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## Spontaneous bacterial peritonitis in patients of cirrhosis of liver with ascites

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**Background**: Spontaneous bacterial peritonitis (SBP) is a common and fatal complication occurring in cirrhotic patients with ascites. It is defined as infected ascites in the absence of any recognisable secondary cause of infection. This study was undertaken to find out the rate of occurrence of SBP in patients of cirrhosis with ascites,to find out relative frequency of variants of ascitic fluid infection, to study clinical presentation and laboratory profile and to determine relationship between MELD score and the occurrence of SBP.

**Methods & Materials**: This hospital based cross-sectional study was carried out in a tertiary care hospital in Nagpur after taking approval from Institute's Ethics Committee. 100 patients of cirrhosis with ascites irrespective of age and gender were enrolled after taking their written informed consent.. 20 ml of ascitic fluid was aspirated in heparinised disposable syringe; out of it 10 ml was immediately inoculated into blood culture bottle at bedside and sent for bacterial culture along with the remaining 10 ml for routine biochemical and cytological examination.

**Results**: Majority of the patients were between 40-49 years of age, mean age of patients diagnosed as SBP was 42.51 years. Out of total 42 cases of SBP, classical SBP was present in 16(38.09%), Culture negative neutrocytic ascites in 14 (33.33%) , Bacterascites in 12 (28.57%) patients with SBP. Escherichia.coli was the most frequently cultured organism isolated in 15 cases (53.570%), followed by pseudomonas in 9 (32.14%), Klebsiella pnuemoniae in 3(10.71%) cases . The common mode of presentation of SBP was abdominal tenderness(65.38%) followed by hepatic encephalopathy(58.82%) associated with abdominal pain(50%) and fever (46.66%) , distention of abdomen (44.30%) hematemesis and malena(45%). Hyponatremia with a serum was found to be associated with severe complications. In (52.63%) patients of SBP ascitic fluid protein was less than 1 mg/dl . MELD score was found to be a reliable index of disease severity .

**Conclusion**: SBP is a fatal complication of cirrhosis with ascites. It has heterogenous clinical presentation. Ascitic fluid should be analysed routinely in all cases of cirrhosis with ascites for the early detection of SBP.

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## Tropical pyomyositis - outcomes and clinical profile

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**Background**: A classical tropical disease, Pyomyositis is a primary suppurative bacterial infection involving the skeletal muscles due to hematological spread, presenting with pain and inflammation in the involved muscles. Incidence is more in an immunocompromised host, with trauma, injection drug use being common predispositions. *Staphylococcus aureus* is the common inciting agent. This study was undertaken to characterise the clinical profile and outcomes of the disease due to a dearth of data from India.

**Methods & Materials**: Methods - Retrospective study was conducted on 66 patients admitted with the diagnosis of primary pyomyositis between January 2013 to January 2015.

Inclusion criteria - Patients with pyomyositis.

Exclusion criteria - Secondary infection, concomitant febrile illnesses, viral myositis

Primary outcome - Response to antibiotic or surgical therapy, relapse or death.

Statistical analysis - Using SPSS 21. Normally data is presented as mean ± standard deviation.

**Results**: The mean age was 37.61 ± 22.25 yrs. Among presenting features, myalgia was in 98.5% patients, fever in 78.8% patients. 54.5% manifested local signs of inflammation and tenderness was in 90.9% patients.

With 24.2% of patients having uncontrolled sugars, Diabetes was the most common risk factor. Trauma was present in 18.2% and 3% were on steroids.

Iliopsoas was involved in 59.1% patients, Quadriceps in 13.6% patients, Hamstrings in 7.5%. Single muscle was involved in 86.4% of the patients and multifocal involvement in 13.6% of patients.

For diagnosis, Ultrasound was used in 56.01% of the patients, Magnetic resonance in 30.03% and Computed tomography in 13.06% of the patients.

10.6% had Acute Kidney Injury.

Microbiologically, 18.2% patients had Methicillin sensitive *Staphylococcus aureus* positivity in the culture. 12.1% patients had Methicillin resistant *Staphylococcus aureus.*

81.8% of the patients recovered with antibiotics and pus drainage. 6.1% had relapse. 3% of the patients died with sepsis.

**Conclusion**: Pyomyositis should be considered in the differential in case of a painful swelling in a muscle in an immunocompromised.

Ultrasound should be used as an adjunct in the diagnosis.

