總校長咖啡早會

暑假最新消息
弘立的未來一年

查永茂博士 – 總校長

2022年9月7日

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暑假活動

我寫給讀者的話：

我是來自弘立書院的潘柏熹，很高興你打開了這本由我拍攝、創作的攝影集。我覺得拍照是一件神奇的事情，因為


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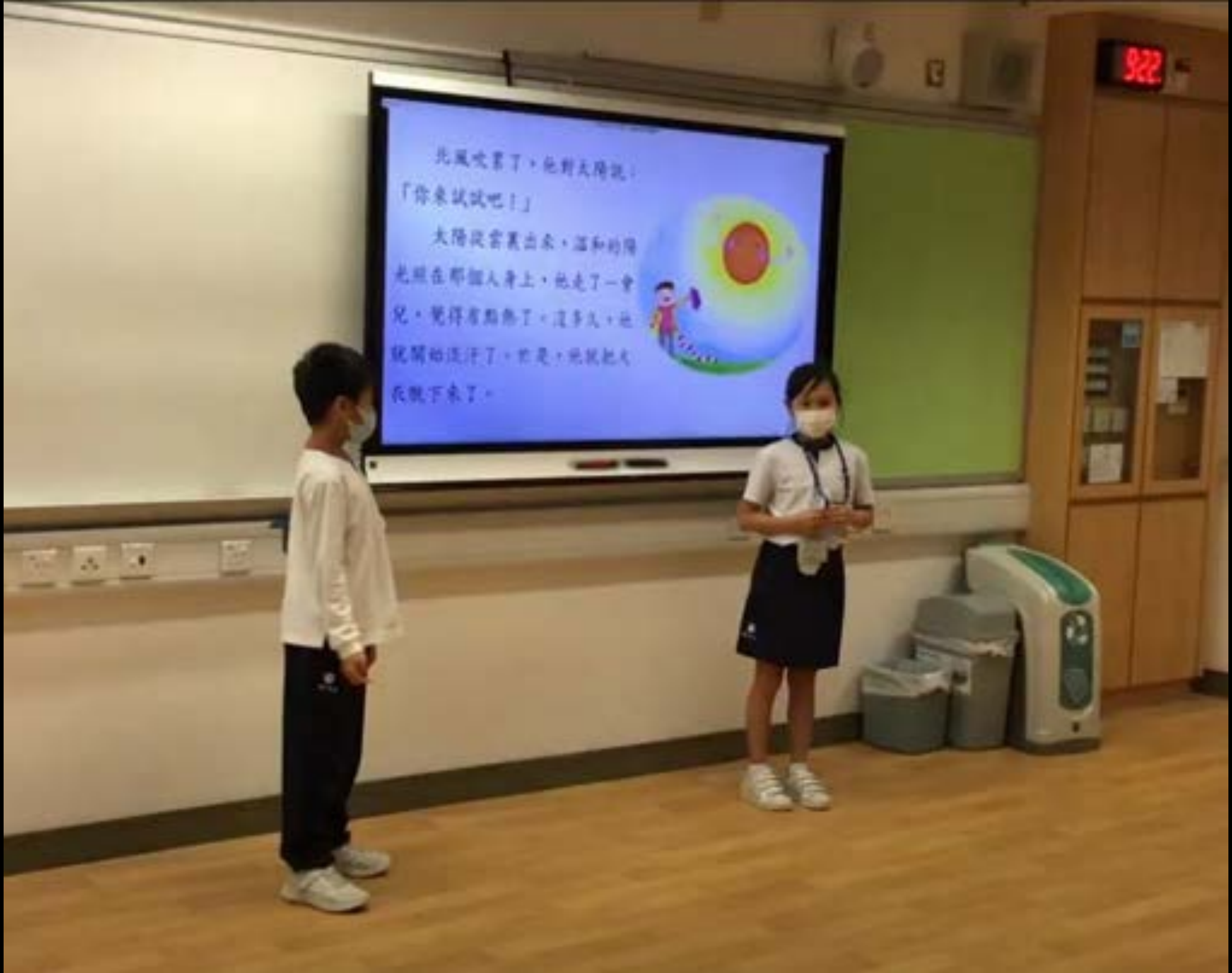

北風吹累了，他對太陽說：「你來試試吧！」

太陽從雲裏出來，溫和的陽光照在那個人身上，他走了一會兒，覺得有點熱了，沒多久，他就開始流汗了，於是，他就把大衣脫下來了。


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體驗學習課程，李約瑟研究所，戶外探索學會和美國微生物學會

#2496
Track: AES05
ASM Microbe
June 2022

Kluyvera sp. CRP a Cellulolytic Isolate from Red Panda Faeces (*Ailurus fulgens*)

Angus C.H. Wai, G. K. K. Lai, S. D. J. Griffin*, F. C. C. Leung
The ISF Academy, Hong Kong *Corresponding author: sgriffin@isf.edu.hk

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Greener biofuels

Biofuels generated from food sources may be 'carbon neutral' but they also have negative consequences for economies and the environment. In contrast, second-generation biofuels from lignocellulosic biomass, such as industrial, agricultural and municipal waste, are more sustainable but require pre-treatment in order to release fermentable sugars.

Biological pre-treatment with isolated enzymes or whole cells is cheap and energy-efficient, so that this project has looked for strongly cellulolytic bacteria in faeces of the Chinese red panda (*Ailurus fulgens*). This species uses bamboo as its major food source, and previous characterisation of its gut microbiota suggests extensive cellulose-degrading pathways [1].

Method:

Red Panda faeces were collected from Ocean Park Hong Kong. 1 g fresh faeces was serial-diluted in 0.9% saline to 0.1% w:v and a 100 µL aliquot spread onto carboxymethylcellulose (CMC) agar and incubated at 27 °C for 48 hours. Isolate CRP grew well on CMC agar and was passaged to purity on Luria agar before DNA extraction (Invitrogen PureLink® Genomic DNA Mini Kit). Cellulolytic activity was checked by incubation on CMC agar followed by staining with Gram's iodine. The complete genome of CRP was generated by hybrid assembly of MiSeq (Illumina) short-reads and MinION long-reads (Oxford Nanopore) using Unicycler v0.4.3 [2]. The sequence was submitted to PATRIC [4] and to NCBI PGAP v5.0 [3] for annotation. GenBank accession no. CP082841.

The complete genomic sequence of CRP totals 5.16 Mbp and Mash/MinHash using PATRIC found it closest to *Kluyvera* genomosp. 3 strain PO2S7 (CP050321) with an average nucleotide identity of 98.83%.

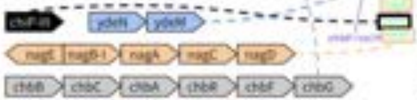
Cellulolytic pathways are strongly represented with four copies of beta-glucosidase, 10 copies of 6-phospho-beta-glucosidase (chbF/celF), together with multiple copies of cellobiose phosphotransferase and the bcs operon.

to save space, only the start and ends of a sequence of proteins are labelled, full sequence can be seen in the colour-coded pathway diagrams

CRP shows resistance to ampicillin consistent with the presence of a CTX-M-40 beta-lactamase.

Disk diffusion assay of CRP on ampicillin

Chitin and GlcNAc Utilization Pathway



Segments of the chitin and GlcNAc utilization pathway

A complete chitin and GlcNAc utilization pathway [5], including a chb operon, was identified around the genome. Compared to the pathway in [5], ydeN and ydeM are in opposite strands in the genome.

Locations of the start and end of each segment of the pathway are squared with respective color.

Cellulose Degradation Pathway

Cellulose degradation pathway as identified in CRP

A complete cellulose degradation pathway was identified in CRP. A cellulase (bcsZ) in CRP sequence is nested within the bcs operon. Four copies of beta-glucosidase in CRP are spread around the genome and each have completely different sequences with no conserved regions. This suggests the four copies might come from different origins.

All four beta-glucosidase in CRP modeled by Phyre2 [7]

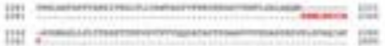
Cellulose Biosynthesis operon

bcs operon

CRP on a CMC plate

A 9 enzyme long bcs operon [6] is present in the sequence. The presence of the *bcs* operon in CRP is consistent with activity shown on CMC agar plates.

Sequence alignment of the *bcs* operon present in genomosp. 3 strain PO2S7 showed a 99% identity (4534/4560 aligned) between the two.



