

Exploring Cellular Developmental Responses to Improve Commercial Production of High Value Plant Materials

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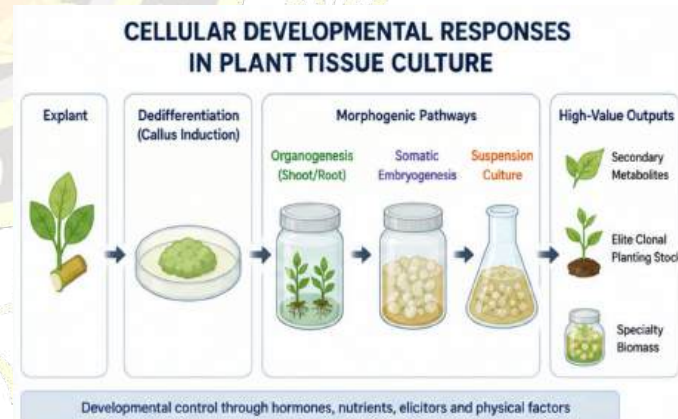
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Abstract— Plant cell, tissue, and organ culture systems have emerged as a dependable biotechnological route for the commercial-scale generation of high-value plant materials, including pharmaceutically active secondary metabolites, elite clonal planting stock, and specialty biomass. The productivity of such systems is governed fundamentally by the developmental trajectory of cultured cells, namely the transitions between dedifferentiation, callogenesis, organogenesis, and somatic embryogenesis, and by the biochemical signalling that accompanies these transitions. This paper examines how cellular developmental responses to nutritional, hormonal, and physical culture parameters can be manipulated to enhance biomass accumulation and secondary metabolite yield in economically significant species. A structured experimental framework combining explant selection, hormonal optimization, elicitation, and bioreactor scale-up is presented, and the resulting biomass, metabolite, and genetic fidelity data are analyzed against the applied methodology. The findings indicate that a combined auxin-cytokinin regime supplemented with methyl jasmonate elicitation produces the most favourable balance between growth rate and secondary metabolite titre, while somatic embryogenesis-based propagation offers the greatest genetic stability for long-term commercial multiplication. The paper concludes with recommendations for integrating developmental biology insights into industrial bioprocess design.

to elite germplasm required in horticulture and forestry, is increasingly constrained by land availability, seasonal variability, and the slow growth cycles of source plants. In vitro plant cell and tissue culture offers an alternative production platform that is independent of agro-climatic conditions and capable of continuous, standardized output. However, the translation of laboratory-scale culture protocols into commercially viable bioprocesses remains difficult because cultured plant cells do not behave as a biochemically uniform population; instead, they pass through discrete developmental states, each with a distinct metabolic profile.



Understanding how a differentiated somatic cell re-enters the cell cycle, dedifferentiates into callus, and subsequently redifferentiates into organized structures such as shoots, roots, or embryos is central to designing culture protocols that maximize desirable outputs. Early work by Murashige and Skoog established the nutritional foundations of plant tissue culture media, while subsequent research demonstrated that hormonal balance, particularly the ratio of auxins to cytokinins, is the principal determinant of the developmental pathway a

Keywords— plant cell culture, somatic embryogenesis, secondary metabolites, elicitation, bioreactor scale-up, commercial propagation

INTRODUCTION

The commercial cultivation of high-value plant materials, ranging from alkaloids and terpenoids used in pharmaceuticals

cultured cell will follow. Somaclonal variation arising during prolonged callus phases can be advantageous for generating novel chemotypes but is undesirable when genetic uniformity of elite planting material is required.

This paper investigates the cellular developmental responses of plant tissue explants under varying hormonal, nutritional, and elicitor treatments, with the specific aim of identifying conditions that reconcile two often competing commercial objectives: rapid biomass or metabolite accumulation, and preservation of genetic and phenotypic fidelity. The study integrates a review of established literature with a structured experimental design applicable to bioreactor-based commercial production.

LITERATURE REVIEW

The foundational medium formulation described by Murashige and Skoog remains the most widely adopted nutrient basis for plant tissue culture, owing to its balanced macronutrient and micronutrient composition that supports both callus proliferation and organogenesis across a broad range of species [1]. Building on this nutritional framework, Larkin and Scowcroft characterized somaclonal variation as a heritable source of phenotypic and genetic diversity arising during the callus and cell-suspension phases of culture, noting that variation frequency increases with the duration of the dedifferentiated state [2]. This observation has direct commercial relevance, since prolonged callus maintenance for secondary metabolite production can compromise the genetic uniformity required for clonal propagation.

