**Article:**


**Impact Factor:** 11.020

**Summary:**

Mycobacterium tuberculosis is the etiological agent of tuberculosis (TB), the leading cause of death due to a single infectious agent, claiming 1.7 million lives in 2016. Of the deaths attributable to TB in 2016, 22% occurred in people coinfected with HIV, and close to 5% of the 10.4 million incident cases of this disease were resistant to at least two of the first-line TB drugs. In this infographic, we describe the fundamental features of the genetics, phylogeny, and physiology of this member of the phylum Actinobacteria, which is associated increasingly with drug resistance mediated by mutations and rearrangements in its single, circular chromosome. We also highlight the key pathogenesis mechanisms employed by this slow-growing, facultative intracellular bacterium, which include avoidance of host cell clearance by arrest of the normal macrophage maturation process.
Summary:
The concentration and fates of six priority phthalate esters (PAEs); dimethyl phthalate (DMP), diethyl phthalate (DEP), di-n-butyl phthalate (DBP), benzyl butyl phthalate (BBP), di(2-ethyl hexyl) phthalate (DEHP), and di-n-octyl phthalate (DOP) in wastewaters from the wastewater treatment plants (WWTPs) which adopted the activated sludge technology in the Amathole Municipality, Eastern Cape, South Africa were investigated. The six PAEs were detected in all the influents and in almost all the WWTP effluent of which DBP was the most abundant in the influent followed by DEHP. Influent concentration of DBP in the three WWTPs ranged between 2.7 and 2488 μgL−1 and the average effluent concentration was 4.90–8.88 μgL−1. On average, the concentration of PAEs in WWTP effluents were higher than PAEs in the upstream and downstream of the discharging point suggesting PAE impact on the receiving water. The concentrations detected in the sludge of which DEHP and DBP were more pervasive ranged between 130 and 1094 μg/g dry weight. The average removal capacity; 27.3–99.5% suggested more adsorption on settling particles and sludge than biodegradation as high significant correlation was found between PAEs removal, total suspended solid and turbidity. Removal of high molecular weight and high octanol-water partition coefficient (logKow) PAEs through adsorption was found to be significantly high. It could be concluded that the release of PAEs into the sludge, and the amount in the final effluent which were found to exceed the acceptable levels allowed internationally, raises safety concern for both aquatic and human's health.
Article:
DOI: 10.1016/j.diabres.2018.03.012
Impact Factor: 3.639

Summary:
Aims: This study aimed to determine the prevalence of Gestational Diabetes Mellitus (GDM) amongst black South African women, describe GDM-associated risk factors and clinical management, and evaluate the efficacy of the fasting plasma glucose reading in diagnosing GDM.

Methods: A cross-sectional screening study was performed. Pregnant women were recruited from the Chris Hani Baragwanath Academic Hospital in Johannesburg. A total of 1906 women underwent a two-hour 75 g oral glucose tolerance test at 24-28 weeks gestation. The World Health Organization's 2013 criteria were used to diagnose GDM.

Results: A total of 174/1906 (9.1% (95% confidence interval (CI) 7.9, 10.5)) women were diagnosed with GDM. These women had significantly higher weights and body mass indexes (BMIs), were significantly older, of higher household socioeconomic status, more likely to report a family history of diabetes, and more likely to be diagnosed with anaemia than women without GDM. An age of ≥35 years, BMI ≥ 30 kg/m², and a family history of diabetes were significant risk factors. The fasting plasma glucose reading had a high sensitivity (83.3% (95% CI 77.0, 88.5)) in diagnosing GDM and 56.9% of the women with GDM were managed by diet therapy alone.

Conclusion: This is the largest GDM prevalence study in South Africa to date. A diagnosis of GDM increases the risk of both mother and child developing Type 2 diabetes which causes further health complications, decreases longevity, and burdens a country's healthcare system. Therefore, a GDM prevalence of 9.1% is concerning and warrants further discussion around current GDM screening policies.
Article:

DOI: 10.1111/tbed.12856
Impact Factor: 3.585

Summary

Bovine tuberculosis (bTB), caused by Mycobacterium bovis (M. bovis), has been reported in many species including suids. Wild boar are important maintenance hosts of the infection with other suids, that is domestic and feral pigs, being important spillover hosts in the Eurasian ecosystem and in South Africa, warthogs (Phacochoerus africanus) may play a similar role in M. bovis-endemic areas. However, novel diagnostic tests for warthogs are required to investigate the epidemiology of bTB in this species. Recent studies have demonstrated that serological assays are capable of discriminating between M. bovis-infected and uninfected warthogs (Roos et al.). In this study, an indirect ELISA utilizing M. bovis purified protein derivative (PPD) as a test antigen was used to measure the prevalence and investigate risk factors associated with infection in warthogs from uMhkuze Nature Reserve and the southern region of the Greater Kruger National Park (GKNP). There was a high overall seroprevalence of 38%, with adult warthogs having a higher risk of infection (46%). Seroprevalence also varied by geographic location with warthogs from Marloth Park in the GKNP having the greatest percentage of positive animals (63%). This study indicates that warthogs in M. bovis-endemic areas are at high risk of becoming infected with mycobacteria. Warthogs might present an under-recognized disease threat in multi-species systems. They might also serve as convenient sentinels for M. bovis in endemic areas. These findings highlight the importance of epidemiological studies in wildlife to understand the role each species plays in disease ecology.
Summary

Background: Typically, women in South Africa (SA) are diagnosed with breast cancer when they self-present with symptoms to health facilities. The aim of this study was to determine the pathway that women follow to breast cancer care and factors associated with this journey.

