rapidly in a simple medium containing yeast extract (0.2%, w/v) plus glucose (2%, w/v). These cultures were in or near to a state of nitrogen limitation and the concentration of secreted aspartate proteinase increased rapidly (within 3–4 h) on addition of BSA. Synthesis and secretion were apparently controlled both positively (induction by albumin or, more probably, the peptides produced from it) and negatively (repression by NH4Cl). A small intracellular pool of the enzyme was detected during production of the enzyme and this pool decreased with the cessation of synthesis and secretion. A stable mutant, IR24, was isolated which secreted less than 0.3% of the amount of the proteinase exported by the parent strain ATCC 10261. The LD50 values for mutant IR24 and the parent strain administered intravenously to mice were >1·0 x 10⁹ and 1·6 x 10⁹ c.f.u. kg⁻¹ respectively.

Introduction

Proposed virulence determinants of the opportunistic pathogen Candida albicans include adhesins, rapid phenotypic variation and antigenic modulations, dimorphism, toxins and secreted hydrolases (for a review see Odds, 1988). Of the secreted hydrolases, an aspartate proteinase is well characterized (Ruchel, 1981); the evidence for its involvement in pathogenesis is convincing but not definitive. Amongst the Candida spp. there is a correlation between secreted proteinase activity and relative virulence (MacDonald, 1984; Ruchel et al., 1983). Schreiber et al. (1985) found no correlation between proteolysis and pathogenicity in a survey of C. albicans isolates from carriers and patients but Cassone et al. (1987) reported that the secreted proteinase activity of isolates from vaginitis patients was 1.7-fold higher than that of the isolates from carriers without symptoms. A correlation has also been reported between secreted proteinase activity and adherence (Ghannoum & Abu Elteen, 1986). Secreted proteinase has been detected in infected tissues by immunofluorescence (MacDonald & Odds, 1980; Ruchel, 1983) and antibodies to the enzyme have been detected in the serum of patients with disseminated candidosis (MacDonald & Odds, 1980). The most convincing evidence for the role of the proteinase in virulence is that proteinase-deficient mutants were found to be significantly less lethal to mice than the parental wild-type strains or a partial revertant of the mutant (MacDonald & Odds, 1983; Kwon-Chung et al., 1985). In both studies the mutants were only partially deficient in proteinase activity (i.e. 10% and 19% of maximum activity of the parent strains) and in both studies proteinase revertants were isolated from mutant cultures. Recently Crandall & Edwards (1987) reported that the wild-type strain ATCC 28366 used by MacDonald & Odds (1983) is heterozygous for proteinase secretion and the proteinase-deficient mutant derived from this strain reverted at a high frequency.

It is well established (Staib, 1965; Rembold et al., 1968; Ruchel et al., 1982) that the proteinase is expressed and secreted when exogenous protein is the sole nitrogen source but it is not secreted when ammonium salts are the nitrogen source or during nitrogen starvation (Crandall & Edwards, 1987). In the present work we have established suitable conditions for the gratuitous expression of the proteinase (i.e. conditions for rapid growth in which proteinase production occurs but is not essential) and have used enzyme activity measurements and immunological assays to study the secretion of the enzyme. These growth conditions and assay systems were also used for the isolation of a stable proteinase mutant which was characterized for its biological and pathological properties.
Methods

Strains. *C. albicans* ATCC 10261, *C. albicans* CA-2, an agermative isolate, *C. albicans* 3151A, the parent from which it was derived (Bistoni et al., 1986) and *Saccharomyces cerevisiae* X2180-1A (Yeast Genetic Stock Center, Berkeley, Calif., USA) were used.