Sequence alignment of CRP and genomosp. 3 strain PO2S7 between bcsA and bcsB by NCBI BLAST [8]

The most significant discrepancy is a gap of 10 acids at the start of *bcsB* in CRP, compared to genomosp. 3 strain PO2S7.

Protein structure modeled by Phyre2 [7] shows no significant difference in structure between the two proteins.

Conclusion:

Kluyvera sp. CRP shows strong activity with chitin and cellulose. Genomic analysis shows prominent chitin and cellulolytic pathways. These could give CRP an advantage in breaking down lignocellulosic waste.

References and supplementary info can be found at: bit.ly/3z24HBI

This work was funded under the ISF Shuyuan research program.

Abstract ID:
BG04-A002
Session: **D3-AM1**
AOGS Aug 2022

Isolation and Characterisation of Plant Growth Promoting Bacteria from Aerial Roots of Hong Kong Plants

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ISF 弘立

Introduction

Similar to many other regions of Southeast Asia, rainfall in Hong Kong surpasses 2200 millimetres per year [1]. In addition, local granite-derived soils are poorly retentive of nutrients, creating oligotrophic conditions with soil total nitrogen concentrations <0.04% in topsoil and negligible concentrations below [2]. Despite such challenges, numerous non-leguminous (and often lithophytic) plants such as *Ficus microcarpa* and *Glochidion hongkongense* are not only abundant but also grow to great size. These high levels of carbon sequestration suggest correspondingly large rates of nitrogen uptake that must depend largely upon microbial nitrogen-fixation.

Method

Aerial root tips ~20 mm in length were collected from common plant species in Hong Kong such as *Ficus microcarpa*. These samples were incubated in nitrogen-free (NF) broth medium for 7 days at 32°C after surface sterilisation using 1% (w/w) 8-hydroxyquinoline sulphate. The incubation was repeated with new NF broth. Next, the top layer was picked and passaged to purity on NF MT10 media to identify potentially nitrogen-fixing bacteria. Complete genomes of *Klebsiella variicola* 9ba2 (from *Philodendron erubescens*), *Gluconobacter thailandicus* ISBL3 (from *Syngonium podophyllum*), as well as *Kosakonia radicincitans* JS2a2 (from *Ficus microcarpa*) were generated by hybrid assembly, using both Illumina MiSeq and Oxford Nanopore MinION platforms. Genomic analyses were performed using NCBI BLAST [3], TYGS [4], PATRIC [5], Uniprot [6] and Clustal Omega [7].

Fig. 1 Roadside *Ficus microcarpa*, source of sample *Kosakonia radicincitans* JS2a 2

Results

Experimental results found that all three samples grow rapidly on NF medium, producing clear, mucoid colonies, and Gram staining revealed that all samples were Gram-negative. Genomic analysis found numerous genes suggesting endophytism, presented in Table 1. How an endophyte may use these genes is presented in the schematic below (Fig. 2) .

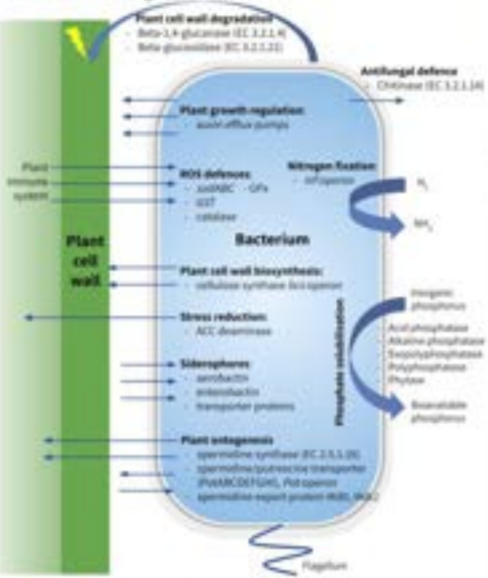

Fig. 2 Schematic of endophytism-associated genes found [10-14]

Genes that allow for both anabolic and catabolic modifications are particularly signifying for endophytism as it suggests host intracellular environment modification capabilities. Nitrogen fixing and phosphate solubilising capabilities in endophytes are also significant given that nitrogen and phosphorus are key limiting nutrients for plant growth [15]. These genes were highly conserved across genera.

Sample ID	9ba2	JS2a2	ISBL3
Taxonomy	*Klebsiella variicola*	*Kosakonia Radicincitans*	*Gluconobacter thailandicus*
Genome size (Mbp)	5.68	~5.26	3.31
G+C Content (%)	57.29	54.55	56.30
Source (aerial roots)	*Philodendron erubescens*	*Ficus microcarpa*	*Syngonium podophyllum*
Plant ontogenesis genes	Pot operon, auxin efflux pumps, spermidine export protein	Pot operon, auxin efflux pumps, spermidine export protein	Pot operon, auxin efflux pumps, ACC deaminase
Cell wall modification genes	*bcs* operon, 2 beta-1,4-glucanases	*bcs* operon, 3 beta-1,4-glucanases	2
Siderophore genes	10	16	2
nif/*pho* operon	☑/☑	☑/☑	☒/☑

Table. 1 High counts of plant growth promoting genes suggest endophytism

Discussion

This study has identified three likely endophytes, possessing genes such as the *nif* operon for nitrogen-fixation, *pho* operon for phosphate solubilisation and polyamine transporters for plant ontogenesis.

The presence of nitrogen-fixing microbes on dominant non-leguminous plant species in Hong Kong, such as *Ficus microcarpa*, may suggest an abundance of growth-promoting endophytes in this region.

Used *in situ* for crop species, such nitrogen-fixing microbes may present a sustainable method for plant growth promotion to reduce dependence on inorganic fertilisers. However, because endophytes are highly adapted to the internal environments of their hosts, the next step in our project will be to investigate pairings of growth-promoting bacteria with potential hosts. Are specific host-related bacterial genes essential for success?

Acknowledgements
This work is funded under the *ISF Shuyuan Research Programme*.

References and Supplementary Materials
can be found at https://tinyurl.com/MLAMAOGS22

#2551
Track: AES06
ASM Microbe
June 2022

Identification of Two *Pseudomonads* with the Potential for Polyester Microfibre Bioremediation

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Introduction

Polyethylene terephthalate (PET) is a sophisticated and stiff plastic with a stable aromatic ring (Fig. 1). With its high tensile strength, PET is now the main ingredient for 60% of plastic for plastic bottles [1] and spun into fabric for polyester-based clothing worldwide, constituting to 42 million tons of microplastic waste per year [2]. In this investigation, aromatic substrates (toluene, sodium benzoate, benzyl benzoate and a suspension of PET microfibres in hexafluoro-2-propanol) were used as carbon sources to screen for polyester-degrading microbes.

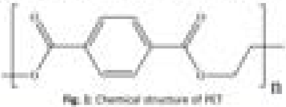

Fig. 1: Chemical structure of PET

Methods

Samples of PET fabric were buried in soil for three months (Fig. 2). After recovery, the fabric was rinsed with 0.9% w:v saline and an aliquot of each extract incubated in minimal medium (at 27 °C with shaking) with 10% v:v toluene as the sole carbon source (Fig. 3). After 7-10 days, viable bacteria (determined by streaking on Luria agar) were transferred to a minimal medium containing 5% w:v sodium benzoate (Fig. 4). Isolates with greatest turbidity were streaked to purity on Luria agar. PET-degrading activity was tested by growth on agar made with Zhang's medium [3] to which a thin layer of PET fibres dissolved in hexafluoro-2-propanol had been applied (Fig. 5). DNA was extracted from two selected isolates using a DNeasy PowerSoil Kit (Qiagen) [4] and sequenced via both Illumina MiSeq [5] and Oxford Nanopore MinIon platforms [6] to generate complete genomes by hybrid assembly (Unicycler v0.4.3) [7]. PATRIC [8], NCBI BLAST [9], Phyre2 [10] and Clustal Omega [11] were used for comparative genomic analysis.


