

The Study of Taiwan Phoridae the addition of Bacillus sk in growth medium elim i nat ed the commonly seen fungal overgrowth, which killed the phoridae generations. Direct observation by scan ning electron microscopy demonstrated that this bacilli were found in the interior of pupa and also in the midgut of larva. Bacillus sk,and other Bacillus spp.DNAs were am pli fied and studied by Random Am pli fi ca tion DNA Polymorphism. Similar but not identical pat terns were found between Bacillus sk and Bacillus subtilis. DNA sequences of 16S rDNA, ITS and 23S rDNA of Ba cil lus sk offered 99% identity to those of Bacillus subtilis. A close evolution relationship with Ba cil lus subtilis was proposed. A protein toxin was secreted by Bacillus sk but not by Bacillus subtilis. Toxin was purified by salt pre cip i ta tion and acetone extraction procedures. This toxin accounts for Bacillus sk's antifungal and worm killing effects. Injections of toxin into larva of ori en tal fruit fly , Bactocera dorsalis, im me di ate ly stop the vessel pulsation and kill the insects. The toxin is nevertheless harmless to Megaselia scalaris larva and fly. Under starvation condition, Megaselia scalaris can even live on washed Bacillus sk bacteria as its only food source. The compensatory symbiosis interactions of Establishment of Artificial Breeding Tech nol o gy The Identification of an Symbiotic Ba cil lus Spe cies [1.Introduction](#) In history,all 54 reported species of Tai wan phoridae had been transferred to Europe, denominated, kept in Hungarian museum , but de stroyed in a big fire in 1965 (1). Accidentally in help ing purification of a bacillus peptide toxin, I ob served a black tiny fly strongly attracted by a protein-rich plate streaked with a toxin-se cret ing Bacillus sk strain. The ex per i ments were repeated several times and 90% of all attracted tiny flies were identified as the long ne glect ed flea fly, Megaselia scalaris. The female Megaselia scalaris flies cop u late with male flies right after meta mor pho sis from pupa and ovulate in 15-45 min utes after reaching the Ba cil lus sk colonies. Further efforts in achieving ar ti fi cial breeding method have dem on strat ed the need of bacillus and high pro tein diet in phoridae growth and maturation.

	水	牛奶	果味	LB	LB	水	煮乳酪	乳酪	蜂
			蠅	plate	plate+	鮭肉		酪	蜜
			培養		Bacill			+	水
存活天數			基		us SK			蜂	
								蜜	
								水	
雄性成蠅	1天	1-2天	2天	2天	1-2天	3-5天	1-2天	2-3天	>14天
雌性成蠅	1-2天	2-3天	3天	2天	2-4天	3-5天	2-3天	3-4天	>20天

Also during long series of passages,

mi cro or gan ism and its insect hosts have been re port ed between flagella protist and termit (2). Re cent ly the identification and analysis of Bacilli DNA from abdominal tissue of some extinct amber-en tombed fossil bees have raised the possibility of bee-Bacillus symbiosis (3). In this study, I presented the evidences from a liv ing example for an acquired symbiotic in ter ac tions be tween Phoridae fly, Megaselia scalaris and a spe cif ic Bacillus strain. Finally for further char ac ter iz ing this very first model of phoridae in Taiwan, its animal behavior, field distribution and rDNA gene struc ture were also issued.[2.Objectives](#) Restore the Taiwan phoridae insect modes which had been collected in Hungarian museum, but de stroyed in the 1965 big fire. Identify the characteristic gene structure

tion and (c). a dif fer en ti a tion and maturation enhancer. [3.Experiment Procedures](#) Phoridae Artificial Breeding Method: Modified Drosophila's growth gel (a mix.of 900c.c.distilled water, 10 gm agar, 30gm yeast powder,40gm crude sugar,100gm corn starch were heated, honey 2% (v/v) ,0.5c.c alcohol and pro pi on ic acid were added and cooled to gel state. Beef -Bacillus SK broth : a mix. of 100 gram ground lean beef , 100 gram D-glucose and 400 gram distilled water ,121°C autoclaved 30 minutes. The supernatent beef extract mixed with Bacillus SK OD 0.3 was cultured at 32°C 24 hours. For breeding, 0.8 c.c. broth was added into a tube con tain ing 5 c.c. mod i fied gel. DNA

