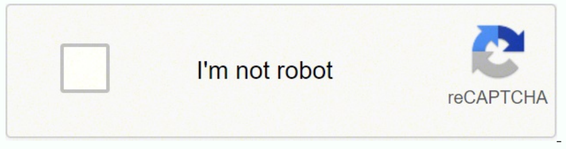

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Sepsis 2018 guidelines ppt

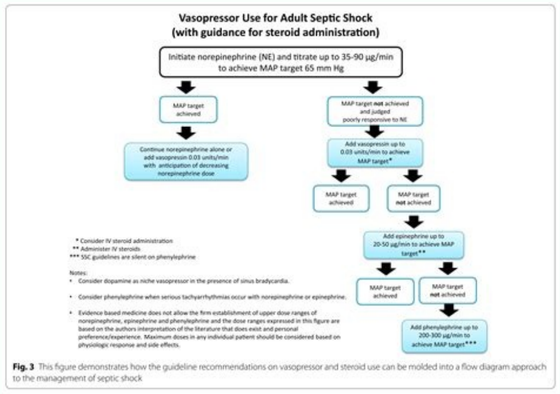
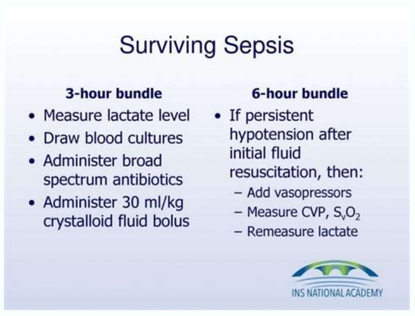
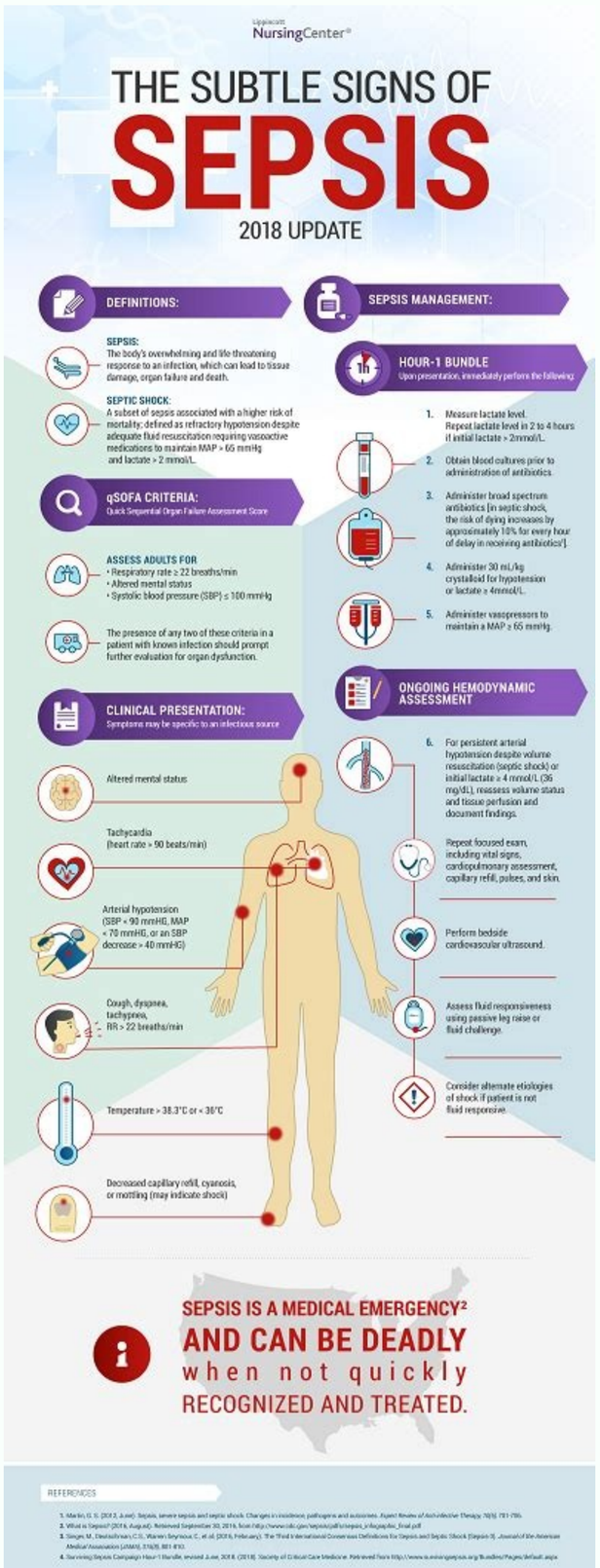
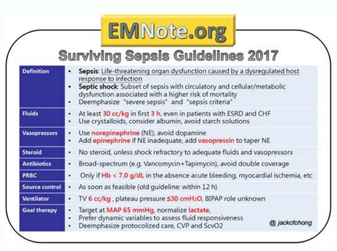