Media. YPD contained (l~1) yeast extract (10 g), peptone (20 g) and glucose (20 g). YBD contained (l~1) yeast extract (2 g), BSA (2 g) and glucose (20 g). YD contained (l~1) yeast extract (2 g) and glucose (20 g). The BSA/glucose and haemoglobin/glucose media used for the isolation of proteinase mutants contained salts, vitamins and trace elements (Wickerham, 1946) except that the (NH$_4$)$_2$SO$_4$ was omitted, either BSA or haemoglobin (2 g l~1) and glucose (20 g l~1). Minimal medium (Shepherd & Sullivan, 1976) contained glucose, salts and biotin. Protein and vitamins were filter-sterilized as 20-fold and 200-fold concentrated stocks respectively. Media for plates contained agar (30 g l~1).

Growth conditions. Cultures were stored on YPD slopes at 4 °C and subcultured at 2 monthly intervals. Plates were incubated at 30 °C. Liquid cultures were grown on a gyratory shaker (200 r.p.m.) at either 30 or 37 °C as indicated. The initial volume was 20% of the nominal fluid volume and the cultures were inoculated from overnight YPD or YD cultures. Growth was measured as OD$_{600}$ with a Cecil CE 373 spectrophotometer (1 OD$_{600}$ unit = 1 x 10$^6$ cells ml$^{-1}$).

Mutagenesis. Cells (5 x 10$^8$) from a YPD culture (OD$_{600}$=1.0) were treated with N-methyl-N-nitro-N-nitrosoguanidine as described by Poulter et al. (1981). After 60 min at room temperature the cells were washed three times with sterile water and stored at 4 °C. The viable cell count on YPD plates was 2.5 x 10$^7$ cells (5% of the treated cells).

Morphological and biochemical characterization of the proteinase mutant. The mutant strain, IR24 (see Results), was subjected to the established morphological and biochemical tests for *C. albicans* identification: in particular, formation of germ-tubes and chlamydo-spires in serum and corn-meal agar respectively, and assimilation and established morphological and biochemical tests for *C. albicans* YD cultures. Growth was measured as OD$_{600}$ with a Cecil CE 373 spectrophotometer (1 OD$_{600}$ unit = 1 x 10$^6$ cells ml$^{-1}$).

Proteinase enzyme assays

(a) Spectrophotometric. Each assay contained 0.6 ml 1-0% (w/v) BSA in 50 mM-sodium citrate, pH 3.2, and 0.15 ml of enzyme solution. After 30 min at 37 °C 0.4 ml 10% (w/v) trichloroacetic acid was added, the tubes were stored on ice for 30 min and then centrifuged (1600 g for 10 min). The absorbance of the supernatant was read at 280 nm and corrected for background using a zero-time control in which the trichloroacetic acid was added prior to the enzyme. One unit of enzyme catalysed a A$_{450}$ of 1.0 min$^{-1}$. With the pure proteinase, the assay was proportional to enzyme concentration over the range A$_{450}$=0.1-0.4 with a reliability of ±12% and a limit of detection of 1 μg.

(b) Radioactivity. BSA (6 mg) was labelled by reductive methylation (Jenthoff & Dearborn, 1979) with 10 μmol [14C]HCHO [12.3 mCi mmol$^{-1}$ (455 MBq mmol$^{-1}$); Amersham]. The labelled protein was recovered by chromatography on a 10 x 1.6 cm column of Sephadex G10, adjusted to pH 1.0 with HCl, dialysed for 12 h against 50 mM-sodium citrate, pH 3.2, and mixed with unlabelled BSA in the same buffer.

Each assay contained 300 μl 1-2% (w/v)[14C]BSA (100000 c.p.m.) in 50 mM-sodium citrate, pH 3.2, and 75 μl of enzyme sample. After 20 min at 37 °C, 0.2 ml 10% (w/v) trichloroacetic acid was added, the tubes were treated as described for the spectrophotometric assay and 100 μl of the supernatant was counted for 2 min in 10 ml of scintillation fluid (33%, v/v, Triton X-100, 67%, v/v, toluene and 0.6% butyl-PBD). One unit of enzyme activity, 5 x 10$^4$ c.p.m. min$^{-1}$ per total assay, was equivalent to the spectrophotometric assay unit. Measurement of activity with 14C-methylated BSA increased the sensitivity to 0.2 μg of enzyme and the assays of crude enzyme samples were not complicated by a high background encountered with the A$_{450}$ system. Both assays, however, were inhibited by peptides and constituents of the growth medium: 14% by 0.5% yeast extract, 10% by 0.2% peptone and 35% by 5 μl of the diffusate collected after ultrafiltration (cut-off filter M, 10000) of YBD or YPD.

