FLAG assay as a novel method for real-time signal generation during PCR: application to detection and genotyping of KRAS codon 12 mutations

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ABSTRACT

Real-time signal generation methods for detection and characterization of low-abundance mutations in genomic DNA are powerful tools for cancer diagnosis and prognosis. Mutations in codon 12 of the oncogene KRAS, for example, are frequently found in several types of human cancers. We have developed a novel real-time PCR technology, FLAG (FLuorescent Amplicon Generation) and adapted it for simultaneously (i) amplifying mutated codon 12 KRAS sequences, (ii) monitoring in real-time the amplification and (iii) genotyping the exact nucleotide alteration. FLAG utilizes the exceptionally thermostable endonuclease PspGI for real-time signal generation by cleavage of quenched fluorophores from the 5'-end of the PCR products and, concurrently, for selecting KRAS mutations over wild type. By including peptide-nucleic-acid probes in the reaction, simultaneous genotyping is achieved that circumvents the requirement for sequencing. FLAG enables high-throughput, closed-tube KRAS mutation detection down to ~0.1% mutant-to-wild type. The assay was validated on model systems and compared with allele-specific PCR sequencing for screening 27 cancer specimens. Diverse applications of FLAG for real-time PCR or genotyping applications in cancer, virology or infectious diseases are envisioned.

INTRODUCTION

Diagnostic methods for the detection of specific gene mutations associated with diseases play an increasingly important role for early cancer diagnosis and prognosis in clinical practice. For example, KRAS codon 12 mutations are a predictor of resistance to tyrosine kinase inhibitors in lung cancer (1) and of non-response to drugs like cetuximab in colon cancer (2). One of the first described methods for detection of known mutations includes PCR-RFLP (3). Subsequently, several other approaches for discriminating specific sequence variations were described including hybridization with allele-specific probes (4,5), allele-specific PCR (6,7), dye terminator incorporation (8–12), oligonucleotide ligation (13), Flap-Endonuclease digestion (14) isothermal amplification assay (15) and others, reviewed by Parsons et al. (16). These methods can be convenient, but require an additional step for end point detection. Analytical methods that reduce sample processing to a single-step procedure were also developed, including nick-translation PCR (17), hybridization with FRET probes (18), melting curves analysis (19–22), fluorogenic allele-specific PCR (23), universal FRET reagents in a single-step Invader assay (24), universal TaqMan probes (25) and others. However, several of these methods cannot deal with detection of a low concentration of mutant target in the presence of a large excess of wild-type DNA that is often found in clinical specimens. The excess wild-type DNA can mask the mutant signal during the detection step of the assay. For these reasons, mutation-selection technologies such as PCR-clamping (26) and restriction endonuclease-mediated selection (REMS)-PCR (27) apply a preliminary step of selective suppression of the wild-type sequences during PCR followed by a mutation detection step. However, the additional detection step increases the risk for contamination and false positives. Furthermore, most methods allow the detection of the presence of a mutation but not characterization of the exact nucleotide change that took place, and sequencing is required as an extra step for genotyping the mutation.

Here we describe a novel real-time PCR signal generation technology (FLAG, FLuorescent Amplicon Generation) that is adapted to the selective amplification of DNA sequences with defined KRAS mutations within a large excess of wild-type DNA, and simultaneously monitors the amplification in real time. In addition, FLAG can genotype the exact nucleotide alteration, thus
circumventing the need for sequencing. We evaluate the specificity and sensitivity of this new assay, and validate its use for real-time KRAS mutation detection and genotyping on cell lines and clinical tumor samples.

MATERIALS AND METHODS

Source and extraction of genomic DNA

Control cell lines. Genomic DNA from cultured cell lines SW480 (KRAS codon 12 homozygous GTT), PL45 (heterozygous GAT/GGT) and CALU1 (heterozygous TGT/GGT) was obtained from the American Type Culture Collection, (Manassas, California, USA) and extracted by the NucleoSpin™ Tissue kit (Macherey-Nagel, Duren, Germany).

