Problem A. Advanced Genetics

Source file name:	`A.c, A.cpp, A.java`
Input:	Standard
Output:	Standard
Author(s):	

Genetics is an interesting biology field which also intersects with other areas of science and is strongly linked with the study of information systems, genetics studies genes, genetic variation, and heredity in living organisms.

Genes contain the information that builds DNA, DNA consists of a chain made from four types of nucleotide subunits : adenine, cytosine, guanine and thymine.

People from Triplonia have found that their DNA string is formed of several gene strings that are merged after a special gene is added to mix. This special gene is called the "Merging factor" . A gene string is a way to represent genes, it is a string that only contains the characters 'A', 'C', 'G' and 'T' each of these characters represents one of the nucleotide subunits that create genes and DNA.

Triplonia genetics researchers have collected a set S of N gene strings and are ready to apply the merging factor M, however, since the merging of the strings occurs after adding the merging factor to the genes mix they want to know how many of the gene strings will be merged so that they are ready to get more samples after this test. Getting genes is an expensive task for them, that's why they have explained the process and are looking for someone who can tell them the number of gene strings that will be merged. Can you help them?

The merging process is as follows :

1. Set $R = M$

2. If suffix of length K of R and the prefix of length K of a string S_i in S are anagrams, then S_i is appended to R.

3. Repeat step 2 with $S = S_{i+1}, S_{i+2}, ..., S_N$ until no more strings can be merged.

One more important thing to know is, if there are more than one way to merge the strings, the resulting DNA will always be the one that merges the most number of strings.

Given N, K, M, and S. Can you help scientists to know, what will be the number of strings merged to create the DNA?

Input

The input starts with a single line containing a single number T . The number of tests cases. Each test case will start with a line containing two integer numbers N and K, the number of genetic strings in the set and the length of the strings merging factor. The next line contains a string M the merging factor used to start the merging process. Each of the next N lines contains a string in the set to merge.

- $2 \leq N \leq 10^3$

- $1 \leq K \leq 10^3$

- All strings will be at least K in length and will not exceed 10^3 characters

Output

For each test case print a single line the maximum number of gene strings that can be merged with process mentioned above.

Example

Input	Output
1 5 2 AC ACTGT TGACC CCGCA CCGGG GGACTG	4

Explanation

In the test case, there are 5 gene strings, the prefixes and suffixes should be of length 2 and the merging factor is AC. The merging factor can be merged with ACTGT (the first gene string). Then it can be merged with TGACC, which can be merged with CCGCA which can not be merged with another string having a total of 3 strings merged, however, if instead of merging CCGCA the string CCGGG is merged then GGACTG can be merged giving a total of 4 strings merged. Since there are no way of merging more than 4 strings then the maximum number of gene strings that can be merged is 4.