IMPLEMENTATION OF A NEW REFERENCE VALUES DATABASE FOR SEMIQUANTIFICATION IN 123I-FP-CIT BRAIN SINGLE EMISION TOMOGRAPHY

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INTRODUCTION

Brain dopamine transporters imaging by Single Emission Tomography (SPECT) with 123I-FP-CIT (DaTScan™) has become an important tool in the diagnosis and evaluation of Parkinson syndromes. This diagnostic method allows the visualization of a portion of the striatum where healthy pattern resemble two symmetric camels, allowing the evaluation of dopamine pre-synaptic system, in which dopamine transporters are responsible for dopamine release into the synaptic cleft, and their reabsorption into the nigrostriatal nerve terminals, in order to be stored or degraded.1,2

In daily practice for assessment of DaTScan™, it is common to rely only on visual assessment for diagnosis. However, this process is complex and subjective as it depends on the observer’s experience and it is associated with high variability intra and inter observer.3

Studies have shown that semiquantification can improve the diagnosis of Parkinson syndromes4,5, for semiquantification, analysis methods of image segmentation using regions of interest (ROIs) are necessary.4 ROIs are drawn, in specific - striatum - and in non-specific – background – uptake areas. Subsequently, specific binding ratios are calculated.4,6

The aim of this investigation was to create and validate a database of healthy controls for Dopamine transporters with DaTScan™ named DBRV. The created database has been adapted to the Nuclear Medicine Department’s protocol, and the population of Infanta Cristina’s Hospital located in Badajoz, Spain.

SUBJECTS & METHODS

1- Sample Selection

A sample of 90 DaTScan™ tests, divided into 3 groups of 30 tests each was used. These were acquired according EANNM guideline.1 The first Group of 30 healthy controls was used for calculation of semiquantification value, therefore, creating a database of reference values (DBRV). The second group of pathological (DBP) tests, and Third Group of 30 healthy studies were used to validate the DBRV. Figure 1 shows the sample selection process.

2- Reconstruction and segmentation of DaTScan™ studies (DBRV, DBB and DBP)

Each DaTScan™ was reconstructed by Filtered Back Projection and processed three times by the same operator. In the summed image of 3 transaxial slices, that identify the full extent of striatal tissue, the average uptake of left and right caudate nucleus (LC and RC) left and right putamen (LP and RP) and occipital (OC) was determined through semiautomatic ROIs.

3- Reference Values Formulas

After segmentation, for each DaTScan™ the Binding Ratios were calculated from the formulas shown in Table 1.

Table 2: Calculation formulas of DaTScan™ semiquantification Binding Ratios

<table>
<thead>
<tr>
<th>Binding Ratio</th>
<th>Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caudate Nucleus</td>
<td>Left Caudate</td>
</tr>
<tr>
<td>Putamen</td>
<td>Left Putamen</td>
</tr>
<tr>
<td>Striatum</td>
<td>Left Striatum</td>
</tr>
</tbody>
</table>

4- Creation of the Database Reference Values (DBRV)

The mean ± standard deviation (x ± SD) for each binding ratio (A-H) of all DaTScan™ studies composing the 30 healthy controls of the first group was calculated. The resulting values for each ratio formed the Database Reference Values.

5- Validation of Database Reference Values (DBRV)

For validation of DBRV control charts (Figure 2-9) were created. An analysis of the distribution of the results obtained for the binding ratios A-H of the DBP and DBR around the reference values was done. For accuracy issues, the value of mean less standard deviation (x - 2 SD) of each reference value was used to differentiate healthy of pathological individuals. Thus the binding ratios A-H from semiquantification of DBP should be above the line x - 2 SD, and the DBP below this same line.

RESULTS

The reference values that comprise the DBRV, semiquantification result of the healthy controls, are shown in Table 2.

Table 2: Database of reference values(± 2) Binding ratios (DBRV)

<table>
<thead>
<tr>
<th>Binding Ratio</th>
<th>Reference Values (± 2 SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>2.40 ± 0.40</td>
</tr>
<tr>
<td>B</td>
<td>2.57 ± 0.36</td>
</tr>
<tr>
<td>C</td>
<td>2.94 ± 0.16</td>
</tr>
<tr>
<td>D</td>
<td>2.13 ± 0.25</td>
</tr>
<tr>
<td>E</td>
<td>1.94 ± 0.25</td>
</tr>
<tr>
<td>F</td>
<td>2.41 ± 0.37</td>
</tr>
<tr>
<td>G</td>
<td>2.44 ± 0.34</td>
</tr>
<tr>
<td>H</td>
<td>0.89 ± 0.07</td>
</tr>
</tbody>
</table>

The following figures (Figure 2-9) represent the control charts of the Binding Ratios A-H, used for validation of the DBRV.

DISCUSSION/CONCLUSION

In DBRV, the binding ratios A-B, C-D and F-G are similar to their striotatal homologous symmetrical structures. The binding ratios F and G are an average value between left and right caudate nucleus and putamen respectively. Through analysis of control charts,4,5 (Figures 2-9) according to the criteria established previously, for diagnostic determination, it was found that 93% of DBP patients are located above the limit (x - 2 SD) and 86% of DBP patients are below the same limit, as a consequence of a decrease in striotatal uptake visible in pathological cases.

BIBLIOGRAPHY

5. Faria DAB. Segmentação, Reconstrução e Quantificação 3D de Estruturas em Imagens Médicas – Aplicações em Imagem Funcional e Metabolismo. 2010:16.