新型冠状病毒信息简报

第 18 期（2020 年 4 月 5 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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免责申明：
本简报仅作为科研参考之用，不构成医疗建议，如您怀疑自己感染新型冠状病毒，请去正规医院或者咨询医生

1. 2020 年 4 月 4 日疫情

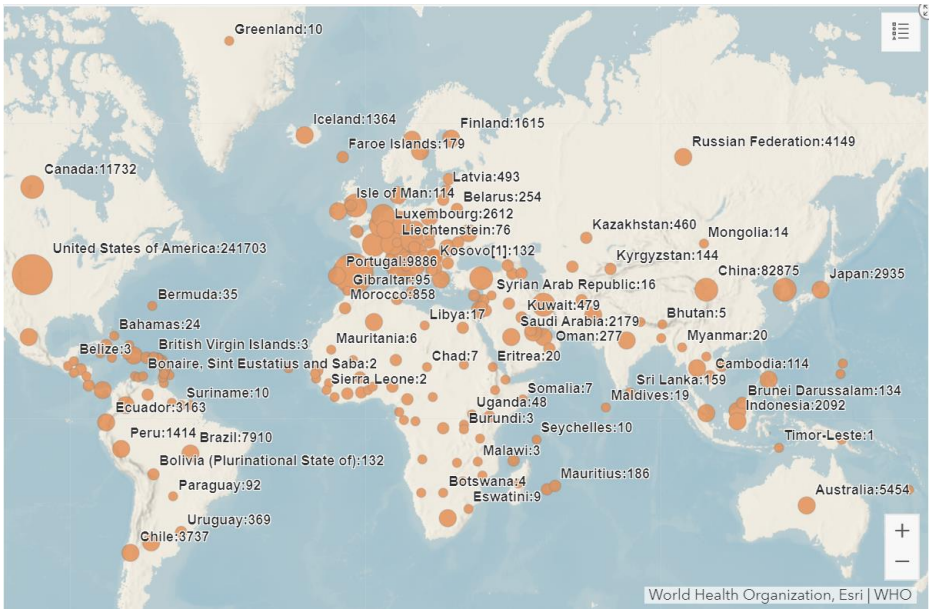
数据来源：WHO

发布时间：2020 年 4 月 4 日北京时间下午 4 点

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

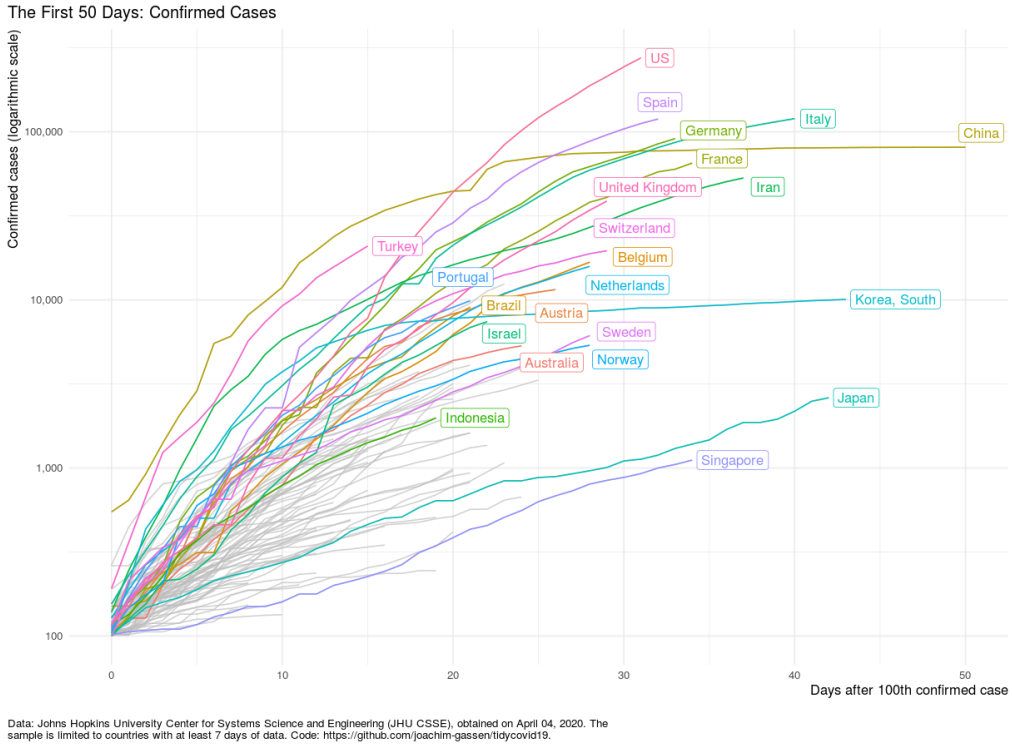
根据 WHO 提供的数据，2020 年 4 月 4 日全球累计确诊新型冠状病毒病人 1051635 例，当日新增确诊 79332 例，累计死亡 56985 例，当日新增死亡 6664。

