
Article:
Shahi, F., Collini, P. and Darton, T. orcid.org/0000-0003-2209-9956 (2023) 53 TRANSLATE TB: Transcriptional signatures for latent TB, Sheffield, UK. Clinical Infection in Practice, 20 (Supplement 1). 100311. ISSN 2590-1702

https://doi.org/10.1016/j.clinpr.2023.100311

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the (V4) of the 16Sr RNA gene was conducted and analysed using QIIME. Nasal swab isolates were cultured and identified using near full-length sequencing of the 16S rRNA gene. Isolates identified as corynebacteria or staphylococci were typed using (rep-PCR). Antagonism was determined using an agar-based inhibition assay.

Results

Four major bacterial phyla (Actinobacteria, Bacteroidetes, Firmicutes, and Proteobacteria) were identified from all volunteers. The typing of cultured staphylococci and corynebacteria suggested that intra-individual strain diversity was limited. Analysis of generated nasal microbiota profiles suggested an inverse correlation in terms of relative abundance between staphylococci and corynebacteria. Despite the apparent antagonism between these genera, it was limited when investigated on agar. Of 1000 pairwise interactions, observable zones of inhibition were only reported between a single strain of C.pseudodiphtheriticum and S.aureus. Imaging under EM revealed this effect to be bactericidal with clear lytic effects on staphylococcal cell morphology.

Conclusion

Nasal microbiota is complex, but culturable staphylococci and corynebacteria were limited in terms of clone type. Analysis of generated nasal microbiota profiles suggested an inverse correlation in terms of relative abundance between these genera suggesting an antagonism or competition between these taxonomic groups.

doi: 10.1016/j.clinpr.2023.100309

52 Bolus vitamin D supplementation did not reduce infection risk, re-occurrence, or symptom duration in young male adults undergoing arduous military physical training: D_SAF, randomised controlled trial

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Evidence suggests that vitamin D status and immune function during physical training may be interrelated. We aimed to investigate the effectiveness of bolus vitamin D supplementation in reducing infections in Royal Marines (RM) recruits undertaking arduous 32-week military physical training.

Methods

Recruits (n = 1815) were randomly allocated into two groups receiving placebo (CON) or 50,000 IU vitamin D3 (VIT-D) at weeks 1, 6, 15, and 24 of the 32-week programme. Serum vitamin D status (25OHD) concentration was assessed at weeks 1, 6, and 31. Upper-Respiratory Tract Infections (URTI) were defined based on self-reported flu-like symptoms and medical notes, and skin and soft tissue infections (SSTI) from medical notes.

Results

The supplementation regimen increased serum 25OHD (Mean ± SD: Baseline CON 62.3 ± 26.5 nmol/L, VIT-D 60.2 ± 23.7 nmol/L; Week 31 CON 54.5 ± 18.6 nmol/L, VIT-D 62.5 ± 15.2 nmol/L), however, sufficiency (≥50 nmol/L) was achieved by 74% of study recruits. VIT-D was not superior to CON in preventing the experience (OR = 0.76, 95% CI 0.50-1.14), or re-occurrence of URTI during follow-up (OR = 0.93, 95% CI 0.75-1.15) or reducing the number of days out of training (B = 0.14, 95% CI −0.50-0.77). Similarly, VIT-D showed no superiority over CON in reducing the occurrence of SSTI (OR = 0.69, 95% CI 0.44-1.07), or re-occurrence during follow-up (OR = 0.72, 95% CI 0.52-1.01), or the number sick days (B = −0.61, 95% CI −1.30-0.09).

Conclusion

In this randomised placebo-controlled trial, we did not find that bolus vitamin D supplementation reduced infectious episodes or sick days compared to placebo in young male adults undertaking arduous military physical training.

doi: 10.1016/j.clinpr.2023.100310

53 TRANSLATE TB: Transcriptional signatures for latent TB, Sheffield, UK

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Background

Latent tuberculosis infection (LTBI) is complex to diagnose as patients have no clinical signs, no detectable bacilli and may be years from exposure. In low incidence settings, interferon-gamma release assays (IGRA) have increased the yield of at-risk patients who might benefit from tuberculosis chemoprophylaxis. Treatment is not without risk, however, and more accurate detection of patients most likely to benefit might be possible using newer approaches, including the detection of host transcription responses. We evaluated the use of proposed host gene-expression signatures in patients presenting to Sheffield Teaching Hospitals NHS Foundation Trust with LTBI.

Methods

We prospectively recruited patients with IGRA-positive LTBI and four additional comparative cohorts of patients with active TB, IGRA-negative inflammatory disease, other acute infections, and healthy controls. Clinical data and whole-blood samples were collected in PAXgene RNA tubes before, during and after treatment. Extracted RNA was probed for 20 genes (7 signatures of interest) by microfluidic qRT-PCR.

Results

78 patients, including 40 with LTBI, were recruited. No patients with LTBI have developed active TB during 10 months of follow-up. All 7 signatures distinguished LTBI, active TB and healthy control cohorts, but did not distinguish TB cohorts from those with other infections or inflammatory conditions.

Conclusion

Early results show that all 7 signatures were sensitive enough to distinguish between patients with LTBI and healthy controls in a UK cohort. However, the specificity of the signatures for TB versus other infective or inflammatory responses appears low and may be of limited use in clinical practice.

doi: 10.1016/j.clinpr.2023.100311