Fig. 3 This figure demonstrates how the guideline recommendations on vasopressor and steroid use can be molded into a flow diagram approach to the management of septic shock







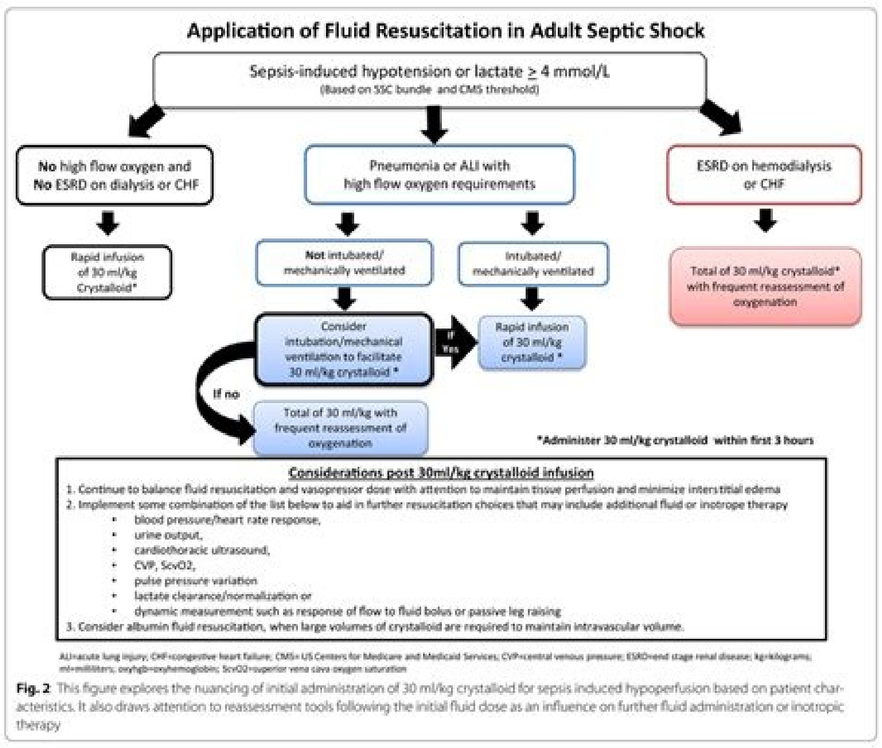


Fig. 2 This figure explores the nuancing of initial administration of 30 ml/kg crystalloid for sepsis induced hypoperfusion based on patient characteristics. It also draws attention to reassessment tools following the initial fluid dose as an influence on further fluid administration or inotropic therapy