中国累计确诊 82875 例，累计死亡 3335 例，当日新增确诊 73 例，新增死亡 4 例。



世界各国家地区累计确诊病例总数，圆圈越大代表总病例数越多

（链接：https://experience.arcgis.com/experience/62c28590b5ae41ef920e4d5a4128504a



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

2. 在少量捐献的血液中检测到 SARS-CoV-2 病毒 RNA

Severe Acute Respiratory Syndrome Coronavirus 2 RNA Detected in Blood Donations

来源：Emerg Infect Dis
发布时间：2020-04-03
来源链接：https://wwwnc.cdc.gov/eid/article/26/7/20-0839_article#tnF1
通讯作者：Lunan Wang，Lan Wang
作者单位：中国医学科学院、武汉血液中心、上海浩源生物科技有限公司
编译：宋张悦
内容摘要：

由于 COVID-19 的爆发，中国血液供应的安全成为一个主要问题。从 2020 年 1 月 25 日开始，研究人员对在武汉血液中心收集的所有捐献品进行筛查。截至 3 月 4 日，通过 RT-PCR 筛查和回顾性分析，发现 4 例无症状献血者的血液样本中病毒 RNA 呈阳性。他们的献血时间和 COVID-19 症状如下图 1 所示。

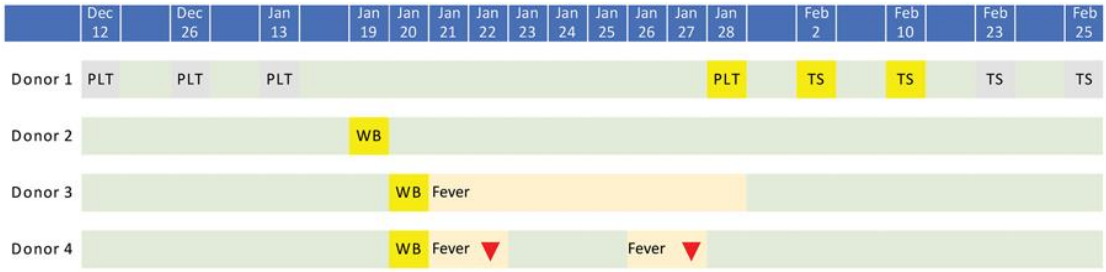


图 1. 4 例献血者的捐献时间和 COVID-19 症状。灰色表示 SARS-CoV-2 RNA 阴性；黄色表示阳性结果。绿色表示供体无症状或体温恢复正常；橙色表示发烧；红色三角形表示捐赠者在服用了退热药后退烧。PLT：血小板；TS：咽喉拭子；WB：全血。

研究人员将 6-8 个血浆样本混合检测或者取 1.6mL 血浆样本单独检测。截至 3 月 4 日，研究人员已经对 2430 例捐献样本进行了筛查，包括 1656 例血小板和 774 例全血。在 1 月 28 日捐献的一份血小板样本中发现了第一例弱阳性样本。研究人员还对 2019 年 12 月 21 日至 2020 年 1 月 22 日期间收集的 4995 份捐赠进行了回顾性检测，采用混合池方法检测。在 1 月 19 日捐献的一份全血样本中检测到了弱阳性。第一例和第二例捐献者都无症状，期间分别在武汉方舱医院和家中进行隔离。1 月 20 日，又发现了 2 名全血捐赠者，结果均为弱阳性，之后出现了发烧症状。通过 ELISA 进一步对这 4 例样本检测 SARS-CoV-2 的特异性抗体 IgG 和 IgM，结果为阴性，提示早期感染的可能性，需要对这些供者进行随访。

在对 1-2 月期间献血的献血者进行电话随访中，研究人员确定了 33 名在献血后出现发烧症状的献血者，他们的捐献品均被停止流通使用。另外，发现阳性的样本集中在 1 月下旬，之后的样本中没有检测到病毒，说明政府对献血者采取的严格管控措施是有效的。随着越来越多的无症状病例的出现，用高灵敏度的检测方法筛选献血者的病毒 RNA，将对确保血液安全至关重要。

Abstract

Because of high rates of 2019 novel coronavirus disease in Wuhan, China, Wuhan Blood Center began screening for severe acute respiratory syndrome coronavirus 2 RNA on January 25, 2020. We screened donations in real-time and retrospectively and found plasma samples positive for viral RNA from 4 asymptomatic donors.

