

Title: New spectral analysis method to identify trait-like features in NREM sleep power spectra.

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Introduction: Variability among individuals in sleep/wake biology and behaviour is pervasive. Sleep/wake-related variability involves individual trait-like features (ITLF). In order to study ITLF, we developed an advanced spectral analysis method (ASAM) to compare in a systematic and reproducible way 3 features of NREM power spectra (PS). As sleep spindles (SS) have been reported several times to be an important ITLF, we focused on a broad range of sigma activity (10 – 18Hz).

Methods: The ASAM is composed of three main steps. First, EEG sleep recording is preprocessed and the NREM PS is computed for each channel of interest. Second, three characteristic features from the NREM PS related to sigma peak activity are extracted: magnitude, peak location and standard deviation. Third, the intra-individual stability and the inter-individual variability of these features, as well as the influence of sleep perturbations, are statistically tested using the Intra-Class Correlation (ICC) coefficient and the Wald Z-test. The performance of the ASAM was assessed using different polysomnography-derived sleep recordings from 16 healthy young male subjects (18-30 years). For each subject, these recordings were acquired in 5 different “sleep contexts”: the acquisition was varied from 4h to 12h and was performed at different circadian phases.

Results: All three features of sigma activity (magnitude, peak location and its standard deviation) were recognized as important ITLFs (ICC = 0.74, 0.94 and 0.63 respectively). Furthermore, the inter-individual variability of these three features was significant different from zero (Wald Z-test $p_s < 0.05$).

Conclusion: Three aspects of NREM PS sigma activity are recognized as important ITLFs. It is also showed that even though these features changed according to sleep context, they remained specific to the individuals. Establishing the trait-specific nature of variability in sleep/wake parameters could elucidate genetic mechanisms.

Disclosures of potential conflict of interest: the authors do not disclose a potential conflict of interest.

Sources of funding: Belgian Fund for Scientific Research (FNRS), European Research Council (ERC-Starting Grant). Actions de Recherche Concertée of the Wallonia-Brussels Federation, University of Liège research funds, Fondation Médicale Reine Elisabeth, Fondation Simone et Pierre Clerdent.