Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

shock. There is little opportunity for pretreatment in this setting and there is invariably a delay to optimum platelet inhibition with even the most effective oral agents.[14] A randomised trial of cangrelor versus placebo on top of optimum dual oral antiplatelet therapy, including either ticagrelor or prasugrel, would help solidify its role in this setting. Second, because patients with high-risk non-STEMI (GRACE score >140) preferentially benefit from early intervention,[15] cangrelor, with its rapid onset and offset, might offer an advantage in this population. Third, in centres where pretreatment is not routine clinical practice, cangrelor will probably become a preferred option. Fourth, cangrelor is an attractive option in patients with high-risk anatomic or clinical features undergoing same-sitting or ad hoc elective PCI for stable coronary artery disease. There is little opportunity to benefit from preloading in these patients and, somewhat surprisingly, neither ticagrelor nor prasugrel has been formally studied in this large group of patients.

Finally, will cangrelor offer value for money? The cost differential between the intravenous infusion of cangrelor and a loading dose of an oral antiplatelet drug (ticagrelor, prasugrel, or clopidogrel) is likely to be substantial. Moreover, the degree to which the reduction in ischaemic events makes cangrelor an overall cost-effective strategy will be a major determinant of how widely it is used. Despite these considerations, its favourable pharmacodynamic profile and effectiveness in reducing periprocedural events makes cangrelor a useful and welcome agent for interventional cardiologists and their patients.

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Tracking the transmission and evolution of MERS-CoV

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See **Articles** page 1993

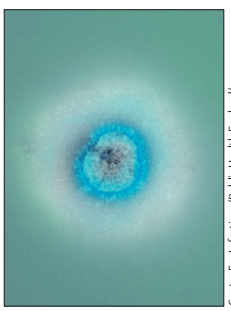
In 2012, Middle East respiratory syndrome coronavirus (MERS-CoV) first emerged in a patient who died of severe pneumonia in Saudi Arabia.[1] Although most cases confirmed so far in the Middle East have been sporadic with an unknown source of infection, human-to-human transmission has been reported in health-care and household settings.[2-4] However, the source of the virus and mode of disease transmission remain unknown despite detection of a small fragment of sequence identical to the EMC/2012 MERS-CoV in a *Taphozous perforatus* bat captured in Saudi Arabia[5] and reports of cross-reactive antibodies to MERS-CoV in dromedary camels in Oman and the Canary Islands.[6]

A hospital outbreak of MERS in the eastern province of Saudi Arabia was previously described,[3] with full genome analysis of four isolates of the Al-Hasa

outbreak combined with five previously identified MERS-CoV genomes. The investigators estimated that the time of most recent common ancestor (tMRCA) was August, 2011 (95% highest posterior density [HPD] November, 2009 to April, 2012), and showed that the four viruses formed a monophyletic clade. The study provided a better understanding of the transmission of MERS-CoV within family clusters[2,7] and in health-care settings.[4] Nevertheless, the four cases selected were closely linked epidemiologically within this outbreak involving four health-care facilities.[3]

In *The Lancet*, Matthew Cotten and colleagues[8] further describe the geographical distribution and phylogenetic relation of MERS-CoV infections across time in Saudi Arabia. This study represents the largest number of MERS-CoV genomes described so far, with 13 complete and eight partial genomes (30–95% genome coverage) from 21 clinical MERS samples taken from the Al-Hasa outbreak and four other sites in Saudi Arabia (Riyadh, Buraidah, Bisha, and Hafr-Al-Batin). Each of the sequences was derived directly from clinical specimens of patients and thus avoided any mutations that would be introduced by tissue culture passage. The authors report three distinct MERS-CoV genotypes, whereas phylogeographic analyses suggest that the MERS-CoV zoonotic reservoir is geographically dispersed. Furthermore, genetic diversity in the Al-Hasa cluster suggests that the hospital outbreak might have been caused by more than one virus introduction. The data obtained from clinical MERS samples from the Al-Hasa cluster and community outbreaks has recorded evolution of the MERS-CoV virus in this epidemic within Saudi Arabia, and the sequence variations also reveal remarkable multiple-tree clusters. The study has provided interesting data supporting circulation of MERS-CoV since the middle of 2011, with the estimated tMRCA as July, 2011 (95% HPD July, 2007 to June, 2012).[8]