(c) ELISA. Samples (up to 30 μl) were placed in microtitre-plate wells, diluted to 90 μl with 50 mM-sodium carbonate, pH 9.5, and incubated overnight at 4 °C. The supernatants were removed, the wells were washed five times with 100 μl of 0.05% casein in PBS (50 mM-potassium phosphate, pH 7.2, containing 150 mM-NaCl, 0.02%, thimerosal and 0.01% Tween 20) and blocked by an incubation with 100 μl 1% (w/v) casein/PBS for 1 h at 37 °C. Rabbit antiserum (100 μl of a 1 in 500 dilution in casein/PBS) was added and after 2 h at 37 °C the wells were washed five times with casein/PBS. Goat anti-rabbit IgG peroxidase conjugate (Caltag Laboratories; 100 μl of a 1 in 8000 dilution in casein/PBS) was added followed by incubation for 1-5 h at 37 °C and washing as above. The substrate mixture for the colour reaction (100 μl) consisted of 50 mM-citric acid, 100 mM-Na$_2$HPO$_4$, 2 mM-H$_2$O$_2$ and 0.4 mg o-phenylenediamine ml$^{-1}$. After 15 min incubation in the dark 50 μl 2 M-H$_2$SO$_4$ was added and the plates were read at 492 nm. Each sample was measured in duplicate and corrected for background (A$_{492}$ = 0.03-0.08) with no antigen. A standard curve (0-300 ng), determined with the purified proteinase for each plate, gave A$_{492}$ readings of 0-1.2.

SDS-PAGE, electrophoresis and immunoblotting. SDS-PAGE (Laemmli & Favre, 1973) was done using 10 x 8 x 0.2 cm gels (Matsudaira & Burgess, 1978) with a 12.5% (w/v) separating gel and a 5% (w/v) stacking gel. Electrophoresis was for 1-2 h at 120 V and 5 mA. The M, markers used were β-galactosidase (116000), phosphorylase b (97000), BSA (66000), ovalbumin (45000), carbonic anhydrase (29000) and cytochrome c (12000). For protein staining, the gels were soaked in a solution of 7.5% (v/v) acetic acid plus 20% (v/v) methanol
for 20 min, stained for 1 h in 0.025% Coomassie blue in 7.5% (v/v) acetic acid and 50% (v/v) methanol and destained in 10% (v/v) acetic acid.

Electrotransfer to nitrocellulose (Towbin et al., 1979) was done at 15°C in 5 litres of precooled buffer consisting of 3 mm-Na$_2$CO$_3$, 10 mm-NaHCO$_3$, and 20% (v/v) methanol. After 4 h at 40 °C and 0.7 A, the transfer of the M, markers was visualized with 0.01% Ponceau S in 0.05% acetic acid. The nitrocellulose was washed with distilled water and soaked overnight in 40 mm-Tris/HCl, pH 7.6, containing 150 mm-NaCl, 0.01% thiomersal, 0.05% Tween 20 and 1% (w/v) casein. The blocked nitrocellulose was probed with a 1 in 3000 dilution of antisera in casein/PBS for 1-5 h at 37°C, washed five times with casein/PBS and then similarly incubated in a 1 in 8000 dilution of goat anti-rabbit IgG peroxidase conjugate. After washing, the bound peroxidase was visualized by incubation in a solution freshly prepared by mixing 6 ml methanol containing 18 mg 4-chloronaphthol and 30 ml 50 mm-sodium citrate/100 mm-sodium phosphate, pH 5.4, containing 3 mm-H$_2$O$_2$. The colour development was for 5 min to 2 h and the reaction was stopped by washing with water.