Fig. 2: Burial site of polyester


Fig. 3: Turbid toluene solution


Fig. 4: Turbid Sodium Benzoate solution

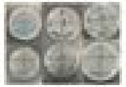
Fig. 5: Samples on Zhang's medium plate

Two *Pseudomonads* show potential for PET degradation

Sample ID	LS_1a	LS_2c
Estimated genome size	5.75 Mbp	6.35 Mbp
% G+C	63.08%	66.46%
Source	soil/leaf litter	soil/leaf litter
GenBank accession	*Pseudomonas* sp. LS.1a CP092827	*Pseudomonas aeruginosa* LS.2c CP092634
Closest genome Source ANI	- *Pseudomonas* sp. 43(2021) - *Oryza sativa* ssp. *japonica* rhizosphere (Italy) ANI 99.41	- *Pseudomonas aeruginosa* AZPAE15026 - clinical UTI (Colombia) ANI 99.99
Key genes for aromatic degradation	- Toluene tolerance proteins - Xylene and sodium benzoate degradation pathway - benzoate transport proteins - benABC operon - dmpK-P operon - Five copies of catechol-1,2-dioxygenase	- Toluene tolerance proteins - Xylene and sodium benzoate degradation pathway - Benzoate transport proteins - benABC operon

Table 1: Details of isolates LS_1a and LS_2c

Similarities with arysterlase

Both isolates possess an arylesterase similar to the PET-degrading enzyme reported by Haernvall *et al.* with the potential to degrade PET through enzymatic hydrolysis [12]. Protein structures found by Phyre2 (Fig. 6, 7, 8) showed similarities in the tertiary structure of enzymes, showing a potential relationship between arysterlase and both isolates.

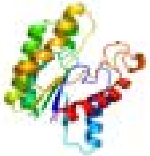
Fig. 6: Sample LS_1a arylesterase structure


Fig. 7: Sample LS_2c arylesterase structure

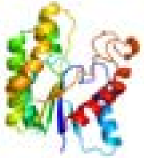
Fig. 8: Arylesterase structure from *Pseudomonas* [illegible]

Comparing LS_1a with *Ideonella sakaiensis* ISF6_4831

Enzymes of the well-known PET-degrading pathway of *Ideonella sakaiensis* ISF6_4831, reported by Yoshida *et al.* [13], share some homology with proteins in LS_1a:

ISF6_4831	LS_1a
PETase (Serine hydrolase)	Dienelactone hydrolase (Cysteine hydrolase)
MHETase	Arylesterase
Teraphthalate dioxygenase	Benzoate 3,4 dioxygenase
Teraphthalate transporter	Benzoate transporter

Fig. 9. Enzymes in LS_1a share some homology with those of the PET-degradation pathway of *Ideonella sakaiensis* (Yoshida et al., 2016)

Although LS_1a can make use of PET to survive, its rate of PET degradation is very slow. Similarities in the enzymes (Fig. 9) of LS_1a and ISF6_4831, however, support the idea that a range of microbes might be actively evolving to make use of the increasingly abundant sources of environmental PET [14].


Fig. 10: Alignment of LS_1a PETase with the ISF6_4831 PETase through Clustal Omega. GWSMG of ISF6_4831 and GICSG of LS_1a are amino acids serine and cysteine respectively

Further investigations of LS_1a

It is significant that LS_1a seems to be more effective than the other isolates in functional tests. Therefore, the next step in investigating the potential of PET degradation in LS_1a is to clone the relevant genes into *E. coli* to verify their activities. Additionally, a later step would be to look further at mutations (particularly within the LS_1a cysteine hydrolase) to see if PET-degrading activities can be enhanced.

Acknowledgements:
This work is funded under the *ISF Shuyuan Research Program.*

Scan QR code for **references** and **supplementary data**:

AES983
 # 2532
ASM Microbe
June 2022

Isolation and characterisation of copper-resistant microbes from a disused mine in Hong Kong

K. M. Leung*, G. R. Wyatt, G. K. K. Lai, S. D. J. Griffin, F. C. C. Leung

The ISF Academy, Hong Kong *Corresponding author: kmleung@isf.edu.hk

Two isolates from sediment samples recovered from a disused tungsten mine in Hong Kong showed remarkable levels of copper tolerance and Cu(II) reduction. *Serratia ureilytica* E1, in particular, shows levels of growth in 80 mM Cu^{2+} only 20% less than control.

Methods

16 sediment samples were collected at different locations in and around the Needle Hill mine (22.387089°N 114.160486°E). Their metal content were determined by ICP-OES. 10 colonies from each plate were screened with 0.5 M $CuSO_4$, 0.5 M $Pb(NO_3)_2$ and 0.1 M $AgNO_3$ by disc diffusion. Isolates demonstrating the greatest metal resistance were passaged to purity before DNA extraction (Qiagen DNeasy PowerSoil Pro Kit) followed by sequencing via the Illumina Miseq platform. Comprehensive Genome Analysis by PATRIC 3.6.12 [1] was used to assemble and analyse the data. Identified metal tolerance genes and proteins were investigated using UniProt [2], NCBI BLAST [3] and Clustal Omega [4]. Phylogenetic trees were generated with AutoMLST [5] and PATRIC [1]. Isolates were exposed to 10 mM to 100 mM of $CuSO_4$ and Cu(II) tartrate to study the level of resistance the genes and pathways provided on both Luria agar and Luria broth.

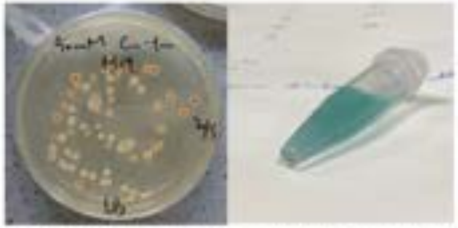

Fig. 1 M14 and E1 reducing copper on agar plate and in Luria broth by M14 (left) and E1 (right) respectively.

Results

Isolates E1 and M14 showed the highest level of tolerance to Cu^{2+}, Ag^+ and Pb^{2+} in culture. They were revealed by BLAST to be strains of *Serratia ureilytica* (E1) and *Pseudomonas putida* (M14), with approx. genome sizes of 5 Mbp and 5.9 Mbp respectively.

Results from NCBI BLAST revealed extensive copper homeostasis genes and pathways. Both isolates contain Cop, Cpx, Cus and the Cut pathways, but E1 carries an extra Scs (suppressor for copper sensitivity) pathway. Both isolates carry cupric reductase genes.

Fig.2 Phylogenetic tree of the *S. ureilytica* E1 (blue box) and *P. putida* M14 (red box).

E1 and M14 were able to grow on agar infused with up to 90 mM $CuSO_4$ and Cu(II) tartrate. Cu(II) tartrate was more easily tolerated, with E1 and M14 producing 80% and 36% of their control-level growth in the presence of an 80 mM infusion. A red-brown precipitate – indicating Cu^{2+} reduction – was given when E1 was incubated in Luria broth containing up to 100 mM Cu(II) tartrate.

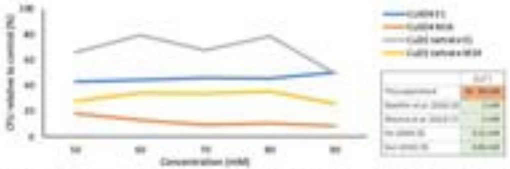

Fig. 3 Percentage difference of in number of colonies of E1 and M14 after exposure to $CuSO_4$ or Cu(II) tartrate on Luria agar plates. The survival rate of the lines were reduced after exposed to Cu^{2+} ions. The table showed the concentration used in other exposure experiments.

Fig.4. Predicted structure of cupric reductase in E1 (left) and M14 (right).

Conclusion

Serratia ureilytica strain E1 and *Pseudomonas putida* strain M14 appear able to survive under heavy copper stress, with E1 showed a higher level of copper tolerance under the same conditions. While this may be consistent with the additional Scs pathway carried by E1, the strong reductive activity is also significant.

The ability to tolerate high concentrations of Cu^{2+} and to reduce the ions to metallic may suggest a role for E1 in copper bio-remediation and bio-mining and this will be the focus of our ongoing work with these isolates. Further studies will also try to further elucidate the major mechanisms operated by E1 in order to understand its notably greater level of tolerance.