Clinical samples. Tissue specimens from sporadic colorectal cancers (SCRCs) were obtained with informed consent from previously untreated patients who underwent surgical resection at the Istituto Nazionale per lo Studio e la Cura dei Tumori of Milan between 1998 and 2000. Tumor specimens and its surrounding normal mucosa were selected by an experienced pathologist from formalin-fixed, paraffin-embedded tissue. Genomic DNA were extracted using QIAamp Tissue Extraction kit (Qiagen, Hilden, Germany) in the Lab of Dr Milo Frattini, Department of Experimental Oncology and Unit of Experimental Molecular Pathology, Istituto Cantonale di Patologia (Locarno, Switzerland).

Selective PNA-mediated FLAG on DNA from cell lines with KRAS mutations and clinical samples

We designed and synthesized four PNA (peptide nucleic acids) probes (Eurogentec, Liege, Belgium) specific for the KRAS codon 12 mutations GTT, GAT, TGT and GCT (PNA_1 NH2-GGACCTGTGTGGCGTA-CON3H, PNA_2 NH2-GGACCTGTGTGGCGTA-CON3H, PNA_3 NH2-GGACCTGTGTGGCGTA-CON3H, PNA_4 NH2-GGACCTGTGTGGCGTA-CON3H, respectively). Concentration of forward (GA112: 5′IAbFQ/TTTCCTGGTTTGAATATA) and reverse (GA111: 5′TTTCCCTGTGTGGACCT 3′) primers was 300 nM (IDT Inc, Coralville, IA, USA). The forward primer carries a C/C mismatch, which allows the creation of a PspGI recognition site only in the presence of wild-type templates.

In each reaction, 68 ng of genomic DNA extracted from clinical samples or from wild-type K562, mutant SW480 (homozygous GGT/GTT), PL45 (heterozygous GAT/GGT) and CALU1 (heterozygous TGT/GGT) cell lines were used as a template. The reaction was performed for 35 cycles (on DNA from cell lines) or 38 cycles (on DNA from clinical samples) as follows: denaturation step at 94°C for 10 s, primers annealing at 56°C for 30 s, primers extension and PNA annealing at 72°C for 60 s in a Chromo™ 4 Detector Real Time PCR machine (MJ research, Waltham, MA, USA) or an ABI 7500 Real Time PCR System (Applied Biosystems, Foster City, CA, USA). The reaction mix contained 0.1× BD Titanium™ Taq polymerase, 1× PCR buffer (BD Biosciences, Franklin Lakes, NJ, USA), 200 μM dNTPs, 1.5 mM MgCl2 in 20 μl total volume. The reaction mix was split into six reactions, performed in parallel and compared to each other: the first reaction is conducted without restriction endonuclease or PNA, while the others are in presence of PspGI (New England Biolabs, Ipswich, MA, USA), 0.5 or 1 U/μl for analysis of DNA extracted from cell lines and clinical samples, respectively.

The third, fourth, fifth and sixth reactions contain also one of the four different PNA probes: 300 nM PNA_1 specific for codon 12 GTT, 200 nM PNA_2 specific for codon 12 GAT, 200 nM PNA_3 complementary to the TGT mutation and 200 nM PNA_4 specific for GCT targets, respectively.

By the comparison between the six parallel reactions, the mutant samples are detected and genotyped.

Detection and genotyping of mutant clinical samples by allele-specific PCR followed by sequencing

Mutations of codon 12 of the KRAS oncogene were detected in clinical samples by allele-specific PCR, and characterized by automatic sequencing in the laboratory of Dr M. Frattini, Department of Experimental Oncology and Unit of Experimental Molecular Pathology, Istituto Cantonale di Patologia (Locarno, Switzerland).

Codon 12 sequence of the KRAS gene was examined as follows: 200 ng of genomic DNA was amplified in 30 μl of final volume reaction with 1× PCR Buffer II, 1.5 mM MgCl2, 0.2 mM dNTPs, 0.5 μM appropriate primer and 2 U of AmpliTaq Gold Polymerase (all from Applied Biosystems, Foster City, CA, USA). PCR amplifications were performed as follows: initial denaturation step of 96°C for 3 min, 45 cycles of 96°C for 30 s, 50°C for 1 min, 72°C for 1 min, and a final elongation step of 72°C for 4 min. Samples were run on 4% polyacrylamide gels and then purified using the Purification Kit Qiagen (Hilden, Germany). Purified products were sequenced in a 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA).

