



Promoter tagging in banana (*Musa* spp.) using the luciferase reporter gene - development and applications

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Objective

Isolate promoters from banana (*Musa* spp.) with constitutive, tissue specific, and cold stress responsive expression patterns

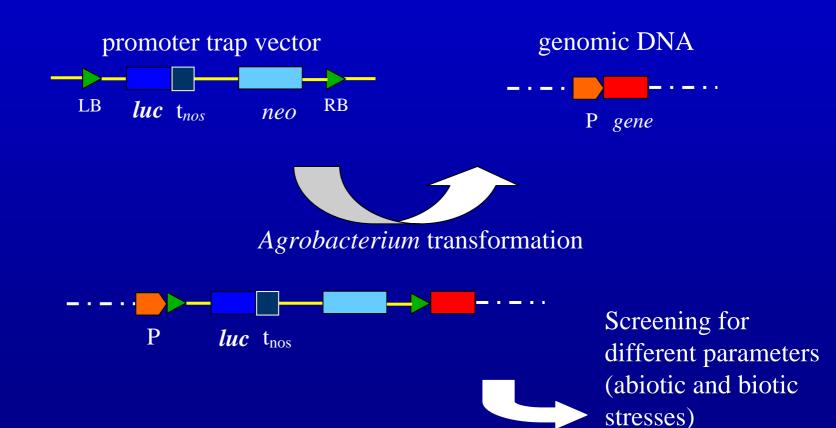
Content

I. The promoter tagging system

II. Luciferase expression patterns

III. Tagging of cold-responsive promoters

IV. Conclusions and perspectives



Luciferase reporter gene



luc

- Highly sensitive
- Non destructive screenings
- Short half-life of enzyme

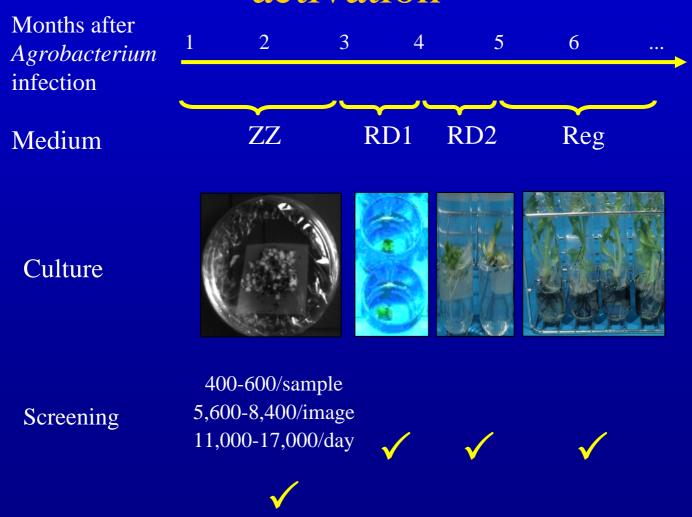
luciferin + ATP + O₂ CO₂ + light (562 nm)

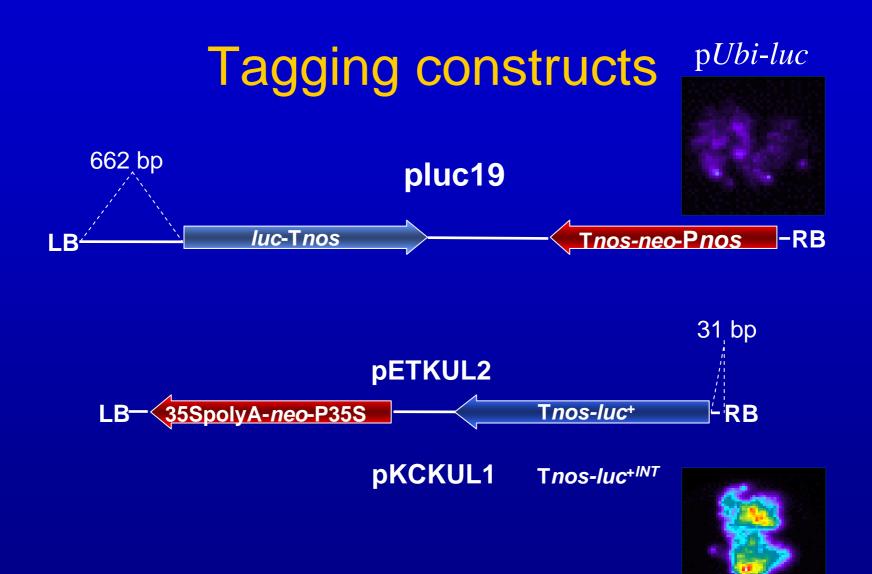
ultrasensitive digital CCD camera system





