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> Superinfection identification and antimicrobial appraisal in COVID-19 patients combined with application of metagenomic sequencing: a Shanghai cohort study

Department of infectious disease, Zhongshan Hospital of Fudan University Qing Miao, MD, PHD candidate Bijie Hu 10/16/2020

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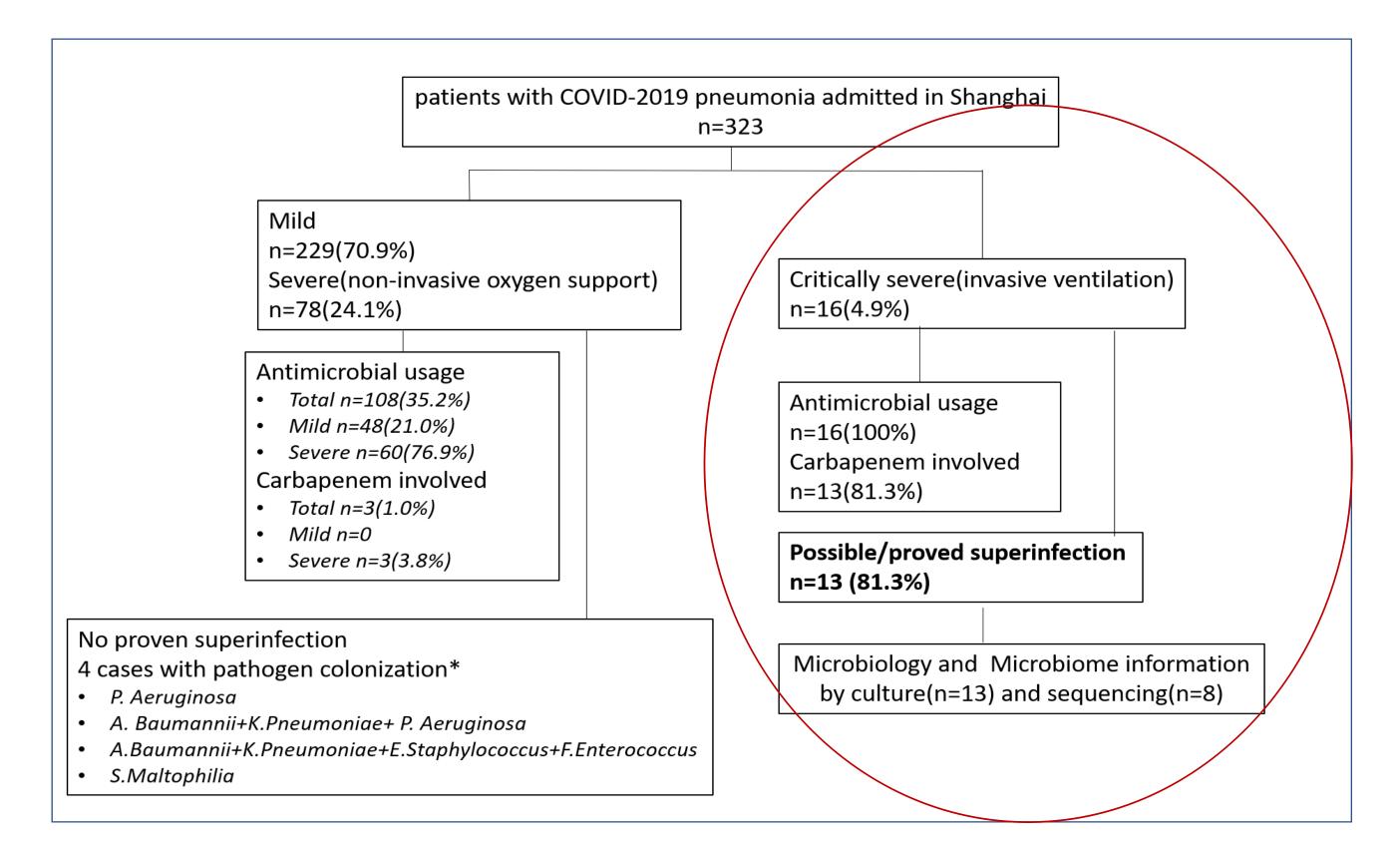
### • No financial conflict of interest

# **BACKGROUND & AIM**

 information regarding coinfection is limited, and the recommendation for use of empirical antimicrobials is challenging

 Whether metagenomics is helpful for revealing more coinfection events and guiding appropriate antimicrobial usage.

