



Application

SNP analysis of aldehyde dehydrogenase by PCR

- Product** KAPATaq EXtra PCR Kit (Cat No. KK3009)
- Manufacturer** KAPA BIOSYSTEMS
- Product** Midori Green Advance (Cat No. MG04)
- Manufacturer** NIPPON Genetics EUROPE
- Product** FAS-Nano (Cat No. GP-06LED)
- Manufacturer** NIPPON Genetics EUROPE

The following data was posted due to the courtesy of Mr Naoharu Takano and Shota Moriya, Biochemistry Dept., Tokyo Medical University, Japan

Introduction

Here, we analyze the SNP (*1) of aldehyde dehydrogenase (ALDH2) gene which determines “strong” or “weak alcohol tolerance.

***1: What is SNP?**

99.9% of the human DNA sequences are the same and it is considered that the difference of genetic information of 0.1% is creating human diversity, such as difference in face, body shape, constitution and character among individuals.

Single nucleotide polymorphism (SNP) refers to a state in which the nucleotide sequence of a gene differs by one site and it is known that the function of in vivo proteins such as enzymes changes slightly depending on the type of SNP.

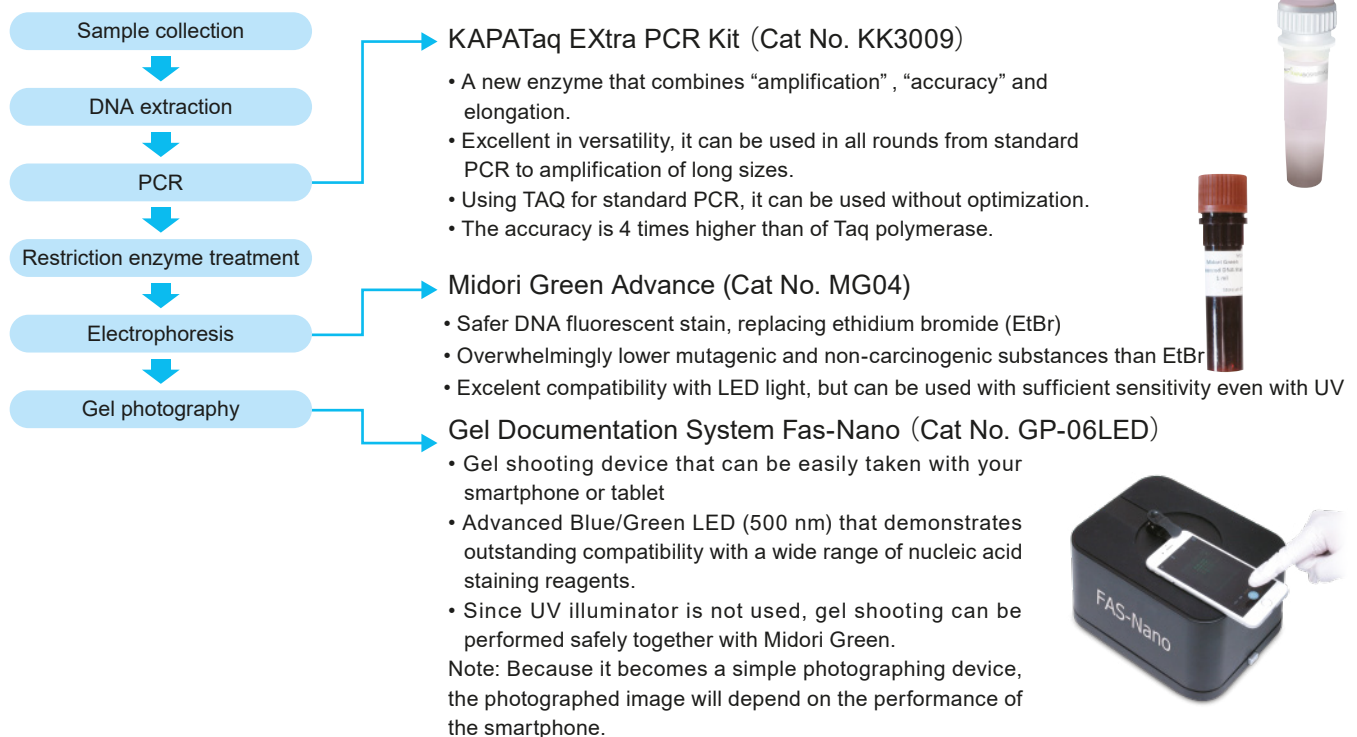
It is known that SNP is susceptible to diseases and the reaction to medicine is different. In the medical field a development of “tailor-made medical”, which offers the optimal treatment for individual patients based on SNP, is expected.