RESULTS

The FLAG assay

FLAG is a novel method for real-time PCR signal generation that utilizes thermostable restriction enzymes (Figure 1). The signal generation strategy consists of amplification of the gene region of interest using a specific primer pair designed to carry an 11-base sequence-tag at the 5′-end, containing the recognition site for an exceptionally thermostable restriction endonuclease, PspGI. The forward primer is doubly labeled at the tag region with a quencher and a fluorophore in 5′ and 3′ positions, respectively. During sequence extension by the polymerase, the sequence-tag region becomes double stranded, resulting to recognition and cleavage by PspGI. Separation of the fluorophore and the quencher leads to generation of fluorescence signal due to loss of quenching. The unusually thermostable PspGI (activity half-life of 2 h at 95°C [28]) resists deactivation during
PNAs with higher thermal stability than DNA/DNA, but which are significantly destabilized in the case of a single mismatch (33). A PNA probe fully complementary to the sequence of a specific KRAS codon 12 mutant prevents annealing and extension of the forward primer, suppressing amplification. In presence of a single mismatch, PNA does not inhibit primer hybridization, which leads to amplification and consequent fluorescence signal generation. Thus, four distinct FLAG reactions are conducted for each mutation-containing sample, each one containing a different PNA probe specific for the four most common KRAS codon 12 mutations (GTT, GAT, GCT, TGT) (Figure 2B). By observing the relative signal intensity from each of these four reactions, the identity of the mutant sequence is inferred, as the resulting signal is weak or non-measurable for the mutation that is fully complementary to the mutation of the target DNA analyzed in the presence of PNA. In summary, in the strategy depicted in Figure 2, the first FLAG reaction identifies and monitors in real time the mutant KRAS DNA sequences, and if the sample is mutated a second set of real-time FLAG assays homogenously genotypes the exact nucleotide alteration, thereby circumventing the need for sequencing.

As an alternative, the 5 FLAG reactions depicted in Figure 2 can be routinely carried out in parallel, thereby obtaining both the mutation and genotyping the information. This results to a single-step procedure at the expense of increasing the overall number of real-time PCR reactions required.

**Selectivity of FLAG-KRAS assay**

To assess the selectivity of FLAG-KRAS assay, genomic DNA from the homozygous GTT mutant cell line SW480 was serially diluted into wild-type KRAS codon 12 DNA from K562 cells to obtain decreasing ratios of mutant-to-wild type sequences. Samples where mutant alleles represented respectively 100, 10, 1, 0.1 and 0.01% of the total DNA were subjected to FLAG-KRAS in the presence of PspGI. Real-time PCR signals (Figure 3, panel A) show that mutant alleles are detectable down to 1:1000 mutant-to-wild type DNA ratio and that there is a linear relation between the threshold cycle (Ct) and the logarithm-dilution factor of the mutant DNA in each sample (Figure 3, panel A) show that mutant alleles are detectable down to 1:1000 mutant-to-wild type DNA ratio and that there is a linear relation between the threshold cycle (Ct) and the logarithm-dilution factor of the mutant DNA in each sample (Figure 3, panel B).

The high level of selectivity of FLAG-KRAS is enabled by the use of PspGI, which is much more thermostable than the isoschizomer restriction endonuclease BstNI commonly used in REMS protocols (13,15,34). To demonstrate this point, we performed the FLAG-KRAS experiment using 1 U/µl PspGI or 1 U/µl BstNI, in parallel. PspGI digested the wild-type codon 12 sequences during all 38 thermal cycles of the FLAG assay, while BstNI lost its activity, resulting in insufficient suppression of the wild-type component of the samples analyzed, thus producing signal indiscriminately from mutant or wild-type samples (Figure 4A and B, respectively). For BstNI to reach a selectivity of 1:100 mutant-to-wild type ratio following 38 PCR cycles, an addition of 10 U of BstNI