This site uses cookies. By continuing to use this site, you consent to the use of cookies. For information about cookies and how to disable them, please visit our Privacy and Cookie Policy. Copy that, thanks! Open peer-reviewed Early diagnosis, precise antimicrobial treatment and subsequent patient stratification may improve sepsis results. Circular biomarkers such as plasma microRNAs (miRNAs) have been shown to be surrogates for the diagnosis, severity and management of infections. The expression of four selected miRNAs (miR-146-3p, miR-147b, miR-155 and miR-223) has been validated for their prognostic and diagnostic potential in a clinically defined co-ordinate of patients with sepsis and septic shock. The expression of plasma miRNA was quantified by quantitative PCR (qPCR) in patients with bacterial sepsis (n= 78), in patients with septic shock (n= 52) and in patients with dengue haemorrhagic fever (DHF; n= 69) and in healthy controls (n= 82). The expression of miRNA studied has been significantly increased in patients with bacterial sepsis and septic shock. MiR-147b plasma was able to differentiate bacterial sepsis from non-septic and septic shock (AUC= 0.77 and 0.8 respectively, p 0.05), while the combination of miR-147b plasma and procalcitonin (PCT) predicted septic shock (AUC= 0.86, p0.05). MiR-147b plasma can be a useful biomarker independently or in combination with PCT to support the clinical diagnosis of sepsis and also prognosis of patients with septic shock. Quote: Trung NT, Lien TT, Sang VV, Hoan NX, Manh ND, Thau NS, et al. (2021) MiR-147b circulating as a diagnostic marker for patients with bacterial sepsis and septic shock. PLoS ONE 16(12): e0261228. Colin Johnson, Oregon State University, UNITED STATESRicevente: 24 May 2021; Accepted: 24 November 2021; 16December 2021 Copyright: © 2021 Trung et al. This is an open access article distributed on terms the Creative Commons Attribution License, which allows unlimited use, distribution and reproduction in any medium, provided that the original author and source are accredited. Availability of data: all data and support materials associated with this study will be shared on request by email to the institutional chairman of the ethics committee pnson@benhvien108.vn.Funding This study was funded by the National Foundation of Vietnam for the Development of Science and Technology (NAFOSTED) under Grant Number 108.06-2017.21 (Dr. Le Huu Song). The financing agency had no role in the design of studies, data collection and analysis, in the decision to publish and/or in the preparation of the manuscript. Competitive interests: all authors do not declare a conflict of interest in this study. Bacterial sepsis is a life-threatening condition in which bacteria enter the blood stream and evoke a systemic inflammatory response that develops a cascade of physiological changes leading to multiple organ failure [1]. There are three phases: sepsis, severe sepsis and septic shock, the latter leads to organ dysfunction involving the cardiovascular system. Most deaths due to sepsis and sepsis are reported from low and middle income countries (LMIC) [2]. With a significant increase in antimicrobial resistance (AMR) especially in LMICs, sepsis management and treatment are increasingly challenging. Early diagnosis, careful antimicrobial treatment and subsequent stratification of patients may improve the outcome of sepsis. Although inflammatory markers such as C-reactive protein (CRP) and procalcitoin (PCT) are useful biomarkers, blood cultures are commonly used in clinical practice as a diagnostic tool to identify aetiologies. Recent progress in the use of automated systems Greater sensitivity and improved culture means facilitate the rapid identification of microbial growth, but positive rates in patients with sepsis vary depending on the gravity of the disease. While blood culture has its own intrinsic limits, such as being laborious laborious Only by identifying microbes growing under optimised culture conditions does the polymer chain reaction (PCR) method have the potential to fill this diagnostic gap [3]. Despite inflammatory markers and diagnostic tools available, a significant proportion of patients still suffer from a sepsis load, as the etiology of sepsis remains unclear in clinical practice [4Â¢ÒÀ]. A recent meta-analysis shows that inflammatory cytokines are not able to distinguish patients with systemic inflammatory response syndrome (SIRS) caused by other non-infectious diseases [7, 8]. In this context, circulating biomarkers such as MicroRNA (miRNA) are proven useful as surrogates for infection diagnosis, severity and case management. MiRNAs, small non-coding RNAs, are secreted from cells and released into the