Prameny odborné literatury

1) Historie a současnost vědeckých časopisů

2) Jak vypadají články - druhy a struktura

Pravidlo druhé:
Základem vědecké práce je studium literatury.

?? Proč ale číst něco, co již bylo objeveno ??

- neopakovat stejný pokus se stejným materiálem
- vlastní nové nápady a myšlenky
- správné postupy vedoucí k výsledku, styl odborného textu
- nelze napsat vědeckou práci

Zdroje:
- ústní
- psané – knihy, časopisy
- elektronické – internet

Historie a současnost vědeckých časopisů

Historie a současnost vědeckých časopisů

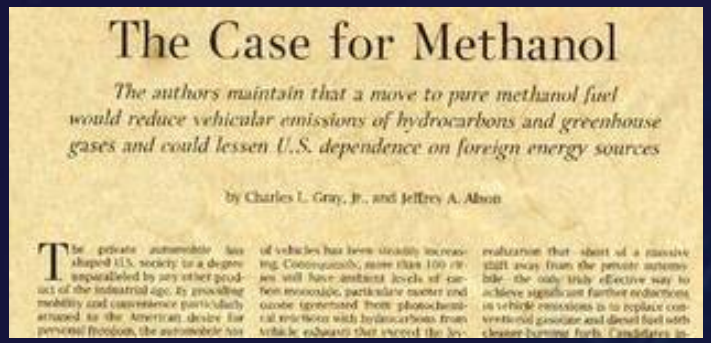
- 17. až 19. století – časopisy obecně vědecké – **přírodovědné** časopisy (1665 F, VB)
- 19. století – specializace na obory – botanika, zoologie, matematika, chemie (1820)
- doposud – další specializace – např. anatomie, fyziologie, genetika fotosyntéza, učení a paměť

!!! Při vyhledávání starších ročníků - u časopisů s dlouhou historií mohlo dojít ke změně jeho názvu např. Plant Physiology and Biochemistry se dříve jmenoval Physiologie végétable nebo Journal of Plant Physiology dříve jako Zeitschrift für Pflanzen-physiologie

- 70. léta 20. století – „Studia Biophysica“ zveřejňuje články jen jako mikrofiše (zmenšeniny na plochém filmu, lze číst pouze ve čtecím přístroji), v tištěné verzi jen rozšířená **abstrakta**

- konec 20. století – CD-ROM – cena stejná jako u tištěné verze, sleva při odběru obou (European Journal of Biochemistry)

- časopisy se začínají objevovat na **internetu** – jen obsah – spíše reklama = bezplatná služba, později kompletní přístup = placená služba



The Case for Methanol

The authors maintain that a move to pure methanol fuel would reduce vehicular emissions of hydrocarbons and greenhouse gases and could lessen U.S. dependence on foreign energy sources

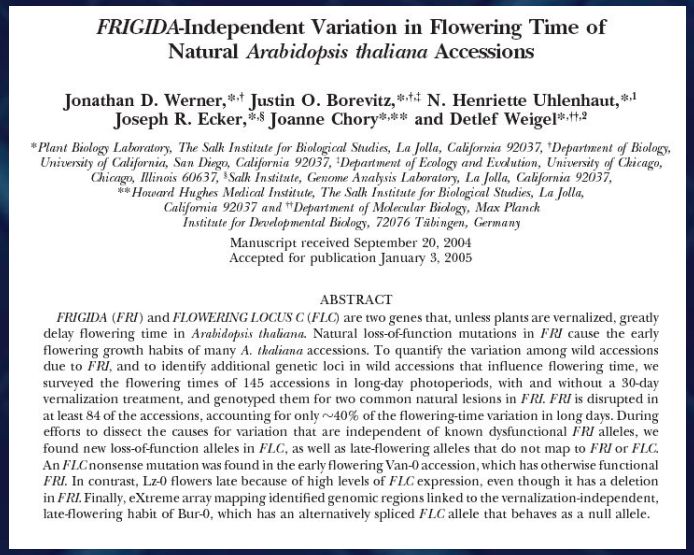
by Charles L. Gray, Jr., and Jeffrey A. Alson