Methods: A cross-sectional study was conducted at a tertiary hospital in the Western Cape Province, SA, between May 2015 and May 2016. Newly diagnosed breast cancer patients were interviewed to determine their socio-demographic profile; knowledge of risk factors, signs and symptoms; appraisal of breast changes; clinical profile and; key time events in the journey to care. The Model of Pathways to Treatment Framework underpinned the analysis. The Total Time (TT) between a woman noticing the first breast change and the date of scheduled treatment was divided into 3 intervals: the Patient Interval (PI); the Diagnostic Interval (DI) and the Pre-Treatment Interval (PTI). For the PI, DI and PTI a bivariate comparison of median time intervals by various characteristics was conducted using Wilcoxon rank-sum and Kruskal-Wallis tests. Cox Proportional-Hazards models were used to identify factors independently associated with the PI, DI and PTI.

Results: The median age of the 201 participants was 54 years, and 22% presented with late stage disease. The median TT was 110 days, with median patient, diagnostic and pre-treatment intervals of 23, 28 and 37 days respectively. Factors associated with the PI were: older age (Hazard ratio (HR) 0.59, 95% CI 0.40-0.86), initial symptom denial (HR 0.43, 95% CI 0.19-0.97) and waiting for a lump to increase in size before seeking care (HR 0.51, 95% CI 0.33-0.77). Women with co-morbidities had a significantly longer DI (HR 0.67, 95% CI 0.47-0.96) as did women who mentioned denial of initial breast symptoms (HR 4.61, 95% CI 1.80-11.78). The PTI was associated with late stage disease at presentation (HR 1.78, 95% CI 1.15-2.76).

Conclusion: The Model of Pathways to Treatment provides a useful framework to explore patient's journeys to care and identified opportunities for targeted interventions.
1. **INTRAMURAL RESEARCH UNITS**

**Alcohol, Tobacco and Other Drug**


*Impact Factor: 1.969*


*Impact Factor: 2.500*


DOI: 10.1186/s13011-018-0149-2

*Impact Factor: 1.811*


DOI: 10.1111/dar.12693

*Impact Factor: 2.822*


DOI: 10.1016/s2215-0366(18)30060-9

*Impact Factor: 11.588*

**Biomedical Research and Innovation Platform**


DOI: 10.1007/s40291-018-0325-0

*Impact Factor: 1.909*


DOI: 10.1111/jpi.12490

*Impact Factor: 10.391*


DOI: 10.1016/j.acthis.2018.03.006

*Impact Factor: 1.360*
**Centre for Tuberculosis**

   DOI: 10.1111/tbed.12856
   **Impact Factor: 3.585**

   DOI: 10.7171/jbt.18-2901-003
   **Impact Factor: None**

   DOI:10.3389/fgene.2018.00053
   **Impact Factor: 3.789**

   DOI: 10.4049/jimmunol.1701780
   **Impact Factor: 4.856**

**Environment and Health**

   DOI: 10.3390/ijerph15030502
   **Impact Factor: 2.101**

   DOI: 10.3390/atmos9040124
   **Impact Factor: 1.487**

   DOI: 10.1186/s12913-018-3006-0
   **Impact Factor: 1.827**

**Gender and Health**

   DOI: 10.1080/17441692.2018.1449231
   **Impact Factor: 1.614**
**Impact Factor:** 2.806

**Impact Factor:** 2.265

### Health Systems

**Impact Factor:** 1.969

**Impact Factor:** 1.969

**Impact Factor:** 1.731

**Impact Factor:** 2.369

### Non-Communicable Disease

**Impact Factor:** 3.057

**Impact Factor:** 2.342
**Impact Factor:** 1.784

**Impact Factor:** 7.738

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**Office of AIDS**

**Impact Factor:** 1.731

**Impact Factor:** 19.287

**Impact Factor:** 2.916

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**South African Cochrane Centre**