Empiric therapy covering *Staphylococcus aureus* is prudent pending culture reports.

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## Virulence gene profile and SCCmec types of clinical MRSA isolates: Is there a fitness cost involved?

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**Background**: The success of methicillin resistant *Staphylococcus aureus* as a pathogen is attributed to its extraordinary repertoire of virulence factors. Based on SCC*mec* types, MRSA isolates can be classified as hospital (HA-MRSA) or community acquired (CA-MRSA). Association of certain virulence genes with particular SCC*mec* types has been previously reported. For instance, *pvl* gene is associated with *SCCmec* types IV or V (CA- MRSA types).

**Methods & Materials**: Two hundred non-repetitive isolates of MRSA from clinical specimens were screened for virulence genes such as *pvl*, *tsst*, *hlg*, enterotoxin A (*sea*), exfoliative toxin A (*eta*), intercellular adhesion (*ica*) genes by PCR. SCC*mec* typing was carried out by multiplex PCR. An attempt was made to find the association between virulence genes and the clinical presentation as well as with the SCC*mec* types to establish the fitness cost, if any.

**Results**: A total of 192 isolates (96%) carried one or more virulence genes while 8 (4%) had none. The commonest virulence gene encountered was *ica* (90%) followed by *hlg* (83%), *sea* (78%), *pvl* (53%), *eta* (12%) and *tsst* (2%). Out of 200 MRSA isolates, only 40% carried single SCC*mec* type, whereas 59% carried multiple SCC*mec* types including a combination of classical HA and CA types. The predominant SCC*mec* type found in our study was III followed by SCC*mec* V. *eta* and *pvl* toxins were mainly encountered in isolates from severe skin and soft tissue infections whereas the isolates which were negative for the virulence genes tested were obtained from mild skin infections. Notably, all the blood isolates (n=12) were negative for *pvl* and *eta*, whereas all were positive for *hlg*. *pvl* gene positivity was significantly associated with SCC*mec* type V followed by type III. Majority of the blood isolates and all the *tsst* positive MRSA isolates carried SCC*mec* III. The single isolate with SCC*mec* type II was negative for all the virulence genes tested.

**Conclusion**: This study documented the presence of virulence genes in various combinations in majority of the clinical MRSA isolates. No strong evidence for fitness cost of SCC*mec* was established as the isolates negative for virulence genes belonged to diverse SCC*mec* types.

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## The human microbiome research in Africa – A systematic review

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**Background**: The explosion of interest in the human microbiome research was sparked in part by two research initiatives launched in 2008, the European and Chinese-led Metagenomics of the Human Intestinal Tract Consortium and the National Institutes of Health (NIH)-sponsored Human Microbiome Project. The new knowledge provided by these initiatives and others worldwide are transforming our understanding of the pathogenesis of several diseases, including asthma, inflammatory bowel diseases, obesity and Type 1 diabetes, as well as the development of the immune response linked to some vaccines. However, African populations are understudied in these initiatives, and there is no "African Microbiome Initiative". This systematic review aimed to summarize and discuss the state of research on the human microbiome in Africa, including the therapeutic role of the microbiome for the management of certain local diseases.

**Methods & Materials**: Using predefined keywords, we searched in six electronic databases for human microbiome studies conducted in Africa. In addition, to find additional articles, we checked references cited in eligible studies. Two authors independently selected eligible studies published until 30 September 2015.

**Results**: Eighty-nine human microbiome papers were identified from six electronic databases and other sources. There were 80 primary microbiome studies (including Khoi San (n= 1) and Hunter-Gatherers (n= 4)) and 9 nested microbiome studies within existing cohorts. 16S rRNA gene sequencing was the technique most widely used to characterize the microbiota. The main body sites studied were the gut (46%), vagina (25%) and the oral cavity (11%). The diseases targeted were malnutrition (n= 4), HIV/AIDS (n= 7), diarrhoea (n= 4), and periodontitis (n= 5). These microbiome studies were performed in individuals of all ages, with most of the studies being conducted in adults. Kenya, Uganda, South Africa and Nigeria were the sites of the majority of studies; however the principal investigators of most of the studies (87%) were from developed countries. The USA NIH was the main funding source (25%), followed by the Bill and Melinda Gates Foundation (9%) and the European Commision (8%).

**Conclusion**: More studies of the microbiome including African participants, focusing on endemic diseases and led by African researchers are needed.

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