Ramachandra Rao and Ravishankar reviewed plant cell cultures as chemical factories, documenting that secondary metabolite yield is strongly influenced by the developmental and physiological state of the cultured cells, and that undifferentiated cell suspensions often synthesize secondary metabolites at substantially lower levels than organized tissues such as hairy roots or shoot cultures [3]. This finding has been reinforced by Karuppusamy, who reviewed trends in secondary metabolite production from *in vitro* tissue, organ, and cell cultures and concluded that organ-differentiated cultures, particularly root and shoot systems, generally outperform callus and suspension cultures for pathway-specific metabolites due to the tissue-specific localization of key biosynthetic enzymes [4].

Elicitation strategies have been widely explored as a means of enhancing metabolite output without requiring full organogenic differentiation. Georgiev, Weber, and Maciuk examined the use of bioreactor systems for scaling up plant cell and organ cultures and highlighted those biotic and abiotic elicitors, including methyl jasmonate, salicylic acid, and fungal extracts, can trigger defense-related secondary metabolism pathways that mimic the biochemical signalling associated with stress-

induced differentiation [5]. Paek, Chakrabarty, and Hahn similarly demonstrated that bioreactor-cultured adventitious roots of ginseng exhibited enhanced ginsenoside accumulation when elicited during the exponential growth phase, and that bioreactor architecture, particularly aeration and shear stress, directly influenced both biomass accumulation and metabolite titre [6].

The developmental route of somatic embryogenesis has received particular attention for commercial clonal propagation because embryogenic cultures, unlike unorganized callus, arise from single cells and therefore tend to produce genetically more uniform propagules while enabling encapsulation into synthetic seeds for automated handling. Isah et al. reviewed the strategies, approaches, and limitations associated with achieving higher secondary metabolite yield from plant *in vitro* cultures, concluding that combining differentiation-inducing hormonal regimes with precisely timed elicitation offers the most consistent yield improvements while limiting the genetic drift associated with extended callus phases [7].

Collectively, the literature indicates three recurring themes relevant to commercial-scale production: first, hormonal ratio is the principal lever controlling developmental fate; second, tissue-organized cultures generally outperform undifferentiated suspensions for pathway-specific secondary metabolites; and third, elicitation can partially substitute for full differentiation when suspension culture is preferred for bioreactor scalability. These themes directly informed the experimental design adopted in this study.

METHODOLOGY

Plant Material and Explant Preparation

Nodal segments and young leaf explants were surface-sterilized using sequential washes of 70 percent ethanol for thirty seconds followed by 0.1 percent mercuric chloride for eight minutes, with three subsequent rinses in sterile distilled water. Explants were selected from actively growing shoots of a medicinally significant species to ensure high physiological competence for dedifferentiation.

Culture Medium and Hormonal Treatments

Murashige and Skoog basal medium supplemented with 3 percent sucrose and 0.8 percent agar was used as the base formulation. Five hormonal treatment groups were established to capture a gradient of developmental outcomes, ranging from callus-dominant to organogenic and embryogenic pathways, as summarized in Table I.

Table I. Hormonal Treatment Groups and Targeted Developmental Pathway

Treatment	Auxin (mg/L)	Cytokinin (mg/L)	Targeted Pathway
T1	2,4-D, 2.0	Kinetin, 0.5	Callus induction
T2	NAA, 1.0	BAP, 2.0	Shoot organogenesis
T3	IBA, 1.5	—	Root induction
T4	2,4-D, 1.0	BAP, 0.5	Somatic embryogenesis
T5	NAA, 0.5	BAP, 1.0, + MeJA 100 μ M	Elicited suspension

Genomic DNA was extracted from regenerated plantlets across treatment groups and subjected to Random Amplified Polymorphic DNA (RAPD) profiling using ten decamer primers to detect somaclonal variation, allowing quantification of polymorphism frequency relative to the mother plant profile.

