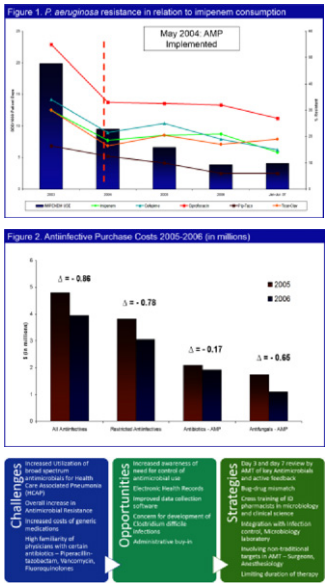
AE. Cost savings exceeded $300,000.

From 2010 to 2014, we have implemented multiple strategies to further control AU.



Conclusion: Since 2004, AMT has implemented strategies that reduced the consumption of RAP agents and *Pseudmonas* resistance has not increased. Re-implementation of AMT responsible for administering institutional guidelines and providing direct feedback resulted in rapid decrease in AE, ACPD. The most gains in the AMT implementation occur early and sustaining an effective AMT requires administrative support and adapting strategies to challenges faced and anticipated.

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Guillain–Barré syndrome in Bangladesh: The role TLR4 Asp299Gly and Thr399Ile polymorphisms

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Background: Bangladesh has achieved a remarkable success to eradicate poliomyelitis, however, Guillain–Barré syndrome (GBS) is frequently diagnosed. GBS is an autoimmune mediated disease of the peripheral nervous system preceded by infections. *Campylobacter jejuni* has been identified as the predominant cause of antecedent infection in GBS. *C. jejuni* lipopolysaccharide (LPS) induces antibodies cross-reactive with gangliosides and has shown nizes mainly lipopolysaccharide (LPS) of gram-negative bacteria. In this study, we investigated functional single nucleotide polymorphisms (SNPs) in the extracellular domain of TLR4 (Asp299Gly and Thr399Ile), and assessed their association for GBS susceptibility, disease pathogenesis and disease outcome.

Methods & Materials: A hospital based case controlled study was conducted in Dhaka Medical College Hospital (DMCH) in Dhaka, Bangladesh in between 2010 to 2013. A total of 210 genomic DNA (105 consecutive patients with GBS and 105 healthy controls of Bangladeshi population) were isolated using QIAGEN (DNA) blood midi kit and genotyped by using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP).

Results: TLR4 (Asp299Gly) polymorphism were significantly associated with GBS patients compared with healthy controls ($p < 0.05$). Gly299Gly homozygote increased the susceptibility of GBS patients compared with healthy controls ($p = 0.0365$, OR = 8.9, 95% CI = 1.1-73.2). Acute motor axonal neuropathy (AMAN) was significantly associated with Gly299Gly homozygote (p=0.0093, OR=14.6, 95% CI = 1.6-130.7). TLR4 variant genotype Asp/Gly ($p = 0.0441$, OR = 2.6, 95% CI = 1.1-6.5) was associated with poor outcome (unable to walk after 6 months); suggesting that these genotype might be one of the factors contributing to a severe form of GBS. No significant association of TLR4 polymorphism (Asp299Gly and Thr399Ile) with anti-ganglioside antibodies was found. In addition, TLR4 Thr399Ile polymorphism had no role in GBS susceptibility as compared with controls.

Conclusion: TLR4 Gly299Gly homozygote is associated with the increased disease susceptibility to GBS. Gly299Gly homozygote is also associated with the axonal variant of GBS. However, TLR4 Asp299Gly polymorphism is prevalently significant with the disease outcome of GBS. Therefore, further study is required to confirm this association using a large cohort.

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Identification of biofilm-stage specific proteins associated with multidrug resistance and quorum sensing pathway in a pandemic strain of Vibrio parahaemolyticus isolated from India

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Background: *Vibrio parahaemolyticus*, a Gram negative halophilic bacterium, is rated as one of the leading etiological agent of food borne diseases in humans. Gastroenteritis is the most common clinical manifestation and specific serotypes of this pathogen were associated with pandemic outbreaks in several parts of the world since 1996. Recent studies conducted in the related Vibrio pathogens has revealed the role of biofilm mode of life in the emergence of multidrug resistance and pathogenicity. Present study was conducted to identify the genes and pathways specific to the biofilm stage of *V. parahaemolyticus* employing high throughput global proteomic approaches.