of Family Phoridae and related gene variation for the different genus of this family. Symbiotic Poly morphism DNA and DNA sequencing: toxic Bacillus sk is a close relative of non toxic Bacillus subtilis. The secreted protein tox in plays an important role for protecting the food from fungal overgrowth, keeping away from natural enemies, saving the larva from animal's intake. Three nontoxic interactions were also identified in this Phoridae-Bacillus symbiosis interactions: Bacillus sk acts as (a). a strong chemical attractant, (b). a spare food in stringent situation, (c). a chemical defense agent. DNA extraction,Random Amplification Polymerase chain reaction (RAPD) DNA and DNA sequencing: These methods were performed as described in all microbiology technology books. DNA data was mainly based of the purification from one larva or adult flea fly instead of many insects. Polymerase chain reaction was performed in Thermocycler 480, (Perkin-Elmer, Netherlands). Sequencing the nuclear rDNA region containing the internal transcribed spacer (ITS) regions and 5.8S rRNA gene and nuclear small (18S) was performed by primers described in Table 1. and ABI PRISM Model 377 DNA Autosequence.Results were compared in website NCBI (www.ncbi.nlm.nih.gov/) and run multiple alignment with the other species by program Vector NT.

4.Results I. Ecology of Megaselia scalarisFigure 1 Three major kinds of phoridae that were attracted by Bacillus sk. 250 Bacillus sk plates were used in 84 different locations .Among 2100 attracted phoridae flies, three different phoridae flies were identified and 90% were megaselia scalaris.

Table 1. primers used in PCR and RAPD reactions

PCR primer	Primer sequence(5'→3')	Target site
NS1	GTAATCATATGCTTGTCTC	18S
NS4	CTTCCGTCAATTCCTTAAG	18S
NS5	AACCTAAAGGAATTGACGGAAG	18S
NS6	GCATCAGACACCGTGTATGCCTC	18S
NS7	GAGGCAATAACAGGTCTGTGATGC	18S
ITS1	TCCGTAGGTGAACCTGC	ITS
ITS2	GCTGCGTTCTTCATCGATGC	ITS
ITS4	TCCTCCGCTTATGATATGC	ITS
ITS5	GGAAGTAAAGTCGTAACAAGG	ITS
FF1	TCGTAAACAGGTTTCCG	ITS
FF2	GTTAGTTTCTTTCTC	ITS
RD1	AAGGAGGTGATCCAGCC	16S
FD1	GAGGTTTGATCTGCTCAG	16S
16SR	ACTGCTGCCTCCGTAG	16S
16ScutF	TAATACGGATAATTTTCAGC	16S
23SR	CAGCACCAGGAGGTGTACACCCC	23S
23ScutF	TAAGTAGGCAATCCGCTTACGT	23S
RAPD primer	Primer sequence(5'→3')	
OPB11	GTAGACCCGT	
OPB12	CCTTGACGCA	
OPB13	TTCCCGCT	
OPB16	TTTGCCGGA	
OPB19	ACCCCGAAG	

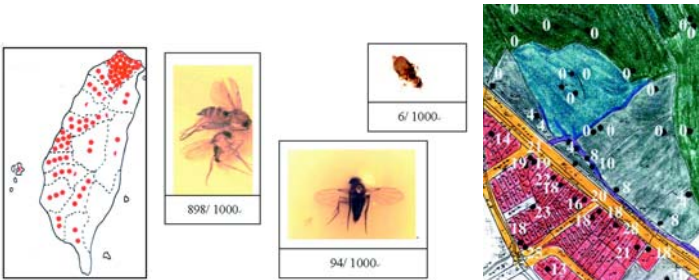
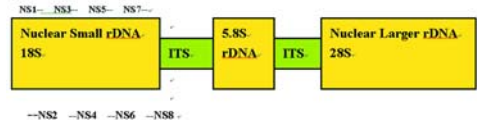