References and supplementary materials
can be found at shorturl.at/muzX6

Acknowledgements

This work is funded under the *ISF Shuyuan Research Program.*

學術簡報2021-2022

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- 取得30分或以上之學生比率：100%（全球：66%）
- 取得40分或以上之學生比率：73%（全球：14%）
- 取得43分或以上之學生比率：35%（全球：5%）
- 科目平均分數：6.4分 （總分為7分）
- 核心項目平均分數：2.6分

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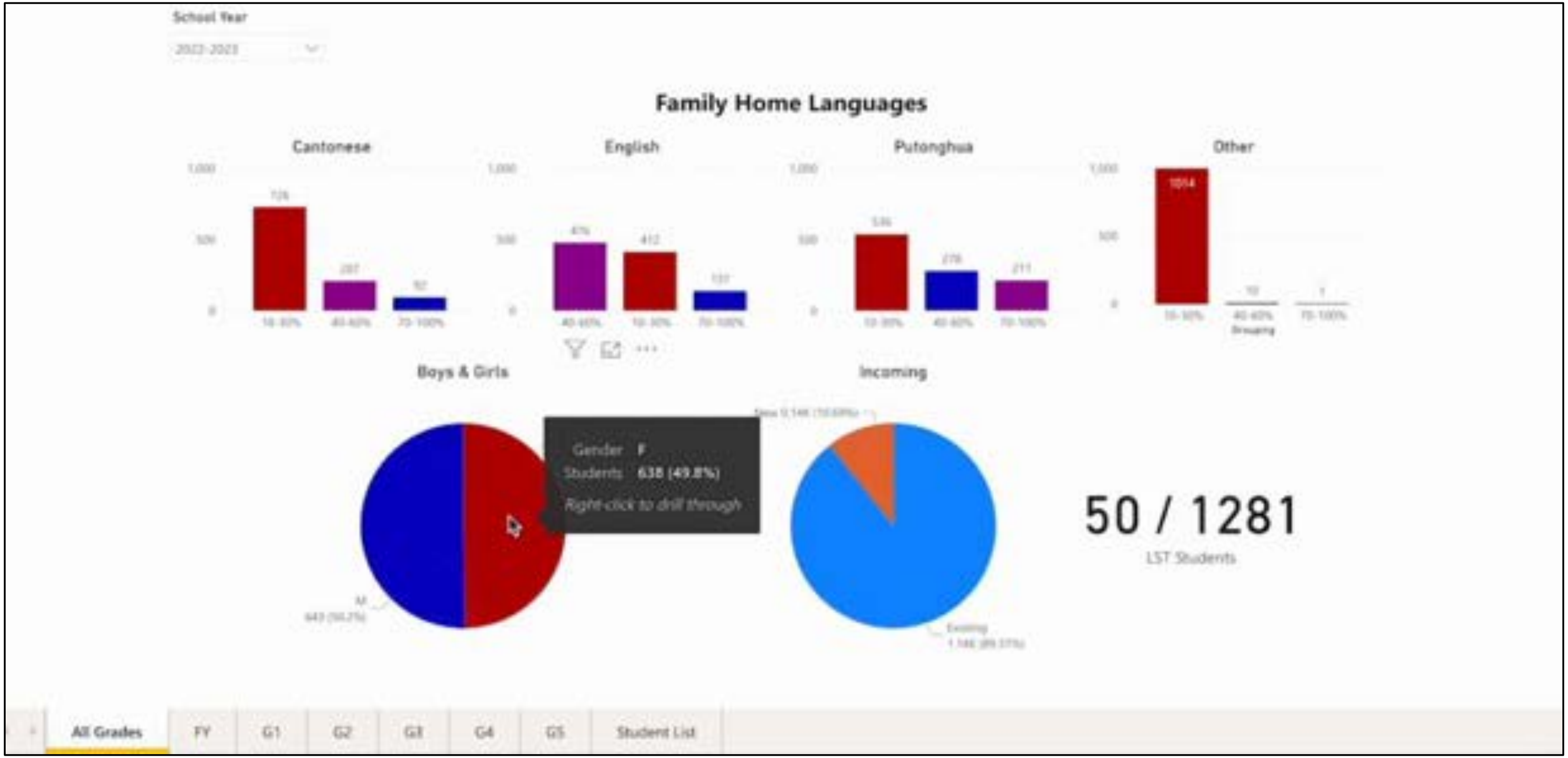
學習分析系統目標

