Abstracts

Nordm.; strains/total (%)

Grape seed extract
7/25 (28%)

Grape seed feed extract
25/25 (100%)

Zone inhibition: 7–14 mm

Grape extract
5

Grape seed feed extract
2

Zone inhibition: 15–20 mm

Grape extract
10

Grape seed feed extract
15

POSITIVE SELECTION IN THE EVOLUTION OF HELICOBACTER PYLORI OUTER MEMBRANE PROTEINS

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Homologous recombination in Helicobacter pylori has been extensively described to occur via Outer Membrane Proteins (OMPs), regulating protein expression and generating allelic diversity, while the importance of single nucleotide polymorphisms (SNP) remains little studied. We used an OMP-encoding gene, homC, as a model to evaluate the weight of positive selection in the evolution of H. pylori, by using ≈200 sequences obtained from strains collected worldwide. N-site and branch-site phylogenetic analysis by maximum likelihood models were used to identify specific codons that may be important in homC evolution, and to evaluate the impact of selective pressure on the geographic segregation of strains, respectively. The N-site overall analysis showed that 14 of the 742 (1.9%) homC codons are likely under positive selection (likelihood-ratio test (LRT), \( p < 10^{-3} \)). Four of these codons are located in the most variable allelic gene middle region, probably reflecting recombination-derived hitchhiking events. On the other hand, eight codons are located in the more conserved 5’ and 3’ gene regions, although the significance of this distribution remains to be clarified. Branch-site analysis revealed 36 codons (4.9%) under positive selection (LRT, \( p < 10^{-3} \)), showing a non-random distribution, and 89% of these particular codons (\( p < 10^{-3} \)) support the phylogenetic segregation of European strains from both African and East Asian strains. The lack of visible recombination within this segment suggests an important biological role of point mutations in the evolution of H. pylori OMPs. In conclusion, homC SNP analysis suggests that, besides recombination, positive selection contributes as well to the evolution of H. pylori OMPs.

Abstract no.: P1.07

ASSEMBLY COMPARISONS: RE-SEQUENCING OF THE H. PYLORI J99 AND 26695 STRAINS USING ION TORRENT AND ILLUMINA MISEQ NEXT GENERATION SEQUENCING TECHNOLOGIES

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Molecular epidemiology by whole genome sequencing is a rapidly growing and evolving area. Benchtop sequencing machines that produce millions of reads of short DNA sequences are becoming standard tools for laboratory analysis. We aimed to understand the accuracy of de novo genome assemblies derived from both the Ion Torrent and the MiSeq sequencing machines. We analysed the accuracy of each coding sequence (CDS) by re-sequencing and assembling the two completely sequenced and finished strains, J99 and 26695. We found that despite high quality data, the genome assemblies displayed limited accuracy and varying results. J99 was assembled more accurately than 26695 by data derived by both machines. The number of coding sequences for that were 100% accurate in the 399 assemblies were 1028 (66%) for Ion Torrent and 1207 (81%) for MiSeq out of the annotated total of 1491. In 26695, the number of correct genes were substantially fewer with 693 (44%) for Ion Torrent and 965 (62%) for MiSeq out of 1566 annotated genes.

Abstract no.: P1.08

SINGLE NUCLEOTIDE POLYMORPHISMS IN PRO- AND ANTI-INFLAMMATORY CYTOKINES AND THE RISK OF GASTRIC CANCER IN IRAN

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Interleukins depending on their tumor promoting or suppressing functions are known to affect cancer risk. IL-2 and IL-4 are respectively known as pro and anti-inflammatory cytokines which are affected by H. pylori infection and involved in predisposition to gastric cancer. We have, herein, investigated the risk of gastric cancer associated with of IL-2 -384G/T and IL-4 -590C/T SNPs and its interaction in H. pylori infection.

Gastric cancer patients (N = 254) and healthy controls (N = 251) were evaluated for H. pylori-specific serum IgG antibodies by ELISA as well as IL-2 -384G/T and