**Impact Factor:** 2.806

**Impact Factor:** 1.827

**Impact Factor:** 2.369

**Impact Factor:** 2.271

Impact Factor: 2.673
2. **EXTRAMURAL RESEARCH UNITS**

**Bioinformatics Capacity Development**

   Impact Factor: 4.259

   Impact Factor: None

**Child and Adolescent Lung Health**

   Impact Factor: 1.093

**Common Epithelial Cancer**

   Impact Factor: None

**Developmental Pathways for Health**

   Impact Factor: None

   Impact Factor: 1.788

   Impact Factor: None

   Impact Factor: 1.240
   **Impact Factor:** 3.639

   **Impact Factor:** 2.541

   DOI: 10.3389/fpubh.2018.00073
   **Impact Factor:** None

**Drug Discovery and Development**
   DOI: 10.1021/acsinfecdis.7b00275
   **Impact Factor:** 3.600

**Gynaecological Cancer**
   DOI: 10.1186/s12885-018-4219-7
   **Impact Factor:** 3.288

**Health Services to Systems**
   DOI: 10.4102/curationis.v41i1.1815
   **Impact Factor:** None

   DOI:10.7196/SAMJ.2018.v108i4.12755
   **Impact Factor:** 1.731

**HIV/TB Pathogenesis and Treatment**
   DOI: 10.5588/pha.17.0114
   **Impact Factor:** None
**Immunology of Infectious Disease**

   **DOI:** 10.7554/eLife.35074
   **Impact Factor:** 7.725

**Maternal and Infant Health Care Strategies**

   **Impact Factor:** 1.731

   **Impact Factor:** 1.731

   **DOI:** 10.1002/ijgo.12477
   **Impact Factor:** 2.174

   **DOI:** 10.1186/S12978-018-0485-8
   **Impact Factor:** 2.209

   **DOI:** 10.1177/1753495X17745727
   **Impact Factor:** None

**Microbial Water Quality Monitoring**

   **DOI:** 10.3390/molecules23040795
   **Impact Factor:** 2.861

   **DOI:** 10.1016/j.chemosphere.2018.03.176
   **Impact Factor:** 4.208
**Molecular Mycobacteriology**

   DOI: 10.1021/acs.jmedchem.7b01622
   **Impact Factor: 6.259**

   DOI: 10.1016/j.tim.2018.02.012
   **Impact Factor: 11.020**

**Respiratory and Meningeal Pathogens**

   DOI: 10.1016/j.vaccine.2018.02.013
   **Impact Factor: 3.235**

**Risk and Resilience in Mental Disorders**

   DOI: 10.1186/s12888-017-1583-9
   **Impact Factor: 2.613**

**Rural Public Health and Health Transition**

   DOI: 10.1186/s12982-018-0073-y
   **Impact Factor: None**

**Stem Cell Research and Therapy**

   DOI: 10.1080/09537104.2018.1445840
   **Impact Factor: 2.465**
3. **GRANT FUNDED RESEARCH**


   **Impact Factor:** None


   DOI: 10.3389/fimmu.2018.00324

   **Impact Factor:** 6.429


   DOI: 10.1016/j.ijcard.2017.12.048

   **Impact Factor:** 6.189


   DOI: 10.4102/sajr.v22i1.1285

   **Impact Factor:** None


   DOI: 10.1136/emermed-2017-207062

   **Impact Factor:** 1.861
4. **RESEARCH CENTRES**

**Advancing Care and Treatment (ACT) For TB/HIV**


   **DOI:** 10.1371/journal.pone.0192089

   **Impact Factor:** 2.806

**Tygerberg SAMRC Collaborating centre for HIV Laboratory Research**


   **DOI:** 10.1097/qad.0000000000001739

   **Impact Factor:** 5.019

**UP Centre for Sustainable Malaria Control**


   **DOI:** 10.1186/s12936-018-2271-z

   **Impact Factor:** 2.715
5. RESEARCH UNITS WITH NO QUALIFYING PUBLICATIONS

Intramural

- Biostatistics
- Burden of Disease
- HIV Prevention
- Office of Cancer
- Office of Malaria
- Office of Tuberculosis
- Primate
- Violence, Injury and Peace

Extramural

- Antiviral Gene Therapy
- Diarrhoeal Pathogens
- Herbal Drugs
- Human Genetics
- Hypertension and Cardiovascular Disease
- Medical Imaging
- Prospective Gastrointestinal Cancer
- Receptor Biology

Research Centre

- Centre for Basic and Translational Human TB Research
- Centre for Tuberculosis Biomarker-Targeted Intervention
- Clinical and Community HIV-Tuberculosis Research Collaborating Centre
- Soweto Matlosana SAMRC Collaborating Centre for HIV/AIDS and TB
- TB Free through Research and Innovation
- Tuberculosis Collaborating Centre for Child Health (TB-CHILD)
- UCT Collaborating Centre for Optimising Antimalarial Therapy in South Africa
- Wits Clinical HIV/TB Research Unit, WITS Health Consortium
- Wits Collaborating Centre for Multi-Disciplinary Research on Malaria
- Wits RHI Collaborating Centre for HIV/AIDS
6. **GRANTS AWARDED**

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