新型冠状病毒信息简报

第 38 期（2020 年 4 月 25 日报）

上海科技大学免疫化学研究所

生物医学大数据平台和高通量筛选平台领衔编译制作

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1. 2020 年 4 月 24 日疫情

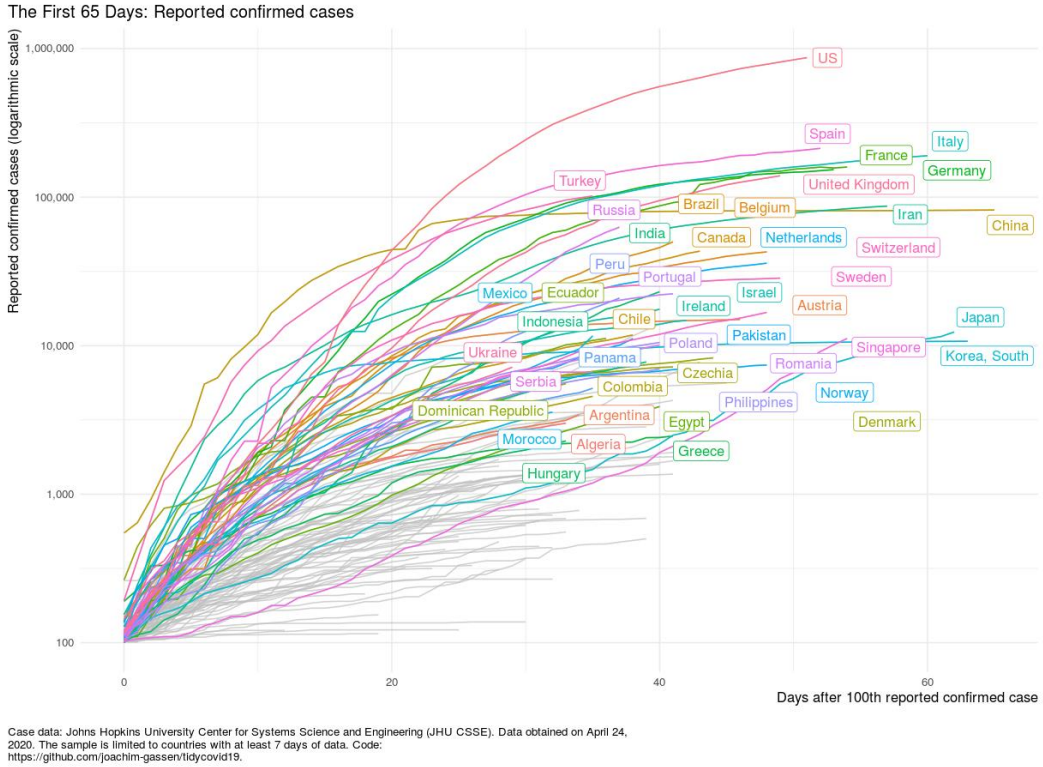
数据来源：WHO

发布时间：2020 年 4 月 24 日北京时间下午 4 点

链接：https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports

根据 WHO 提供的数据，2020 年 4 月 24 日全球累计确诊新型冠状病毒病人 2626321 例，当日新增确诊 81529 例，累计死亡 181938 例，当日新增死亡 6260。

中国累计确诊 84311 例，累计死亡 4642 例，当日新增确诊 9 例，新增死亡 0 例。



重点国家确诊数量曲线（https://jgassen.shinyapps.io/tidycovid19/，数据截止 4 月 24 日北京时间下午 4 点）

全国新型冠状病毒肺炎新增确诊病例分布图（4 月 24 日，来源：http://2019ncov.chinacdc.cn/2019-nCoV/）

2. 根据 SARS-CoV-2 全球循环分支的基因组变异全景定义的一个遗传条形码方案

The genomic variation landscape of globally-circulating clades of SARS-CoV-2 defines a genetic barcoding scheme

来源：biorxiv

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中文摘要：

该研究描述到 2020 年 3 月 31 日为止，2058 个高质量 SARS-CoV-2 基因组（来自 GISAID）的 15 个主要突变事件。这些突变事件定义了全球循环病毒种群的五个主要分支（G、I、S、D 和 V），占所有测序病例的 85.7%，可以通过使用 10 个核苷酸的遗传分类码或条形码进行识别。五个主要分支按照氨基酸突变命名（图 1）：S(Orf8, L84S)，V (Orf3a, G251V)，I(Orf1ab, V378I)，D (Orf1ab, G392D)和 G(S,D614G)。之后，该研究将条形码（图二）应用于 3 月 31 日至 4 月 15 日期间发布的另外 4000 个基因组，成功地对 95.6%的基因组进行了分类，说明该方法的实用性。对 SARS-CoV-2 中 ORFs 中氨基酸变异的分析提供了病毒蛋白在宿主进入和基因组复制中的替代事件的证据。根据对来自 GISAID（截止 2020 年 3 月 31 日）的 2058 个基因组的分析，发现 S、N 和 Orf3a 基因积累的突变明显多于随机漂移预期。对 SARS-CoV-2 病毒基因组的动态变化进行长时间系统监测，有助于协助监测病毒循环中的遗传多样性，可以指导治疗和预防策略来管理和控制该病毒，并帮助指导使用有效的抗病毒药物和疫苗。条形码可增加必要的基因分辨率，以便于跟踪和监测感染群，以区分输入和本地病例，从而有助于公共卫生措施在不需要实时完整基因组测序的情况下设法中断传播链。