Assessment of the antisera used. The specificity and sensitivity of the antisera was assessed by Western blot analyses. With fresh preparations of pure proteinase, 1 ng was detected as one band with a 1 in 3000 dilution of antisera. Older preparations of the enzyme exhibited multiple bands of proteolytic degradation products (Fig. 1b). No bands were detected with YBD medium, with a cell-free extract from cells grown in YPD or with 0.5 mg of the vacuolar aspartate proteinase from S. cerevisiae (Sigma). No bands were detected with preimmune serum. An antisera to the S. cerevisiae aspartate proteinase at a 1 in 3000 dilution reacted specifically with the enzyme from this organism and there were no cross-reactions with the samples listed above.

Mouse infections. Mice were infected as described previously (Bistoni et al., 1986). Briefly, groups of eight inbred male CD2F1 mice (18-21 g; Charles River Breeding Laboratories) were injected intravenously with different doses of C. albicans strains and the mortality was assessed over 30 d. In other experiments, mice were killed by cervical dislocation at intervals during the experimental infection, the organs removed aseptically and immediately fixed in 10% (v/v) formalin. Sections of paraffin-embedded organs were examined after treatment with periodic acid/Schiff (PAS) and Van Gieson stains.

Results

Conditions for proteinase synthesis and secretion

The C. albicans aspartate proteinase has commonly been produced by growth in minimal medium with BSA as the sole nitrogen source (MacDonald & Odds, 1980; Buchel, 1981). These cultures have an extended lag phase (10-15 h) and proteinase secretion only reaches a maximum after 4-7 d. We therefore sought conditions for rapid growth and secretion. Fig. 1(a) shows that C. albicans ATCC 10261 grew rapidly in YBD medium (2.5 OD$_{600}$ units h$^{-1}$) but this was interrupted by a decreased growth rate around OD$_{600}$ 12-13 followed by a second phase of growth. Proteinase was secreted from 4 h and the concentration of the enzyme in the culture supernatant changed rapidly resulting in peaks (enzyme activity and ELISA) at 12 h and a peak (enzyme activity) at 20 h (Fig. 1a). The amount of proteinase in the culture supernatant relative to the cell density was constant from 4 to 10 h [5 µg (OD unit)$^{-1}$]; it then rose to 14 µg (OD unit)$^{-1}$ at 14 h, decreased to 2.3 µg (OD unit)$^{-1}$ at 18 h and returned to 5 µg (OD unit)$^{-1}$ at 20 h. These data were confirmed by a Western blot analysis of the culture medium (Fig. 1b) which showed changes in the concentration of the intact proteinase with growth and proteolytic degradation of the enzyme (8-14 h). Pure proteinase, freshly prepared, showed one band in Western blots but the pattern of multiple bands exhibited by stored preparations (Fig. 1b, c) was essentially the same as the pattern for the culture supernatant samples. The spheroplast extracts from cells grown in YBD medium contained a small pool of the proteinase (Fig. 1c) but there was no intracellular accumulation of the enzyme during growth and the pool decreased at 16 h prior to the second phase of growth and proteinase production.

When BSA was omitted from the medium (YD) C. albicans grew at 1.5 OD$_{600}$ units h$^{-1}$ with a low level of proteinase secretion (Fig. 2a); the growth rate was increased only slightly when 0.2% BSA was added at 4.5 h (1.8 OD$_{600}$ units h$^{-1}$) but secretion of the proteinase increased rapidly between 7 and 8.5 h resulting in peaks of enzyme concentration at 8.5 and 10 h (Fig. 2b). Under these conditions secretion of the proteinase was repressed by NH$_4$Cl (Fig. 2c). L-Leucine (80 mM) also decreased secretion of the proteinase and the maximum concentration at 10 h was 22 µg ml$^{-1}$ compared with 45 µg ml$^{-1}$ for BSA added alone. When BSA was added at 4 h and NH$_4$Cl at 4.5 h there was only a small transient increase in the concentration of the secreted proteinase (Fig. 2d) compared with the culture supplemented with BSA alone (Fig. 2b).

