## SUPPORTING INFORMATION

Detection of Terminal Mismatches on DNA Duplexes with Fluorescent Oligonucleotides<br>Ulysse Asseline*, Marcel Chassignol, Yves Aubert and Victoria Roig<br>Centre de Biophysique Moléculaire, CNRS UPR 4301, affiliated with the University of Orléans and with INSERM.<br>Rue Charles Sadron, 45071 Orléans Cedex 02, France<br>asseline@cnrs-orleans.fr

## Influence of the presence of mismatches at the penultimate or last two positions of the duplex



Fig. 9. Fluorescence duplex/fluorescence free probe. Concentrations were $[C]=1 \mu \mathrm{M}$ (each strand) in a 5 mM sodium cacodylate buffer, $\mathrm{pH}=6$, containing 50 mM NaCl .45 min hybridization at room temperature.

As previously observed at $6^{\circ} \mathrm{C}$ (Figure 5), the discrimination factor between the perfectly matched duplexes (red bars) and those involving terminal mismatches (green bars) on the same lines was also superior to 2 at room temperature $\left(25^{\circ} \mathrm{C}\right)$. The values observed for the perfectly matched duplexes (red bars) were also inferior to those obtained for the duplexes involving a perfectly matched terminal base-pair and a penultimate mismatched one (blue bars on the same histograms) and also for the duplexes involving two terminal mismatched base-pairs (white bars). Among the combinations studied, the greatest fluorescence increases were observed when a CT mismatch was present at the penultimate position of the duplexes. Another observation was that the hybridization of the four ODN-TO' probes (each column of histograms) with each of the corresponding complementary target sequences gave, in all cases, the lowest fluorescence ratio for the perfect duplexes.

Variation of the nucleic base $V$ on the target sequences adjacent to the terminal base-pair of the duplex (on the side of TO' attachment):



Fig. 10. Fluorescence duplex/fluorescence free probe. Concentrations were $[C]=1 \mu \mathrm{M}$ (each strand) in a 5 mM sodium cacodylate buffer, $\mathrm{pH}=7$, containing 50 mM NaCl .30 min hybridization at room temperature.

Sixteen possibilities were studied. A comparison of the results showed that the perfect duplexes formed with the target studied above $\mathbf{V}=\mathrm{G}$ (red bars) and the perfect duplexes formed with the other three targets $\mathbf{V}=\mathrm{C}, \mathrm{A}$ or T (yellow bars) could be discriminated from the corresponding mismatched ones [green bars $(\mathbf{V}=\mathbf{G})$ and white bars $(\mathbf{V}=\mathrm{C}, \mathrm{A}$ or T$)$ ]. The fluorescence ratio for the duplexes involving terminal mismatches were higher than those corresponding to the perfect duplexes. The discrimination factor was at least equal or superior to 2 except when $\mathbf{X}$ and $\mathbf{V}$ were cytosines leading to a reduced value (between 1.7 and 1.4).