3. 生活污水可以揭示冠状病毒的爆发范围

对生活污水进行检测也可以提供病毒重新回来的预警信号

How sewage could reveal true scale of coronavirus outbreak

Wastewater testing could also be used as an early-warning sign if the virus returns.

来源：nature

发布时间：2020.4.3

https://www.nature.com/articles/d41586-020-00973-x

由于大部分的人可能不会接受结合病毒检测，世界各地 10 多个课题组开始通过对污水的分析来估计社区里总感染人数。目前为止，科学家们已经在荷兰、美国和瑞典的污水里检测到病毒的踪迹。

一个污水处理场处理的污水可能来自于百万以上的人。对污水的检测可以覆盖轻症和无症状的人进而能更好的估计新型冠状病毒到底传播到什么范围了。

为了对感染得范围进行定量，科学家们需要知道根据污水里的病毒 RNA 浓度以及粪便里的 RNA 含量来推断有多少人受到感染。

科学学也需要确保取样具有代表性，而不是只是个别的事件点的取样。另外，他们用的测试需要能够检测低浓度的病毒。

由于大学和实验室关门以及缺少检测相关的试剂，一些检测病毒的努力被搁置了。

疫情控制后，对污水的常规检测，也可以作为病毒再次爆发的无创性早期预警信号。

科学家在荷兰 Tilburg 的医院确诊第一例 COVID-19 病人的 4 天之后就在该城的 Schiphol 机场的污水中检测到了 SARS-CoV-2。科学家们正在将对污水的检测扩展到荷兰的 12 个省的首会城市以及 12 个还没有病例的城市。在 Amersfoort 城中，科学家在发现社区中第一例病人之前就从污水中检测到了病毒。

有研究表明，感染之后的 3 天之内病人的粪便里面就可能出现 SARS-CoV-2，但此时离病人发生任何症状以及严重到要去医院还有好长一段时间—可能长达 2 周。检测污水里的病毒可以给公共卫生官员 7 到 10 天的提前量去决定是否应该采取诸如封城之类的措施。

更早的检测到病毒，可以减少 COVID-19 引起的健康和经济损失。特别是对明年而言。

亚利桑那大学环境微生物学家讲污水检测在过去几十年里被用来监测骨髓非质炎的疫苗是否成功。这个方法同样可以拿来检验现在的抗疫手段比如社交距离的有效性。

More than a dozen research groups worldwide have started analysing wastewater for the new coronavirus as a way to estimate the total number of infections in a community, given that most people will not be tested. The method could also be used to detect the coronavirus if it returns to communities, say scientists. So far, researchers have found traces of the virus in the Netherlands, the United States and Sweden.

Analysing wastewater — used water that goes through the drainage system to a treatment facility — is one way that researchers can track infectious diseases that are excreted in urine or faeces, such as SARS-CoV-2.

One treatment plant can capture wastewater from more than one million people, says Gertjan Medema, a microbiologist at KWR Water Research Institute in Nieuwegein, the Netherlands. Monitoring influent at this scale could provide better estimates for how widespread the coronavirus is than testing, because wastewater surveillance can account for those who have not been tested and have only mild or no symptoms, says Medema, who has detected SARS-CoV-2 genetic material — viral RNA — in several treatment plants in the Netherlands. “Health authorities are only seeing the tip of the iceberg.”

But to quantify the scale of infection in a population from wastewater samples, researchers

say the groups will need to find out how much viral RNA is excreted in faeces, and extrapolate the number of infected people in a population from concentrations of viral RNA in wastewater samples.

Researchers will also need to ensure that they are looking at a representative sample of what is being excreted by the population and not just one snapshot in time, and that their tests can detect the virus at low levels, say scientists representing the Queensland Alliance for Environmental Health Sciences in Australia, a research centre that advises the state government on environmental-health risks. And it's important that wastewater surveillance, should it be feasible, does not take away resources from the testing of individuals, the group says.

Some efforts to monitor the virus have been stalled by university and laboratory shut-downs and the limited availability of reagents to conduct tests — the same ones used in clinics, which are already in short supply, says Kyle Bibby, an environmental engineer at the University of Notre Dame in Indiana. “We don't want to contribute to the global shortage,” he says.