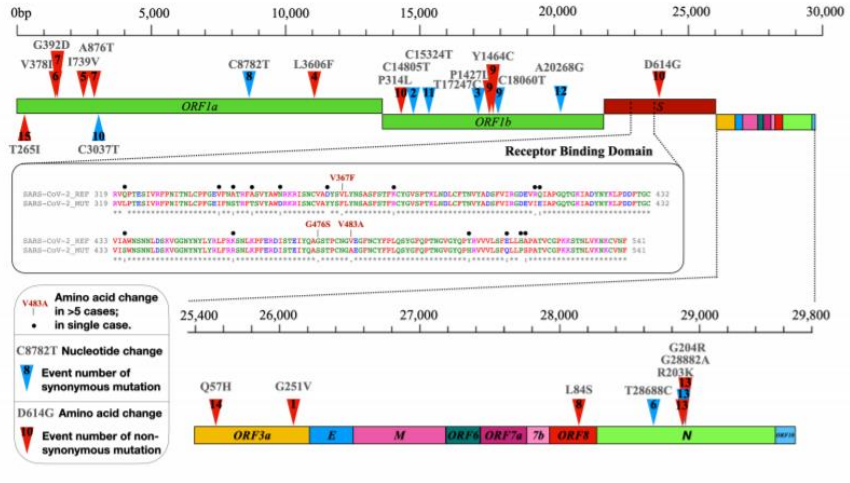
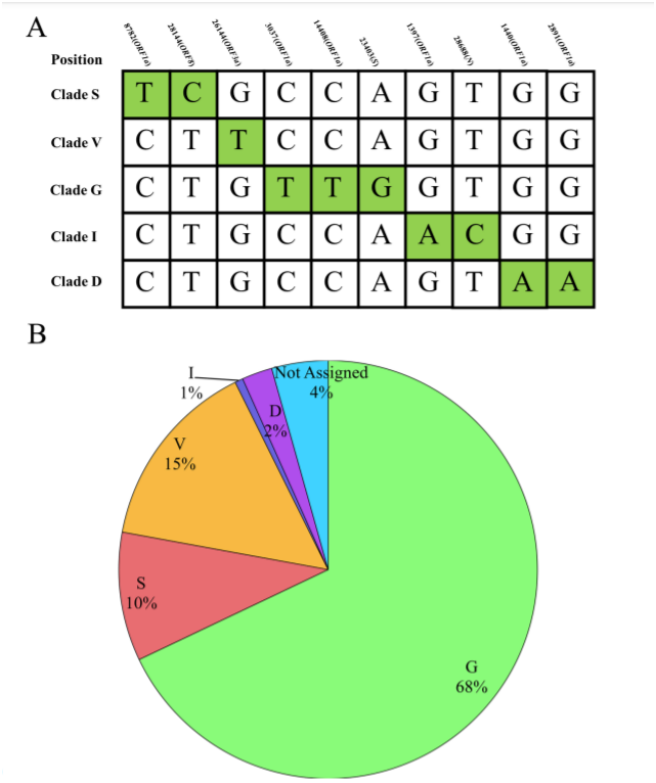


Figure 2. Major mutations and associated variation in globally circulating SARS-CoV-2 genomes (n=2,058). Genomic localisation of major mutation events as defined within our study. SARS-CoV-2 mutations in the receptor-bing domain (RBD) sequence contain all amino acid substitutions from 2,058 genomes available up until March 31st 2020.

图一



图二 Major mutations and associated variation in globally circulating SARSCoV-2 genomes (n=6,058) available until April 15th 2020. (A) A 10 nucleotide SNP genetic barcode that defines the 5 clades of SARS-CoV-2. (B) By applying this barcode we are able to classify 95.6% of the cases published between March 31st and April 15th 2020 during the early phase of the pandemic. Pie charts showing the percentage of each major clade by applying a 10 nucleotide genetic classifier to 4,000 new genomes downloaded from GISAID.