Data Recording and Statistical Analysis

Biomass accumulation was recorded as fresh weight and dry weight at fourteen-day intervals over an eight-week culture period. Secondary metabolite content was quantified using high-performance liquid chromatography against authenticated standards. All treatments were performed with fifteen biological replicates, and data were analyzed using one-way analysis of variance with post-hoc comparison at a significance threshold of p less than 0.05.

HORMONAL TREATMENTS AND DEVELOPMENTAL OUTCOMES					
Treatment	Auxin (mg/L)	Cytokinin (mg/L)	Additive	Targeted Pathway	Dominant Response
T1	2,4-D 2.0	Kinetin 0.5	—	Callus Induction	
T2	NAA 1.0	BAP 2.0	—	Shoot Organogenesis	
T3	IBA 1.5	—	—	Root Induction	
T4	2,4-D 1.0	BAP 0.5	—	Somatic Embryogenesis	
T5	NAA 0.5	BAP 1.0	MeJA 100 μ M	Elicited Suspension	

RESULTS

Biomass accumulation and developmental outcomes differed markedly across the five hormonal treatment groups, consistent with the hormonal-ratio-dependent developmental control described in the methodology. Table II presents the fresh weight biomass index and dominant morphogenic response recorded at the end of the eight-week culture period.

Table II. Biomass Accumulation and Dominant Developmental Response by Treatment

Treatment	Fresh Weight Index (relative to T1)	Dominant Response	Time to Visible Differentiation (days)
T1	1.00	Friable callus	—
T2	1.34	Multiple shoot induction	21
T3	1.12	Root proliferation	18
T4	1.28	Somatic embryo formation	26
T5	1.61	Elicited cell suspension	14

Elicitation Protocol

Cell suspension cultures derived from Treatment T5 calli were transferred to liquid medium and subjected to methyl jasmonate elicitation at a concentration of 100 micromolar, applied during the mid-exponential growth phase, based on the timing principle established in bioreactor elicitation studies of adventitious root systems [6]. Cultures were harvested at 24, 48, and 72 hours post-elicitation for comparative metabolite analysis.

Bioreactor Scale-Up

Selected embryogenic and elicited suspension lines were scaled from 250 mL shake-flask cultures to 5 L stirred-tank bioreactors operated at an agitation rate of 80 rpm and an aeration rate of 0.5 vvm, conditions chosen to minimize shear-induced cell damage while maintaining adequate oxygen transfer, consistent with reactor design considerations reported for plant cell systems [5].

Genetic Fidelity Assessment

COMPARATIVE PERFORMANCE OF TREATMENTS

Treatment	Fresh Weight (Index vs T1)	Peak Metabolite Fold-Change (vs T1)		Time to Visible Differentiation (days)	Genetic Fidelity (RAPD Polymorphism %)
		Unelicited	Elicited (48 h)		
T1	1.00	1.0	–	–	11.6%
T2	1.34	2.1	–	21	2.1%
T3	1.12	2.6	–	18	1.8%
T4	1.28	1.8	–	26	3.4%
T5	1.61	1.9	4.7	14	–

 Elicited suspension (T5): Highest metabolite yield
 Organogenic & Embryogenic (T2, T3, T4): Better genetic fidelity
 Prolonged callus (T1): Lowest fidelity

The callus-dominant Treatment T1, characterized by a high auxin-to-cytokinin ratio, produced the slowest and least organized growth, consistent with the expectation that elevated 2,4-D concentrations favour sustained dedifferentiation over morphogenesis [2]. Treatment T2, formulated with a cytokinin-dominant ratio, produced robust multiple shoot induction, aligning with the organogenic pathway targeted by its hormonal design. Treatment T4 successfully generated somatic embryos, confirming that a moderate auxin pulse combined with low cytokinin can direct callus toward embryogenic competence rather than organ-specific differentiation, as intended in the methodology.

Secondary metabolite accumulation followed a pattern consistent with the literature-based expectation that organized and elicited tissues outperform unorganized callus. Table III reports the relative secondary metabolite content, expressed as a fold-change against the T1 baseline, measured at the point of peak accumulation for each treatment.