Early-warning sign

Infection-control measures, such as social distancing, will probably suppress the current pandemic, but the virus could return once such measures are lifted. Routine wastewater surveillance could be used as a non-invasive early-warning tool to alert communities to new COVID-19 infections, says Ana Maria de Roda Husman, an infectious-disease researcher at the Netherlands National Institute for Public Health and the Environment in Bilthoven. The institute has previously monitored sewage to detect outbreaks of norovirus, antibiotic-resistant bacteria, poliovirus and measles.

de Roda Husman’s group detected traces of SARS-CoV-2 in wastewater at Schiphol Airport in Tilburg only four days after the Netherlands confirmed its first case of COVID-19 using clinical testing. The researchers now plan to expand sampling to the capitals of all 12 provinces in the Netherlands and 12 other sites that have not had any confirmed cases. Medema’s group found viral RNA in the city of Amersfoort before infections had been reported in the community.

Studies have also shown that SARS-CoV-2 can appear in faeces within three days of infection, which is much sooner than the time taken for people to develop symptoms severe enough for them to seek hospital care — up to two weeks — and get an official diagnosis, says Tamar Kohn, an environmental virologist at the Swiss Federal Institute of Technology in Lausanne. Tracking viral particles in wastewater could give public-health officials a head start on deciding whether to introduce measures such as lockdowns, she says. “Seven to ten days can make a lot of difference in the severity of this outbreak.”

Earlier identification of the virus’s arrival in a community might limit the health and economic damage caused by COVID-19, especially if it comes back next year, says Bibby. Wastewater monitoring has been used for decades to assess the success of vaccination campaigns against poliovirus, says Charles Gerba, an environmental microbiologist at The University of Arizona in Tucson. The approach could also be used to measure the effectiveness of interventions such as social distancing, says Gerba, who has found traces of SARS-CoV-2 in raw sewage in Tucson

4. IL-6 水平可预测住院有症状 COVID-19 患者的呼吸衰竭

Level of IL-6 predicts respiratory failure in hospitalized symptomatic COVID-19 Patients