The private automobile has shaped U.S. society to a degree unparalleled by any other product of the industrial age. By providing mobility and convenience particularly attuned to the American desire for personal freedom, the automobile has

of vehicles has been steadily increasing. Consequently, more than 100 cities still have ambient levels of carbon monoxide, particulate matter and ozone generated from photochemical reactions with hydrocarbons from vehicle exhausts that exceed the fed-

evaluation that short of a massive shift away from the private automobile, the only truly effective way to achieve significant further reductions in vehicle emissions is to replace conventional gasoline and diesel fuel with cleaner-burning fuels. Candidates in-

Jak vypadají vědecké články



FRIGIDA-Independent Variation in Flowering Time of Natural *Arabidopsis thaliana* Accessions

Jonathan D. Werner,[*,†] Justin O. Borevitz,[*,†,‡] N. Henriette Uhlenhaut,[*,1] Joseph R. Ecker,[*,§] Joanne Chory[*,] and Detlef Weigel[*,††,2]**

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ABSTRACT

FRIGIDA (*FRI*) and *FLOWERING LOCUS C* (*FLC*) are two genes that, unless plants are vernalized, greatly delay flowering time in *Arabidopsis thaliana*. Natural loss-of-function mutations in *FRI* cause the early flowering growth habits of many *A. thaliana* accessions. To quantify the variation among wild accessions due to *FRI*, and to identify additional genetic loci in wild accessions that influence flowering time, we surveyed the flowering times of 145 accessions in long-day photoperiods, with and without a 30-day vernalization treatment, and genotyped them for two common natural lesions in *FRI*. *FRI* is disrupted in at least 84 of the accessions, accounting for only ~40% of the flowering-time variation in long days. During efforts to dissect the causes for variation that are independent of known dysfunctional *FRI* alleles, we found new loss-of-function alleles in *FLC*, as well as late-flowering alleles that do not map to *FRI* or *FLC*. An *FLC* nonsense mutation was found in the early flowering Van-0 accession, which has otherwise functional *FRI*. In contrast, Lz-0 flowers late because of high levels of *FLC* expression, even though it has a deletion in *FRI*. Finally, eXtreme array mapping identified genomic regions linked to the vernalization-independent, late-flowering habit of Bur-0, which has an alternatively spliced *FLC* allele that behaves as a null allele.

„Short communication“

(Krátký článek k zajištění priority objevu nebo zveřejnění výsledků omezeného rozsahu, nové využití metod atd.)

Původní vědecké sdělení

Přehledné referáty - reviews

Původní vědecké sdělení

- nemá shrnující charakter oproti review
- podává zprávu (protokol) o konkrétním výzkumném úkolu s konkrétními cíly a závěry
- struktura takových článků je pevně daná:

Nadpis (**T**itle)
Jména autorů s adresami
Abstrakt (**A**bstract)
Úvod (**I**ntroduction)
Materiál a metody (**M**aterials and Methods)
Výsledky (**R**esults)
Diskuse (**D**iscussion)
Poděkování (Acknowledgements)
Seznam literatury (References)

TAIMRD x IMRAD

- jsou ale i odchylky dle zvyklostí časopisu
  - Materials and methods na konci článku (Cell)
  - Results and Discussion společně (viz. IMRAD)
  - + Summary na konci článku (nebo součástí Diskuse)
  - Key words pod abstraktem

Co najdeme v jednotlivých částech

Nadpis (Title) – vypovídá o obsahu samotné práce – hledání a výběr článku na základě slov uvedených v nadpise + o čem článek je

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Co najdeme v jednotlivých částech

Jména autorů s adresami – lze využít při objednávání článku, případně při vyhledávání dalších publikací podle jména autora

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Co najdeme v jednotlivých částech

Abstrakt (Abstract) – nejdůležitější částí – výstižně sděluje **co** a **na čem** se zkoumalo, jakých bylo dosaženo **výsledků** a co z toho vyplývá (**závěr**) = strukturovaný

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- vyhledávání článků probíhá i na základě slov v abstraktu,
- na základě abstraktu se rozhoduji o objednání článku
- **!!! Nestačí však čerpat informace pouze z abstraktů !!!**

