



## Efficiency of Indigenous Fungi for Controlling Pathogenic Bacteria in a Swine Natural Farming System

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### Introduction

Indigenous microorganisms (IMOs) such as fungi are used in 'Cho Han Kyu' natural farming systems to reduce the rate of both air and water pollution. Different kinds of fungi are therefore added to the bedding to support the production of organic fertilizer. Fungi synthesize enzymes, lactic acid and antibiotics that might inhibit the growth of pathogenic bacteria. However, no information about the type and special property of the IMOs used in the swine natural farming.

### Materials and Methods

Indigenous fungi were collected under bamboos at 13 places located in five provinces of Northern Thailand (Chiangmai, Lamphun, Lampang, Chiangrai and Phrae). The fungi were pure culture and genus or species was identified by Kiffer and Morelet method (Kiffer and Morelet, 1999). Antibacterial performance was test using the fungi culture filtrate and co-culture methods. Cellulase activities was test on Carboxyl methyl cellulose (CMC) agar and measured by Miller's method (Miller, 1959).

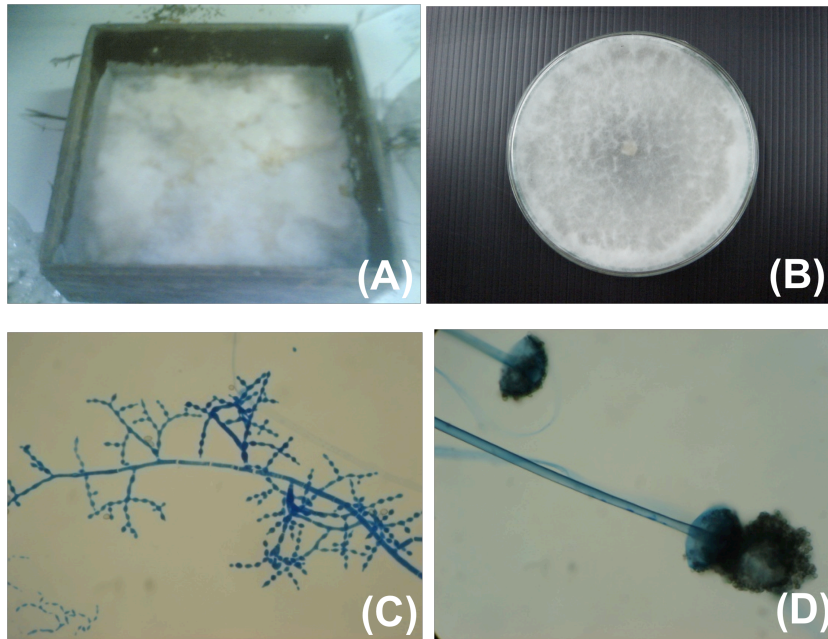
### Results and Discussion

**IMOs Identification:** These results indicated that the majority of fungi belonged to *Geomyces* sp. and *Rhizopus* sp. (Fig 1). The origin of the further fungi remained unknown.

**Antibacterial Performance:** This study, using *Salmonella* spp., *E. coli* and *Staphylococcus aureus* revealed that three of the 13 fungi affect bacterial growth (23.1%). The fungi collected at Lamphun (LPM01 isolate) and at Chiangmai (CMSM02 and CMSM03 isolate) hold the power to inhibit bacterial growth at 61.5%, 38.5% and 38.5% of all bacteria tested, respectively. Co-culture experiments revealed that all fungi strains were capable to inhibit *Salmonella Typhymurium* at bacterial concentrations of less than  $10^6$  CFU/ml. Growth rates of *Salmonella* spp. taken from pig faeces were inhibited at a concentration of 10 CFU/ml ( $p < 0.01$ ) (Table 1).

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**Fig. 1** Fungi collection and identification (A) IMOs were collected under bamboos used steaming rice as baiting medium (B) Colony of purified fungus on Potato Dextrose Agar (PDA) (C) *Geomyces* under microscope (400x) (D) *Rhizopus* under microscope (400x).

**Table 1** Inhibition of fungi to control bacteria growth by co-culture experiment

Concentration of bacteria (10 <sup>x</sup> CFU/ml)	% Inhibited <i>Salmonella Typhimurium</i> (Standard)	% Inhibited <i>Salmonella spp.</i> (from Feces No.193A)
0	92.31 <sup>a</sup>	46.15
2	100.00 <sup>b</sup>	0.00
4	46.15 <sup>c</sup>	0.00
6	7.69 <sup>d</sup>	0.00
8	0.00	0.00

