

Result: Out of 267 samples, 133 gave positive results for *B. abortus* by real-time PCR.

Conclusion: These results indicate a high presence of this pathogen in this area of the country and that this method is considerably faster than current standard methods.

PP-041 Computational prediction of type III secreted proteins using labeled and unlabeled data

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Background: The type III secretion system (T3SS) is a specialized protein delivery system that injects proteins (effectors) directly into the eukaryotic host cytosol and facilitates bacterial infection. T3SS plays a key role in pathogens, but its secretion mechanism has not been fully understood yet and the type III secreted effectors (T3SE) are notoriously difficult to identify.

We propose to predict T3SEs with a bioinformatics method since the wet-bench approaches, e.g., functional screen and protein secretion assay, are laborious and time-consuming. Moreover, because the confirmed effectors and non-effectors are very few, our method is based on semi-supervised learning utilizing both labeled and unlabeled data to improve the prediction accuracy.

Methods: We adopted SVMlin as the predictor. It implements linear SVMs and also extensions of standard SVMs to incorporate unlabeled data. The feature vectors involve amino acid composition, secondary structure and solvent accessibility information.

Result: We have built a non-redundant data set from *Pseudomonas syringae*, including 108 positive samples and 3424 negative samples. This data set was divided into five subsets, four of which for training and the left one for test. In addition, 3000 unlabeled data were used in the semi-supervised learning. The results are listed in Table 1. Three measures were examined. We observe that using the unlabeled data helps to improve the recall nearly 20%. Although the precision decreases, the total accuracy is still improved. Overall, the semi-supervised learning has a better performance.

Table 1. Accuracy comparison

Method	Recall, TP/(TP+FN)	Precision, TP/(TP+FP)	Total accuracy
Supervised	52.4%	78.5%	98.1%
Semi-supervised	71.4%	71.5%	98.3%

TP: true positive; FP: false positive; FN: false negative.

Conclusion: We propose a computational method based on semi-supervised learning to predict type III secreted effectors. The experimental results demonstrate the superiority of the method.

PP-042 Comparison of three methods for the detection of biofilm forming microorganisms isolated from a tertiary care hospital in Pakistan

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Background: Biofilm are described as matrix of extrapolymeric substances in which are embedded bacterial cells. Microorganisms growing in a biofilm are highly resistant to antimicrobial agents and associated with several human diseases. There are various methods to detect biofilm production. These include tissue culture plate (TCP), tube method (TM), congo red agar method (CRA), bioluminescent assay and fluorescence microscopic examination.

Objective: The study was conducted to detect the prevalence of biofilm forming microorganisms isolated from clinical specimens in our laboratory by three different methods, that include TCP, TM and CRA and to compare these three methods for biofilm production.

Place and duration of study: The study was carried out from October 2009 to March 2010, at the Department of Microbiology, Army Medical College/National University of Sciences and Technology, Rawalpindi, Pakistan.

Materials and Method: A total of 112 organisms isolated from blood, pus, intravenous and urinary catheter tips, urine, and sputum were investigated for biofilm production. Isolates were identified by standard microbiological procedures. Biofilm detection was done by TCP method, tube method and CRA method.

Results: Out of 112 isolates, 73 were Gram positive organisms, and 39 were Gram negative organisms. Among 73 Gram positive organisms, 78% were producing biofilm. Among 39 Gram negative organisms, 61% were positive for biofilm production. *Staphylococcus epidermidis* is highly isolated organism. TCP detected more accurately biofilm producers than TM and CRA methods. High resistance to conventional antibiotics was seen by biofilm producers.

Conclusion: TCP method, a quantitative method, is more reliable and accurate method to detect biofilm forming microorganisms.

PP-043 First-line antituberculosis drugs induce long-term alterations in diabetic rats' liver

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Background: Isoniazid, rifampicin, ethambutol and pyrazinamide during short-course chemotherapy for tuberculosis can result in liver injury. The coexistence of tuberculosis and diabetes is common. Availability of the rodent diabetic models offers a unique opportunity to uncover mechanisms of clinical interest in averting human diabetic sensitivity to antituberculosis drug-induced hepatotoxicity.

Methods: Effects of co-administration of first-line antituberculosis drugs, isoniazid, rifampicin, ethambutol, pyrazinamide in therapeutic doses have been investigated in male rats with streptozotocin diabetes. *p*-nitrophenol hydroxylase, glutathione-S-transferase (GST) activity, reduced glutathione (GSH) level, intensity of DNA fragmentation in liver and biochemical indices of blood serum were measured. Histomorphology of liver was provided.

Results: Co-administration of antituberculosis drugs caused increase of liver injury. CYP P-450 2E1 marker – *p*-nitrophenol hydroxylase activity rose in 2 time as compared with untreated diabetic rats and in 5.7 time as compared with positive control. GST activity was significantly elevated and GSH level was consistently descended in diabetic rats liver. Under antituberculosis agents treatment GST activity extended to rise, but GSH level increased to positive control rate. In 24 hours after final medicines co-administration hyperbilirubinemia and increase of alkaline phosphatase (ALP) activity were observed in blood serum, that indicate cholestasis. Investigations after 45 days recovery (without treatment) showed *p*-nitrophenol hydroxylase activity decrease, bilirubin and ALP activity level normalization as compared with previous experiments. But GST activity and GSH level kept tendencies to vary as before. Morphological changes and intensity of DNA fragmentation in liver of treated and untreated diabetic rats were too high in both series of experiments.