Figure 2 The distribution of Megaselia scalaris in The Taipei Suburban area. 50 traps were evenly sit ed over a mixed area of three or more different regions: red, residential; yellow, public transport paths; purple: a trench; gray: factory; green: farmland; light blue: water pond. The black dots represent the sites of the traps, the white number denotes the number of the Megaselia scalaris flies caught in 6 hours. Although in Taipei city life, healthy-looking and vi va cious Megaselia scalaris are often seen here and there. It is difficult to catch this fly at mountain or farmland. This plus the finding t that Megaselia scalaris often lay eggs at the brim of some opened beef extract cans. Megaselia scalaris may have long adapted to human civilization and become used to live with our artificial waste and junk stuff environment. II.The characteristic phoridae rDNA gene structure In the past 100 years, Taiwan flea flies were col lect ed and transferred to Europe, studied by for eign researchers. Recent study on these reported animal models were extremely difficult due to the huge de struc tion in a big fire. In this paper, the es tab lish ment of artificial breeding method and cross fer til i za tion (at least five generations) provides me large quantities of Megaselia scalaris with iden ti cal mor phol o gy and gene structures. The ap pli ca tion of 18S,28S ribosome DNA probes with PCR method re flects the specific DNA sequence about Megaselia scalaris (Chen,Taipei). To begin with ribosomal DNA primer set FF1: TCG,TAA,CAA,GGT,TTC,CG; FF2:GGT,AGT,TTC,TTT,TTC,TC, I obtained the first DNA segment sequence by an ABI prism Model 377 DNA

autosequencer . Since not any DNA sequence re lat ed to flea fly has been published before, I tried various sets of primers to elucidate the whole se quence of 18S and ITS1 regions(Figure 3). Figure 3 Phoridae Megaselia scalaris 18S rDNA gene structure. Comparison between several different living or gan isms was performed bycomputer search. Care ful study on the gene struc ture of phoridae rDNA has indicated the following events:(1) The closer two organisms appear in evolution, the more their



