MYCOBACTERIUM TUBERCULOSIS FROM EXTRA PULMONARY SITES
NEXT-GENERATION WHOLE GENOME SEQUENCING: OPPORTUNITIES &
CHALLENGES

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Tuberculosis (TB) remains one of the leading causes of morbidity and mortality worldwide. Extrapulmonary tuberculosis (EPTB) constitutes around 15–20% of TB cases in immunocompetent individuals. Extrapulmonary sites that are affected by TB include bones, lymph nodes, meningitis, pleura, and genitourinary tract. Whole genome sequencing has emerged as a powerful tool to map genetic diversity among Mycobacterium tuberculosis (MTB) isolates and identify the genomic signatures associated with drug resistance, pathogenesis, and disease transmission. Several pulmonary isolates of MTB have been sequenced over the years. However, availability of whole genome sequences of MTB isolates from extrapulmonary sites is limited. Some studies suggest that genetic variations in MTB might contribute to disease presentation in extrapulmonary sites. This can be addressed if whole genome sequence data from large number of extrapulmonary isolates becomes available. In this study, we have performed whole genome sequencing of five MTB clinical isolates derived from EPTB sites using next-generation sequencing platform. We identified 1434 nonsynonymous single nucleotide variations (SNVs), 143 insertions and 105 deletions. This includes 279 SNVs that were not reported before in publicly available datasets. We found several mutations that are known to confer resistance to drugs. All the five isolates belonged to East-African-Indian lineage (lineage 3). We identified 9 putative prophage DNA integrations and 14 predicted clustered regularly interspaced short palindromic repeats (CRISPR) in MTB genome. Our analysis indicates that more work is needed to map the genetic diversity of MTB. Whole genome sequencing in conjunction with comprehensive drug susceptibility testing can reveal clinically relevant mutations associated with drug resistance.

Key words: coding DNA sequence, lineage, lymphadenitis, nonsynonymous, octal code

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IRON METABOLISM PROTEINS DURING PREGNANCY

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Iron-deficiency (ID) is the most common nutritional deficiency worldwide. ID anaemia, a condition in which circulating haemoglobin (Hb) levels are reduced, is estimated to affect 1.2 billion people globally; the prevalence of latent ID, in which no overt signs of anaemia exist, is undoubtedly higher. Global rates of anaemia in pregnant women are estimated to be 38%, with 22% of pregnant women in developed nations affected, emphasizing the importance of iron status assessments in vulnerable groups regardless of geographical location. ID during pregnancy and the postnatal developmental period causes altered growth trajectories, and is associated with long-term cognitive deficits, cardiovascular perturbations, and metabolic dysfunction [1]. To study iron metabolism markers during the pathogenesis of IDA in pregnant women is important for the developing of new principles of treatment [2].
Materials and Methods. We study some indicators of iron metabolism in pregnant women in anaemia. The venous blood of 85 pregnant women with anaemia was examined. Serum iron, ferroportin, transferrin, serum ferritin and hepcidin were investigated. The comparison group consisted of 19 pregnant women without anaemia, as well as control group consisted of 15 non-pregnant practically healthy women.

The haemoglobin concentration was measured by using “Mythic-18” haematological autoanalyzer. The serum transferrin level was established by using an immunoturbidimetry method with “Cormay” (Poland) reagent kits. The concentrations of hepcidin and ferroportin were determined by using “Cloud-Clone Corp.” (USA), and ferritin concentrations were determined by using “Pishtaz teb” (Iran) reagents through enzyme-linked immunosorbent assay (ELISA) method.

Results. The study revealed a significant decrease in the level of lactoferrin, ferritin level. The study also revealed a significant decrease in the level of hepcidin in the blood serum of pregnant women with IDA. There was a tendency to increase the concentration of hepcidin in the third trimester. An increase the hepcidin level in the blood can be a natural reaction of the body to an increase in intestinal absorption of iron. In this period, an increased content of this protein leads to a lack of iron for the synthesis of Hb. A change in hepcidin level in anemia can be mediated by tissue hypoxia, an increase in erythropoietin, or a decrease in serum and tissue iron level due to its consumption by red blood cell precursors. The synthesis of hepcidin is suppressed by erythropoietin, which ensures the supply of a sufficient amount of iron to the bone marrow and active erythropoiesis. An increase in hepcidin level in the third trimester of pregnancy can be caused by changes in the cytokine profile that occur during preparation of the body for childbirth.

According to the results of our study, in the blood serum of pregnant women with IDA there is a significant increase in the content of ferroportin compared with the data of pregnant women without anemia. A comprehensive definition of various indicators of iron metabolism provides important information not only for understanding the pathogenesis of iron deficiency anaemia in pregnancy but also for early diagnosis of the disease and the appointment of the correct treatment.

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COMPARATIVE MONITORING OF THE ENZYME ACTIVITY OF BONE METABOLISM IN PATIENTS AFTER DENTAL IMPLANTATION

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The balance of bone regeneration processes helps to reduce the resorption and increase mineralization. The imbalance mechanism of bone recovery depends on which process is currently the leading: increased bone resorption or decreased bone regeneration. Comparative monitoring of the activity of bone metabolism enzymes is important for predicting the results of treatment and reduction the inflammatory process. The aim is to carry out a comparative analysis of enzymes activity in bone metabolism in patients after dental implantation.