運用為學生、在學生身上和由學生生成和收集的大量數據和信息，深入了解學生的成長、發展和個人需求，並以此為行動提供基礎。

此工具正處於開發階段，將參考持份者的意見，用於支持我校的發展。

實時互動工具

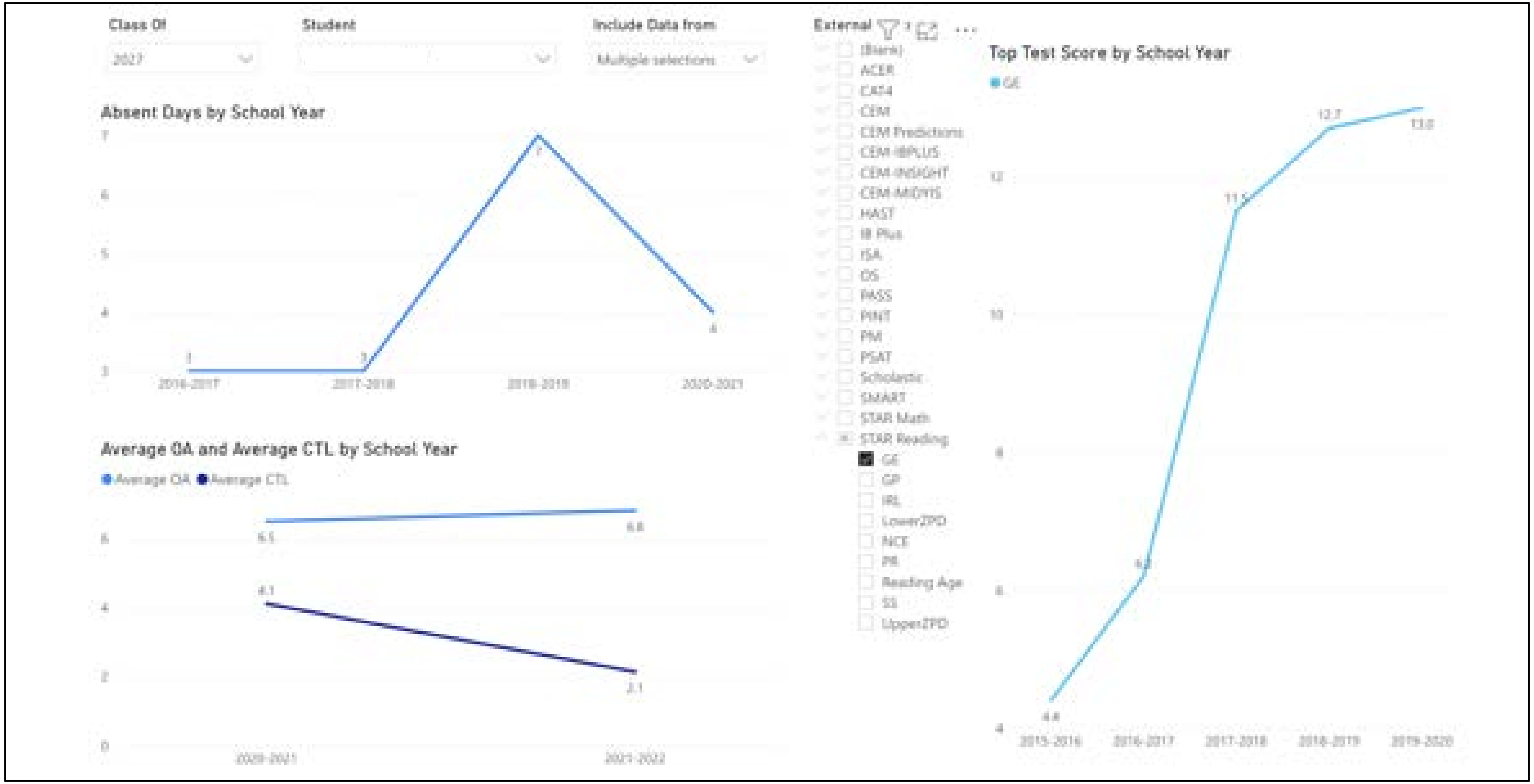


School Year: 2022-2023

Gender F
Students 638 (49.8%)
Right-click to drill through

50 / 1281
LST Students

個別學生資訊

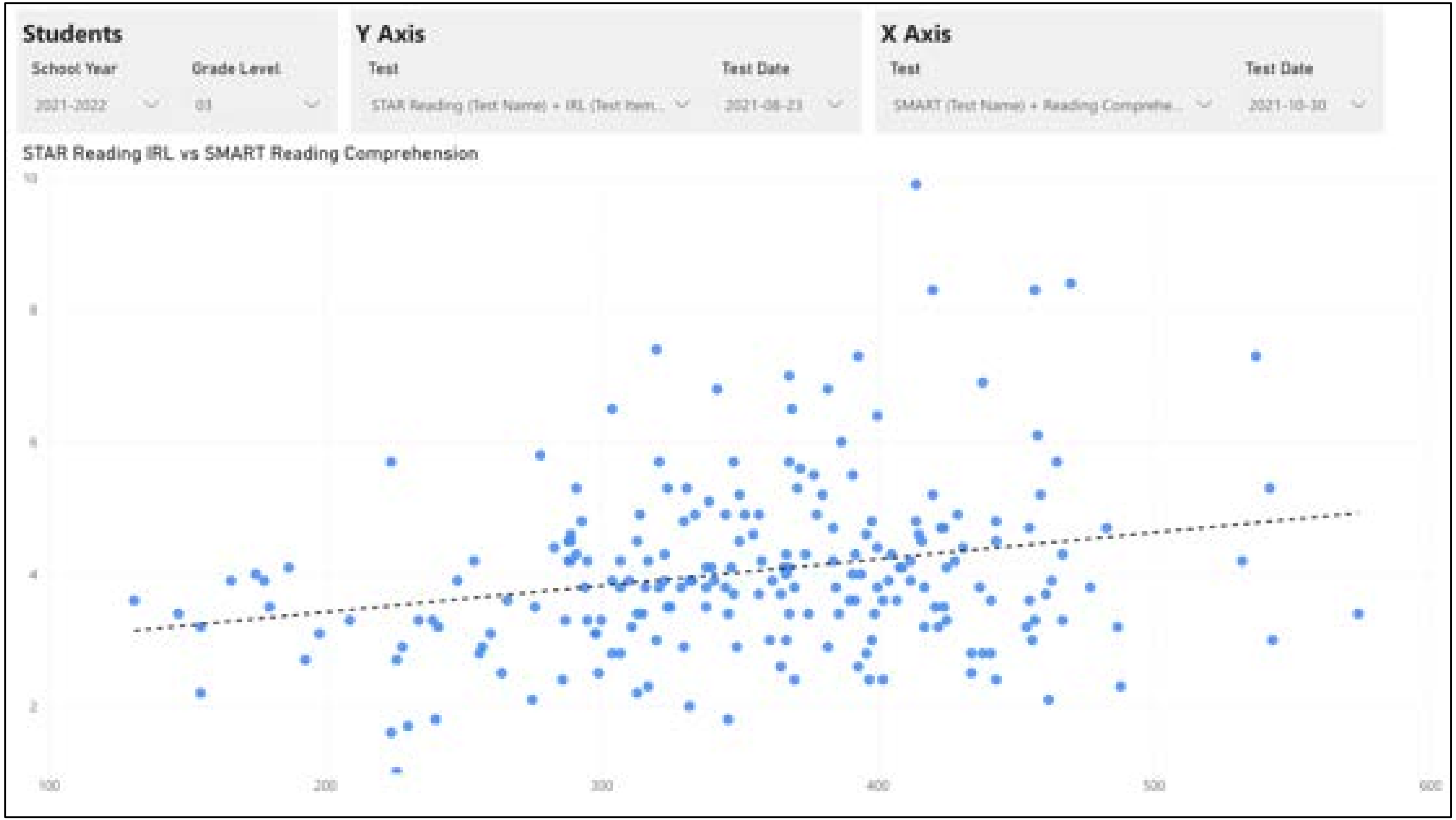


Class Of: 2027

Student:

Include Data from: Multiple selections

外部數據



Students

School Year: 2021-2022

Grade Level: 03

Y Axis

Test: STAR Reading (Test Name) + IRL (Test Item...

Test Date: 2021-08-23

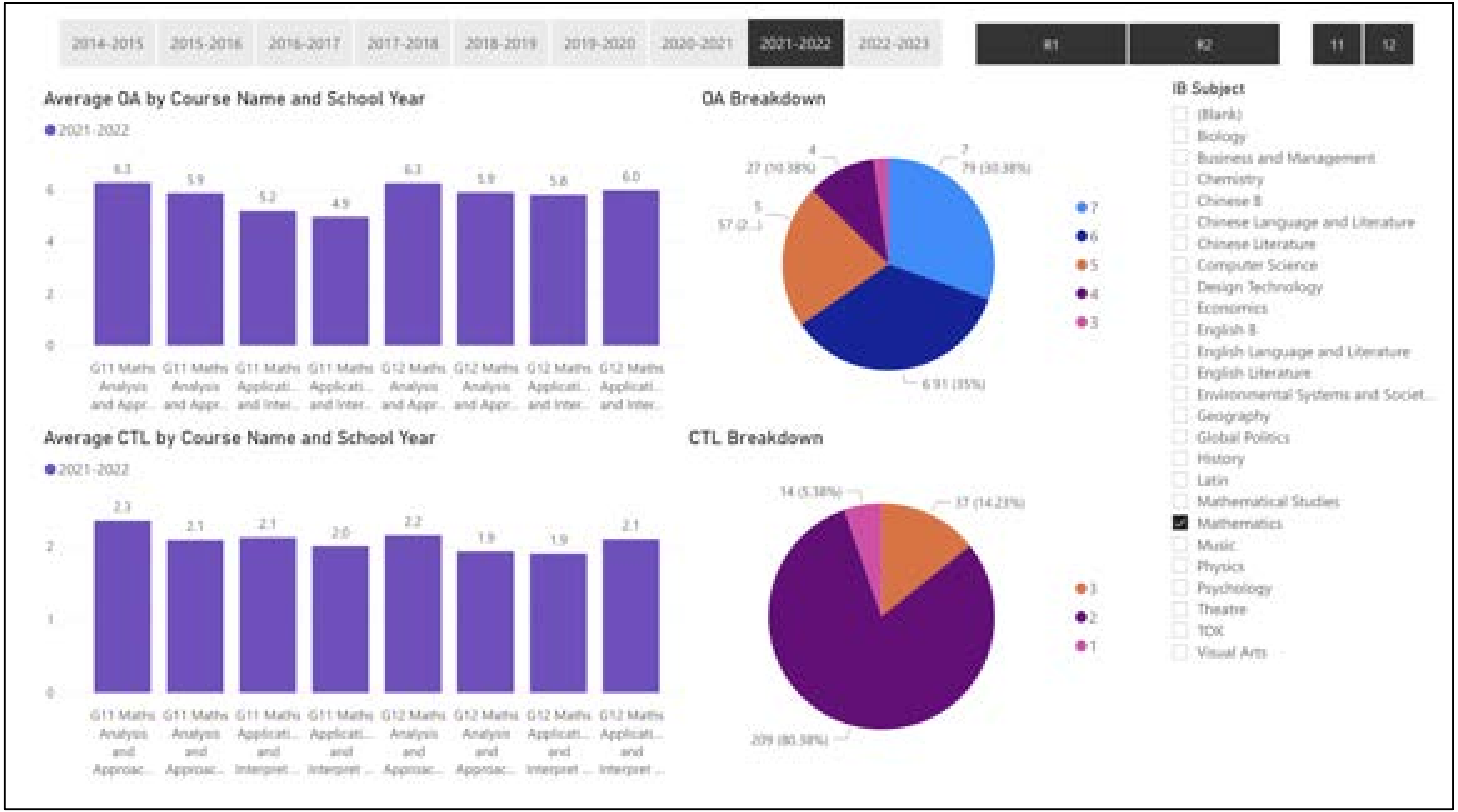
X Axis

Test: SMART (Test Name) + Reading Comprehe...