Experiment

In this experiment, genomic DNA is extracted from buccal mucosa cells and the ALDH2 gene which is involved in alcohol metabolism is amplified by PCR. After that, amplified fragments are treated with restriction enzymes and the genotype of ALDH2 is determined by agarose electrophoresis, thereby confirming the tolerance of alcohol.

References: Helminen A, Väkeväinen S, Salaspuro M.

ALDH2 genotype has no effect on salivary acetaldehyde without the presence of ethanol in the systemic circulation.
 PLoS One. 2013;8:e74418.
 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3772811/>)





Experimental method

• Sample

Oral mucosa was collected with physiological saline from human who obtained informed consent and genomic DNA was extracted with InstaGene (BIO-RAD)

PCR reaction

• PCR reaction composition

KAPATaq EXtra DNA Polymerase (5 U/ μ L)	0.2 μ L
5 \times KAPATaq EXtra buffer (Mg^{2+} free)	8 μ L
25mM $MgCl_2$	2.8 μ L
dNTP Mix (10 mM each)	1 μ L
PrimerF (10 μ M)	2 μ L
PrimerR (10 μ M)	2 μ L
Template DNA	20 μ L
PCR grade Water	4 μ L
Total	40 μL

• Thermal cycler conditions

Taq activation, denaturing	94°C	5min	} 40 cycles	
↓	Denaturing	94°C		30sec
↓	Annealing	60°C		30sec
↓	Extension	72°C		60sec
↓	Final extension	72°C	2min	

Thermal cycler: BIO-RAD MyCycler

• Primer sequence:

Forward Primer: TCAAATTACAGGGTCAACTGCT

Reverse Primer: GGCTGGGTCTTTACCCTCTC

References: Helminen A, Väkeväinen S, Salaspuro M. ALDH2 genotype has no effect on salivary acetaldehyde without the presence of ethanol in the systemic circulation. PLoS One. 2013;8:e74418.

Digestion

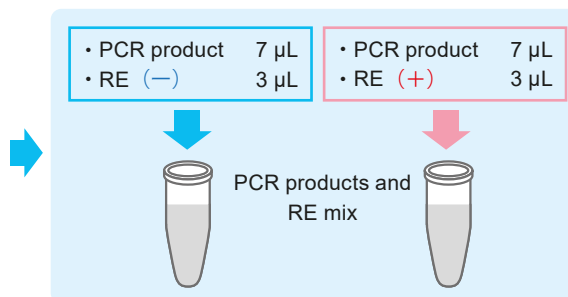
Restriction enzyme (RE) (-)		Restriction enzyme (RE) (+)	
Ultra pure water	2.8 μ L	Ultra pure water	2 μ L
10xCutSmart Buffer	1.6 μ L	10xCutSmart Buffer	1.6 μ L
1.6mM S-adenosyl-methionine*	0.4 μ L	1.6mM S-adenosyl-methionine*	0.4 μ L
total	4.8 μL	total	4.8 μL

* final concentration 40 μ M

Acu I : NEB

10xCutSmart Buffer and S-adenosyl-methionine are attached to Acu I

S-adenosyl-methionine used 1.6 mM as a stock solution



Electrophoresis

Agarose: Agarose (NIPPON Genetics EUROPE: Cat No. AG01)

Nucleic acid stain reagent: Midroi Green Advance

(NIPPON Genetics EUROPE Cat No. MG04)

Electrophoresis conditions: 100V

Stop electrophoresis when 1/2 of the gel is proceeded

Buffer: TBE

Electrophoresis device: Mupid-2plus



Loading dye has better results with NIPPON Gene: 313-90111 (SDS containing, BPB, XC) SDS containing cleaner results.

In particular, in this experiment many impurities such as Taq and restriction enzyme are contained in the electrophoresis sample, so there is a possibility that the band pattern is disturbed unless SDS entry is used.