>18s rRNA gene of FF

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ATTCTGGTGTGATCCTCTCGTCGGGACGGGCTGTAGNCTATGCTTGTCTGCTTACG
GAATTGACGGAGATGATCATTATGCTTGTTCCTTAAAGGAATGACGGAGGAGT
ACTGATGTGCTTGTATAGCTAATACATGCAATTATAGCAGGACCTTTTGAACGTG
TGCTTTTATTAGGCTAAACCAACGATCTTTTCGGGAATCGTGAATGGTGAATCT
CTAGATAACTTGCAGATCGTATGCTTGTACCGACGACAGATCTTCAAAATGCTG
CCCTATCAACTATTGATGATGATATCTAGGACTACCATGGTGCACACGGTAAACGGG
GAATCAGGGTTCGATTCGGAGGGGAGCTGAGAAACGGCTACCACTCTAAGGAA
GGCAGCAGGGCGCTAAATACCCACTCCGACGACGGGAGGTAGTACGAAAAAATAA
CAATACAGGAGCTGATTCGGAGGGCTGTAATTTGAATGAGTACACTTTAAATCCTT
TAACAGGACCTATTGGAGGGCAAGTCTGGTCCGACGACGGCGGTAAATTCAGCTT
CAATAGCGTATATTAAAGTTGTTGGGTAAACGTTCTGATGTGAACTTGTGCTCC
ATACGGGTAGTACACCCATCAATTTGGGTGTGATCTACTCTATGATGTGAGCGT
ATTACCGGTGGAGTTCTTATATGTTATGGTACTGTATTATAGCGTATTCCTCTAT
TCAAACTACTTTCAGTGCTCTTCTATCGAGTGTGTTGTGGGCGGTACAAATCTTT
GAACAAATTAGAGTGTCTAAAGCAGGCTTCAAAATGCTGAATATTTGTGATGGAAAT
AATGAATATAGACCTCTGTTCTACTTTCATTTGGTGTATAGATCAAGAGGTAAATGATT
AATAGAGGCTGTTTGGGGCATTAGTATTACGACGCGAGAGGTGAATTTCTTGGACC
GTCTGAAGACTAATCTTAAACGAGAGCTTTCCCAAGAGTGTTCATTAATCAAGAA
CTAAAGTTAGAGGTTCCAGAGGATCAGATACCGGCTAGTTCTTAAACATAAAGCAT
GCCAGCTAGCAATTTGGGTGTAGCTACTTTTATGGCTCTCTCAGTCCCTTCCGGAAA
CCAAAGCTTTTGGGCTCCGGGGAGATATGGTTCCAAAGCTGAATCTTAAAGGAAT
TGACGGAAGGGCACCAACGAGGTGGAGCCTTGGGCTTAATTTGATCAACACGGG
GAACCTCACAGGTCACAGCTTCTGTAGATTTGACGATTTGGCGATGCTTCATGATT
AGAAGGGTGGTGGTGCATGGCCGTTCTTATGTTGTGACGTAAAGTTGTCTGCTTATT
GGGTAACGAGCGAGACCTCGGCCGCTAGTTGCCAGAACTCACACTTTGTGAGTCTT
TGCTCTTACGGGGACTACCGGAGACAAATTCGGGGAGGTTGAGGCAATAACAGGT
CTGTGATGCTACTAGATGCTCGGGCTGCACGCGCGCTACACTGACGAGCGACGGA
GTTAATCCTTGTCCGAAAGGAACGGGTAACTTTGTTAACTGCTCGTGAATGGGAT
AGAAGCTTTGAATTTTGTCTTGAACGAGGAATCTAGTAAGCTAAGTCATCAA
CTTGGTTGATTACGCTCCGCTGCTTTGTACACACGCGCGTCTACTACCGATTG
AATGGCTTATGAGGTCTTAGGAGGATTTTGCACGAGGCGACCTCTAGCGAGAAA
CCAAATTCGATCAAACTTGTGCTATTAGAGGAATACAAGTCGTAAACAAGTTTCCG
TAGGTGAACCTCGGGAGGATCATT
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ITS1of rRNA gene of FF:

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TCTGAAGGCTTTTTCGCAAAACCACTGTGAACAGCTTAGACTTCGGTCTTTGCAATT
GCTTGGGTGTGAAAGGCGCCACCTCTTAAACCTTTAATATTGTTCTGAAACAAAT
GAAATTTTAAACCTTTCACACAGGAGCTCTTGGTCTCGTATCGATGAAGAACGCA
GCAAGCGCATAGGTAAATGCAATTCGAGCGTGAATCATTAATTTTGAACGCA
TATTGCGCTATATGTTTGTCTTAATAGCATGCTTGTGGAATGATAAATCTTCCTCTCA
ACCATTTTGTATGAGGCTTGTCTCTTTAGGAGTAAAAATCATGGAAGTGACACA
CGTTAATTAACCTGTGCGATATACACTTTTATCTCTCCAAATCAAGCAAGGATACC
CCCTGAATCTAAGCATATTAAATAGCGGGGAAAGAACTAACA*
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gene structures resemble.(2) There are two kinds of dif fer ent domains in rDNA 18S region,one fair ly con stant (base 300-500) and others very variable among different species. (3) The ITS 1 regions are com posed of many DNA fragments with con ser vative sequences. Fig 5