# **Overview of superinfection and antimicrobial usage**



# Comparison of infection-associated indexes between survivors and deaths in critically ill patients

	Total(n=16)	Die(n=7)	Survive(n=9)	p value				
Possible and proven Infection <sup>c</sup>	12(75)	5(71.4)	7(77.8)	1				
Proven infection	5(31.3)	4(57.1)	1(11.1)	0.1058				
Site of all infection								
Respiratory	11(91.7)	5(100)	6(85.7)	0.839				
Urinary	7(58.3)	2(40)	5(71.4)	0.28				
Bloodstream	3(25)	3(60)	1(14.3)	0.146				
Site of improven infectlion								
Respiratory	1(20)	1(25)	Improved in	nfection of				
Urinary	1(20)	0	Improved infection o					
Bloodstream	1(20)	1(25)	funcua waa	associated				
SYSTEMIC	2(40)	2(50)	fungus was associated					
Pathogen of all infection			• .1	•				
NFB	10(83.3)	5(100)	with poor prognosis					
Enterobacteriaceae	8(66.7)	4(80)						
G+ microbe	8(66.7)	4(80)						
Fungus	8(66.7)	3(60)	(۲۰۰۰)	0.017				
Pathogen of improven infection								
Enterobacteriaceae	2(40)	1(25)	1(100)	0.849				
G+ microbe	1(20)	1(25)	0(0)	0.242				
Fungus	3(60)	3(75)	0(0)	0.063				
Non-COVID-19 virus detection by MS	8	4	4					
virus colonization	8(100)	4(100)	4(100)	0.614				
virus activation	6(75)	1(25)	4(100)	0.197				

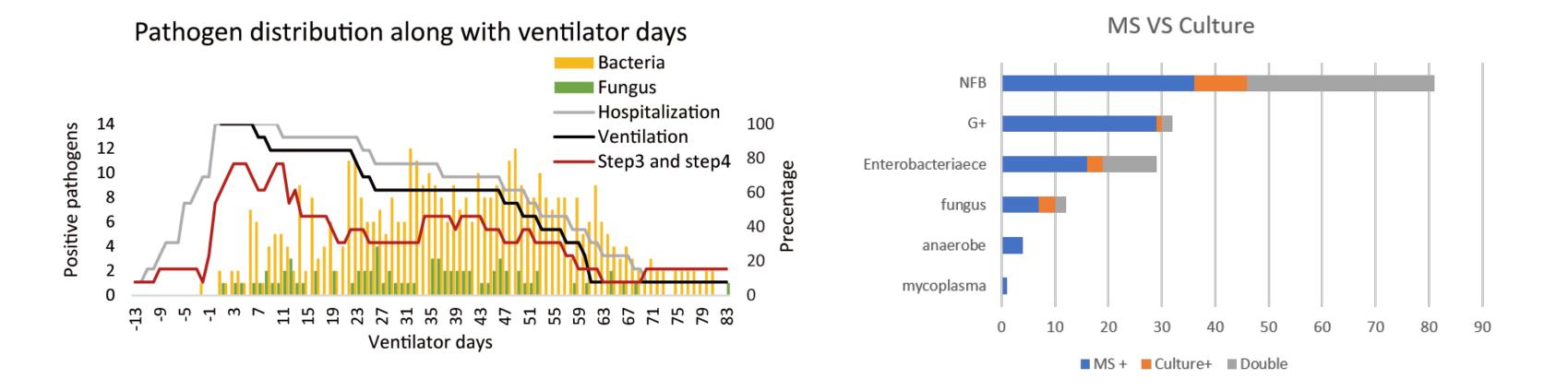
No significant difference with:

