ANALYSIS OF GTP CYCLOHYDROLASE I GENE (GCH1) BY MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION (MLPA) FOR DIAGNOSIS OF SEGAWA DISEASE

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Objective:

To evaluate the efficacy in diagnosis of Segawa disease by using MLPA (Multiplex Ligation-dependent Probe Amplification) method which can detect large deletions in patients who have no mutations by the direct sequencing method.

Patients and Methods

We diagnosed 25 patients with Segawa disease by clinical symptoms and pteridines analysis in cerebrospinal fluid (CSF). Among 25 patients with Segawa disease 22 patients were confirmed genetically by direct gene analysis of *GCH1*. In the other 3 patients we performed gene analysis by using MLPA methods.

Results

All 25 patients with Segawa disease showed significantly lower levels of both neopterin (N:6.59±4.09 nM) and biopterin (B:5.20±2.85 nM) in CSF than controls (N:19.5±2.10, B:23.7±8.50 nM). Twenty-two patients diagnosed by direct sequencing method had a point mutation or two bases deletion in one allele and the other 3 patients had a large deletion in their one allele which detected by MLPA method. Both N and B levels in CSF were significantly lower in the former 22 patients (N:6.92±3.92, B:5.58±2.74 nM) than in the latter 3 patients (N:1.98±0.94, B:1.67±1.46 nM).

Conclusions

All patients with Segawa disease had very low N and B levels in CSF. Especially patients who had large deletion showed significantly lower levels of both N and B in CSF than the other patients who had a point mutation or 2 bases deletion. Patients suspected to be Segawa disease who had very low N and B levels in CSF should be analyze GCH1 gene by MLPA method.