**Figure 1.** FLAG principle for real-time PCR signal generation. The FLAG assay utilizes a primer pair carrying a tag sequence at the 5’ end that contains the recognition site for the highly thermostable enzyme PspGI. (A) One of the primers is doubly labeled at the tag region with a quencher Q and a fluorophore F. (B) During the primer extension, the primer tag becomes double stranded, becoming available for recognition and cleavage by the endonuclease. (C) The digestion leads to generation of fluorescence due to loss of quenching.
Figure 2. PNA-mediated FLAG-KRAS assay. FLAG-KRAS assay leads to selective amplification of mutant codon 12 KRAS sequences during the real-time fluorescent reaction through a REMS-PCR approach. (A) a mutagenic (underlined base) primer introduces a variation that creates the recognition site for PspGI (circle) in the wild-type codon 12 (X = C, ACC) target sequence, thereby suppressing the exponential amplification of the wild-type allele. The mutant alleles escape digestion and this enables their exponential amplification. (B) to assess the exact nucleotide alteration of the target amplified, the FLAG-KRAS assay is repeated in four parallel reactions in the presence of PNA probes (dotted lines) specific for the most common mutations of codon 12. When the reaction is conducted in the presence of the fully complementary PNA (4), no exponential amplification is allowed. In presence of a mismatched PNA (1–3) the probe is destabilized and the primer can consequently anneal and extend causing an exponential amplification and generation of FLAG fluorescent signal as explained in Figure 1.
to the solution was needed every 10 cycles of reaction (Figure 4C).

**FLAG-KRAS combined with PNA for genotyping**

FLAG-KRAS was combined with PNA, as described in Figure 2, for genotype determination via suppression of mutant alleles carrying specific mutations. To demonstrate the principle, we performed PNA-mediated FLAG-KRAS reactions in parallel for DNA extracted from wild-type K562 and mutant SW480 (homozygous GTT/GTT), PL45 (heterozygous GGT/GAT) and CALU1 (heterozygous GGT/TGT) cell lines and the PCR products were run on an ethidium-stained agarose gel. As shown in Figure 5, all cell lines generate PCR product in the absence of PspGI (first panel), while no product from K562 sample is visible in the presence of PspGI (second panel). When the reaction is conducted in the presence of PNA probe specific for GTT codon 12 sequence, no amplification product is obtained from SW480 DNA (Figure 5, panel 3). Similarly, no product from PL45 DNA was obtained when PNA specific for GAT was used (Figure 5, panel 4), and no product for CALU1 DNA was obtained when PNA specific for TGT was used (Figure 5, panel 5).

**Analysis of clinical samples by PNA-mediated FLAG-KRAS assay**

The PNA-mediated FLAG-KRAS assay was applied on 27 clinical samples from patients diagnosed with sporadic colorectal cancers, previously analyzed for codon 12
Out of 27 samples tested, we identified 22 concordant techniques show 81.5% concordance (Supplementary Table 1). Compared with those obtained by ASP-S. The two techniques are complementary to that specific PNA. The results were and we therefore assigned to the sample the genotype probe fully complementary to the KRAS mutated sequence indicates suppression of the amplification by the PNA.

The excess positives identified via FLAG-KRAS may potentially be a result of the high selectivity of the FLAG method that allows the detection of four mutated samples missed by ASP-S due to the very low-abundance KRAS mutations. Overall, there is a satisfactory agreement between the two independent methods.

**DISCUSSION**

FLAG provides a novel, simple method for real-time signal generation during PCR that is based on the use of the exceptionally thermophilic enzyme PspGI acting on the formed double-stranded PCR amplicons. FLAG does not require fluorogenic probes as the Taqman or Molecular Beacons approaches (4,5,25) since the fluorophores are on the PCR primers, thus providing an alternative platform for multiplexing real-time PCR reactions. As with other non-probe-based real-time PCR approaches (33–36), the basic requirement for a specific signal generation by FLAG is avoiding primer–dimer formation, which would result in false positive calls. We addressed this problem by designing our primers taking advantage from accurate simulations performed by the VisualOMP4 Software to exclude any problematic primer pairs. Because PspGI remains active during the entire PCR course, fluorescence is generated continuously during the reaction resulting to robust signals. A potential limitation of FLAG is that the amplified region must not contain PspGI sites other than those incorporated at the 5'-ends of the primers. This requirement restricts the application to amplicons that are devoid of 5'-CCWGG-3' sequence strings. Given that the amplicons are short, we found that this is not a severe limitation.