Co najdeme v jednotlivých částech

Úvod (Introduction) – stručný přehled literatury, úvod do problematiky, co je již známého v dané problematice – **citace**, které využijeme při hledání další literatury o daném tématu, na jeho konci většinou ***cíl*** publikované práce nebo nosná **hypotéza** výzkumu

A plant's decision to initiate reproductive development is an important event that is controlled by the intersection of an endogenous program with environmental factors such as temperature and light. Biotic and abiotic factors affecting plant growth and survival are variable across habitats, requiring plants to specialize in sensing environmental stimuli and adapting their development accordingly. Presumably, natural selection has optimized this program to time the transition to flowering to provide optimal fitness in a given environment. Indeed the existence of latitudinal clines in many species, including *Arabidopsis thaliana*, is strongly indicative of adaptive variation in flowering (Mikola 1982; Hurme *et al.* 1997; Van Dijk *et al.* 1997; Stinchcombe *et al.* 2004) or light response (Maloof *et al.* 2001).

The study of floral induction in *A. thaliana* has long been approached through the isolation and characterization of mutants with altered flowering times. A large number of flowering-time genes have been identified and a scaffold of the underlying molecular network has been constructed (for review, see Mouradov *et al.* 2002; Simpson and Dean 2002; Searle and Coupland 2004; Sung and Amasino 2004). As may be expected, this network is complex. On the basis of an extensive body of physiological, genetic, and molecular studies, four main pathways that regulate the key floral identity genes have been outlined: photoperiod, vernalization, autonomous, and gibberellin. The photoperiod pathway utilizes photoreceptors in conjunction with the circadian clock to strongly accelerate flowering in the presence of long-day photoperiods. Flowering is also accelerated when plants with high levels of the floral inhibitor *FLC* are exposed to an extended period of winter-like temperatures. This process, called vernalization, causes epigenetic silencing of the *FLC* locus and thereby relieves repression of flowering. Independently of vernalization, *FLC* is also negatively regulated by the autonomous pathway, which was originally thought to function independently of the environment. Recently, however, it has been found that this pathway may also mediate response to ambient growth temperature (Blázquez *et al.* 2003).

Sequences data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY781906–AY785055, AY849982–AY850002, AY854371, AY854372, and AH014566.

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E-mail: weigel@weigelworld.org

Genetics **170:** 1197–1207 (July 2005)

Co najdeme v jednotlivých částech

Materiál a metody (Materials and Methods) – jaké metody se v řešení dané problematiky používají

MATERIALS AND METHODS

Plant material: A list of accessions and their phenotypes can be found at http://naturalvariation.org/werner. Most accessions were obtained from the Arabidopsis Biological Resource Center or Lehle Seeds. The L*er*K and CviK accessions are parents of the L*er*/Cvi recombinant inbred line set in which the *EDI* allele of *CRY2* was identified (El-Assal *et al.* 2001) and were kindly provided by Maarten Koornneef (Wageningen, The Netherlands). Combinations of functional and nonfunctional *FRI* and *FLC* alleles in Col (Lee *et al.* 1994b; Michaels and Amasino 2001) were kindly provided by Rick Amasino (Madison, WI). All lines were propagated prior to genotypic and phenotypic analysis.

Growth conditions: Seeds were suspended in 1 ml of 0.1% phytagar (Invitrogen, San Diego) and imbibed at 4° in darkness for 4 days. Seeds were then sown onto presoaked Sunshine Mix no. 5 (McConkey, Garden Grove, CA) and thinned after 5 days. Plants were grown in a growth room at 22° under 16 hr of light provided by a 3:1 mixture of Cool-white and Gro-Lux (Sylvania) fluorescent bulbs, followed by 8 hr of darkness. For the long-day surveys, six plants for each line were raised in one pot, except for several control genotypes grown in three blocks of six plants. Over the course of the experiment, the pots were randomized across all flats several times and flats were rotated across and between shelves on a daily basis. Vernalization treatments were performed at the seedling

Co najdeme v jednotlivých částech

Výsledky (Results) – shrnuje a popisuje hlavní výsledky

of Col, and two replicates each for the early and late-flowering pools. Analysis of the hybridization data was similar to that described previously (Wolyn *et al.* 2004). For the Bur-0 × *fle*-3 F_2 population (n = 330), the 65 earliest and the 65 latest plants, as measured by days to flowering, were pooled and processed similarly. A total of eight samples were prepared and hybridized: three replicates of Bur-0 and *fle*-3 and one sample each for the pools.