 $\checkmark$  Infection site

✓ Pathogens

 ✓ Antibiotics such as anti-G-, anti-G+, anti-fungus and anti-CD

# Pathogen distribution

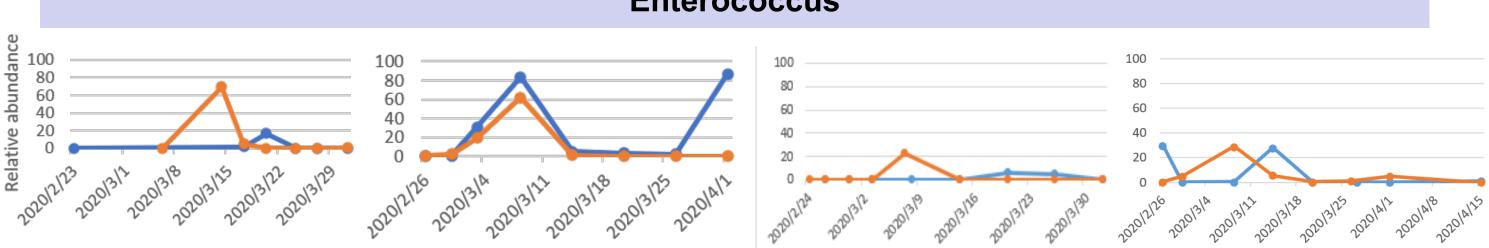


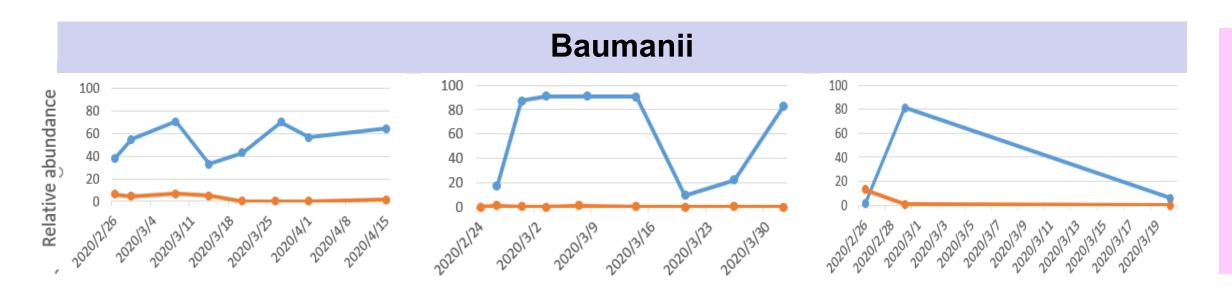
- ✓ The peak bacterial yield rate was between day 35 to 51 post-ventilation, suggesting that most co-bacteria infection were secondary to prolonged ventilation.
- MS showed higher sensitivity rate than culture, especially for mycoplasma and anaerobe.  $\checkmark$
- $\checkmark$  No unexpected organism were identified by MS.

### Plasma vs airway surveillance by MS



### **Enterococcus**







Due to higher sensitivity and semi-quantity, MS was helpful for:

