CDC A-Z INDEX Y

Q

## Public Health Genomics and Precision Health Knowledge Base (v6.8)

**PHGKB** 

About

**MyPHGKB** 

Specialized PHGKB

Genomics (A-Z)

Office of Genomics and **Precision Public Health** 

State Public Health Genomics Programs Map

My Family Health Portrait

Genomics & Health Impact Weekly Scan

(Current Edition) Advanced Molecular

**Detection Weekly Clips** (Current Edition)

**Non-Genomics Precision** Health Update

**CDC-authored Publications** Update

**COVID-19 Genomics** Precision Health Update

All Databases

Release Note

Contact Us

**DataSet Download Center** 

Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

Tweet

Published on 10/15/2020

Recommend

COVID-19 Genomics and Precision Public Health Weekly Update Content

• Pathogen and Human Genomics Studies

 Non-Genomics Precision Health Studies News. Reviews and Commentaries

Pathogen and Human Genomics Studies

AK Banerjee et al, Cell, October 8, 2020

**Share** 

 Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing. Joung Julia et al. The New England journal of medicine 2020 Oct (15) 1492-1494

polymerase-chain-reaction (RT-qPCR) assays. STOP (SHERLOCK testing in one pot) is a streamlined assay that combines simplified extraction of viral RNA with isothermal amplification and CRISPR-mediated detection. This test can be performed at a single temperature in less than an hour and with minimal equipment. SARS-CoV-2 disrupts splicing, translation, and protein trafficking to suppress host defenses

We describe a simple test for detection of SARS-CoV-2. The sensitivity of this test is similar to that of reverse-transcription-quantitative

We define the interactions between SARS-CoV-2 proteins and human RNAs. NSP16 binds to the mRNA recognition domains of the U1 and U2 splicing RNAs and acts to suppress global mRNA splicing upon SARS-CoV-2 infection. NSP1 binds to 18S ribosomal RNA in the mRNA entry

channel of the ribosome and leads to global inhibition of mRNA translation upon infection. Finally, NSP8 and NSP9 bind to the 7SL RNA in the Signal Recognition Particle and interfere with protein trafficking to the cell membrane upon infection. Disruption of each of these essential cellular functions acts to suppress the interferon response to viral infection. Our results uncover a multipronged strategy utilized by SARS-CoV-2 to antagonize essential cellular processes to suppress host defenses. Large-scale Multi-omic Analysis of COVID-19 Severity KA Overmeyer et al, Cell Systems, October 7, 2020

We surveyed biomolecules in 102 COVID-19 and 26 non-COVID-19 patient blood samples. We found 219 biomolecules strongly associated

Brandsma Eelke et al. The Journal of infectious diseases 2020 Oct

Genomic evidence for reinfection with SARS-CoV-2: a case study

RL Tillet et al, Lancet Inf Diseases, October 12, 2020

sacrificing sensitivity/specificity.

with COVID-19 status and severity. We observed pronounced dysregulation of lipid transport and neutrophil degranulation.

 Clinical impact of molecular point-of-care testing for suspected COVID-19 in hospital (COV-19POC): a prospective, interventional, nonrandomised, controlled study NJ Brendish et al, Lancet Resp Medicine, October 8, 2020

This is a prospective, interventional, non-randomized, controlled study of molecular point-of-care testing in patients aged 18 years or older presenting with suspected COVID-19. Point-of-care testing was associated with large reductions in time to results and could lead to

Evaluation of a genetic risk score for severity of COVID-19 using human chromosomal-scale length variation. Toh Christopher et al. Human genomics 2020 Oct (1) 36

improvements in infection control measures and patient flow compared with centralized laboratory PCR testing.

We compared 981 patients from the UK Biobank dataset who had a severe reaction to SARS-CoV-2 infection before 27 April 2020 to a similar number of age-matched patients drawn for the general UK Biobank population. For each patient, we built a profile of 88 numbers characterizing the chromosomal-scale length variability of their germ line DNA. Rapid, sensitive and specific SARS coronavirus-2 detection: a multi-center comparison between standard qRT-PCR and CRISPR based DETECTR.

