Identification of a novel genomic mutations through a next-generation sequence among 51 Japanese Cystinuria patients (Look for a missing piece of Genotype Criteria?)

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Back Grounds: Unique Characteristics of Japanese Cystinuria

- Autosomal recessive disorder
- Cause recurrent Urinary Stone
- Impair transport of Cystine and dibasic amino acids (Lys, Arg, Orn)
- Defect in Cystine transporter BAT1(Defect in Cystine transporter BAT1) and rBAT (Defect in Cystine transporter BAT1) will cause Cystinuria

40% Slc7a9 mRNA
30% Slc3a1 mRNA
60%

- Hypothesis
- 30% = Unclassified!
- New mutation in exon

30% = Unclassified!

- Method
- 1. RNA Splicing?
- 2 Missed by Direct Seq

New mutation in exon

- Results
- Table 1. Result of selected 14 patients with novel mutations or no mutation among 51 Cystinuria patients by Next Seq

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Direct Seq</th>
<th>Nxt Seq</th>
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Table 2. List of novel mutations by Next seq

**Clinical Question of Cystinuria**

- **Objectives and Methods**
- **Results**
- **Conclusion**

Future direction

- Determine the transcriptional level of Intron-exon boundary mutations in Slc7a9 and Slc3a1 gene (possibly by WBC).
- Study the further genomic analysis of Cystinuria patient’s genome by next generation sequence (get a big grant).
- International collaboration to determine the global landscape of Cystinuria mutation.

- **Figure 1. Genotype Classification**

- **Figure 2. Cystine Concentration based on Genotype / Mutants**

- **Figure 3. % of P482L related mutations**

- **Table 1. Result of selected 14 patients with novel mutations or no mutation among 51 Cystinuria patients by Next Seq**

- **Table 2. List of novel mutations by Next seq**

- **Table 3. Result of selected 14 patients with novel mutations or no mutation among 51 Cystinuria patients by Next Seq**