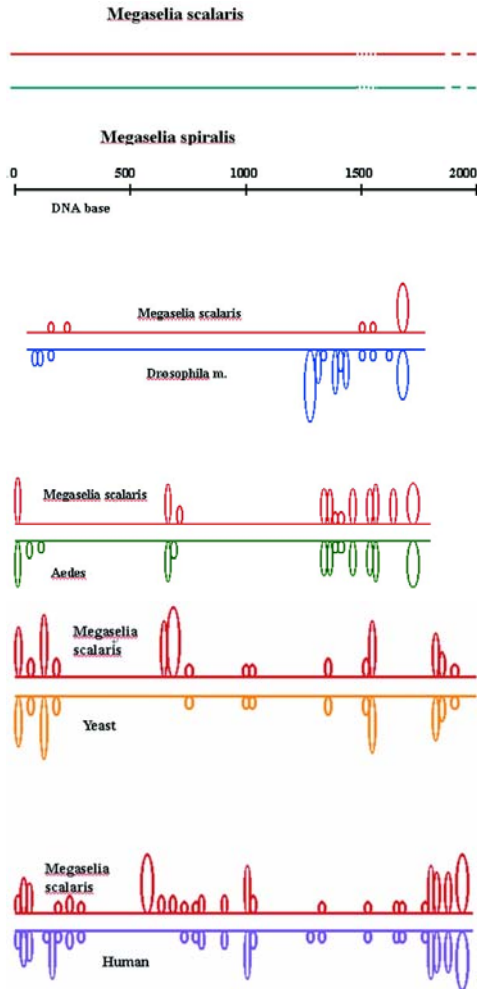
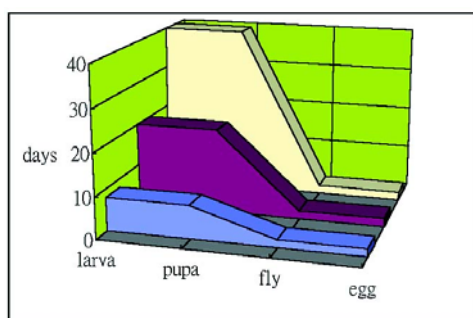


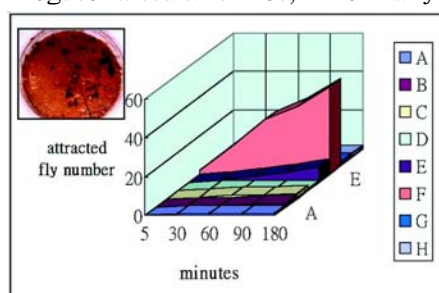
Figure 6 Comparison of Phoridae 18S rDNA gene structure with those of Drosophila, Human, and Yeast

Nontoxic Effects of Bacillus sk Under optimal growth condition, the life cycle of Megasela Scalris can be as short as 18 days. The time intervals in each stages are approximately 2 days for egg to hatch larva, 2 days for new flies to lay eggs, 7 days for pupa development and 7 days for larva growth. The presence of Bacillus sk promotes the rapid maturation and fast growth of Megaselia scalaris at each stages. Beef extract alone or the addition of antibiotic to kill the bacteria significantly slow down the fly growth and maturation. The changes were mainly due to the prolonged pupa and larva stages (7 days to 40 days, 7 days to 35 days). Figure 7 Effect of Bacillus SK on Phoridae Mat u ra tion In each group, 20 fly eggs were incubated with dif fer ent growth gel supplemented with one of the followings: Blue, bacillus sk; Red,beef extract; White: beef extract +ampicillin 0.2mM. Average lengths(Z axis) of each stages (X axis)



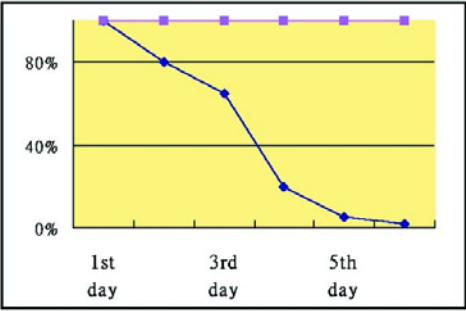
were measured.