来源：medrxiv 发布时间：2020.4.4

链接：https://www.medrxiv.org/content/10.1101/2020.04.01.20047381v1

通讯作者：Tobias Herold MD, Vindi Jurinovic PhD 作者单位：慕尼黑大学附属第三医院、德国环境卫生中心、慕尼黑大学

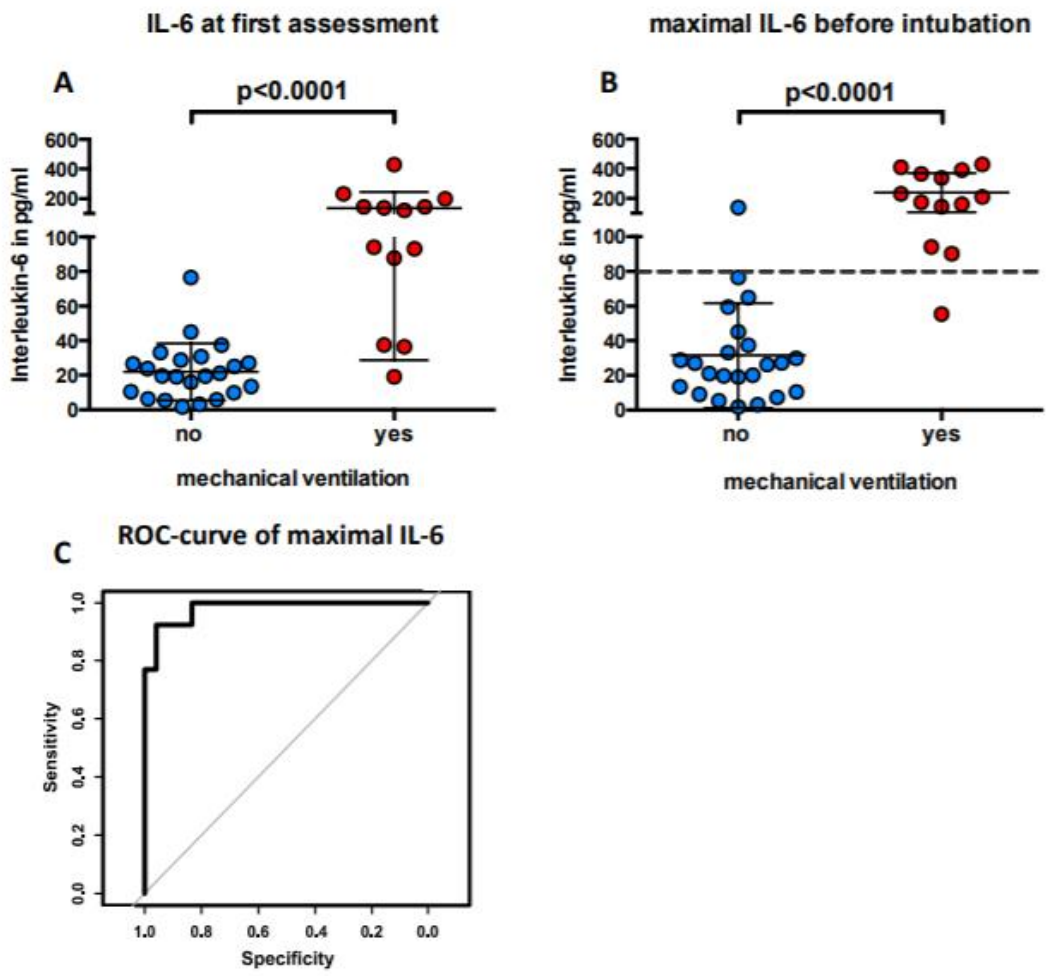
编译：张丽双

摘要：这篇文章希望能够确定一些 COVID-19 重症（呼吸衰竭，需要机械通气）相关的因素，帮助医生分流患者，减轻重症病房负担。文中分析了 2020 年 2 月 29 日至 3 月 27 日 PCR 确诊的 40 位 COVID-19 感染患者。需要机械通气的患者 13/40（32.5%）在年龄、合并症、影像学发现、呼吸频率或 qSofa 评分方面无差异。然而 IL-6 的升高与机械通气需求密切相关（p = 1.2.10-5）。与此同时，疾病期间每位患者的最大 IL-6 水平（临界值 80 pg / ml）可准确预测呼吸衰竭（p = 1.7.10-8，AUC = 0.98）。 IL-6 水平≥80 pg / ml 的患者的呼吸衰竭风险是 IL-6 水平较低患者的 22 倍。这项研究表明 IL-6 是一种有效的标志物，并且有可能能够高度准确地预测即将发生的呼吸衰竭并帮助医生在早期正确分流患者。

Abstract：The pandemic Coronavirus-disease 19 (COVID-19) is characterized by a heterogeneous clinical course. While most patients experience only mild symptoms, a relevant proportion develop severe disease progression with increasing hypoxia up to acute respiratory distress syndrome. The substantial number of patients with severe disease have strained intensive care capacities to an unprecedented level. Owing to the highly variable course and lack of reliable predictors for deterioration, we aimed to identify variables that allow the prediction of patients with a high risk of respiratory failure and need of mechanical ventilation.

Patients with PCR proven symptomatic COVID-19 infection hospitalized at our institution from 29th February to 27th March 2020 (n=40) were analyzed for baseline clinical and laboratory findings. Patients requiring mechanical ventilation 13/40 (32.5%) did not differ in age, comorbidities, radiological findings, respiratory rate or qSofa score. However, elevated interleukin-6 (IL-6) was strongly associated with the need for mechanical ventilation (p=1.2.10-5). In addition, the maximal IL-6 level (cutoff 80 pg/ml) for each patient during disease predicted respiratory failure with high accuracy (p=1.7.10-8, AUC=0.98). The risk of respiratory failure for patients with IL-6 levels of ≥ 80 pg/ml was 22 times higher compared to patients with lower IL-6 levels. In the current situation with overwhelmed intensive care units and overcrowded emergency rooms, correct triage of patients in need of intensive care is crucial. Our study shows that IL-6 is an effective marker that might be able to predict upcoming respiratory failure with high accuracy and help physicians correctly allocate patients at an early stage.

Figure 1



5. Ruxolitinib 治疗 COVID-19 的临床试验

根据诺华公司官网的消息，Novartis 在 4 月 2 日宣布和 Incyte 合作开始一项三期临床试验，研究 Jakavi（ruxolitinib）治疗 COVID-19 病人里发生的严重免疫过激也叫做细胞因子风暴，这是一项危及病人生命的呼吸系统并发症。today announced plans to initiate a https://www.novartis.com/news/media-releases/novartis-announces-plan-initiate-clinical-study-jakavi-severe-covid-19-patients-and-establish-international-compassionate-use-program

Ruxolitinib 又叫 JAKAVI，是 JAK1 和 JAK2 的抑制剂，是一种获批可以治疗骨髓纤维化，多囊性血症，和移植排异的药物。该药物在 101 个国家获得批准用于治疗这些适应症中的一种或者多种。

4 月初有两项 Ruxolitinib 治疗 COVID-19 的临床试验注册。

注册 1 链接：https://clinicaltrials.gov/ct2/show/NCT04331665

试验的名称是：

A Single Arm Open-label Clinical Study to Investigate the Efficacy and Safety of Ruxolitinib for the Treatment of COVID-19 Pneumonia