✓ Early warning for BSI

✓ Ruling out secondary BSI

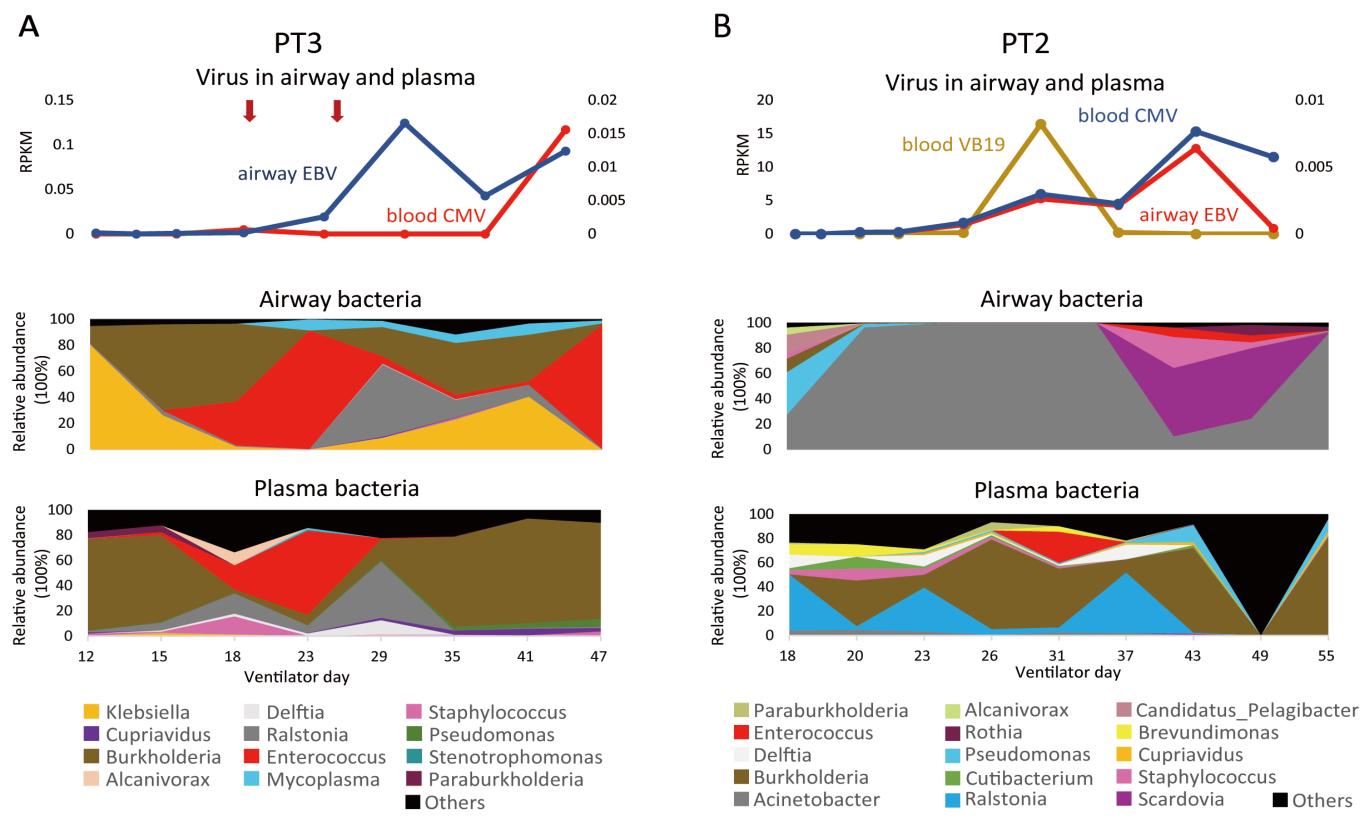
## **Non-COVID-19 virus detection by MS**

	CMV		HSV1		EBV		HSV7		HSV6		TTV		PV19		JCV		activation
	blood	airway	blood	airway	blood	airway	blood	airway	blood	airway	blood	airway	blood	airway	blood	airway	episode
PT1	√	√	√	<b>√</b> *	√	√		√			<b>√</b> *	<b>√</b> *	<b>√</b> *	√			3
PT2e	<b>√</b> *	√	√	√		<b>√</b> *		√	√		√	√	<b>√</b> *	1	√		3
PT3e	<b>√</b> *	√		<b>√</b> *		√		√									2
PT4e	√*	√	√			√*		√				√					2
PT5a	√	√	√	√					√								2
PT6ea	√*	√				√											1
PT7ea	√	√	√					√									0
PT9ea	√			√				√		√	√						0
virus detection	8	/8	6	/8	5	/8	4	/8	3	/8	3	/8	2	/8	1	/8	
virus activation	5	/8	3	/8	2	/8	0	/8	0	/8	1	/8	2	/8	0	/8	
e:ecmo,a:die																	
√: detection																	
*: activation																	