Lz-0 × L*er* QTL mapping: A total of 178 F_2 plants from the cross of Lz-0 to L*er* were grown in long days and genotyped for 32 markers distributed across all five chromosomes with an average distance of 15 cM, and a genetic map was determined using MapMaker/EXP 3.0 (Lander *et al.* 1987). Marker order was as expected from the physical locations of the markers in the Col reference sequence.

For QTL analysis presented in the text, composite interval mapping was performed with QTL Cartographer 1.16c (Basten *et al.* 2002) using model 6 with a window size of 4.00

RESULTS

Association of *FRI* deletions with flowering-time effects: We measured the flowering times of 145 single-seed descent accessions in long-day photoperiods and genotyped them for the Col and Ler *FRI* deletions. As observed in previous surveys (Johanson *et al.* 2000; Le Corre *et al.* 2002; Stinchcombe *et al.* 2004), the *FRI* deletions first described in the Col and L*er* laboratory strains occur with considerable frequency among accessions, with 34 having the L*er*-type and 46 the Col-type deletion (Figure 1). No accession has both deletions, as expected due to their very tight linkage (253 bp). The effect of these deletions on flowering was obvious,

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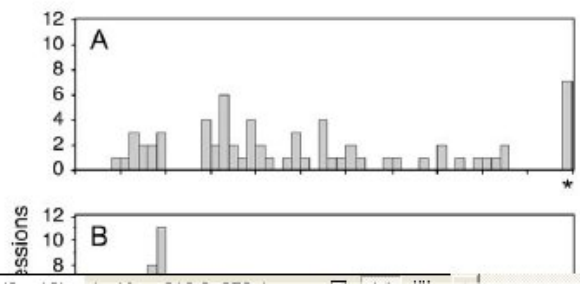

is likely identical to "Indel2" found in the BUI accession (Le Corre *et al.* 2002). Accession Or-0 was found to have a novel 1-bp deletion in exon 2 of *FRI*, causing a frameshift in the coding sequence that leads to a premature stop codon.

While we found variation at the nucleotide and amino acid level in the remaining seven early accessions [Da(1)-12, Dra-0, Est, Shahdara, Van-0, Wa-1, Wil-1], none had

Co najdeme v jednotlivých částech

Diskuse (Discussion) – diskutuje - kriticky hodnotí a porovnává výsledky s výsledky jiných autorů a hypotéz

- ověření správného pochopení obsahu abstraktu – uvádím citaci ve správném kontextu?

DISCUSSION

Previous studies of natural variation in flowering time in *A. thaliana* either have focused on a small number of accessions (*e.g.*, GAZZANI *et al.* 2003) or did not include genetic analyses (*e.g.*, STINCHCOMBE *et al.* 2004). Here, we examined variation of flowering time in a large collection of single-seed descent accessions available from stock centers. We have confirmed and extended previous observations regarding the frequency and magnitude of effect of two natural *FRI* deletions. Furthermore, we not only have estimated the extent of variation likely to be due to genetic loci other than *FRI*, but also have carried out initial genetic and molecular analyses of accessions that have interesting flowering phenotypes with respect to their genotype at *FRI*.

With the identification of the Or-0 *fri* allele, there are now at least 10 different mutations known to disrupt the *FRI* coding region (JOHANSON *et al.* 2000; LE CORRE *et al.* 2002 ; GAZZANI *et al.* 2003). At least 84 of the 145 accessions that we surveyed carry *FRI* loss-of-function alleles, with the Col and L*er* deletions being, by far, the most prevalent. At a minimum, the presence or absence of natural *fri* alleles are responsible for 40% of the variation in long-day flowering time seen in our experiment.

Co najdeme v jednotlivých částech

Seznam literatury (References) – úplný výpis citovaných prací

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Gazzani, S., A. R. Gendall, C. Lister and C. Dean, 2003 Analysis of the molecular basis of flowering time variation in *Arabidopsis* accessions. Plant Physiol. **132:** 1107–1114.