Abstract:
We describe fifteen major mutation events from 2,058 high-quality SARS-CoV-2 genomes deposited up to March 31st, 2020. These events define five major clades (G, I, S, D and V) of globally-circulating viral populations, representing 85.7% of all sequenced cases, which we can identify using a 10 nucleotide genetic classifier or barcode. We applied this barcode to 4,000 additional genomes deposited between March 31st and April 15th and classified successfully 95.6% of the clades demonstrating the utility of this approach. An analysis of amino acid variation in SARS-CoV-2 ORFs provided evidence of substitution events in the viral proteins involved in both host-entry and genome replication. The systematic monitoring of dynamic changes in the SARS-CoV-2 genomes of circulating virus populations over time can guide therapeutic and prophylactic strategies to manage and contain the virus and, also, with available efficacious antivirals and vaccines, aid in the monitoring of circulating genetic diversity as we proceed towards elimination of the agent. The barcode will add the necessary genetic resolution to facilitate tracking and monitoring of infection clusters to distinguish imported and indigenous cases and thereby aid public health measures

seeking to interrupt transmission chains without the requirement for real-time complete genomes sequencing

3. 在 COVID-19 患者中 SARS-CoV-2 核衣壳抗体检测的敏感性高于刺突蛋白抗体

Detection of Nucleocapsid Antibody to SARS-CoV-2 is More Sensitive than Antibody to Spike Protein in COVID-19 Patients

来源：medRxiv

发布时间：2020-04-20

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中文摘要：

背景：SARS-CoV-2 是 2019 年冠状病毒病（COVID-19）的病因，与呼吸相关的发病率和死亡率有关。检测病毒特异性抗体对于了解感染的流行情况和免疫应答过程具有重要意义。

方法：通过萤光素酶免疫沉淀分析系统（LIPS）对核衣壳和刺突蛋白的血浆或血清抗体进行了定量测量，纵向和横向分析了 100 例 SARS-CoV-2 感染患者的样品。

结果：症状发作后十五天或更长时间，针对 SARS-CoV-2 核衣壳蛋白的抗体显示 100％的敏感性和 100％的特异性，而针对刺突蛋白的抗体检测到的敏感性为 91％和 100％的特异性。通过样品的热灭活，抗体水平和血清阳性率均未显着降低。对六名 COVID-19 患者的每日样本进行分析，发现抗核衣壳和刺突抗体在出现初始症状后的第 8 天至第 14 天之间出现。与免疫功能正常的患者相比，免疫受损的患者通常对 SARS-CoV-2 的抗体反应延迟。

结论：SARS-CoV-2 核衣壳蛋白抗体对早期感染的检测比刺突蛋白抗体敏感。通过 LIPS 分析热灭活的样品是安全,敏感的检测 SARS-CoV-2 抗体的方法。

Abstract:

Background: SARS-CoV-2, the cause of coronavirus disease 2019 (COVID-19), is associated with respiratory-related morbidity and mortality. Assays to detect virus-specific antibodies are important to understand the prevalence of infection and the course of the immune response. Methodology: Quantitative measurements of plasma or serum antibodies by luciferase immunoprecipitation assay systems (LIPS) to the nucleocapsid and spike proteins were analyzed in 100 cross-sectional or longitudinal samples from SARS-CoV-2-infected patients. A subset of samples was tested with and without heat inactivation.

Results: Fifteen or more days after symptom onset, antibodies against SARS-CoV-2 nucleocapsid protein showed 100% sensitivity and 100% specificity, while antibodies to spike protein were detected with 91% sensitivity and 100% specificity. Neither antibody levels nor the rate of seropositivity were significantly reduced by heat inactivation of samples. Analysis of daily samples from six patients with COVID-19 showed anti-nucleocapsid and spike antibodies appearing between day 8 to day 14 after initial symptoms. Immunocompromised patients generally had a delayed antibody response to SARS-CoV-2 compared to

immunocompetent patients.
Conclusions: Antibody to the nucleocapsid protein of SARS-CoV-2 is more sensitive than spike protein antibody for detecting early infection. Analyzing heat-inactivated samples by LIPS is a safe and sensitive method for detecting SARS-CoV-2 antibodies.