一个研究 Ruxolitinib 治疗 COVID-19 的安全性和有效性的单臂开放标签临床试验。

这项试验由 University Health Network, Toronto（加拿大）主持，注册于 4 月 2 日，将于 4 月 6 日开始，试验完全结束的事件是 2021 年 1 月。
试验涉及要招募的病人是 12 岁以上 COVDI-19 核酸阳性，并且需要吸氧保持血氧饱和度 93%的病人。计划招募的病人数目是约 64 名。
试验的主要临床终点是 6 个月内 COVID-19 病人变成危重症的比例（需要机械通气、以及动脉氧饱和比（FiO2） 超过 60%）。

注册 2 链接：
https://clinicaltrials.gov/ct2/show/NCT04334044
试验名称：Treatment of Severe Acute Respiratory Syndrome Caused by COVID-19 With Ruxolitinib
用 Ruxolitinib 治疗 COVID-19 引起的严重急性呼吸综合症
这个 phase I, II 试验由 Grupo Cooperativo de Hemopatías Malignas（墨西哥）主持，注册于 4 月 3 日，计划开始于 2020 年 4 月 1 日，结束于 2020 年 6 月 1 日。是一个单臂开放试验。
试验计划招募 20 名 18 岁以上的病人。入组条件是核酸检测阳性，呼吸急促或者困难，存在胸部影像学改变。
试验的主要终点是考察用药 14 天内病人呼吸症状的缓解。

6. 冠状病毒能让你生多严重的病？答案可能是你的基因

How sick will the coronavirus make you? The answer may be in your genes
来源：Science
发布时间：2020-03-27
来源链接：https://www.sciencemag.org/news/2020/03/how-sick-will-coronavirus-make-you-answer-may-be-your-genes?from=timeline&isappinstalled=0#
内容摘要：
COVID-19，由新的大流行性冠状病毒引起，具有怪异的选择性。只有部分感染者得病，虽然大多数危重病人都是老年人，或有心脏病等复杂问题，但部分死亡的 COVID-19 病人以前是健康的，甚至是相对年轻的。研究人员现在正准备对病人的基因组进行 DNA 变异的研究，以解释这一谜团。这些发现可以用来确定那些最有可能患重病的人和那些可能受到保护的人，也可以指导寻找新的治疗方法。
这些项目包括：正在进行的数千名参与者的 DNA 研究，其中一些人现在感染了冠状病毒；新工作包括在意大利等重灾区收集 COVID-19 患者 DNA。目的是比较没有糖尿病、心脏病或肺病等潜在疾病的 COVID-19 重症患者，与轻症或无症状患者的 DNA。“我们看到临床结果和各国之间的巨大差异。这其中有多少是由遗传易感性解释的，这是一个疑团。”芬兰赫尔辛基大学分子医学研究所（FIMM）的遗传学家 Andrea Ganna 说。
一些研究人员认为，很难预测这些基因搜索会产生什么结果。但是，国家过敏和传染病研究所的免疫学家 Philip Murphy 提出“编码细胞表面蛋白血管紧张素转换酶 2（ACE2）的基因，冠状病毒利用它进入气道细胞。ACE2 基因的变异可能使病毒进入细胞变得更容易或者更难。”他的实验室在另一种人类细胞表面蛋白 CCR5 中发现了一种相对常见的突变，这使得一些人不易感染艾滋病病毒。
同时也隶属于美国 Broad 研究所的 Ganna 领导了一项汇集来自世界各地的 COVID-19 患者基因数据的工作。Ganna 说，这个想法“很自然地”出现在大约两周前，当时“每个人都坐在电脑前看着这场危机”。

Ganna 和 FIMM 主任 Mark Daly 很快为他们的项目 COVID-19 宿主遗传学计划（Host Genetics Initiative）创建了一个网站（https://www.covid19hg.org/），并联系了负责大型生物库研究的同事，这些研究跟踪了数千名志愿者多年，寻找他们的 DNA 与健康之间的联系。至少有十几家生物银行（主要来自欧洲和美国）表示有兴趣，愿意在 COVID-19 患者同意后提供他们的数据。其中包括 FinnGen，该公司拥有 500 万芬兰人口中 5%的 DNA 样本和健康数据，以及西奈山伊坎医学院（Icahn School of Medicine）生物库，拥有 5 万名参与者的数据。