Test Date: 2021-10-30

STAR Reading IRL vs SMART Reading Comprehension

學科領域及年級信息



IB Subject
- ☐ (Blank)
- ☐ Biology
- ☐ Business and Management
- ☐ Chemistry
- ☐ Chinese B
- ☐ Chinese Language and Literature
- ☐ Chinese Literature
- ☐ Computer Science
- ☐ Design Technology
- ☐ Economics
- ☐ English B
- ☐ English Language and Literature
- ☐ English Literature
- ☐ Environmental Systems and Societ...
- ☐ Geography
- ☐ Global Politics
- ☐ History
- ☐ Latin
- ☐ Mathematical Studies
- ☑ Mathematics
- ☐ Music
- ☐ Physics
- ☐ Psychology
- ☐ Theatre
- ☐ TOK
- ☐ Visual Arts

Applied Life Skills
應用生活技能

Creative Arts
創意藝術

Nurturing Health and Resilience
培育健康與抗逆能力

Empowering Global Stewardship
有能力成為地球護育者

Exploring History, Language and Culture
歷史、語言及文化探索

Science, Technology, Engineering and Mathematics (STEM)
数理科工 (STEM)

2022-23年「好學」課程

金庸作品及影視劇賞析
Playwriting - ScriptLab
Making Theatre
Ceramics
華語歌曲歌詞賞析課程
中國藝術與文化
Fashion
Vocal
Piano
Chinese crosstalk 相聲趣多多
From Pen to Print: Creative Writing Workshop for Beginners
思辨萬花筒
Physical Geography & Environmental Management
Film and Literature
Introduction to Spanish
Pop Lit:
Competitive swimming
Squash
Digital Design Pro
Global Politics
Film vs. Novel: What Makes Them Different?
The Beauty of Mathematics
Experimental Portrait Painting
中醫小學堂 Chinese Medicine
普通話播音主持 Putonghua Broadcast Hosting

Marketing and Advertising
Digital Art and Design
Film & Filmmaking
日劇教我們的事
Makerspace
Digital Art and Graphic Design
An Introduction on Guangdong Mahjong
Global Challenges
Exploration of Environmental Science Topics
Home Science
Metallic Jewelry Masterclass
Our Universe: Science, History, and the Way Forward
Enriching Hearts and Minds
The Art of Graphic Novels
Underwater Robotics
中國女紅傳承
Service Learning
Jazz / Popular Music / improvisation Workshop
Wind Ensemble
One Act Play Production.
戲劇人生
Glass enameling
Write perform a pantomime
Project Journeys
Hands-on Photography!
iLEAD / AYP Silver Expedition Course
Living Seas

故事新編：基於經典的創意寫作
中華文化學會（高級）：宋元明清的藝術、生活與科技
中華文化學會（中級）：魏晉隋唐的藝術、生活與科技
中華文化學會（初級）：先秦兩漢的藝術、生活與科技
閱讀與藝術創作（和諧粉彩）
Reading and artistic creation(Pastel Nagomi Art)
The House Science
Chinese Fashion of Life 中式生活時尚
Basketball; Netball; Squash; Swimming
Aesthetics and Design in Film
Sports Leaders
思辨萬花筒
Marketing Ideas
Movie and Literature電影與文學
Theatre
Global issues: discussing the world around me
Makerspace HX
Theatrical Stagecraft
Athens vs. Sparta
Science Fiction Publishing and Editorial
Ancient Greek Mythology
Student-athlete; Netball
Student-athlete; Basketball
String ensemble
Starting a Business (Group 1)
Starting a business (Group 2)

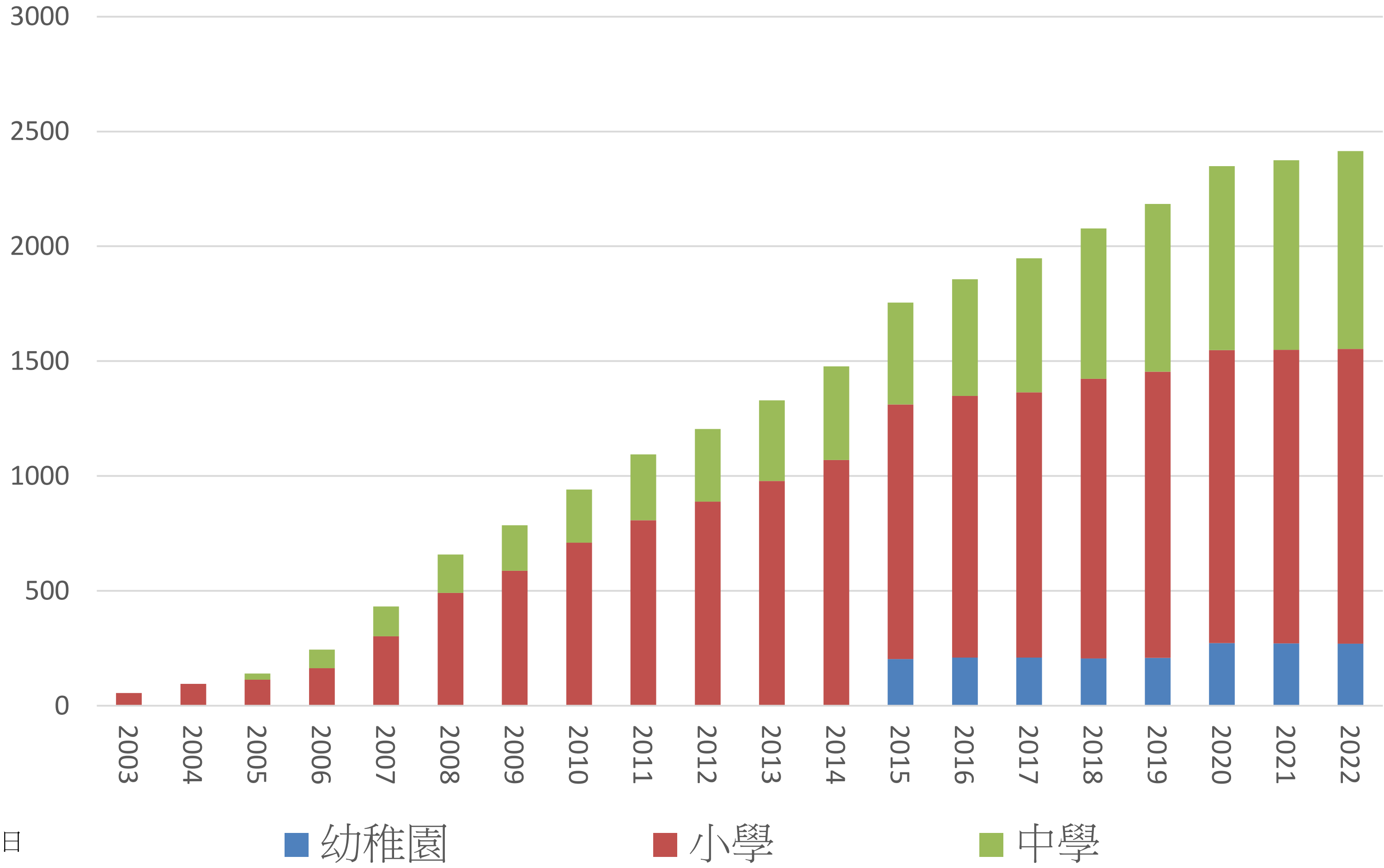
學校營運

學生人數：弘立書院

學年	小學	中學	總計
2022/23	**1,283**	**862**	**2,145**
2021/22	1,277	826	2,103
2020/21	1,275	801	2,076
2019/20	1,245	731	1,976
2018/19	1,215	655	1,870
2017/18	1,154	584	1,738
2016/17	1,138	512	1,650
2015/16	1,100	444	1,544
2014/15	1,063	413	1,476
2013/14	960	347	1,307
2012/13	884	314	1,198
2011/12	808	289	1,097
2010/11	705	226	931