High throughput screening for LUC activation





p*Ubi-luc*+

Effect of tagging constructs on activation frequency

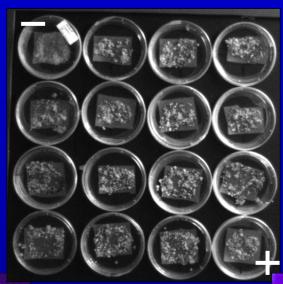
Exp.	Tagging constructs	Total # of cell colonies screened	BLA frequency* (%)		
1	pluc19	1,550	0.06		
	pET2	19,000	2.50		
2	pET2	4,695	0.90		
3	pET2	8,862	0.93		
	pKC1	33,390	2.03		

^{*} Baseline luciferase activity

II. Luciferase expression patterns

Cell colony stage

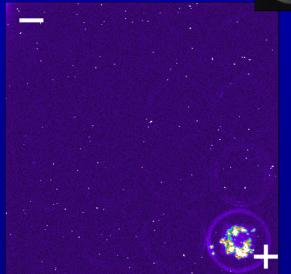


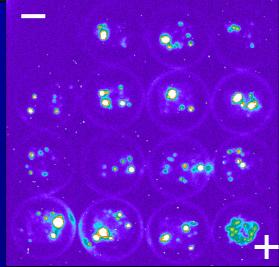


11,000 – 17,000 colonies/day

pluc19 (*luc*) 0.06%

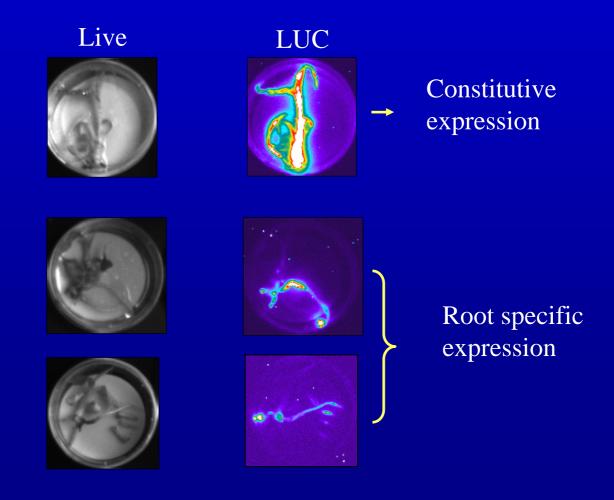


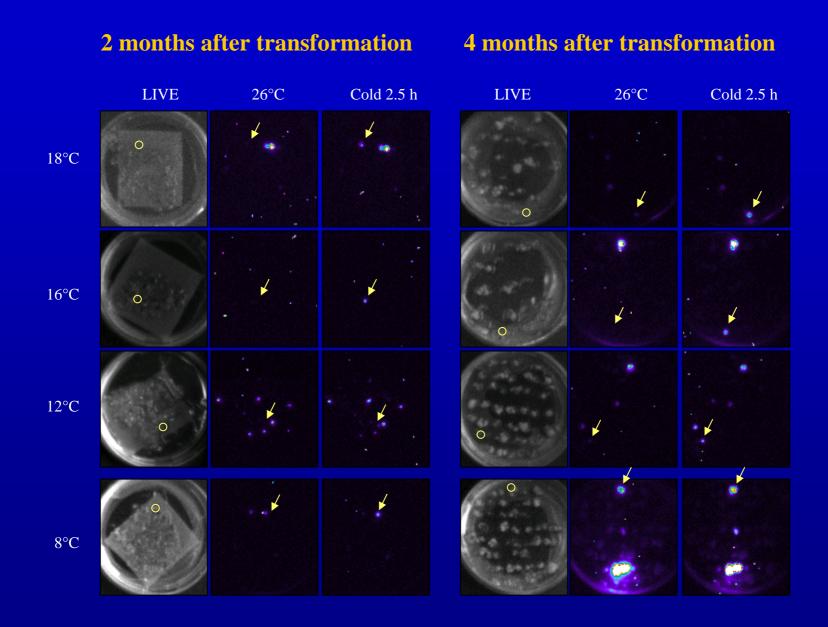




II. Luciferase expression patterns

In vitro plantlet stage

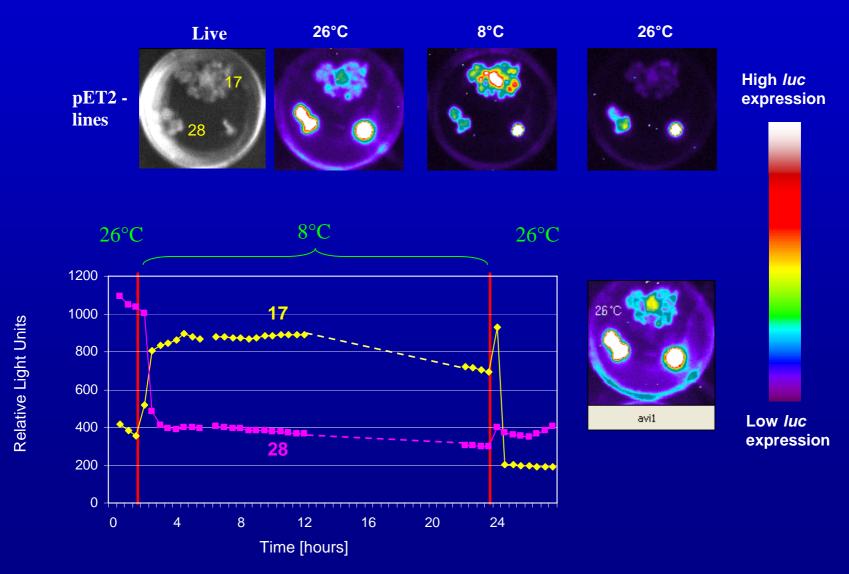




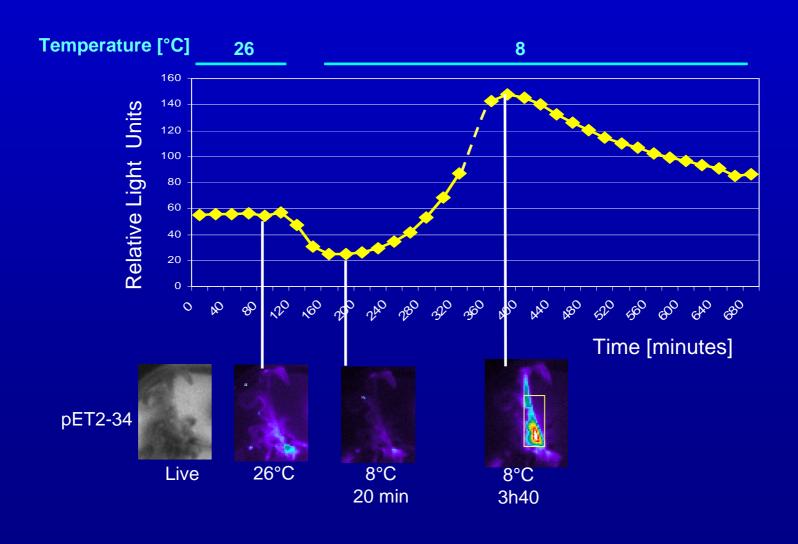
Cold responsive luciferase activity (CRLA) at 8°C of transgenic cultures (~16,000) during regeneration