4. **透明质酸浓度快速升高作为高危 COVID-19 患者发病率和死亡率的主要驱动因素：口服透明质酸抑制剂预防“诱导透明质酸风暴”综合征**

Accelerated hyaluronan concentration as the primary driver of morbidity and mortality in high-risk COVID-19 patients: with therapeutic introduction of an oral hyaluronan inhibitor in the prevention of "Induced Hyaluronan Storm" Syndrome
来源：medRxiv
发布时间：2020-04-24
链接：https://www.medrxiv.org/content/10.1101/2020.04.19.20071647v2
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编译者：雷颖
中文摘要：
背景：到目前为止，超过 161,000 人死于 2019 年冠状病毒病(COVID-19)，但发病率和死亡率的根本驱动因素仍然不确定。世界各地的临床医生似乎无法知道如何有效地预防和治疗这些患者的严重呼吸窘迫。因此，需要紧急发现和处理导致 COVID-19 高危患者死亡的基本机制。尽管现在尸检的频率明显下降，但尸检仍然是发现特定个体死亡原因的重要方法，也是促进疾病的科学和治疗的重要部分，尤其是在 SARS-CoV-2 等新病原体的情况下。尸检的目的是利用宏观/微观调查来发现死亡原因(COD)。传统上，完整的器官被仔细移除、检查和称重。由于肺的重量经常受到死亡原因的影响，而且最后一次呼吸即使不是发生在死亡时刻也是在非常接近的时候，因此肺的评估是任何 COD 调查的起点之一。
方法：对 COVID-19 患者的所有报告尸检结果进行全面的搜索，以更好地了解导致死亡的潜在疾病机制。然后，作者将这些发现与透明质酸与急性呼吸窘迫综合征(ARDS)的靶向文献综述的结果进行了比较。
结果：共鉴定出 181 例尸体解剖数据。其中，选择 6 例 COVID-19 患者的尸检进行详细的回顾和统计分析。那些被确定死于 SARS-CoV-2 的人的平均肺重为 2196g——大约是正常肺重的 2.5 倍。透明膜一致在组织学切片上被鉴定。对文献的回顾表明，透明质酸自 1967 年以来一直与 ARDS 的病理生理学有关。然而，它在驱动疾病发病率和死亡率方面的关键作用迄今尚未得到充分认识。
结论：作者认为，诱导透明质酸风暴综合征或 IHS 是解决迄今令人困惑的呼吸衰竭的最好的模型，这是少数但不断增加的患者死亡的近端原因。除了治疗和预防目前感染的人的 IHS 之外，还应进行积极的研究工作，以发现为什么大多数暴露于病毒的人要么是轻微或无症状的，而少数高风险的人却迅速进展到呼吸衰竭和死亡。
Abstract
Background: To date, more than 161,000 people have died from the coronavirus disease 2019 (COVID-19) yet the fundamental drivers of the morbidity and

mortality remain uncertain. Clinicians worldwide appear to be at a loss to know how to prevent and treat the severe respiratory distress in these patients effectively. Consequently, the fundamental mechanisms leading to death in high-risk patients with COVID-19 need to be discovered and addressed with urgency. Despite a marked drop in frequency, the post-mortem autopsy remains an essential part of both discovering the cause of death in a particular individual, but also in advancing the science and treatment of disease, especially in the case of novel pathogens such as SARS-CoV-2. The goal of an autopsy is to discover the cause of death (COD) using a macro/microscopic investigation. Traditionally, the intact organs are carefully removed, inspected, and weighed. Because lung weight is often affected by the cause of death and the last breath occurs very near if not at the moments of death, the evaluation of the lungs is one of the starting points of any COD investigation.

Method: A comprehensive search was performed to systematically review all reported autopsy findings in COVID-19 patients in order to better understand the underlying disease mechanisms resulting in death. We then compared these findings with the results of a targeted literature review of hyaluronan in relationship to acute respiratory distress syndrome (ARDS).

Results: In total, data from 181 autopsies were identified. From this group, 6 autopsies of COVID-19 patients were selected for a detailed review and statistical analysis. The average lung weight of those who were determined to have died as a result of SARS-CoV-2 was 2196g-approximately 2.5x normal lung weight. Hyaline membranes were consistently identified on histologic sections. A review of the literature reveals that hyaluronan has been associated with the pathophysiology of ARDS since 1967. However, its key role in driving the morbidity and mortality of the condition has heretofore not been fully recognized.

Conclusions: We propose that the induced hyaluronan storm syndrome or IHS, is the model that best addresses the heretofore perplexing respiratory failure that is the proximal cause of death in a minority, but ever rising number, of patients. In addition to treating and preventing IHS in currently infected individuals now; an aggressive research effort should be undertaken to discover why the majority of individuals who are exposed to the virus are either minimally or asymptomatic, while a minority of high-risk individuals rapidly progress to respiratory failure and death.

5. STAT2 信号是一把双刃剑，一方面限制了病毒的传播，另一方面却使感染了 SARS-CoV-2 的仓鼠患上了严重的肺炎

STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters

来源：biorxiv

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编译者：张怡

中文摘要：
自从 SARS-CoV-2 的出现引发了 COVID-19，无数人住院治疗，预计将有数十万人死亡。为了寻找有效治疗的关键靶点，迫切需要模拟人类 COVID-19 的强健动物模型。本文中，作者证明了小鼠肺部产生的 SARS-CoV-2 感染受早期 I 型干扰素反应的限制。相比之下，叙利亚仓鼠对 SARS-CoV-2 非常宽容。在野生型仓鼠中，SARS-CoV-2 感染可引发支气管肺炎和肺部的强烈炎症反应，伴有中性粒细胞浸润和水肿。在 STAT2 或者 IL28R-a 基因敲除的仓鼠肺部病毒 RNA 量和野生型没用显著差异。(Fig. 2B). 但是 STAT2 基因敲除仓鼠肺部有更高滴度的有感染性病毒(Fig. 2C)，更高的病毒血症 (Fig. 2E)。另外在 STAT2 基因敲除仓鼠的脾、肝、以及上下肠道都有更多的病毒 RNA。作者通过临床应用的 micro-CT 进一步分析 SARS-CoV-2 诱导的仓鼠肺病理学。最后，作者确定了旺盛的先天免疫反应是免疫发病机制的关键，其中 STAT2 信号在其中起着双刃剑的作用，一方面导致了严重的肺损伤，另一方面又限制了系统病毒的传播。他们的结果支持仓鼠作为临床前模型，以合理化和评估新的抗病毒药物或免疫调节剂对 COVID-19 患者的治疗效果。