Isolation of proteinase-deficient mutants

The proteinase indicator plates were initially tested with positive and negative controls for proteinase secretion. C. albicans ATCC 10261 produced 2-3 mm cleared zones around each colony after 3, 5 and 7 d growth on plates containing YBD, haemoglobin/glucose and BSA/glucose respectively. After 7 d growth S. cerevisiae X2180-1A produced minute colonies on BSA/glucose and good growth on the other two media; there were no cleared zones on any of the plates.

Mutagenized cells were grown on YPD plates and 3000 colonies were selected for screening on proteinase indicator plates. Of the isolates, 93 (3.1%) showed no zone of clearing in an initial screening on haemoglobin/glucose. After more than ten replatings on the various indicator plates with passages onto YPD plates the collection was reduced to 23 with the elimination of
Fig. 1. Growth of C. albicans and secretion of the proteinase. YBD medium was inoculated to OD$_{600}$ = 0.2 with a 12 h YPD culture (OD$_{600}$ = 10.0) of C. albicans ATCC 10261. At the times indicated (a) 1.0 ml samples of the culture were measured for growth (●) and culture supernatant proteinase by enzyme activity (○) and ELISA (■). SDS extracts of the culture supernatant (b) and cell lysates (c), equivalent to 37.5 µl of the culture at the times indicated, were analysed in Western blots for the proteinase. Each blot shows a lane containing 1 µg of the purified proteinase and the characteristic pattern of autodegradation. Std, stored preparation.
isolates that showed proteinase secretion or altered growth characteristics (colony size and morphology).

These 23 isolates were then screened on minimal medium plates and various liquid media. Six isolates finally selected from the screening included three proteinase-deficient mutants, an unusual mutant that secreted the proteinase at 37 °C but not at growth temperatures below 30 °C and two revertants that arose late in the screening process. One isolate, IR24, exhibited the most suitable phenotype: no detected reversion, and a growth rate in minimal medium comparable with that of the parent strain; growth in YBD and YD was slightly impaired. Isolate IR24 developed germ-tubes in serum, chlamydospores in cornmeal agar medium and it also formed mycelia in vivo to an extent comparable to that of the parental strain ATCC 10261 (see also Fig. 4). In fermentation and assimilation tests the parent and mutant strains were identical.

With isolate IR24 no proteinase was detected in YBD medium by either the enzyme assay or ELISA but a faint band was detected by immunoblotting a sample of the culture medium (Fig. 3). The limit of detection of pure proteinase by immunoblotting was 1 ng (data not shown) and on this basis the immunoreactive proteinase secreted by IR24 was less than 0.3% that of C. albicans ATCC 10261 (Fig. 3, lanes 2 and 4).

Virulence for mice of IR24 and wild-type strains of C. albicans

The experimental pathogenicity of C. albicans ATCC 10261 and its proteinase-deficient derived mutant IR24 were assessed in a systemic infection of
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Fig. 3. Proteinase secretion by C. albicans ATCC 10261 and IR24. Flasks of YBD medium were inoculated to OD_600 = 0.2 with 12 h YD cultures of C. albicans ATCC 10261 and the proteinase mutant IR24. The culture supernatants were analysed for secreted proteinase after 2 h and 7 h growth by ELISA and in a Western blot (2 h, lanes 1 and 3; 7 h, lanes 2 and 4). Each lane contained 15 μl of medium and the amounts of proteinase per lane as estimated by ELISA are given in parentheses. Lanes 1 and 2, ATCC 10261 (1.3 pg and 1.9 pg); lanes 3 and 4, proteinase mutant IR24 (no proteinase detected).

Table 1. Mortality of mice challenged intravenously with different strains of C. albicans

The results are shown as the LD_{50}, the median survival time (MST) in days and as dead mice at 30 d over total number of animals tested (D/T). Groups of eight mice were used for each dose of cells administered. The experiments for the calculation of the mortality after a challenge with 10^6 cells were done separately from the experiment to determine LD_{50} value.