	Screening for CRLA						
	1st (Colony)	2nd (Cult)	3rd (Cult)	4th (Cult)	5th (Cult)	6th (Cult)	7th (Plantlet)
Number of lines showing CRLA	106	98	42	42	42	28	26
Percentage of lines showing CRLA	0.67%	0.62%	0.26%	0.26%	0.26%	0.18%	0.16%

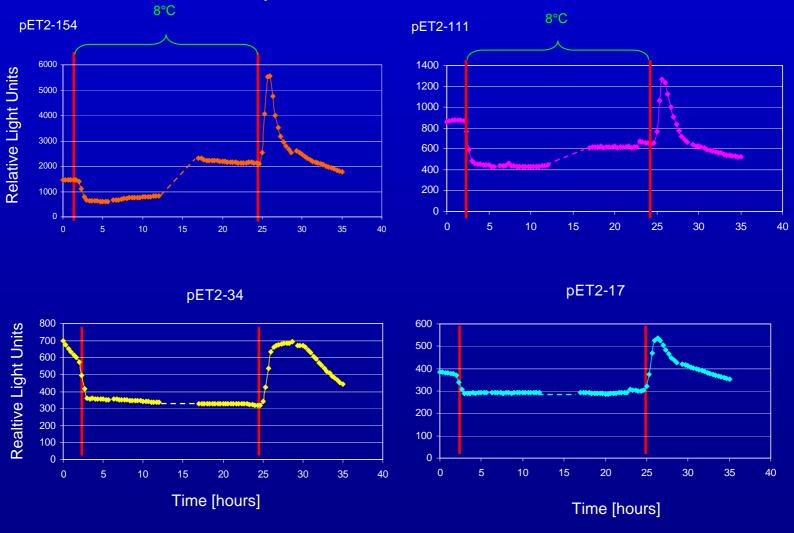
Cell culture stage



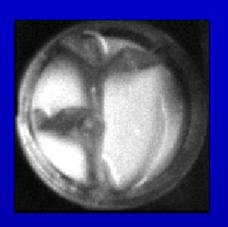
In vitro plantlet stage

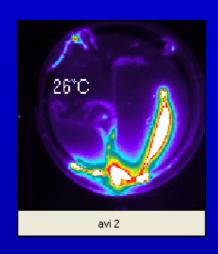


Quantification of localized LUC expression in pseudostems of *in vitro* plantlets under cold stress



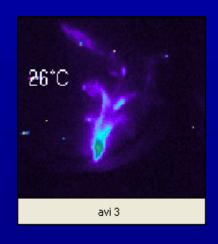
pET2-111





pET2-17





Conclusions

- Tagging constructs optimized
- Cold screening system developed
- Candidate lines obtained with enhanced and repressed CRLA patterns

Perspectives

- Confirmation of CRLA patterns in greenhouse plants
- Isolation of putative promoter sequences
- Bioinformatic analysis of promoter sequences