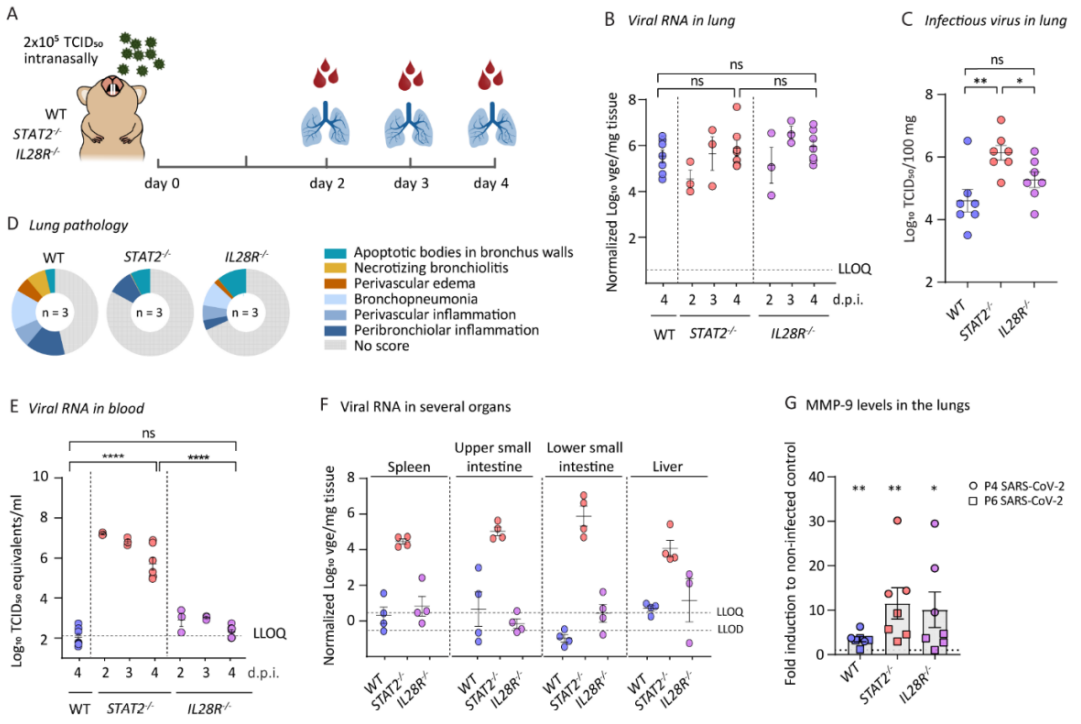

Figure 2. Exuberant innate response by STAT2 drives SARS-CoV-2-induced lung pathology in hamsters. (A) Schematic representation of SARS-CoV-2 inoculation

schedule. WT, STAT2-/- and IL28R-a -/- hamster strains were intranasally inoculated with 2 × 105 TCID50 of passage 4 or 2 × 106 of passage 6 SARS-CoV-2. On the indicated days post inoculation (d.p.i.), organs and blood were collected to determine viral RNA levels, infectious virus load and score for lung damage. Viral loads in the indicated organs were quantified by RT-qPCR (B, E and F) or virus titration (C). (B,F) Viral RNA levels in the indicated organs were normalized against β-actin mRNA levels and transformed to estimate viral genome equivalents (vge) content per weight of the lungs (Figure S5). (C) Infectious virus loads in the lung are expressed as the number of infectious virus particles per 100 mg of lung tissue. (E) Viral RNA levels in the blood were calculated from a standard of infectious virus and expressed as TCID50 equivalents per ml blood. Dotted lines indicate lower limit of quantification (LLOQ) or lower limit of detection (LLOD) (D) Histopathological scoring of lungs. Hamsters were sacrificed on day 4 p.i. with passage 4 SARS-CoV-2 and lungs were stained with H&E and scored for signs of lung damage (apoptotic bodies, necrotizing bronchiolitis, edema, pneumonia and inflammation). Scores are calculated as percentage of the total maximal score. (G) Levels of matrix metalloproteinase (MMP)-9 levels in lung homogenates of SARS-CoV-2 infected hamsters, relative to non-infected controls of the same strain. Values for infected animals (n=7 each) compiled from two independent experiments using either P4 (n=3, circles) and P6 (n=4, squares) SARS-CoV-2. Statistical significance was calculated between infected and noninfected animals within each group. The data shown are mean ± SEM. Statistical significance between groups was calculated by the nonparametric Mann-Whitney U-test (ns $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$).