Co najdeme v jednotlivých částech

Význam (shrnutí):

- dle nadpisu vyhledávám
- dle abstraktu se rozhoduji, zda článek objednám
- na základě rychlého čtení (obrázky a tabulky s příslušnými popiskami) se rozhoduji, zda-li má pro mne článek nějaký význam a zda budu číst dál

Přehledné referáty – reviews (přehled literatury)

- podává přehled o současném stavu problému na základě již publikovaných článků - shrnující review

nebo

- informuje o hlavních oblastech pokroku, ukazuje budoucí směr výzkumu, vytyčuje nové hypotézy

- ideální přehled literatury skloubí oba typy dohromady

- existují ještě další typy přehledných referátů a také tzv. minireview

Přehledné referáty – reviews (přehled literatury)

- člení se na: Úvod (Introduction), vlastní text členěný na kapitoly, Závěr (Shrnutí), příp. Závěr a nastínění budoucnosti; součástí může být i abstrakt

Severe acute respiratory syndrome (SARS)—paradigm of an emerging viral infection☆

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[b] *Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany*

Accepted 9 March 2003

Abstract

An acute and often severe respiratory illness emerged in southern China in late 2002 and rapidly spread to different areas of the Far East as well as several countries around the globe. When the outbreak of this apparently novel infectious disease termed severe acute respiratory syndrome (SARS) came to an end in July 2003, it had caused over 8000 probable cases worldwide and more than 700 deaths.

Starting in March 2003, the World Health Organization (WHO) organised an unprecedented international effort by leading laboratories working together to find the causative agent. Little more than one week later, three research groups from this WHO-coordinated network simultaneously found evidence of a hitherto unknown coronavirus in SARS patients, using different approaches. After Koch's postulates had been fulfilled, WHO officially declared on 16 April 2003 that this virus never before seen in humans is the cause of SARS.

Ever since, progress around SARS-associated coronavirus (SARS-CoV) has been swift. Within weeks of the first isolate being obtained, its complete genome was sequenced. Diagnostic tests based on the detection of SARS-CoV RNA were developed and made available freely and widely; nevertheless the SARS case definition still remains based on clinical and epidemiological criteria. The agent's environmental stability, methods suitable for inactivation and disinfection, and potential antiviral compounds have been studied, and development of vaccines and immunotherapeutics is ongoing.

Despite its grave consequences in humanitarian, political and economic terms, SARS may serve as an example of how much can be achieved through a well-coordinated international approach, combining the latest technological advances of molecular virology with more "traditional" techniques carried out to an excellent standard.

Keywords: Severe acute respiratory syndrome (SARS); Coronavirus; SARS-associated coronavirus (SARS-CoV); Laboratory diagnosis; Transmission; Emerging infection; Epidemiology; Antiviral treatment; World Health Organization (WHO)

1. Introduction

Severe acute respiratory syndrome (SARS) is the latest in a series of emerging infectious diseases, and certainly one of the most widely publicised. This acute and often enormous scales, and when the disease's ability to spread to distant areas within a very short period of time became obvious (World Health Organization, 2003d). A definition was developed for suspected and probable SARS cases, based on clinical and epidemiological criteria; it has since

2. Search for the causative agent

On 17 March 2003, the WHO set up a worldwide network of virological laboratories investigating SARS cases (World Health Organization, 2003a). The investigations conducted by the members of these networks were coordinated by WHO's Department of Communicable Disease Surveillance and Response (CSR) through normally daily telephone conferences and a password-protected internet website. Thus results and planned further studies were communicated and views and comments exchanged almost in "real-time" which made possible the rapid progress in elucidating the aetiological agent. In its final form, this network comprised 13 participating laboratories from ten countries (World Health Organization Multicentre Collaborative Network for Severe Acute Respiratory Syndrome Diagnosis, 2003).