We adapted FLAG to the single-step detection and genotyping of somatic KRAS mutations within a large excess of wild-type sequences, starting directly from genomic DNA. The KRAS mutation selection is enabled by the primer-mediated formation of restriction sites that are recognized by the same enzyme used for signal generation, the exceptionally thermophilic PspGI. The KRAS mutation genotyping is enabled by the novel use of PNA probes designed to interrogate specific nucleotide changes in a set of real-time FLAG reactions. While PNA

**Figure 5.** Selective PNA-mediated FLAG on cell lines. The FLAG assay was performed on cell lines K562 (GTT/GGT), SW480 (GTT/GTT), PL45 (GTT/GAT) and CALU1 (GTT/GTT), or in absence of DNA target, B. **Panel 1:** FLAG assay without PspGI restriction endonuclease or PNA (positive controls). An amplification product is produced from all the reactions performed. **Panel 2:** FLAG assay in presence of PspGI to detect mutant versus wild-type samples. The wild-type sample K562 was digested by the enzyme, while the cell lines containing a mutation are exponentially amplified. **Panels 3–5:** FLAG assay with addition of PspGI and PNA specific for GTT, GAT or TGT. No amplification product is obtained from wild-type sample K562 (digested by PspGI) and from the cell lines that are suppressed by the fully complementary PNA present in the reaction.

**Figure 6.** Representative PNA-mediated FLAG-KRAS obtained from analysis of clinical samples. Four FLAG-KRAS reactions were performed on clinical sample TL132 in presence of different PNA probes, specific for GTT, GAT, TGT or GCT mutations. The assays produced fluorescent amplicons in presence of all PNA, except for the one specific for GCT mutation. The data indicate that sample T132 contains the mutation GCT.
is frequently employed for suppression of wild-type KRAS alleles (37,38), the present adaptation extends the use of PNA to the genotyping of specific nucleotide changes, thus circumventing the need for di-deoxy-sequencing. This application can either be performed in two steps (single FLAG-KRAS reaction to determine presence of mutation, followed by a set of four parallel reactions for genotyping, if mutation-positive) or in a single step of five parallel real-time PCR reactions. The first approach reduces the total number of reactions performed, as the wild-type samples are not processed for a second step. The second approach provides the advantage of speed and a closed-tube approach since no PCR tube needs to be opened to perform a second reaction. The closed-tube approach used for PNA-mediated FLAG-KRAS decreases the risk of contamination that is more elevated for alternative technologies based on multi-step reactions (16,39–41). The selectivity of the assay was demonstrated to be 0.1% (detection of 1 mutant sequence in presence of 999 wild-type alleles). Current protocols based on thermophilic enzymes other than PspGI (42) require multi-step approaches to reach similar sensitivity (43). The high selectivity of the assay can potentially be useful for homogenous detection and genotyping of mutations present at low prevalence in plasma samples. Nanogram quantities of circulating DNA are present in the plasma of normal individuals (44), and increased quantities circulate in patients with cancer (45–47). Detection of mutated DNA in plasma DNA may precede conventional cancer diagnosis (48,49) resulting to a non-invasive tool for initial detection of malignancy as well as an indicator of recurrence during follow-up. Detection of specific KRAS nucleotide changes in plasma using PNA-mediated FLAG-KRAS could contribute to a more accurate prognosis and therapy choice in certain cancers (24,25).

In summary, PNA-mediated FLAG-KRAS is a novel and practical method for simultaneous selection and genotyping of KRAS sequence alterations in clinical samples. The technology has the specificity and the selectivity required for analysis of surgical/biopsy tumor samples and can be potentially used for identification of KRAS codon 12 variations in fluid specimens (needle aspiration, plasma-circulating DNA). In principle it should also be applicable for additional somatic mutations. However, using a mutagenic primer may also reduce the priming efficiency of the PCR reaction. Therefore adaptation of the FLAG assay to additional mutations may need substantial optimization and remains to be proven in practice.

Finally, besides KRAS mutation detection, FLAG provides a generally applicable new method for fluorescent signal generation in real-time PCR and could be used for multiple additional applications (e.g. in genetic testing, infectious diseases or virology).

SUPPLEMENTARY DATA
Supplementary data are available at NAR Online.

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