Abstract

Since the emergence of SARS-CoV-2 causing COVID-19, the world is being shaken to its core with numerous hospitalizations and prospected hundreds of thousands of deaths. In search for key targets of effective therapeutics, robust animal models mimicking COVID-19 in humans are urgently needed. Here, we show that productive SARS-CoV-2 infection in the lungs of mice is limited and restricted by early type I interferon responses. In contrast, we show that Syrian hamsters are highly permissive to SARS-CoV-2. In wild-type hamsters, SARS-CoV-2 infection triggers bronchopneumonia and a strong inflammatory response in the lungs with neutrophil infiltration and edema. We further assess SARS-CoV-2-induced lung pathology in hamsters by micro-CT alike used in clinical practice. Finally, we identify an exuberant innate response as key player in immune pathogenesis, in which STAT2 signaling plays a double-edged role, driving severe lung injury on the one hand, yet restricting systemic virus dissemination on the other. Our results endorse hamsters as pre-clinical model to rationalize and assess the therapeutic benefit of new antivirals or immune modulators for the treatment of COVID-19 patients.

6. SARS-CoV-2 进入因子与先天免疫基因一起在鼻上皮细胞中高度表达

SARS-CoV-2 entry factors are highly expressed in nasal epithelial cells together

with innate immune genes
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发布时间：2020-04-23
链接：https://www.nature.com/articles/s41591-020-0868-6
第一作者：Waradon Sungnak
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DOI 或 PUBMED ID：https://doi.org/10.1038/s41591-020-0868-6
编译者：宋张悦
中文摘要：
本研究通过检测来自健康人供体的多个组织的单细胞 RNA 测序数据中病毒进入相关基因（ACE2 和 TMPRSS2）的表达，研究了 SARS-CoV-2 的潜在趋向性。本研究中的单细胞 RNA 测序数据来自人类细胞图谱(HCA)联盟和其他资源中生成的多个 scRNA-seq 数据集。数据集取自多个人体组织中已发表和未发表的数据集，包括呼吸道、角膜、骨骼肌、回肠、结肠、胰腺、肝脏、胆囊、心脏、肾脏、胎盘/蜕膜、睾丸、前列腺、大脑、皮肤、视网膜、脾脏、食道和胎儿组织。研究团队在特定的呼吸道、角膜和肠上皮细胞中共同检测到了这些基因的转录本，这可能解释了 SARS-CoV-2 的高效传播性。这些基因在鼻上皮细胞中与参与先天免疫的基因共同表达，强调了细胞在初始病毒感染、传播和清除中的潜在作用。这项研究为进一步的研究来自 COVID-19 患者的有价值的临床样本提供了有用的资源，研究团队在 www.covid19cellatlas.org 上，以全面、开放和用户友好的方式提供了他们的数据。
Abstract:
We investigated SARS-CoV-2 potential tropism by surveying expression of viral entry-associated genes in single-cell RNA-sequencing data from multiple tissues from healthy human donors. We co-detected these transcripts in specific respiratory, corneal and intestinal epithelial cells, potentially explaining the high efficiency of SARS-CoV-2 transmission. These genes are co-expressed in nasal epithelial cells with genes involved in innate immunity, highlighting the cells' potential role in initial viral infection, spread and clearance. The study offers a useful resource for further lines of inquiry with valuable clinical samples from COVID-19 patients and we provide our data in a comprehensive, open and user-friendly fashion at www.covid19cellatlas.org.
编者注：
相关研究可以参考 4 月 23 日简报 12、13 条，以及 4 月 24 日简报第 10 条。

7. Y 染色体丢失引起的 X 染色体单倍体嵌合可能带来免疫缺陷以及心血管病风险：老年男性对 COVID-19 更脆弱的原因？

Immune defects and cardiovascular risk in X chromosome monosomy mosaicism mediated by loss of chromosome Y. A risk factor for SARS-CoV-2 vulnerability in elderly men?
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DOI:
编译者：蒋立春
中文摘要：
COVID-19 的死亡率根据中国的数据看大约为 1.38%，死亡率在男性中比女性中高出 53%，并且随着年龄增加呈指数增加。通过对英国生物样品库的数据进行分析，发现由于 Y 染色体在男性中的缺失导致的 X 染色体单体嵌合现象（XCM/LOY）在老年人群中也有类似的指数增加趋势。而且 X 染色体单体嵌合现象(XCM/LOY)和全因性死亡率增加相关。

通过对爱沙尼亚生物样品库中的 530 个成年男性的外周血样品进行比较转录组学分析，作者们发现 X 染色体单体嵌合现象(XCM/LOY)和外周血中的前体细胞数目下降，血细胞计数异常，以及多个免疫系统功能损害的生物标志物、促凝血活性以及心血管风险增加有关。在 530 例分析的样品中， 一共有 28 个样品发生了 X 染色体单体嵌合现象(XCM/LOY)。研究者发现这些样品中一些下调表达的基因参与了宿主对 SARS-CoV-2 的起始免疫应答（和已经报道的 SARS-CoV-2 感染人肺部上皮细胞以及肺癌细胞 A549 得到结果）。这些基因主要是可能参与宿主抑制病毒的干扰素诱导基因。这个研究提示 X 染色体单体嵌合现象(XCM/LOY)至少部分地参与了老年 COVID-19 病人中有性别偏向性的重症率和病亡率。

