★★★ ＜第31回知的財産翻訳検定試験【第15回英文和訳】＞ ★★★
≪１級課題 -バイオテクノロジー-≫

【解答にあたっての注意】
１．問題の指示により和訳してください。
２．解答語数に特に制限はありません。適切な箇所で改行してください。
３．課題文に段落番号がある場合、これを訳文に記載してください。
４．課題は４題あります。それぞれの課題の指示に従い、４題すべて解答してください。

問１． ***START***から***END***までを和訳してください。

START
In the autumn and winter, rainfall triggers spore release from the stubble. Within two weeks of spores landing on canola cotyledons and young leaves, clearly visible off-white coloured lesions develop, within the lesion pycnidial fruiting bodies (dark coloured dots) release rain-splashed spores. Blackleg infections may occur on cotyledons, leaves, stems and pods. The plant is susceptible to blackleg infection from the seedling to pod-set stages. Lesions occurring on the leaves are dirty white and are round to irregularly. On stems, blackleg lesions can be quite variable, but are usually found at the base of the stem, or at points of leaf attachment. Once a lesion has formed, the fungus grows within the plants vascular system to the crown where it causes the crown of the plant to rot, resulting in a canker. Severe canker will sever the roots from the stem, whereas a less severe infection will result in internal infection of the crown restricting water and nutrient flow within the plant. Stem lesions may be up to several inches in length, and are usually white or grey with a dark border. Stem lesions may also appear as a general blackening at the base.
END

問２．***START***から***END***までを和訳してください。

START
A "recombinant polynucleotide" or "recombinant nucleic acid" comprises a combination of two or more chemically linked nucleic acid segments which are not found directly joined in nature. By "directly joined" is intended the two nucleic acid segments are immediately adjacent and joined to one another by a chemical linkage. In specific embodiments, the recombinant polynucleotide comprises a polynucleotide of interest or a variant or fragment thereof such that an additional chemically linked nucleic acid segment is located either 5', 3' or internal to the polynucleotide of interest. Alternatively, the chemically-linked nucleic acid segment of the recombinant polynucleotide can be formed by deletion of a sequence. The additional chemically linked nucleic acid segment, or the sequence deleted to join the linked nucleic acid segments, can be of any length, including for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20 nucleotides or more. Various methods for making such recombinant polynucleotides include chemical synthesis, and the manipulation of isolated segments of polynucleotides by genetic engineering techniques. In specific embodiments, the recombinant polynucleotide can comprise a recombinant DNA sequence or a recombinant RNA sequence.
END

問３．***START***から***END***までを和訳してください。

START
The functionality of PTG1 and PTG2 was confirmed by examining the insertion/deletion (indel) mutations introduced by non-homologous end joining (NHEJ) repairing at the predicted Cas9:gRNA cleavage site. Because gRNA1 and gRNA2 targets contain the KpnI and SacI restriction enzyme (RE) sites (Example 2, Fig. 5A), respectively, the mutations induced by PTG1/Cas9 and PTG2/Cas9 could be readily analyzed by the digestion of

PCR products encompassing the targeted sites with corresponding RE (PCR/RE assay). In rice protoplasts transfected with PTG1/Cas9 and PTG2/Cas9, 15% and 9% of the target sites were found to carry indels, respectively (Fig. 2I), which are slightly higher than the mutation rate of sgRNA:Cas9 constructs we used previously (24). In consistence with our hypothesis that tRNA may function as a transcriptional enhancer for Pol III, the quantitative RT-PCR with gRNA specific primers revealed that the transcript levels of PTG1 and PTG2 were about 3 and 31 times higher than those of sgRNA1 and sgRNA2 in protoplasts (Fig. 2J), respectively. Taken together, our results demonstrated that the endogenous tRNA system could be utilized as a precise and robust tool to produce gRNAs from PTG for Cas9-mediated genome editing.
END

問４．***START***から***END***までを和訳してください。

START
Claim 1. A method for determining the presence or absence of one or more fetal chromosomal aneuploidies, said method comprising:
(a) obtaining a maternal sample comprising a mixture of fetal and maternal cell-free DNA (cfDNA);
(b) isolating said mixture of fetal and maternal cfDNA from said sample;
(c) preparing a sequencing library from said mixture of fetal and maternal cfDNA; wherein preparing said library comprises the consecutive steps of dA-tailing and adaptor ligating said cfDNA, and wherein said preparing excludes end-repairing said cfDNA;
(d) massively parallel sequencing at least a portion of said sequencing library to obtain sequence information for said fetal and maternal cfDNA in said sample;
(e) storing in a computer readable medium, at least temporarily, said sequence information;
(f) using said stored sequence information to computationally identify a

number of sequence tags for each of said one or more chromosomes of interest and for a normalizing sequence for each of said any one or more chromosome of interest;

(g) computationally calculating, using said number of sequence tags for each of said one or more chromosomes of interest and the number of sequence tags for said normalizing sequence for each of said one or more chromosomes of interest, a chromosome dose for each of said one or more chromosomes of interest; and

(h) comparing said chromosome dose for each of said one or more chromosomes of interest to a corresponding threshold value for each of said one or more chromosomes of interest, and thereby determining the presence or absence of said fetal chromosomal aneuploidy in said sample, wherein steps (e)-(g) are performed using one or more processors.

END

－－－注（下記の文章は翻訳不要）－－－

Note: The term “adaptor-ligating (DNA)” herein refers to an enzymatic process that ligates an adaptor to DNA. The term “dA tailing (DNA)” herein refers to an enzymatic process that adds a dA tail to the 3′ end of DNA.