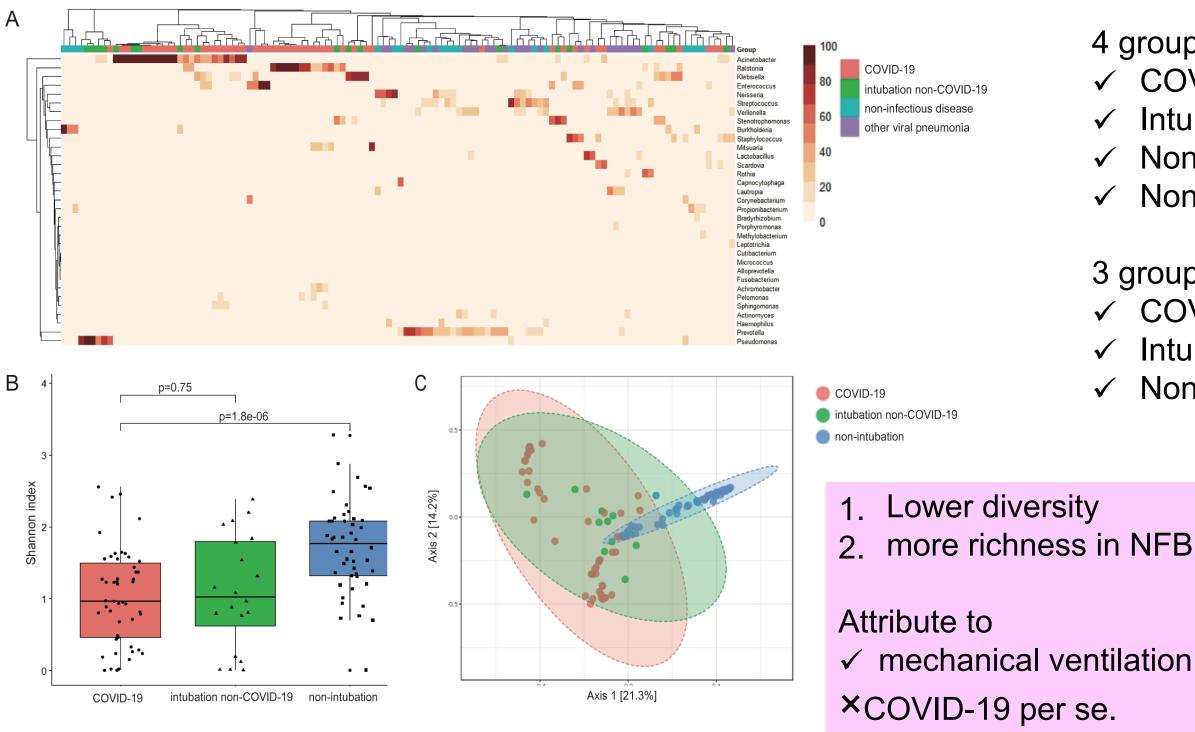
MS has revealed a high prevalence of virus colonization (8/8, 100%) and activation (5/8, 62.5%) CMV, HSV, EBV, HPVB-19, JCV, TTV



## **Clinical benefit of MS for antimicrobial usage**



# **Airway microbiome comparison of COVID-19**



4 groups for clustering analysis: ✓ COVID-19 ✓ Intubation non-COVID19 Non-COVID-19 virus infection ✓ Non-infection

3 groups for comparison: ✓ COVID-19 Intubation non-COVID19 ✓ Non-COVID-19

2. more richness in NFB, G+ and Enterobacteriaceae

# CONCLUSION

- In our cohort, superinfection **exclusively occurs** in critically ill COVID-19 patients, with a proven infection rate of **31.3%**.
- Fungal coinfection deserves intensive attention due to the high mortality risk.
- The clinical benefit of MS in guiding antimicrobial management warrants further investigation.

