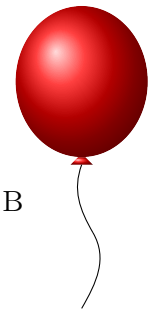
E Evolution of Weasels



Time limit: 2.0s
Memory limit: 2048MB

A wild basilisk just appeared at your doorstep. You are not entirely sure what a basilisk is and you wonder whether it evolved from your favorite animal, the weasel.

How can you find out whether basilisks evolved from weasels? Certainly, a good first step is to sequence both of their DNAs. Then you can try to check whether there is a sequence of possible mutations from the DNA of the weasel to the DNA of the basilisk.

Your friend Ron is a talented alchemist and has studied DNA sequences in many of his experiments. He has found out that DNA strings consist of the letters `A`, `B` and `C` and that single mutations can only remove or add substrings (a substring is a contiguous sequence of characters). The substrings that can be removed or added by a mutation are `AA`, `BB`, `CC`, `ABAB` or `BCBC`. During a sequence of mutations a DNA string may even become empty.

Ron has agreed to sequence the DNA of the weasel and the basilisk for you, but finding out whether there is a sequence of possible mutations that leads from one to the other is too difficult for him, so you have to do it on your own.

Input

Each test contains multiple test cases. The first line contains an integer t ($1 \leq t \leq 100$) — the number of test cases. The descriptions of the t test cases follow.

The first line of each test case contains a string u ($1 \leq |u| \leq 200$) — the DNA of the weasel.

The second line of each test case contains a string v ($1 \leq |v| \leq 200$) — the DNA of the basilisk.

The values $|u|$, $|v|$ denote the lengths of the strings u and v. It is guaranteed that both strings u and v consist of the letters `A`, `B` and `C`.

Output

For each test case, print `YES` if there is a sequence of mutations to get from u to v and `NO` otherwise.

Samples

Sample input 1	Sample output 1
8 A B B C C A AA BB BB CC CC AA ABAB BCBC ABC CBA	NO NO NO YES YES YES YES NO