J Diabetes Metab 2016, 7:8(Suppl)
http://dx.doi.org/10.4172/2155-6156.C1.052

12th European Diabetes Congress

Screening aerobic micro-biome in diabetic foot ulcers

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A prospective study was carried on diabetic foot patients to deduce clinical attributes, the gamut of aerobic microbial flora and to appraise their comparative *in vitro* susceptibility to the customarily used antimicrobials. A detailed clinical chronicle and physical examination was carried out in each patient. The study also pivoted on assessing potential risk factors involved in development of non-healing ulcers. A total of 87 organisms were isolated from 70 specimens, and an average of 1.2 isolates per case was reported. Polymicrobial infection was found in 17% of subjects. In this study, *Escherichia coli* among the gram-negative (19.5%) and *Staphylococcus aureus* among the gram-positive (18.3%) were the predominant aerobes explored. *Pseudomonas aeruginosa* and *Escherichia coli* were pre-dominant isolates of non-healing ulcers. Amikacin exhibited highest sensitivity to gram-positive cocci (90.7%) and Enterobacteriace (86%). All strains of *Pseudomonas aeruginosa* were sensitive towards Imipenem (100%). Deplorable glycemic status, altered lipid spectra, existence of neuropathy and peripheral vascular disease possessed the potentiality for development of non-healing lesions. There is a need for continuous surveillance of bacteria and their antimicrobial sensitivity blueprints to provide the basis for empirical therapy and minimize the risk of complications. Also ardent clinical evaluation and history will aid in revealing the risk of developing non-healing status in DFUs.

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Hypoxia and extra-cellular matrix gene expression in adipose tissue associates with reduced insulin sensitivity in black South African women

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Objective: Black South African (SA) women are more insulin resistant and have increased gluteal subcutaneous adipose tissue (SAT) hypertrophy than white SA women. We tested the hypothesis that adipose tissue hypoxia and extracellular matrix (ECM) gene expression in gluteal and abdominal SAT is higher in black than white women, and associates with reduced insulin sensitivity (SI) in black women.

Methods: SI (frequently sampled intravenous glucose tolerance test), gluteal and abdominal SAT mRNA levels of hypoxia- and ECM-related genes were measured in normal-weight and obese premenopausal black (n=30) and white (n=26) SA women at baseline, and in black women, at 5-year follow-up (n=10).

Results: Compared to obese white women, obese black women had higher expression of hypoxia inducible factor 1 (*HIF-1α*), collagen type Vα1 (*Col5a1*) and collagen VIα1 *Col6a1* and reduced vascular endothelial growth factor-α (*VEGFα*) expression in gluteal ($p<0.05$) but not abdominal SAT depots. Independent of body fatness, gluteal expression of *HIF-1α* ($r=-0.55$; $p=0.01$), *Col5a1* ($r=-0.41$; $p=0.05$) and *Col6a1* ($r=-0.47$; $p=0.03$) correlated with reduced S_I in black women only. Over a 5-year follow-up, changes in gluteal *HIF-1α* ($r=0.58$; $p=0.01$), *Col5a1* ($r=0.82$; $p=0.02$), and *Col6a1* ($r=0.88$; $p<0.00$) expression correlated positively with the change in fasting insulin concentrations in black women.

Conclusion: Compared to their white counterparts, black women expressed higher levels of genes associated with hypoxia and collagen deposition, and that the associations between these genes and SI differed by ethnicity. We thus propose that insulin resistance in black women may be related to higher ECM and hypoxia gene expression.

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