<table>
<thead>
<tr>
<th>Strain</th>
<th>10^6 × LD_{50} (c.f.u. kg^{-1})*</th>
<th>Mortality after challenge with 10^6 cells</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>MST (d)</td>
</tr>
<tr>
<td>3153A</td>
<td>0.60 ± 0.12</td>
<td>3</td>
</tr>
<tr>
<td>CA-2</td>
<td>158 ± 2.7</td>
<td>&gt;30</td>
</tr>
<tr>
<td>ATCC 10261</td>
<td>1.6 ± 0.1</td>
<td>5</td>
</tr>
<tr>
<td>IR24</td>
<td>&gt;1000</td>
<td>&gt;30</td>
</tr>
</tbody>
</table>

* ± Standard error.

CD2F1 mice given graded numbers of Candida cells by the intravenous route. For comparison, two additional strains of C. albicans were included in the experiment: strain 3153A and its derivative CA-2, previously characterized as an agerminative proteinase producer with low virulence (Bistoni et al., 1986). The data in Table 1 show that strains 10261 and 3153A of C. albicans were highly pathogenic for mice with LD_{50} values of about 10^6 cells kg^{-1} and a median survival time of less than 1 week after an intravenous injection of 1 × 10^6 cells. In contrast, mutant IR24 was much less pathogenic, being unable to kill any animal after a challenge with 10^6 cells (the LD_{50} was about three orders of magnitude higher than for the wild-type strains). Table 1 also shows that the proteinase mutant was less pathogenic than the agerminative CA-2 strain. Strain CA-2, however, produces secreted proteinase at approximately 50% of the amount secreted by strain 3153A. Fig. 4 shows heart sections of animals infected with the parent strain ATCC 10261 and the mutant IR24. Extensive hyphal development was noted with both strains. C. albicans isolates were also recovered from kidneys and...
hearts of the infected mice. The isolates from mice infected with mutant IR24 showed no proteinase activity on YBD plates but the isolates from mice infected with ATCC 10261 were all proteinase-positive.

Discussion

Previous studies suggested that the production of the *C. albicans* secreted proteinase is induced by protein (MacDonald & Odds, 1981; Ruchel et al., 1982; Crandall & Edwards, 1987), stimulated by 0.01%, yeast extract (Germaine et al., 1978) or the iron content therein (Crandall & Edwards, 1987), stimulated by glucose (Samaranayake et al., 1984) and repressed by (NH₄)₂SO₄ (Crandall & Edwards, 1987). The enzyme was not secreted during nitrogen starvation (Crandall & Edwards, 1987) and the evidence for induction and repression has not been clearly documented.

In the present work we found that YD medium (yeast extract plus glucose) contained sufficient nutrients for rapid growth of *C. albicans* but the cultures were apparently in or near to nitrogen limitation. In YD cultures the concentration of the secreted proteinase was low (2-5% of the maximum) but this amount of the enzyme could contribute to the provision of nitrogen for growth. The growth rate did not change markedly on the addition of other nitrogen sources but the concentration of the proteinase increased 20 to 50-fold within 4 h after addition of BSA. This response was strongly repressed by NH₄Cl and to a lesser extent by leucine. The repression by leucine may have been mediated via other metabolites such as NH₄⁺ and further experiments are needed to establish whether other amino acids and low-molecular-mass nitrogen metabolites also repress production of the proteinase.