截至2022年8月1日

弘立書院入學招生: 2003-2022



截至2022年8月1日

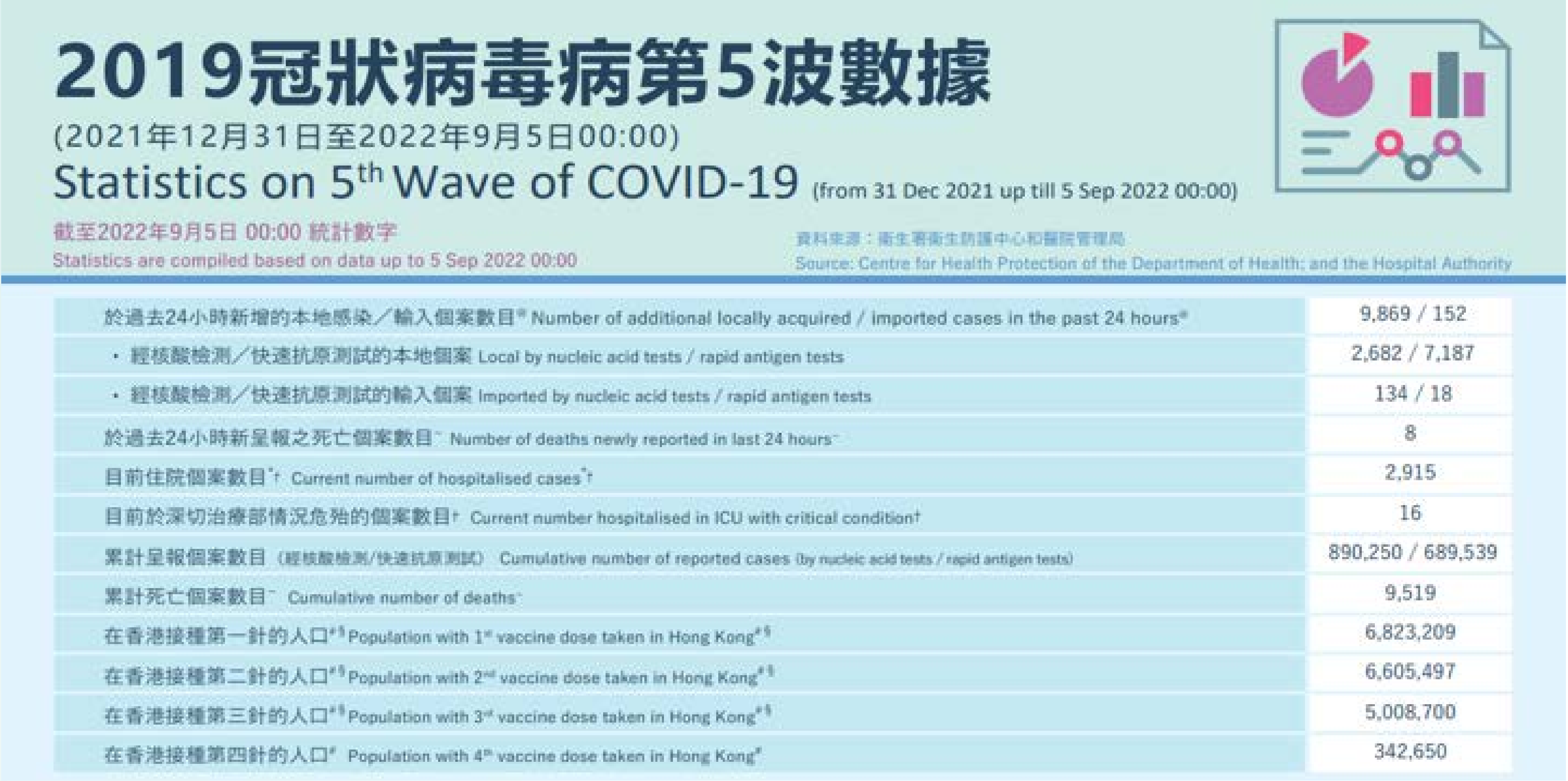
主要目標: 人力資源

教師留任率(>90%)	91%
師生比例	1:7.5
教職員學歷的提升(進行中) (>20)	24

No Stopping 切勿停留
No Parking 不准泊車
No Right-Hand Turns 不准右轉

No Parking at Primary Gate
小學閘門前不准泊車


香港特別行政區政府
同心抗疫 Together, We Fight the Virus!
本地情況互動地圖
最新消息
新聞短片
病毒資訊
澄清
實用資訊
疫情概覽
健康資訊
資源中心
社區參與
第5波最新疫情
死亡個案分析
हिन्दी
नेपाली
اردو
ไทย
Bahasa Indonesia
Tagalog
සිංහල භාෂාව
বাংলা ভাষা
Tiếng Việt
EN
简
字型大小
輸入關鍵詞



2019冠狀病毒病第5波數據

(2021年12月31日至2022年9月5日00:00)

Statistics on 5th Wave of COVID-19 (from 31 Dec 2021 up till 5 Sep 2022 00:00)

截至2022年9月5日 00:00 統計數字

Statistics are compiled based on data up to 5 Sep 2022 00:00

資料來源：衞生署衞生防護中心和醫院管理局

Source: Centre for Health Protection of the Department of Health; and the Hospital Authority

於過去24小時新增的本地感染／輸入個案數目[@] Number of additional locally acquired / imported cases in the past 24 hours[@]	9,869 / 152
• 經核酸檢測／快速抗原測試的本地個案 Local by nucleic acid tests / rapid antigen tests	2,682 / 7,187
• 經核酸檢測／快速抗原測試的輸入個案 Imported by nucleic acid tests / rapid antigen tests	134 / 18
於過去24小時新呈報之死亡個案數目[~] Number of deaths newly reported in last 24 hours[~]	8
目前住院個案數目[*†] Current number of hospitalised cases[*†]	2,915
目前於深切治療部情況危殆的個案數目[†] Current number hospitalised in ICU with critical condition[†]	16
累計呈報個案數目（經核酸檢測/快速抗原測試） Cumulative number of reported cases (by nucleic acid tests / rapid antigen tests)	890,250 / 689,539
累計死亡個案數目[~] Cumulative number of deaths[~]	9,519
在香港接種第一針的人口[#§] Population with 1st vaccine dose taken in Hong Kong[#§]	6,823,209
在香港接種第二針的人口[#§] Population with 2nd vaccine dose taken in Hong Kong[#§]	6,605,497
在香港接種第三針的人口[#§] Population with 3rd vaccine dose taken in Hong Kong[#§]	5,008,700
在香港接種第四針的人口[#] Population with 4th vaccine dose taken in Hong Kong[#]	342,650

https://www.covidvaccine.gov.hk/pdf/5th_wave_statistics.pdf

過去14天的2019冠狀病毒病個案和死亡個案數目

https://www.coronavirus.gov.hk/chi/index.html

三針
10月1日

衞生防護中心事項

- 每天檢查體溫：<37.5度
- 每天進行快速抗原測試：陰性或陽性
- 觀察孩子的身體狀況：不適，喉嚨痛，咳嗽？
- 如有疑問，請聯絡醫生！
- 在學校進行抗原測試：如有需要，駐校護士將會安排
- 負責清潔：項目設施管理處和惠康
- 衞生防護中心停課指標：班級、年級、學部：學校的 5% 或班級的 10%

呈報快速抗原測試結果

- 7:30前提交結果
- 弘立於10:00前向衛生防護中心呈報
- 法律責任將由家長承擔
- 衛生防護中心建議時刻跟進隔離個案
- 衛生防護中心每日會向傳媒公布停課消息

學校出現 2019冠狀病毒病個案 呈報表格

學校出現 2019冠狀病毒病個案 呈報表格

* 必須回答

一切學校資料以教育局分區學校名冊為準

請按此查看教育局分區學校名冊

Education Bureau
School List by District

Date: 31/03/2022
Page: 1

ISLANDS
離島區

AIDED SECONDARY SCHOOLS
資助中學

No.	Name & Address of School 學校名稱及地址	Tel. 電話 Fax 傳真	Chairman of SMC 學校管理委員會主席 Head of School 校長	AM PM WD 上午 下午 全日
1	CHEUNG CHAU CHAN TAI MAN MEMORIAL COLLEGE 385D SCHOOL ROAD CHEUNG CHAU NEW TERRITORIES 長洲陳大文紀念中學 新界長洲學校路 385D School No./Location ID: 812345 / 0001	Tel. 電話: 21345678 Fax 傳真: 21345679	Chairman of SMC 學校管理委員會主席: MR CHAN TAI MING 陳大明先生 Head of School 校長: MR CHAN SIU MING 陳小明先生	* CO-ED 男女
	Website 網址 : http://www.ccgss.edu.hk			*

🟨 學校名稱 🟩 學校地址 🟪 學校編號 🟦 地址編號

隨著馬鞍遠離香港，本港普遍風力將逐漸減弱。天文台會視乎本港風力減弱的程度，考慮改發一號戒備信號，或取消所有熱帶氣旋警告信號。

初時本港西南部離岸及高地仍會間中吹烈風，海面有大浪及湧浪，市民應遠離岸邊並停止所有水上活動。

在過去一小時，長洲、青洲及橫瀾島分別錄得的最高持續風速為每小時73、65及64公里，最高陣風分別為每小時85、81及85公里。

熱帶氣旋路徑資訊 - 地理信息系統版

熱帶氣旋： 馬鞍

✔ 可能路徑範圍 預測時間標籤 衛星雲圖 雷達圖像

名稱： 強烈熱帶風暴 馬鞍

日期： 2022 年 8 月 25 日 **香港時間：** 10 時

位置： 北緯 21.2 度, 東經 111.7 度 (即香港之 西南偏西 約 280 公里)