该项目本月在推特上发布消息称，拥有 50 万参与者 DNA 数据的全球最大生物银行之一的 UK Biobank 也计划将参与者的 COVID-19 健康数据添加到其数据集中。冰岛公司 deCODE Genetics，为冰岛的大部分人口提供了新冠检测，该公司首席执行官说，政府已经许可他们将这些相关数据和任何随后的 COVID-19 症状添加到其数据库中，该数据库包含冰岛 36.4 万居民中一半的基因组和健康数据。

另一项鉴定保护性或易感 DNA 变异的工作是由哈佛大学 eorge Church 领导的个人基因组项目，该项目招募愿意分享完整基因组、组织样本和健康数据的人进行研究。本月早些时候，它向数千名参与者发送了问卷，询问他们的 COVID-19 状态。600 多位美国人在 48 小时内作出了回应。但他的团队还没有加入甘纳的合作。

与 Ganna 计划合作的其他研究人员正在医院内直接招募 COVID-19 患者进行基因组学研究。意大利锡耶纳大学的遗传学家 Alessandra Renieri 提到，预计，意大利至少有 11 家医院将向她的团队给予了伦理认可，在患者同意后，她的团队可以从患者身上采集 DNA 样本。她认为（宿主）基因差异是导致严重急性肺炎易感性的关键因素。

洛克菲勒大学的儿科医生 Jean-Laurent Casanova 专门研究能使健康的年轻人易患某些严重疾病的罕见基因，他正在利用世界各地的儿科医生网络，寻找相对较少的能发展成 COVID-19 重症的年轻人。他解释说："我们只研究以前健康的患者"和 50 岁以下的患者，因为他们的 COVID-19 重症更可能有遗传基础。

除了 ACE2 受体的基因变异外，科学家还想了解影响免疫系统对病毒和细菌反应的人类白细胞抗原基因的差异是否会影响 COVID-19 的严重程度。斯坦福大学人类遗传学家 ManuelRiva 的团队希望跟进一项中国研究小组在预印本中的发现：O 型血的人可能对病毒不易感。

随着冠状病毒的迅速传播，可用于基因搜索的 COVID-19 患者的数量也会快速增长。Ganna 预计，第一批易感基因可能在几个月内被鉴定出来。

Abstract

COVID-19, caused by the new pandemic coronavirus, is strangely—and tragically—selective. Only some infected people get sick, and although most of the critically ill are elderly or have complicating problems such as heart disease, some killed by the disease are previously healthy and even relatively young. Researchers are now gearing up to scour the patients' genomes for DNA variations that explain this mystery. The findings could be used to identify those most at risk of serious illness and those who might be protected, and they might also guide the search for new treatments.

The projects range from ongoing studies with DNA for many thousands of participants, some now getting infected with the coronavirus, to new efforts that are collecting DNA from COVID-19 patients in hard-hit places such as Italy. The goal is to compare the DNA of people who have serious cases of COVID-19 (which stands for coronavirus disease 2019)—but no underlying disease like diabetes, heart or lung disease—with those with

mild or no disease. “We see huge differences in clinical outcomes and across countries. How much of that is explained by genetic susceptibility is a very open question,” says geneticist Andrea Ganna of the University of Helsinki’s Institute for Molecular Medicine Finland (FIMM).

It’s hard to predict what will pop out from these gene hunts, some researchers say. But there are obvious suspects, such as the gene coding for the cell surface protein angiotensin-converting enzyme 2 (ACE2), which the coronavirus uses to enter airway cells. Variations in the ACE2 gene that alter the receptor could make it easier or harder for the virus to get into cells, says immunologist Philip Murphy of the National Institute of Allergy and Infectious Diseases, whose lab identified a relatively common mutation in another human cell surface protein, CCR5, that makes some people highly resistant to HIV.

Ganna heads up a major effort to pool COVID-19 patients’ genetic data from around the world. The idea “came quite spontaneously” about 2 weeks ago when “everyone was sitting at their computers watching this crisis,” says Ganna, who is also affiliated with the Broad Institute, a U.S. genomic powerhouse.

He and FIMM Director Mark Daly quickly created a website for their project, the COVID-19 Host Genetics Initiative, and reached out to colleagues who run large biobank studies that follow thousands of volunteers for years to look for links between their DNA and health. At least a dozen biobanks, mostly in Europe and the United States, have expressed interest in contributing COVID-19 data from participants who agreed to this. Among them are FinnGen, which has DNA samples and health data for 5% of the 5 million–person Finnish population, and the 50,000-participant biobank at the Icahn School of Medicine at Mount Sinai.