bloodstream during infection, inflammation and sepsis [9]. Their presence in plasma and/or serum indicates the role of circulating (cell-free) miRNAs in pathogenesis and are thought to be the key gene modulators of distinct inflammatory responses [10]. A number of myRNAs are expressed differentially in the peripheral blood of patients with bacterial sepsis [10Ã¢Â]. Among the well-identified, miR-146-3p, miR-147b and miR-155 were involved in NF-206 activation;Âo B marker, a key mediator of inflammatory responses [11, 12] and miR-223 involved in the regulation of macrophagia monocyte differentiation, neutrophil recruitment and pro-inflammatory responses, and is a key regulator of innate immunity [17]. In addition to existing diagnostic tools, we hypothesize that the aberrant expression of such miRNA-stimulated inflammation (miR-146-3p, miR-155, miR-147b, miR-223,) is associated with bacterial sepsis and can be used as a surrogate that has added value in diagnosing blood infections. In this study we have the expression of four selected myRNAs (miR-146-3p, miR-147b, miR-155 and miR-223) in a clinically defined cohort of patients with and compared their MiRNA expression with healthy controls. In addition, the prognostic and diagnostic potential of these selected miRNAs is validated in a subset of patients with sepsis and septic shock using their respective MiRNA expression levels and PCT values. The study was approved by the Institutional Review Board and the Independent Ethics Committee of 108 of the Central Military Hospital, Hanoi, Vietnam. Informed written consent was obtained from all study patients. A total of 130 blood plasma samples for sepsis (n = 78), septic shock (n = 52) and dengue hemorrhagic fever (DHF; N = 69) were collected from patients admitted to 108 Central Military Hospital in Hanoi, Vietnam, between 2017 and 2019. In addition, plasma from healthy controls (n = 82, healthy blood donors) was also included in this study. Patients were evaluated on clinical signs, sequential organ failure scores (sequence), biochemical parameters, white blood cell count (WBC), platelet count (PLT), procalcitonin (PCT), liver enzymes including total bilirubin, Alanine Aminotrans (ALT), Aspartate Aminotransferase (AST), serum creatinine, and lactation levels in subgroups who had sepsis or septic shock, based on guidelines of the third consensus definition of sepsis and septic shock (SEPSIS-3) [1]. Total and direct bilirubin, Alanine Aminotransferase (ALT), As Partate aminotransferase (AST), procalcitonin (PCT), serum creatinine and lactation levels were measured on a self-analyzer (BECKMAN Coulter AU5800 äï¬ “Singapore). Total RNA, including miRNA, was isolated from 500 Î1⁄4l plasma with trizol and was reconstituted in 50 Î1⁄4l of water treated with Diethyl Pyrocarbonate (DEPC). Approximately 100 ng of total RNA were used for reverse transcription (RT) by Reverseaid First Strand Synthesis Kit (ThermoFisher Scientific Inc., Singapore) following the manufacturer's instruction. The primers used for cDNA synthesis were designed according to stelo-loop theory as aspreviously [18] and are given in Table 1. After the reverse transcription, the quantitative PCR was performed in real time (qPCR). In short, the reaction mixtures consisted of 10th; ldi 2x SYBR-Green I master mix (Applied Biosystems, Foster City, CA, USA), 5; Idi preparation of cDNA, 5ptol of the universal reverse primer of the miRNA GTGAGRAGCGCGGT and 5pdol of the primary forward specific to miRNA (Table 1). The qPCR reaction was performed using the Stratagne M3000p (Stratage, San Diego, CA, USA) device with a pre-incubation phase 50th C for 15 minutes, initial denaturation to 95th 176C for five minutes, followed by 45-cycles 95th 176C for fifteen seconds and 60; 6C for 60 seconds. The cycle threshold values (Ct) were recorded and analysed according to the comparative method Ct [19], where the Ct value of miRNA-16 was used as a normalisation factor as recommended [20]. The statistical analyses were carried out by R v3. 5.2. The values were presented as average with standard deviation (SD), average with interval, if applicable. Non-parametric Mann-Whitney U-Test or Kruskal-Wallis tests were used to compare quantitative variables between different groups, where appropriate. Receiving operational curves (ROC) have been generated on the basis of random forest models to assess the predictive value of individual or combined mesRNA panels when discriminating sepsis or septic shock from another clinical state (not sepsis and sepsis without shock respectively) by calculating the area under the ROC curve (AUC). The level of meaning has been fixed to a value p on two sides of

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