Although the human exposures that result in infection remain unknown, this study has added the novel finding of three distinct MERS-CoV genotypes in Riyadh, with at least two distinct lineages probably circulating in Riyadh in October, 2012. Disease transmission patterns in the epidemic suggest both human-to-human transmission and sporadic zoonotic events. The current genome sequence set is not adequate to discriminate definitively between single or multiple zoonotic introductions, but the description of the pair of related genomes from Riyadh and Bisha and the description of cases in east and west Saudi Arabia in both major lineages of the tree suggest many zoonotic events. Overall, this is an interesting study that extends earlier findings.[2,3] Although this report provides neither direct evidence of animal transmission nor the precise mechanism of transmission, the information is useful in tracing the source and transmission of MERS-CoV.[8]



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There are some examples of the historical role and scientific value of molecular methods in tracing emerging severe acute respiratory infections. After the major outbreaks of SARS-CoV in 2003, researchers in many countries had applied molecular genome analysis to track the viral evolution and spread of the disease.[9–11] PCR has provided the scientific basis for direct examination of clinical samples for evidence of infection. Similar to MERS-CoV, sequence variations were reported in SARS-CoV obtained from different patients in this epidemic.[9–11] Cotten and colleagues[8] have effectively shown that sequence variations in the MERS-CoV genome can be applied as a powerful molecular method in tracing the route of transmission, when used in conjunction with standard epidemiology. Furthermore, using the publicly released full genomic sequences of SARS-CoV in 2003, various molecular detection methods based on RT-PCR were developed. Most of the diagnostic assays were initially focused on RNA extracted from nasopharyngeal aspirates, urine, and stools, but assays based on the analysis of RNA extracted from plasma and serum were later developed.[12,13] Such blood RNA assays (with one targeted at the nucleocapsid region and the other the polymerase region of the virus genome) allowed the more standardised quantitative expression of viral loads and became useful for early SARS diagnosis, with a detection rate of up to 80% during the first week of illness, when serology diagnosis of SARS was not sensitive at the early stage.[12,13] These quantitative systems, if available, might be useful for the early diagnosis of MERS-CoV and can provide viral load information that might facilitate prognostic assessments of an infected individual.

With the increasing number of sporadic cases of MERS in the Middle East, more research is needed into the mode of transmission and exposures responsible for the sporadic introductions of MERS-CoV into human populations. Development of rapid and reliable

diagnostic assays is also urgently needed so that health authorities can take appropriate public health measures to interrupt disease transmission and contain the virus.

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I declare that I have no conflicts of interest.

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Effects of a short-term mass-media campaign against smoking

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See **Articles** page 2003

Although the benefits of continuous antismoking media campaigns are clear,[1] little is known about the effects of short-term programmes on attempts to quit smoking by the general population. In *The Lancet,* Timothy McAfee and colleagues[2] report on a national antismoking campaign funded by the US Centers for Disease Control and Prevention, called "Tips from Former Smokers" (Tips), which was delivered via television, print, digital, and other media outlets for 3 months. Development of advertisements for the Tips campaign was rigorous and considered a diverse set of smokers' opinions about what would help them quit. Hard-hitting, emotional, and graphic real-life stories were produced that emphasised the effects of smoking-related disease on quality of life, rather than focusing on risk of death.

The effectiveness of this public-health education programme was assessed by baseline and follow-up surveys of a nationally representative sample of 3051 adult smokers and 2220 non-smokers. The prevalence of smokers reporting a quit attempt rose over the period of the campaign (adjusted odds ratio 1·20, 95% CI 1·02–1·40; p=0·02). McAfee and colleagues estimated that, nationwide, 1·64 million additional smokers made a quit attempt during the 3-month Tips campaign, and 220 000 (95% CI 159 000–282 000) remained abstinent at follow-up. Furthermore, 4·7 million additional non-smokers recommended a cessation service (telephone helpline or quit assistance website) and more than 6 million discussed the hazards of smoking with family and friends. These study findings could be deemed population-specific, but they should nonetheless encourage low-income and middle-income countries that are facing major tobacco epidemics—such as China, India, Bangladesh, Egypt, Malaysia, Indonesia, and Russia—to develop appropriate and cost-effective strategies for tobacco control.[3]

Tobacco dependence has been defined as a chronic disease,[4] and the process of quitting smoking is dynamic; therefore, a prolonged campaign might have had a greater effect. Globally, many long-term antismoking programmes have been delivered.[1,5] However, Tips was the first federally funded, high-exposure, national antismoking media campaign in the USA, and it reached almost 80% of the US population. McAfee and colleagues used a conservative approach to estimate the possible long-term effect of the Tips campaign. Their findings suggested that more than 100 000 smokers were likely to have become sustained quitters because of the Tips campaign, possibly adding a