DETECTR, a combination of isothermal reverse transcriptase loop mediated amplification (RT-LAMP) and subsequent Cas 12 by stander nuclease activation by amplicon targeting ribonucleoprotein complexes, could be a faster and cheaper alternative to qRT-PCR without

A 25-year-old man who was a resident of Washoe County in the US state of Nevada presented to health authorities on two occasions with symptoms of viral infection. The patient had two positive tests for SARS-CoV-2, separated by two negative tests done during follow-up. Genomic analysis of SARS-CoV-2 showed genetically significant differences between each variant associated with each instance of infection.

SARS-CoV-2 sequencing reveals rapid transmission from college student clusters resulting in morbidity and deaths in vulnerable populations

CS Richmond et al, MEDRXIV, October 14, 2020 La Crosse County, Wisconsin experienced a substantial SARS-CoV-2 outbreak (2,002 cases in September 2020) that coincided with the return

more vulnerable populations. • Safety and Immunogenicity of Two RNA-Based Covid-19 Vaccine Candidates EE Walsh et al, NEJM, October 15, 2020

195 participants underwent randomization. In each of 13 groups of 15 participants, 12 participants received vaccine and 3 received placebo.

BNT162b2 was associated with a lower incidence and severity of systemic reactions than BNT162b1. The vaccine candidates elicited similar

to in-person instruction at three local academic institutions. Genomic sequencing found rapid expansion of two viral substrains. Although the

majority of cases were among college-age individuals, from a total of 111 genomes sequenced we identified rapid transmission of the virus into

dose-dependent neutralizing geometric mean titers, which were similar to or higher than the geometric mean titer of a panel of convalescent serum samples.

Non-Genomics Precision Health Studies Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing.

We describe a simple test for detection of SARS-CoV-2. The sensitivity of this test is similar to that of reverse-transcription-quantitative

of viral RNA with isothermal amplification and CRISPR-mediated detection. This test can be performed at a single temperature in less than an

polymerase-chain-reaction (RT-qPCR) assays. STOP (SHERLOCK testing in one pot) is a streamlined assay that combines simplified extraction

NJ Brendish et al, Lancet Resp Medicine, October 8, 2020

hour and with minimal equipment.

SARS-CoV-2 disrupts splicing, translation, and protein trafficking to suppress host defenses

Joung Julia et al. The New England journal of medicine 2020 Oct (15) 1492-1494

AK Banerjee et al, Cell, October 8, 2020 We define the interactions between SARS-CoV-2 proteins and human RNAs. NSP16 binds to the mRNA recognition domains of the U1 and U2 splicing RNAs and acts to suppress global mRNA splicing upon SARS-CoV-2 infection. NSP1 binds to 18S ribosomal RNA in the mRNA entry channel of the ribosome and leads to global inhibition of mRNA translation upon infection. Finally, NSP8 and NSP9 bind to the 7SL RNA in the

Signal Recognition Particle and interfere with protein trafficking to the cell membrane upon infection. Disruption of each of these essential

cellular functions acts to suppress the interferon response to viral infection. Our results uncover a multipronged strategy utilized by SARS-

CoV-2 to antagonize essential cellular processes to suppress host defenses. Large-scale Multi-omic Analysis of COVID-19 Severity

characterizing the chromosomal-scale length variability of their germ line DNA.

Brandsma Eelke et al. The Journal of infectious diseases 2020 Oct

Genomic evidence for reinfection with SARS-CoV-2: a case study

Safety and Immunogenicity of Two RNA-Based Covid-19 Vaccine Candidates

KA Overmeyer et al, Cell Systems, October 7, 2020 We surveyed biomolecules in 102 COVID-19 and 26 non-COVID-19 patient blood samples. We found 219 biomolecules strongly associated with COVID-19 status and severity. We observed pronounced dysregulation of lipid transport and neutrophil degranulation. Clinical impact of molecular point-of-care testing for suspected COVID-19 in hospital (COV-19POC): a prospective, interventional, nonrandomised, controlled study

This is a prospective, interventional, non-randomized, controlled study of molecular point-of-care testing in patients aged 18 years or older

Evaluation of a genetic risk score for severity of COVID-19 using human chromosomal-scale length variation. Toh Christopher et al. Human genomics 2020 Oct (1) 36

number of age-matched patients drawn for the general UK Biobank population. For each patient, we built a profile of 88 numbers

We compared 981 patients from the UK Biobank dataset who had a severe reaction to SARS-CoV-2 infection before 27 April 2020 to a similar

Rapid, sensitive and specific SARS coronavirus-2 detection: a multi-center comparison between standard qRT-PCR and CRISPR based DETECTR.

presenting with suspected COVID-19. Point-of-care testing was associated with large reductions in time to results and could lead to

improvements in infection control measures and patient flow compared with centralized laboratory PCR testing.