Investigations had soon ruled out a novel influenza virus strain, possibly of avian origin, as the cause of SARS, and then focussed on members of the *Paramyxoviridae* family, including human metapneumovirus (hMPV), and *Chlamydia*-like organisms, including *Chlamydia pneumoniae*. However, further investigations did not confirm these findings; the said agents were indeed found in a number of SARS patients but not in all (WHO multicentre collaborative networks for severe acute respiratory syndrome (SARS) diagnosis, 2003). Almost nobody knew at that stage that virologists in Beijing had already discovered a new virus in samples from some of the earliest SARS patients. However, the official line in China at the time was that the novel

underwent seroconversion against this coronavirus, using cells infected with patient isolates as antigen for indirect immunofluorescent antibody tests (Drosten et al., 2003a; Ksiazek et al., 2003; Fig. 1). Furthermore, no evidence of present or past infection with this agent could be detected in limited surveys of healthy control individuals not suffering from SARS (Ksiazek et al., 2003). This strengthened the case for the novel coronavirus being the cause of SARS, but only after it had been shown to cause a similar illness in artificially infected macaques could it be regarded as fulfilling all four of Koch's postulates (Fouchier et al., 2003; World Health Organisation Multicentre Collaborative Networks for Severe Acute Respiratory Syndrome Diagnosis, 2003). On April 16, 2003, less than a month after the laboratory network had been brought into existence, WHO officially announced that a new coronavirus, never before seen in humans or animals and now provisionally termed SARS-associated coronavirus (abbreviated as SARS-CoV), was the cause of SARS (Kuiken et al., 2003).

3. Virology

Coronaviruses are large, enveloped, positive-stranded RNA viruses with a diameter of 60–220 nm. Most but not all viral particles display the characteristic appearance of surface projections, giving rise to the virus family's name (corona, Latin, = crown). They have the largest genomes of all RNA viruses. Based on their unique transcription strategy that involves the formation of "nested" mRNA molecules

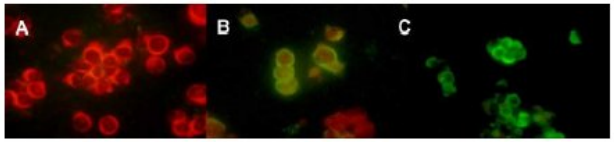

Fig. 1. Seroconversion during the course of SARS demonstrated by IFA using SARS-CoV-infected Vero cells. Serum samples from wife of Frankfurt index

Přehledné referáty – reviews (přehled literatury)

- člení se na: Úvod (Introduction), vlastní text členěný na kapitoly, Závěr (Shrnutí), příp. Závěr a nastínění budoucnosti; součástí může být i abstrakt

8. Antiviral treatment

No specific treatment recommendations can be made at this time. Primary measures include isolation and the implementation of stringent infection control measures to

9. Conclusions and outlook

The rapid success in identifying the causative agent of SARS results from a collaborative effort—rather than a

competitive approach—by high-level laboratory investigators making use of all available techniques, from cell culture through electron microscopy (Hazelton and Gelderblom, 2003) to molecular techniques, in order to identify a novel agent. Hopefully this approach, coordinated by WHO, will serve as a model for future instances of emerging infections that will undoubtedly take place (Ludwig et al., 2003).

Despite the exemplary efforts that led to the identification of the causative novel coronavirus and allowed enormous knowledge about it to be accumulated within only a few months, it is maybe surprising that this success in terminating the outbreak has to be attributed to "old-fashioned" measures such as rapid and strict isolation of suspect cases and thorough contact tracing (World Health Organization, 2003c); one is left wondering whether the same might also have been achieved without knowledge of the aetiology.

For this purpose, WHO has defined three geographical zones according to their presumed risk for a SARS recurrence: a potential zone of re-emergence, comprising Guangdong and other areas where animal-to-human of SARS-CoV might occur; nodal areas, comprising Hong Kong, Vietnam, Singapore, Canada, and Taiwan, with sustained local transmission in spring 2003 or entry of numerous persons from the potential zone of re-emergence; and low risk areas. SARS-related vigilance should be staged according to the zone in which a particular area is situated; for low risk areas, surveillance should be for clusters of "alert" cases among health care workers, other hospital staff, patients and visitors in the same health care unit. A SARS Alert is defined as two or more health care workers or hospital-acquired illness in at least three individuals (health care workers and/or other hospital staff and/or patients and/or visitors) in the same unit