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compared to progressing (34.9%) individuals ($P < 0.001$, OR = 0.17).
Conclusions: The E3K SNP is likely to affect both CXCR6 cell surface expression and/or binding of its ligand. Thus, we hypothesize that the high prevalence and interplay of both these mutations in Black South African individuals may be masking the effect of the rs2234358 SNP on LTNP within this population.

P37.07
Cytokines Genes Polymorphisms in Ukrainian HIV-1 Infected Individuals

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Background: The objective of the research was to study distribution character of the allelic variants of cytokines genes in HIV-1 infected Ukrainians.
Methods: Data for the study were DNA samples, received from 200 inhabitants of Ukraine: 78 HIV-infected, 22 - HIV-negative individuals from the group of high risk of contamination, 100 healthy blood donors. IL-4 (–590C/T), IL-10 (–592C/A) and TNF-α (–308G/A) genes polymorphisms detection was made with PCR-RLFP method.
Results: By analysis of frequency of IL-4 gene allelic variants it has been discovered that homozygotes by the main allel were the dominant variant. Among people with HIV T/T minor gene carriers were 4.5 more often met in comparison with control group ($p < 0.05$) that can prove the tendency to association of the mentioned genotype with infection.
Distribution of allelic variants of IL-10 gene promoter region in position – 592 is characterized by homozygote dominance by the main gene. Among the individuals with HIV A/A minor allel carriers were 3.4 more often met in comparison with control group ($p < 0.05$). Individuals with A/A genotype were not identified in group of high risk of virus infection. The above-mentioned proves the tendency to association of minor allel carrier state with HIV infection.
The occurrence of the homozygous combination of the allelic variant G/G of the promoter of TNF-α has been shown to prevail almost twofold over the occurrence of the variant G/A among all groups. High frequency of heterozygote by the main allel has been recorded among the individuals with HIV. Thus, G/A genotype frequency in group of HIV-infected people 2 and 1.5 exceeded the appropriate indices of group of high risk of infection and comparison group correspondingly ($p < 0.05$) that points to the tendency to association of the mentioned variant with infection.
Conclusions: Cytokines genes variations may contribute to the acquisition of HIV infection and encourages carrying out of further populations studies in this sphere of HIV-infection immunogenetics.

P37.08
Multiple T-cell Epitopes of HIV-1 Nef Containing Positively Selected Mutations Associated with Different Disease Outcome

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Background: HIV-1 Nef plays a major role in enhancing the pathogenicity of the virus through various mechanisms such as down-regulation of CD4 and HLA class I surface expression and interfering with cell signaling pathways. Identifying and characterizing CD8+ T cell epitopes in Nef that are under host immune selection can help in selecting targets for an effective vaccine.
Methods: 326 subtype A Nef sequences from treatment naïve patients of a Kenyan sex-worker cohort were generated using 454 pyrosequencing. Positively selected (PS) mutations were determined using a bioinformatics approach, quasi analysis. Peptides were designed with mutation placed in anchor position 2, 5, 8, 9 of epitopes of HLA class I alleles for validation with ELISpot assay using patient PBMCs.
Results: E70D, I109V and I176M were associated with rapid CD4 decline ($p = 0.010$, 0.015, 0.025 respectively). H124N and K190M were associated with slow CD4 decline ($p = 0.001$ and 0.029). The five PS mutations were significantly associated with HLA class I alleles including A*23:01 (E70D, $p = 0.002$; I176M, $p = 0.003$), A*02:01 (I109V, $p = 0.028$; H124N, $p = 0.021$), B*58:01 (I109V, $p = 0.048$), A*3002, B*57:03 and C*02:01 (H124N, $p = 0.026$, 0.0004, and 0.011 respectively) and C*06:02 (K190M, $p = 0.037$). ELISpot analysis identified 27 novel epitopes containing either the consensus or the PS mutations. Six new epitopes contained E70D, five epitopes contained K190M, and I109V and H124N were each contained by eight new epitopes. No epitopes containing I176M was confirmed by ELISpot. It is possible that I176M represents compensatory mutations due to functional requirements under host immune selective pressure.
Conclusions: Identification and characterization of epitopes containing beneficial and detrimental PS mutations can provide important insight for selecting immunogens for an effective HIV vaccine. More detailed investigation of T-cell responses, such as poly-functionality and proliferation to these mutations will be conducted to further characterize these Nef epitopes.

Innovations in Vaccine and Microbicides Studies in Lab and Monitoring

P38.01
Operational Challenges for the Set-up of Gram Stain Analysis for Diagnosing Bacterial Vaginosis in a Local Laboratory in Durban, South Africa

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Background: Studies have demonstrated the association between BV and HIV acquisition in woman. The prevalence of BV reported in clinical trials conducted by the Medical Research Council HIV Prevention Research Unit (MRC HPRU) is between 5–9%. In an attempt to reduce turnaround time for results, enable direct contact with research clinics, facilitate staff capacitation and reduce costs, the HPRU was selected by the Protocol Reference Laboratory to perform in-house testing for diagnosing BV. We report here on the operational challenges associated with the set-up of the laboratory to perform the analysis.