Reaction condition optimization to minimize hydrolysate formation in a maleimide-NHS esteroligonucleotide conjugation reaction

Shiva P Adhikari¹, Jiaqi Zhang¹, Adeline Espinasse¹, Pierre Barratt¹, & Derek Gauntlett¹

¹LGC Axolabs, 2199 South McDowell Blvd, Petaluma CA 94954, USA

DoE design, and

shiva.adhikari@lgcgroup.com

Abstract

Maleimide chemistry is unique in the tool-kit of bioconjugation because of its ease of synthesis and remarkable reactivity. 3-(Maleimido)propionic acid N-hydroxysuccinimide ester (A) reacts with the amine group of amino-modified DNA (B), in a basic environment leads to the incorporation of maleimide into oligonucleotide strand (C), Fig. 1. The newly introduced maleimide is susceptible to base catalyzed hydrolysis in aqueous environments, producing hydrolysate (D) – an impurity. By altering three key reaction parameters - temperature, time, and pH - we set out to optimize the reaction conditions to slow down the formation of hydrolysate during conjugation reaction. We employed design of experiments (DOE) with the JMP software to minimize the number of experiments required for this study.



Oligo conjugated with maleimide (DNA+maleimide) Figure 1. Conjugation reaction

Background **Raw Results** 3 outputs of the design The conjugation reaction requires basic condition. However, in aqueous condition the maleimide rings is %DNA+Maleimide [%(C)], desirability maximum opened by hydrolysis forming hydrolysate (D). %Hydrolysate [%(D)], desirability minimum Hydrolysis rate increases with high pH. %Amino-modified-DNA [%(B)], desirability minimum Table 1. 12 experiments proposed by JMP (B1 - B12) 0.30 0.28 Rxn Condition (Input) Normalized Value (Output) 0.26 Hydrolysis in %Aminc (D) Sample Malein %Hydrol Aqueous buffer 0.24 Name Rxn Temp. Time modified de-DNA DNA pН min (%D) (%C) 0.22 (%B) -NH2 0.20 B3 5.5 60 179 0.5 81.6 (B) B11 6 120 77.7 19.9 0.18 2.4 (C) 20 B6 6.5 30 92.0 2.3 5.6 0.16 2 B12 7.2 30 96.5 3.5 0.0 0.14 B9 5.5 30 20.1 0.5 79.4 0.12 **B**8 6 60 83.0 2.4 14.6 25 0.10 B5 6.5 120 95.0 4.5 0.6 0.08 B7 7.2 120 92.5 7.5 0.0 0.06 B1 5.5 120 35.0 0.9 64.1 0.04 B10 6 85.9 2.7 11.5 30 35 B4 6.5 60 94.1 5.4 0.4 0.02 B2 72 60 90.2 9.8 0.0 0.00 -0.02 5 00 10 00 30 00 35 00 15 00 25 00 0 00 Predicted optimal conditions

Figure 2. Example of LE IPRP chromatogram displaying peaks representing (B), (C), and (D). Solution of (A) in DMSO and aqueous solution of (B) were mixed at 20 ± 5 °C for 60 min.

Reactions parameters for DoE

Design of Experiment (DOE) with JMP was used to assess process parameters deemed potentially influential for successful conjugation of (A) with (B) to (C) while keeping hydrolysate (D) low.

For conjugation reaction, JMP used to generate a weighted D-optimal assessment to evaluate the following parameters: pH, temperature, and time.

3 Factor design were utilized with the following levels for each Discrete numeric factor (3 inputs)

- pH = 4 (5.5, 6, 6.5, 7.2)
- Temp = 3 (20°C, 25°C, 35°C)
- Time = 3 (30 min, 60 min, 120 min)



Confirmation Experiments

Table 2. Optimal pH and time wasinvestigated at 20 °C

Sample Name	Rxn Condition		Normalized Value		
	Rxn pH	Time, min	%Malei mide- DNA (%C)	%Hydrol ysate (%D)	%Amino- modified- DNA (%B)
S1	6.5	30	87.2	2.1	10.7
S2		60	91.4	2.6	6.0
S3		120	94.1	3.5	2.4
S4	6.9	30	96.7	2.4	0.8
S5		60	96.4	3.3	0.3
S6		120	95.5	4.5	0.0
S7	7.2	30	96.5	3.5	0.0



Figure 3. DNA+Maleimide profile

Complete or near-complete conversion observed while hydrolysis rate limited to ~ 2-3% (S3 - S7).

Manufacturing optimal conditions for 60 mmol:, pH 6.9, 60 min, 20 °C.

Conclusion and Outlook

For the conjugation reaction, optimal reaction conditions were designed using DOE/JMP

Utilization of statistical software have potential to decrease time spent to perform experiments while evaluating a wide range of parameters.