鉴于 X 染色体单体嵌合现象(XCM/LOY)可能和疾病的预后以及对治疗的响应有关系，作者们建议在药物和疫苗临床试验中对确诊病人要实施相应的生物标志物检测。对 X 染色体单体嵌合现象(XCM/LOY)的检测也可能鉴定出人群中最容易发展出 COVID-19 重症的人。

Abstract

The ongoing pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2, COVID-19) has an estimated overall case fatality ratio of 1.38% in China, being 53% higher in males and increasing exponentially with age. Mosaicism for X chromosome monosomy (XCM) shows a similar increase in aging population mostly driven by loss of chromosome Y in males (LOY), and is associated with a raise in all-cause mortality. Using comparative transcriptomic data, we have defined that XCM/LOY is associated with abnormal peripheral blood cell counts with decreased progenitor cells and multiple biomarkers of immune system dysfunction, pro-coagulation activity and increased cardiovascular risk.Several differentially down-regulated genes in XCM/LOY individuals are involved in the initial immune response to SARS-CoV-2 (OR of enrichment=7.23, p=1.5x10-7), mainly interferon-induced genes that code for inhibitors of viral processes. Thus, our data suggest that XCM mosaicism underlies at least part of the sex-biased severity and mortality of COVID-19 in aging patients. Given its potential relevance for modulating prognosis and therapeutic response, we propose that evaluation of LOY and XCM by currently established methods should be implemented as biomarkers in infected patients, including currently ongoing clinical trials with different medications and vaccines for COVID-19. Testing for LOY/XCM at large scale among elderly people may also be helpful to identify still unexposed people who may be especially vulnerable to severe Covid-19 disease.

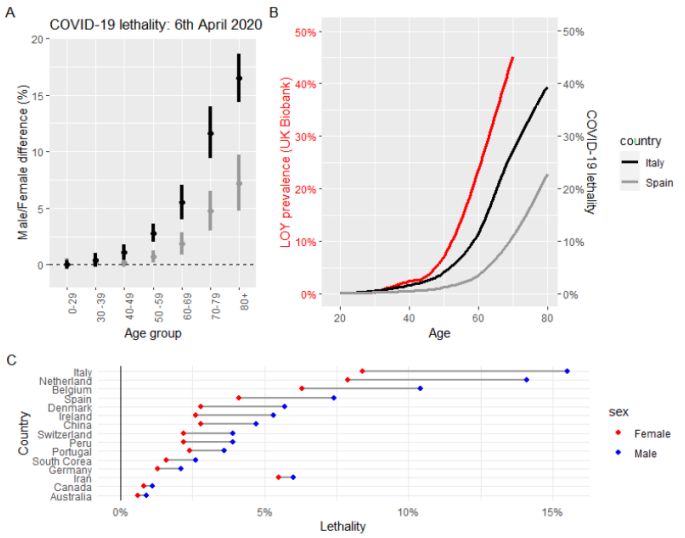

Fig1 (**A**) Increasing male to female difference in mortality rate (hospital deaths) for SARS-CoV-2 in Italy and Spain in the different age intervals (6th April, 2020). (**B**) Curves of mortality rate in Italy (black) and Spain (grey), as well as the prevalence of LOY in men by age (red)[4]. (**C**) Consistent sex-bias in mortality in multiple countries despite non-uniform reporting.

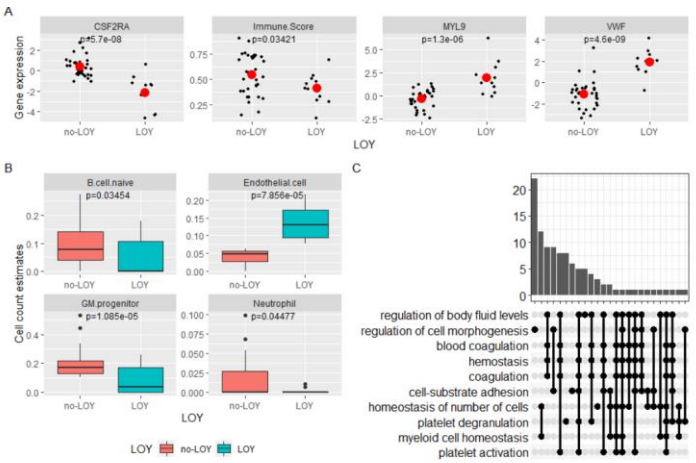

Figure 2: (**A**) Decreased expression of *CSF2RA* mRNA and an increased expression of *MYL9* and *VWF* in individuals with LOY compared with controls with no LOY (mean gene expression in red dot). (**B**) Different predicted cell counts underlying the transcriptomic differences between LOY cases and control individuals (normal). (**C**) Gene Ontology (GO) enrichment of top differentially expressed genes.