Bacillus SK has a remarkable chemotaxis effect on *Megalotia scalaris* adult fly. *Streptococcus*, *Staphylococcus*, and different species of *Bacillus* *Escherichia coli*, *Klebsiella* were streaked on each Miller Hinton plate and evaluated their potency on attracting flies. Phenomenal difference was discovered with *Bacillus* SK as described in the following figure. Figure 8 *Bacillus* sk acts as a strong chemical attractant to *Megalotia scalaris*. A. *Streptococcus faecalis* B. *Staphylococcus aureus*, C. *Bacillus cereus*, D. *Bacillus thuringiensis*, kurstaki, E. *Bacillus subtilis* F. *Bacillus* sk G. *Escherichia coli* K12, H. *Klebsiella pneumoniae aerogenes* were streaked on each Miller Hinton plate and incubated to 80% saturation. The plate put in a 80 cubic cm plastic box containing 50 male and 50 female *Megalotia scalaris* flies were examined for their positive chemotaxis effect. The number of trapped flies was measured at different time points. III. Toxic Effects of *Bacillus* sk In laboratory, it is very common to identify that the contamination of fungi in growth medium will prohibit the growth and maturation of *Drosophila* fly larva. Interestingly, during the passages of *Megalotia scalaris* flies, little if any fungi contamination has been observed.



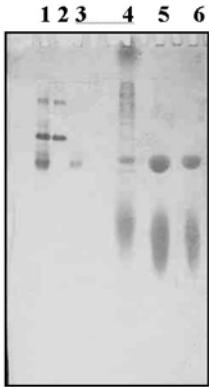
In my Electron microscopy study, very short fungi fragments were surrounded by a rod bacteria. Further studies reflect an unusually strong anti-fungal property with *Bacillus* sk. Tests were performed to study the antifungal spectrum and all the following included *Agaricus arvensis* CCRC 36371 *Aspergillus ochraceus* CCRC 300101 *Aspergillus fumigatus* CCRC 30099 *Aspergillus niger* ATCC 9642 *Aspergillus flavus* CCRC 30119 *Aspergillus vesicolor* CCRC 30225 *Aspergillus candidus* CCRC31129 *Aspergillus terreus* CCRC 32664 (terrium production) *Aspergillus terreus* CCRC32653 *Saccharmyces cerevisiae* *Zygosacchomyces rouxii* were prohibited by this specific *Bacillus* sk. Figure 9 Antifungal effects of *Bacillus* sk A horizontal streak of *Bacillus* sk was applied on a Miller Hinton II plate. A second vertical streak of fungus (include *Agaricus*, *Aspergillus*, *Saccharmyces* and *Zygosacchomyces*) was applied at right angle

across the first Bacillus streak). An ti fun gal Result of Ba cil lus sk was identified as a miss ing upper part of cross + symbol.



Figure

10 Worm killing effect of Bacillus sk on Bactocera dorsalis larva Bactocera larvae were breed in guajava (Psidium guajava) jelly with (blue dots) or without (pink dots) Bacillus sk bacteria at OD 0.3.The sur viv al per cent age was measured at different time points. (X axis : % of survived Bactocera dorsalis larva , Y axis: days after the addition of Bacillus sk). Figure 11 10% PAGE of Bacillus sk and Bacillus subtilis secreted proteins A toxin with antifungi property was purified by salt precipitation and acetone extraction as described in Materials and Methods in this paper(Chinese Edition). 10% PAGE demonstrates the location of this purified toxin. Well 1:Bacillus sk secreted



proteins, well 2: *Bacillus subtilis* secreted Proteins, well 3: Acetone washed *Bacillus sk* protein profile well 4: Salt precipitation of total *Bacillus sk* secreted Proteins well 5: Acetone washed 4. Ppt. 6. As 5. Figure 12 Worm killing effect of purified *Bacillus sk* toxin on larva of *Bactocera dorsalis* Larva of *Bactocera dorsalis* was lightly pressed on a glass plate with a transparent tape and vessel pulsation can be clearly observed through a reverse phase contrast microscopy. Purified toxin (100ug/ml) was injected into the tail portion of the worm body. IV. What's *Bacillus sk*? *Bacillus sk* is classified as a morphology I, Gram-positive endospore containing rod bacteria. Its colony on sheep RBC plate gives a beta-hemolytic picture. *Bacillus sk* like *Bacillus subtilis* on many enzymatic activities : glucose fermentation positive and mannitol fermentation positive. There are many similar PCR bands between *Bacillus sk* and *Bacillus subtilis* (Fig.); however there are also some distinguished band found in one bacillus but not the other. Study about 16S rDNA of these two reflect two 99% identical sequences (Fig.).