DETECTR, a combination of isothermal reverse transcriptase loop mediated amplification (RT-LAMP) and subsequent Cas 12 by stander nuclease activation by amplicon targeting ribonucleoprotein complexes, could be a faster and cheaper alternative to qRT-PCR without sacrificing sensitivity/specificity.

RL Tillet et al, Lancet Inf Diseases, October 12, 2020 A 25-year-old man who was a resident of Washoe County in the US state of Nevada presented to health authorities on two occasions with

symptoms of viral infection. The patient had two positive tests for SARS-CoV-2, separated by two negative tests done during follow-up.

Genomic analysis of SARS-CoV-2 showed genetically significant differences between each variant associated with each instance of infection.

to in-person instruction at three local academic institutions. Genomic sequencing found rapid expansion of two viral substrains. Although the

majority of cases were among college-age individuals, from a total of 111 genomes sequenced we identified rapid transmission of the virus into

SARS-CoV-2 sequencing reveals rapid transmission from college student clusters resulting in morbidity and deaths in vulnerable populations CS Richmond et al, MEDRXIV, October 14, 2020 La Crosse County, Wisconsin experienced a substantial SARS-CoV-2 outbreak (2,002 cases in September 2020) that coincided with the return

EE Walsh et al, NEJM, October 15, 2020 195 participants underwent randomization. In each of 13 groups of 15 participants, 12 participants received vaccine and 3 received placebo.

BNT162b2 was associated with a lower incidence and severity of systemic reactions than BNT162b1. The vaccine candidates elicited similar

dose-dependent neutralizing geometric mean titers, which were similar to or higher than the geometric mean titer of a panel of convalescent

SARS-CoV-2 disrupts splicing, translation, and protein trafficking to suppress host defenses AK Banerjee et al, Cell, October 8, 2020

hour and with minimal equipment.

News, Reviews and Commentaries

Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing.

Joung Julia et al. The New England journal of medicine 2020 Oct (15) 1492-1494

more vulnerable populations.

serum samples.

channel of the ribosome and leads to global inhibition of mRNA translation upon infection. Finally, NSP8 and NSP9 bind to the 7SL RNA in the Signal Recognition Particle and interfere with protein trafficking to the cell membrane upon infection. Disruption of each of these essential cellular functions acts to suppress the interferon response to viral infection. Our results uncover a multipronged strategy utilized by SARS-CoV-2 to antagonize essential cellular processes to suppress host defenses. Large-scale Multi-omic Analysis of COVID-19 Severity

We surveyed biomolecules in 102 COVID-19 and 26 non-COVID-19 patient blood samples. We found 219 biomolecules strongly associated

with COVID-19 status and severity. We observed pronounced dysregulation of lipid transport and neutrophil degranulation.

Clinical impact of molecular point-of-care testing for suspected COVID-19 in hospital (COV-19POC): a prospective, interventional, non-

We describe a simple test for detection of SARS-CoV-2. The sensitivity of this test is similar to that of reverse-transcription-quantitative

polymerase-chain-reaction (RT-qPCR) assays. STOP (SHERLOCK testing in one pot) is a streamlined assay that combines simplified extraction

of viral RNA with isothermal amplification and CRISPR-mediated detection. This test can be performed at a single temperature in less than an

We define the interactions between SARS-CoV-2 proteins and human RNAs. NSP16 binds to the mRNA recognition domains of the U1 and U2

splicing RNAs and acts to suppress global mRNA splicing upon SARS-CoV-2 infection. NSP1 binds to 18S ribosomal RNA in the mRNA entry

characterizing the chromosomal-scale length variability of their germ line DNA.