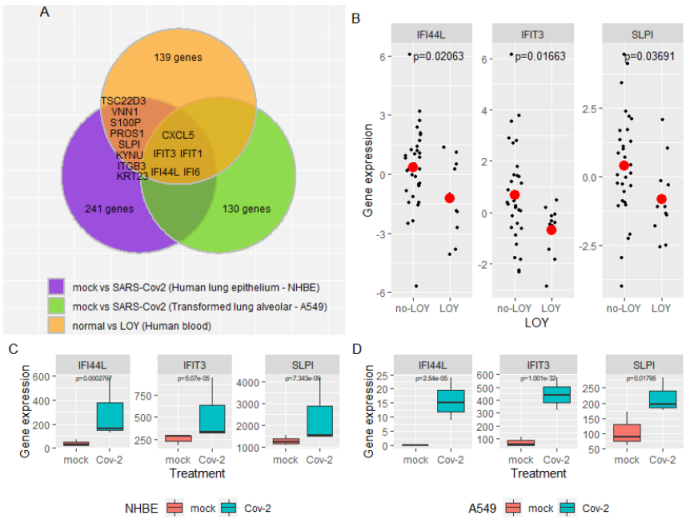

Fig 3: (**A**) overlap between top differentially expressed genes in individuals with LOY and deregulated genes in SARS-CoV-2 infected cells. Panels **B**, **C** and **D** show detailed gene expression patterns of some of these overlapping genes, down-regulated in individuals with LOY (**B**), and over-expression in NHBE (**C**) and A549 (**D**) cell lines infected with SARS-CoV-2.

编者注：很多疾病在男性和女性中有很大的差异。本研究为 COVID-19 宿主遗传学研究提供了一个非常重要的思路。另外，需要了解的是遗传学研究一般会关注 germline 遗传本身，不会特别关注体细胞出现的突变。

8. 英国生物样本库

英国生物样品库是一个国家以及国际的健康资源库，是一个独立的注册慈善组织，目的在于提高预防、诊断以及治疗一系列严重危及生命的包括癌症、心脏并、中风、糖尿病、风湿疾病、骨质疏松、眼睛疾患、抑郁以及不同类型的痴呆。英国生物样品库在 2006 到 2010 年间从不同的国家招募了 50 万名 40-69 岁的志愿者参与到项目。这些志愿者通过了各种检查并且提供了血液、尿液以及口水样品供将来进行研究。支援者没呢也提供了关于他们的详细信息也同意进行健康随访。经过很多年的工作，这个生物样品库会成为一个帮助科学家 q 什么一些人后来发展出特定的疾病而另一些人不会的强大的资源。

来源：https://www.ukbiobank.ac.uk/

UK Biobank is a major national and international health resource, and a registered charity in its own right, with the aim of improving the prevention, diagnosis and treatment of a wide range of serious and life-threatening illnesses – including cancer, heart diseases, stroke, diabetes, arthritis, osteoporosis, eye disorders, depression and forms of dementia. UK Biobank recruited 500,000 people aged between 40-69 years in 2006-2010 from across the country to take part in this project. They have undergone measures, provided blood, urine and saliva samples for future analysis, detailed information about themselves and agreed to have their health followed. Over many years this will build into a powerful resource to help scientists discover why some people develop particular diseases and others do not.

UK Biobank was established by the Wellcome Trust medical charity, Medical Research Council, Department of Health, Scottish Government and the Northwest Regional Development Agency. It has also had funding from the Welsh Government, British Heart Foundation, Cancer Research UK and Diabetes UK. UK Biobank is supported by the National Health Service (NHS). UK Biobank is open to bona fide researchers anywhere in the world, including those funded by academia and industry. The medical research project is a non-profit charity which had initial funding of about £62 million.

UK Biobank has had additional funding for extra baseline measurements (such as the eye measures and saliva samples) and has core funding (currently until 2022) that covers storage of samples, and developing the on line access facility that allow scientists to use the resource. In addition to information collected during the baseline assessment, 100,000 UK Biobank participants have worn a 24-hour activity monitor for a week, and 20,000 have undertaken repeat measures. A programme of online questionnaires is being rolled out (diet, cognitive function, work history and digestive health) and UK Biobank has embarked on a major study to scan (image) 100,000 participants (brain, heart, abdomen, bones & carotid artery). UK Biobank is linking to a wide range of electronic health records (cancer, death, hospital episodes, general practice), and is developing algorithms to accurately identify diseases and their sub-sets. Blood biochemistry

is being analysed (such as hormones & cholesterol).

Genotyping has been undertaken on all 500,000 participants and these data are being used in health research. GSK & Regeneron have successfully applied to exome sequence the samples. Data are made available for approved researchers undertaking health research in the public good. They are obliged to return their findings to UK Biobank when their work is complete, so that other scientists can benefit. UK Biobank hopes to follow its participants for many years, since this strengthens the resource. Though only people aged 40-69 years were recruited into the project, there is no upper age limit for participants.

UK Biobank's Principal Investigator and Chief Executive is Rory Collins, who is also British Heart Foundation (BHF) Professor of Medicine and Epidemiology at the University of Oxford.