The UK Biobank, one of world’s largest with DNA data for 500,000 participants, also plans to add COVID-19 health data from participants to its data set, the project tweeted this month. And the Icelandic company deCODE Genetics, which is helping test much of the nation’s population to see who is infected with the new coronavirus, has received government permission to add these data and any subsequent COVID-19 symptoms to its database, which contains genome and health data on half of Iceland’s 364,000 inhabitants, says its CEO Kári Stefánsson. “We will do our best to contribute to figuring this out,” Stefánsson says.

Another effort to identify protective or susceptibility DNA variants is the Personal Genome Project led by Harvard University’s George Church, which recruits people willing to share their full genome, tissue samples, and health data for research. Earlier this month, it sent questionnaires to its thousands of participants, asking about their COVID-19 status. More than 600 in the United States responded within 48 hours. “It seems that most people want to do their part,” says Church, whose group isn’t yet part of Ganna’s collaboration.

Other researchers working with Ganna’s initiative are recruiting COVID-19 patients directly within hospitals for such genomics studies. Italian geneticist Alessandra Renieri of the University of Siena expects at least 11 hospitals in the nation to give ethics approval for her team to collect DNA samples from willing patients. “It is my opinion that [host] genetic differences are a key factor … for susceptibility to severe acute pneumonia,” Renieri says. Pediatrics researcher Jean-Laurent Casanova at the Rockefeller University, who specializes in identifying rare genes that can make healthy young people susceptible to

certain serious diseases, is drawing on a network of pediatricians around the world to look for the relatively few young people who develop COVID-19 serious enough to get admitted to intensive care. “We study exclusively patients who were previously healthy” and under 50, as their serious COVID-19 illness is more likely to have a genetic basis, he explains.

In addition to genetic variants of the ACE2 receptor, scientists want to see whether differences in the human leukocyte antigen genes, which influence the immune system’s response to viruses and bacteria, affect disease severity. And some investigators want to follow up a finding, which a Chinese team reported in a preprint: that people with type O blood may be protected from the virus. “We’re trying to figure out if those findings are robust,” says Stanford University human geneticist Manuel Rivas, who is contributing to Ganna’s initiative.

The catastrophic spread of the coronavirus should soon increase the number of COVID-19 patients available to these gene hunts. And that could speed findings. Ganna expects the first susceptibility genes could be identified within a couple of months.

7. FDA 批准的药物 Ivermerctin 在体外实验中可以抑制 SARS-CoV-2 的复制

The FDA-approved Drug Ivermectin inhibits the replication of SARS-CoV-2 in vitro

来源：Antiviral Research

发布事件：2020.4.3

链接：https://www.sciencedirect.com/science/article/pii/S0166354220302011

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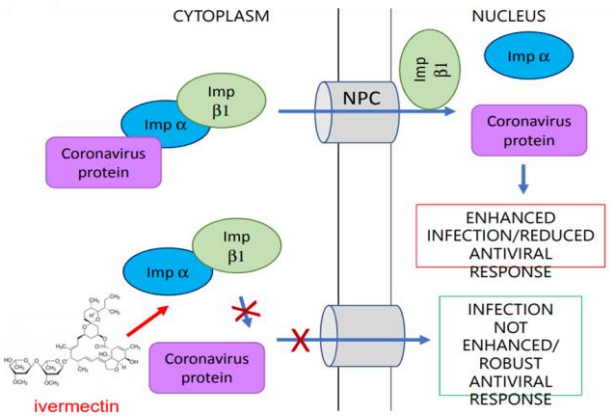
近些年作者和其他课题组发现 FDA 批准的抗寄生虫的的药物 Ivermectin 在体外有广谱的抗病毒活性，并对该药物的抗 HIV 的机制进行了初步的研究。该研究中作者发现该药物也有抑制 SARS-CoV-2 的活性。在感染 2 小时后的绿猴细胞系 Vero-hSLAM 培养体系中加入一次药物，就可以将 48 小时 RNA 病毒量降低 5000 倍。Ivermectin 是 WHO 必备药物的名单上，所以在全世界各地容易获得。基于以上原因，作者建议进一步在临床中对该药治疗 COVID-19 的有效性进行研究。

作者提出的 Ivermectin 可能的抗病毒机制



Although several clinical trials are now underway to test possible therapies, the worldwide

response to the COVID-19 outbreak has been largely limited to monitoring/containment. We report here that Ivermectin, an FDA-approved anti-parasitic previously shown to have broad-spectrum anti-viral activity in vitro, is an inhibitor of the causative virus (SARS-CoV-2), with a single addition to Vero-hSLAM cells 2 hours post infection with SARS-CoV-2 able to effect ~5000-fold reduction in viral RNA at 48 h. Ivermectin therefore warrants further investigation for possible benefits in humans.