中心附近最高持續風速： 每小時 110 公里

馬鞍會在今日大致移向廣東西部沿岸。

EDB

特別通告

2022年8月25日 (星期四) 09:20

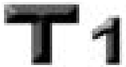
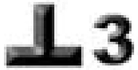
內地高校港生入境內地便利措施

擬於2022年8月至9月入境內地升讀高等院校，並需香港特別行政區政府協助的香港學生，請按此進入並填寫電子表格。

幼稚園、肢體傷殘兒童學校、智障兒童學校、中小學的上午及全日制學校今日繼續停課。中小學的下午校及夜校今日將恢復上課。

停課期間線上學習安排

間距	**幼稚園**	**小學**	**中學**
第一天	選擇性的雙語自主學習活動將會刊登在 Moodle。 不設 Google Meet 課堂	提供已修改的時間表，學生可選擇性出席。校務處將以電郵通知家長 / 學生查看 Google Calendar	依照平常的時間表出席線上課堂。學生必須出席
第二天	依照 meet.google.com 上的線上學習時間表**選擇性**出席不涉及評估的 Google Meet 課堂。應使用學生帳戶登入 Google Meet 課堂	提供已修改的時間表，學生必須出席	
第三天起	提供完整線上教學計劃，學生必須出席		

一號熱帶氣旋警告信號 	除非教育局另有指引，否則學校會照常上課		
三號熱帶氣旋警告信號 	**幼稚園及小一預備班：** 面授課堂將會取消 **一至十二年級：** 課堂將照常進行	除非教育局另有指引，否則學校會照常上課	**幼稚園及小一預備班：** 聯課活動將會取消 **一至十二年級：** 聯課活動將照常進行
八號或以上熱帶氣旋警告信號 	取消所有面授課堂，學生應留在家中進行線上學習	取消所有面授課堂，乘搭校車的學生將於校車抵達後離開，家長／監護人應盡快前往平日接放學的地點接回學生	聯課活動將會取消

警告信號	上課前	上課途中	聯課活動
黃色暴雨警告信號 	除非教育局另有指引，否則學校會照常上課		
紅色暴雨警告信號 	取消所有面授課堂。學生應留在家中進行線上學習	學生應留在學校至放學時間，並在安全的情況下方可回家；家長無需即時到學校接領子女。校車服務將會在改發較低警告信號及路面情況許可下回復正常	聯課活動將會取消
黑色暴雨警告信號 			

EDB

課堂無邊界 停課不停學

https://www.edb.gov.hk/tc/about-edb/press/insiderperspective/insiderperspective20200212.html

停課不是額外的學校假期，大家應該善用時間，持續學習，做到「停課不停學」。

楊潤雄先生
教育局局長

Fully Accredited by WASC ACCREDITING COMMISSION FOR SCHOOLS

WE ARE A CIS INTERNATIONALLY ACCREDITED SCHOOL

ISF 弘立

未來一年：2022-23

9月

- 返校活動：9月1，2，8日
- 咖啡早會（總校長，小學，中學）
- 中秋節：9月12日

10月

- 國慶日假期 / 學期中假期：10月1至4日
- 三方會談
- 體驗學習課程1（中學）
- 咖啡早會（總校長，小學，中學）

11月

- 體驗學習課程1（小學四至五年級）
- Jam 2022
- 專業進修日
- 成績報告1（小學）

12月

- 弘立書展
- 冬季慶祝活動
- 美國地球物理聯盟
- 冬季假期：12月19日至1月2日

1月

- 第二學期開始：1月3日
- 第二學期聯課活動開始：1月3日（中學 / 「書院」）；1月9日（其他）
- 農曆新年假期：1月16至27日
- 教師招聘（全校）
- 參觀大學及院校

2月

- 教師招聘（全校）
- 參觀大學及院校
- 十二年級家長教師學生三方會談

3月

- 咖啡早會（總校長，小學，中學）
- 成績報告2（小學）
- 六至十年級家長教師學生三方會談
- 學生主導會議（小學）

4月

- 復活節 /春季假期：4月3至10日
- 咖啡早會
- 國際學校委員會 / 美國西部院校協會準備評估

5月

- 國際文憑大學預科考試
- 中學項目電子評估
- 體驗學習課程2（小學）
- 十一年級家長教師學生三方會談
- 專業進修日

6月

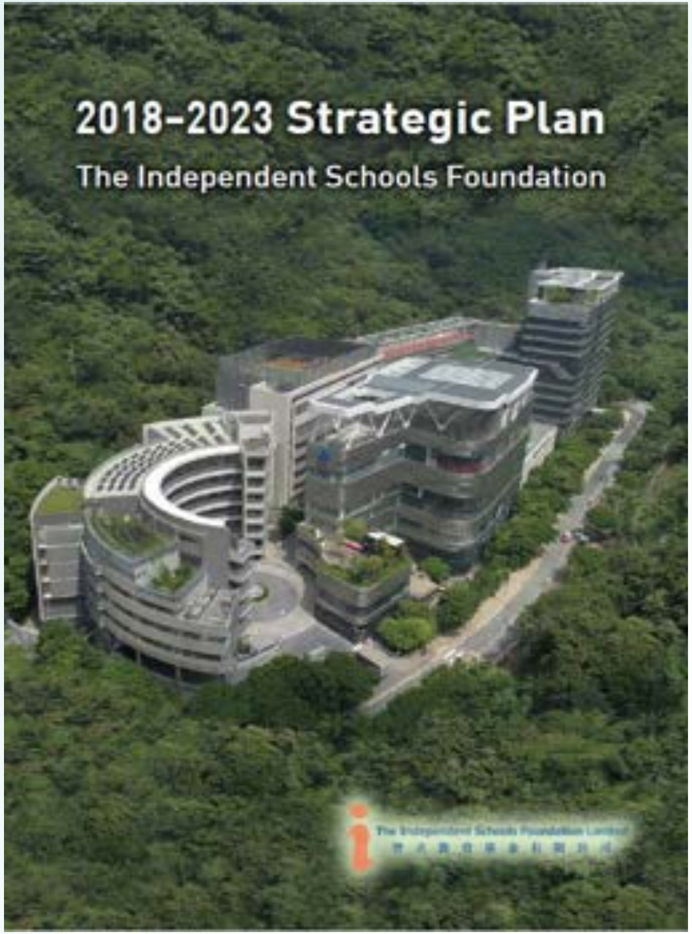
- 聯課活動註冊
- 體驗學習課程2（中學：5月29日至6月2日）
- 十二年級畢業典禮及進階典禮
- 學年結束
- 暑期延伸課程

7月

- 暑期課程
- 劍橋李約瑟研究所
- 牛津比較哲學
- 哥倫比亞

8月

- 2023-24學年開始



2018-2023 Strategic Plan

The Independent Schools Foundation

The Independent Schools Foundation Limited

2024–2029年
策略規劃

ISF 弘立

主要策略方向

- 中英雙語、雙語文、雙文化
- 「八德一智」
- 國際文憑大學預科項目和中學項目
- 「書院」（「數理科工」、古代經典、工作室、合作夥伴）
- 體驗學習（石壁營地）
- 八德課程框架

SAVE THE DATE!

HEALTHY FASHION
2022
康健★新尚
FASHIONABLY HEALTHY

約定您！

ISF ANNUAL SCHOOL FAIR
弘立校園遊藝會

Community & Celebration ｜ 社群和慶典

A fun filled day of games, activities & food galore!

屆時有一連串的攤位遊戲及豐富的食物，為您帶來歡樂的一天！

Saturday, November 19, 2022
11:00a.m. - 4:00p.m.

2022年11月19日(星期六)
上午11:00 - 下午4:00

For ISF Community Only

僅限弘立社群參與

JAM ON!

1 Kong Sin Wan Road, Hong Kong

ISF 弘立

香港鋼綫灣道1號

謝謝！

下次總校長咖啡早會
2022年10月12日(星期三)