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Acquisition, Processing and Quantification of DaTSCAN studies

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Brain imaging using radioactive tracers provides particular technical challenges and studies using DaTSCAN are no exception. DaTSCAN is licensed for the differential diagnosis of Parkinson's disease and Essential Tremor and relies primarily on the visual interpretation of the radioactive distribution in the caudate and putamen following Single Photon Emission Tomographic (SPECT) imaging. This technique has shown high diagnostic sensitivity and specificity, however, technically poor studies will tend to produce distributions which will be interpreted as abnormal and therefore produce a false positive diagnosis of Parkinson's Disease. This potential outcome makes it essential that all aspects of the acquisition and processing of these studies are optimized. The EANM has published guidelines (1) for the conduct of DaTSCAN studies and provides the basis for high quality studies. However, each gamma camera, data processing combination produces images of different characteristics and quality depending particularly on patient positioning capabilities and collimator characteristics. The key choices for acquisition characteristics are the choice of collimator, the pixel size and the energy window used and for SPECT the number of projection images and total scanning time. The uptake of tracer is known to be dependent on age and time post injection and physical acquisition parameters must be linked to a consistent and methodical approach to patient preparation and post injection study time to provide studies with adequate signal to noise ratio.

The reconstruction of the transaxial sections provides another set of choices which include the use of either Filtered Back Projection or Iterative methods, the selection of smoothing filter, the choice of transaxial slice thickness and the reconstructed pixel size. The above options must be chosen primarily to retain resolution within the diagnostic images. It is essential that the images are presented for visual interpretation using standard planes in order to optimize the visualization of the caudate and putamen.

Whilst visual interpretation has proven to be effective for clinical interpretation considerable interest exists in quantifying the specific uptake of the tracer within the striatum or each caudate and putamen. It is important to define the question to be answered in seeking to optimize the quantification process which may include the differentiation of disease entities, the monitoring of disease progression or the effectiveness of drug interventions. Quantification will require, as a minimum, the application of an attenuation correction within the reconstruction process followed by the application of a volume of interest assessment of the specific and non-specific binding in the brain. The differentiation of disease states requires the user to establish normal ranges of uptake and considerable interest exists as to the possibility of establishing normal ranges which can be translated across all acquisition and processing systems (2). The evaluation of reconstruction software (3) has shown that all systems exhibit different responses to input signal and provide differing signal to noise ratios from test data. These variations are compounded by the different physical characteristics of the gamma camera systems. It has been proposed that universal normal ranges may be generated by ensuring that all system variables are corrected using an iterative reconstruction process (4,5). The parameters to be corrected will include system resolution and scatter as well as attenuation correction, preferably using a measured attenuation correction map.

Following the application of an optimized reconstruction algorithm quantification must be undertaken using a reproducible and sensitive methodology which minimizes inter and intra operator variability whilst maximizing patient group differentiation. Several volume of interest based techniques have been proposed, however, the application of pixel based techniques such as SPM are of particular interest as they provide a methodology which is virtually operator independent and into which can be incorporated other study variables (6). Whilst all of these methods have demonstrated potential, published applications have been performed on single systems utilizing normal ranges or populations from the same system. Global normal ranges are not yet available and it remains vital that users carefully validate

each quantification method and establish system specific normal ranges. Local practice will determine such parameters as test/retest variability which will impact upon the usefulness of the methodology to monitor disease progression and treatment interventions. Quantification of DaTSCAN studies remains a significant challenge. This presentation will review the current guidance and the latest research using quantitative methods.

References

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