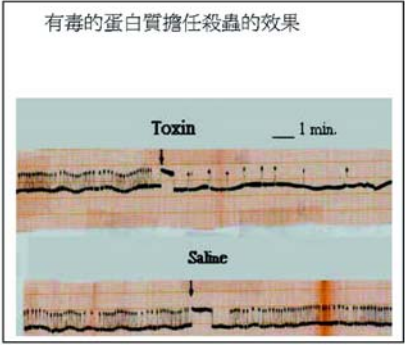
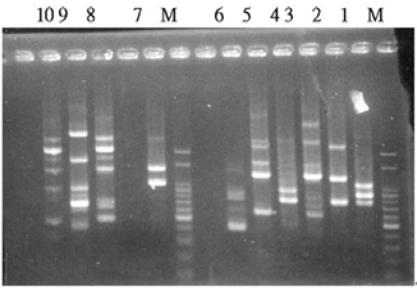


Figure 13 RAPD of Various *Bacillus* spp. Experiment was performed as described in procedures. M: DNA marker, 100bp DNA ladder 1. *Bacillus.licheniformis* 2. *Bacillus.thuringiensis* sp.israelensi 3. *Bacillus subtilis* 4. *Bacillus thuringiensis* subsp.kurstaki 5 *Bacillus SK* 6. *Bacillus popill* 7. *Bacillus larvae* 8 *Bacillus* spp. (isolated from *Drosophila* gut) 9. *Bacillus* spp. unspecified 10. *Bacillus popillae* Figure 14,15 RAPD comparison of three *Bacillus* spp. Different PCR probes were used to elucidate the differences between *Bacillus* spp. B.s.: *Bacillus subtilis*; B.sk:



Bacillus sk B.t. : *Bacillus thuringiensis* M: molecular marker

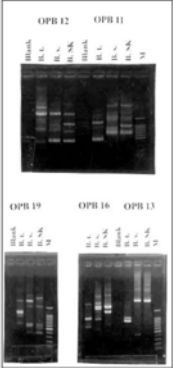
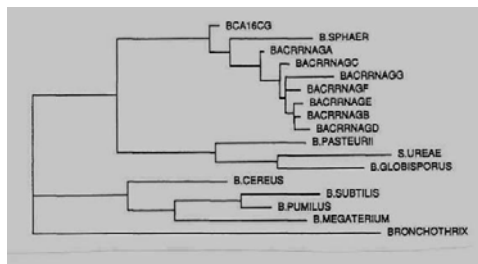


Figure 16, 17 Identical ribosome DNA sequences were found in *Bacillus subtilis* and *Bacillus sk*. The evolution of phoridae makes *Megaselia* *Bacillus sk*:upper; *Bacillus subtilis*:lower. A

[illegible]

5. Conclusions

1. *Megaselia scalaris* appears to be the most abundant fly species in Taiwan cities. 2. An artificial breeding method is established by adding digested beef extract into starch/yeast

Phylogenetic tree showing the relationship between SF1 and FF1. The tree indicates that SF1 and FF1 are sister taxa, with SF1 being the outgroup to FF1. The tree is rooted at the bottom left, with branches leading to SF1 and FF1. The labels 'Drosophila1', 'Aedes1', 'Saccharomyces1', and 'Homo' are listed below the branches, indicating the species used for each sequence.

Poinar, H., Poinar, G.O., Jr and Cano, R.J. *Nature*, 363, 677, 1993.

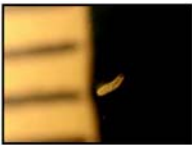


Coin:2.5cm ,House fly: 0.7cm

Size Comparison



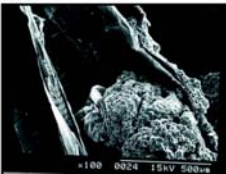
Megaelia scalaris: adult fly



egg,larva(just hatched):0.4mm
larva (longest before metamorphosis)
8mm



wing length:1.8-2.0mm



M.scalaris cell size: 8-15 μm