Proteinases of eukaryotic micro-organisms (North, 1982) and in particular *S. cerevisiae* (Achstetter & Wolf, 1985) have been extensively reviewed. The production of extracellular proteinases is often controlled by catabolite repression only, e.g. *Aspergillus nidulans* (Cohen, 1981) and *Schizosaccharomyces pombe* (Sessoms & Lilly, 1986). In these organisms proteinase secretion increases under conditions of nitrogen limitation and in the absence of exogenous protein. The production of exocellular proteinases in *Neurospora crassa* (Cohen & Drucker, 1977) and *Mucor miehei* (Lasure, 1980) is also repressed by NH₄⁺ and amino acids but nitrogen limitation does not result in proteinase production unless protein is present in the growth medium. The production of the *C. albicans* proteinase is apparently also controlled by repression and induction. It is noteworthy that in *N. crassa* exocellular proteinase activity is required before induction can occur (Drucker, 1973) and a similar requirement in *C. albicans* would account for the extended lag phase encountered when the organism is transferred to media with BSA as the sole nitrogen source.

Measurement of the concentration of the secreted proteinase was difficult because of the relative insensitivity of the enzyme activity assays, the inhibition of the enzyme by constituents of the growth medium and the inherent inability of ELISA to distinguish between intact and degraded forms of the enzyme. Enzyme activity was not directly proportional to enzyme concentration as measured by ELISA but three methods of analysis (activity, ELISA and Western blotting) showed that the concentration of the secreted proteinase oscillated during growth in YBD (Fig. 1). Several factors could have contributed to this result. The changes in proteinase concentration coincided with the decreased growth rate in YBD around OD₆₀₀ 12-14, the cell density at which YD cultures entered stationary phase (Fig. 2a). This suggests that the YBD cultures undergo a nutritional adaptation at this time. The synthesis of the proteinase decreased during this phase as judged by the decreased intracellular pool. Western blot analysis of the culture supernatant revealed a pattern of proteinase degradation similar to that observed with the purified enzyme. These data suggest that autodegradation contributed to the decreased concentration and enzyme activity in the culture supernatant. It is not known whether any of the proteolytic breakdown products have enzyme activity.

YBD was a suitable medium for screening proteinase-deficient mutants because the organism was not dependent on the secreted enzyme for growth but the proteinase synthesis was not repressed. Only a trace of immunoreactive proteinase was secreted by the mutant IR24 and this was well below the levels of detection of the ELISA and enzyme activity assays. The nature of the mutation in IR24 has not been determined. It is possible that the mutagenesis procedure used could have produced other undetected mutations but IR24 was not auxotrophic for any nutrient and the slight decrease in the growth rate in YD and YBD could be due to the proteinase deficiency itself. The mutant isolated by MacDonald & Odds (1983) showed an initial lag phase but then grew rapidly in a medium with BSA as the sole nitrogen source. Initial growth of the mutant isolated by Kwon-Chung et al. (1985) was rapid in a synthetic medium with haemoglobin as sole nitrogen source (possibly due to low-molecular-mass nitrogen compounds in the medium); this was followed by a lag phase (from 15-20 h) and then by growth to the same cell density as the parent strain.

Importantly, IR24 and the parent strain grew at comparable rates at 37 °C; both formed germ tubes *in vitro* and *in vivo* and the mutation affecting proteinase secretion was stable.
The pathogenicity experiments showed that strain IR24 was 1000-fold less virulent than the wild-type proteinase-secreting strains and about 10-fold less virulent than a low virulence, proteinase-positive, agerminative strain. MacDonald and Odds (1983) reported a 10-fold difference in the LD_{50} values of a proteinase mutant and its parent strain. The proteinase mutant IR24 can be regarded as a non-pathogenic strain of _Candida_ albicans. In contrast, the proteinase mutants isolated by MacDonald and Odds (1983) and Kwon-Chung et al. (1985) retained appreciable pathogenicity for mice, interpreted as due to a partial in vivo reversion to proteinase production. The lack of pathogenicity of mutant IR24 can be accounted for by the stability of the proteinase mutation in _vivo_. It may, however, differ from strain ATCC 10261 in virulence-related properties other than proteinase secretion. Our data indicate more strongly than the previous studies (MacDonald & Odds, 1983; Kwon-Chung et al., 1985) that the secreted aspartate proteinase plays a role in the pathogenicity of _Candida_ albicans but unequivocal proof will require the construction of a proteinase-negative mutant by a specific gene disruption.

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References