Brandsma Eelke et al. The Journal of infectious diseases 2020 Oct

Genomic evidence for reinfection with SARS-CoV-2: a case study

Safety and Immunogenicity of Two RNA-Based Covid-19 Vaccine Candidates

RL Tillet et al, Lancet Inf Diseases, October 12, 2020

CS Richmond et al, MEDRXIV, October 14, 2020

NJ Brendish et al, Lancet Resp Medicine, October 8, 2020

KA Overmeyer et al, Cell Systems, October 7, 2020

randomised, controlled study

sacrificing sensitivity/specificity.

presenting with suspected COVID-19. Point-of-care testing was associated with large reductions in time to results and could lead to improvements in infection control measures and patient flow compared with centralized laboratory PCR testing. • Evaluation of a genetic risk score for severity of COVID-19 using human chromosomal-scale length variation. Toh Christopher et al. Human genomics 2020 Oct (1) 36

We compared 981 patients from the UK Biobank dataset who had a severe reaction to SARS-CoV-2 infection before 27 April 2020 to a similar

Rapid, sensitive and specific SARS coronavirus-2 detection: a multi-center comparison between standard qRT-PCR and CRISPR based DETECTR.

This is a prospective, interventional, non-randomized, controlled study of molecular point-of-care testing in patients aged 18 years or older

DETECTR, a combination of isothermal reverse transcriptase loop mediated amplification (RT-LAMP) and subsequent Cas 12 by stander nuclease activation by amplicon targeting ribonucleoprotein complexes, could be a faster and cheaper alternative to qRT-PCR without

number of age-matched patients drawn for the general UK Biobank population. For each patient, we built a profile of 88 numbers

symptoms of viral infection. The patient had two positive tests for SARS-CoV-2, separated by two negative tests done during follow-up. Genomic analysis of SARS-CoV-2 showed genetically significant differences between each variant associated with each instance of infection.

A 25-year-old man who was a resident of Washoe County in the US state of Nevada presented to health authorities on two occasions with

SARS-CoV-2 sequencing reveals rapid transmission from college student clusters resulting in morbidity and deaths in vulnerable populations

La Crosse County, Wisconsin experienced a substantial SARS-CoV-2 outbreak (2,002 cases in September 2020) that coincided with the return

to in-person instruction at three local academic institutions. Genomic sequencing found rapid expansion of two viral substrains. Although the majority of cases were among college-age individuals, from a total of 111 genomes sequenced we identified rapid transmission of the virus into more vulnerable populations.

EE Walsh et al, NEJM, October 15, 2020 195 participants underwent randomization. In each of 13 groups of 15 participants, 12 participants received vaccine and 3 received placebo. BNT162b2 was associated with a lower incidence and severity of systemic reactions than BNT162b1. The vaccine candidates elicited similar

serum samples.

**Disclaimer**: Articles listed in COVID-19 Genomics and Precision Public Health Weekly Update are selected by the CDC Office of Public Health Genomics to provide current awareness of the scientific literature and news. Inclusion in the update does not necessarily represent the views of the Centers for Disease Control and Prevention nor does it imply endorsement of the article's methods or findings. CDC and DHHS assume no responsibility for the factual accuracy of the items presented. The selection, omission, or content of items does not imply any endorsement or other position taken by CDC or

dose-dependent neutralizing geometric mean titers, which were similar to or higher than the geometric mean titer of a panel of convalescent

DHHS. Opinion, findings and conclusions expressed by the original authors of items included in the Clips, or persons quoted therein, are strictly their own and are in no way meant to represent the opinion or views of CDC or DHHS. References to publications, news sources, and non-CDC Websites are provided solely for informational purposes and do not imply endorsement by CDC or DHHS. Content source: Office of Genomics and Precision Public Health, CDC Office of Science

× **Follow CDC About CDC** 

Mission and Vision

Using this Site

All Languages

Page last reviewed: Oct 1, 2020

Page last updated: Jan 14, 2021

Legal **Contact CDC Employment** Link to Us Policies Newsroom Training/Education FOIA

No FEAR Act

**CDC Media** 

You

Centers for Disease Control and Prevention 1600 Clifton Rd. Atlanta, GA 30333 USA 800-CDC-INFO (800-232-4636) Contact CDC-INFO Funding Accessibility CDC's Organization Privacy