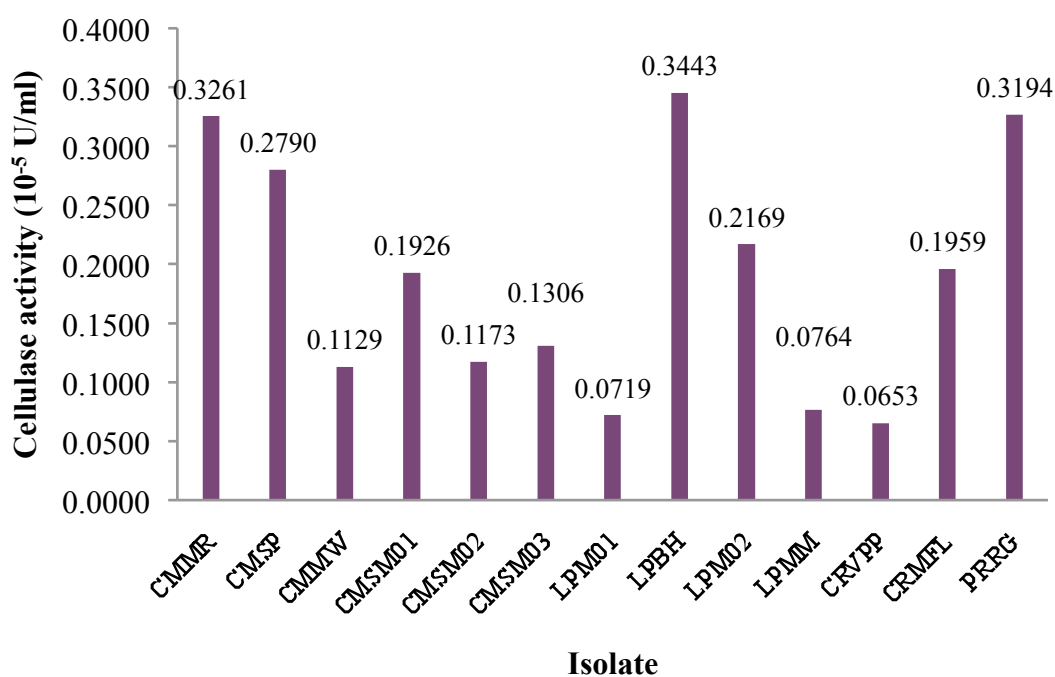
<sup>a,b,c,d</sup> Within a column, values having no superscript letter in common differ at  $p < 0.01$

**Cellulose Degradation Performance:** A high efficiency to degrade CMC has been found in isolates collected in Phrae (PRRG isolate), Chiangrai (CRMFL isolate), Chiangmai (CMSP isolate), Lampang (LPM02 isolate), and Lamphun (LPBH isolate) ( $p > 0.05$ ) (Table 2). Therefore, the fungus extracted from the LPBH isolate showed the highest cellulase activity ( $0.344 \times 10^{-5}$  U/ml) followed by the CMMR (Chiangmai), the PRRG (Phrae) and the CMSP isolate (Chiangmai) ( $0.326 \times 10^{-5}$  U/ml,  $0.319 \times 10^{-5}$  U/ml and  $0.279 \times 10^{-5}$  U/ml), respectively. The lowest activity was found in the CRVPP isolate (Chiangrai) ( $0.065 \times 10^{-5}$  U/ml) ( $p < 0.05$ ) (Fig. 2).

**Table 2** The efficiency of the fungi isolate to degrade carboxyl methyl cellulose (CMC)

No. of fungi isolate	Fungi isolate	Average of CMC diameter (cm)
1	PRRG	8.57 <sup>a</sup>
2	CRMFL	8.22 <sup>a</sup>
3	CMSP	7.97 <sup>a</sup>
4	LPM02	7.80 <sup>a</sup>
5	LPBH	7.72 <sup>a</sup>
6	CMMR	5.72 <sup>b</sup>
7	LPM01	3.92 <sup>c</sup>
8	LPM01	2.77 <sup>d</sup>
9	CMSM01	2.72 <sup>d</sup>
10	CRVPP	2.55 <sup>d</sup>
11	CMSM02	2.47 <sup>d</sup>
12	CMSM03	2.00 <sup>de</sup>
13	CMMW	1.45 <sup>e</sup>

<sup>a,b,c,d,e</sup> Within a column, values having no superscript letter in common differ at  $p < 0.05$



**Fig. 2** Cellulase activity of each fungi isolate

### Conclusion and Outlook

- 1) The majority of fungi belonged to *Geomyces* sp. and *Rhizopus* sp.
- 2) The IMO can inhibited bacterial growth at a low bacterial concentration.
- 3) The cellulase activity of each fungi isolate follows an unique pattern varying from 0.3261 to 0.00653, depending on the environment difference.

4) To gained basic knowledge about the indigenous fungi, we will start to characterize these species on the molecular level. The final goal will be to assess their potentials to be used in the swine natural farming system.

### **References**

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