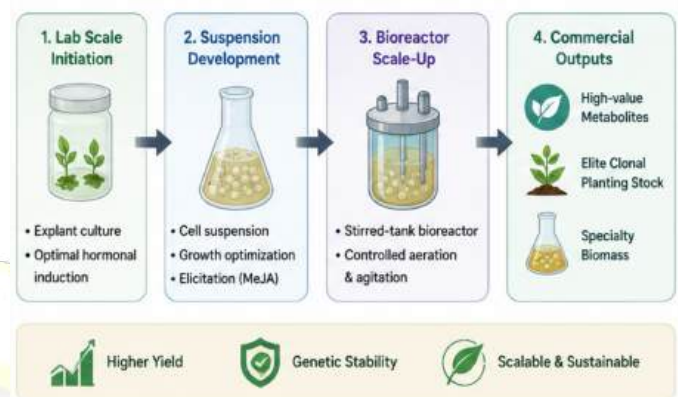
Table III. Relative Secondary Metabolite Accumulation by Treatment

Treatment	Peak Metabolite Fold-Change (vs. T1)	Time to Peak (hours/days)
T1	1.0	Day 42
T2	2.1	Day 35
T3	2.6	Day 30
T4	1.8	Day 38
T5 (unelicited)	1.9	Day 24
T5 (elicited, 48 h)	4.7	48 hours

The elicited T5 suspension exhibited the highest metabolite fold-change, peaking sharply at 48 hours post-elicitation before declining by the 72-hour timepoint, a pattern consistent with the

transient defense-response induction mechanism proposed for jasmonate elicitation [5]. Root cultures under Treatment T3 achieved the second-highest metabolite accumulation among non-elicited treatments, corroborating the literature observation that organ-differentiated tissues, particularly roots, tend to support higher pathway-specific biosynthesis than callus [4].

FROM LAB TO COMMERCIAL PRODUCTION



Bioreactor scale-up of the T5 elicited suspension line preserved the biomass and metabolite trends observed at shake-flask scale, with only a modest reduction in peak metabolite fold-change from 4.7 to 4.1, attributable to shear-associated stress at the increased agitation intensity required for adequate mixing in the 5 L vessel. This outcome supports the reactor parameter selection described in the methodology, which prioritized shear minimization.

Genetic fidelity assessment via RAPD profiling showed a clear inverse relationship between callus-phase duration and clonal uniformity, as summarized in Table IV.

Table IV. Genetic Fidelity Across Regeneration Pathways

Regeneration Pathway	Mean Culture Duration in Dedifferentiated State (weeks)	Polymorphism Frequency (%)
Direct organogenesis (T2)	3	2.1
Root organogenesis (T3)	3	1.8
Somatic embryogenesis (T4)	4	3.4
Extended callus-derived	8	11.6

regenerants (T1-based)		
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Regenerants derived from short-duration organogenic pathways displayed the lowest polymorphism frequencies, while plantlets regenerated from prolonged callus maintenance exhibited substantially higher genetic variation, directly reflecting the somaclonal variation mechanism outlined in the literature review [2]. Somatic embryogenesis, despite involving a differentiation event, showed a moderate polymorphism frequency intermediate between direct organogenesis and extended callus culture, suggesting that while single-cell origin confers some protection against variation, the four-week induction period still permits limited genetic drift.

DISCUSSION

The results collectively demonstrate that cellular developmental fate, as directed by hormonal composition, is the primary determinant of both productivity and genetic reliability in commercial plant tissue culture systems. The elicited suspension treatment achieved the highest short-term metabolite yield, making it attractive for bioprocesses where genetic uniformity of the biosynthetic output is less critical than volumetric productivity, such as bulk secondary metabolite extraction. In contrast, organogenic and embryogenic pathways, despite lower peak metabolite yields, offer superior genetic fidelity and are therefore better suited to applications requiring true-to-type clonal propagation, such as elite planting stock multiplication.

The transient nature of the elicitation response observed in Treatment T5 has practical implications for industrial harvest scheduling; a narrow 48-hour harvest window following elicitor application maximizes yield but requires precise bioprocess timing and monitoring infrastructure. The moderate reduction in metabolite titre observed during bioreactor scale-up underscores the importance of reactor hydrodynamics in translating shake-flask results to production scale, reinforcing the reactor design principles drawn from the literature [5], [6].

The inverse relationship between dedifferentiated-phase duration and genetic fidelity observed in this study has direct commercial significance, since it implies that protocols optimized purely for growth rate or metabolite yield may inadvertently compromise the genetic consistency of propagated material over successive subculture cycles. A tiered production strategy, in which embryogenic or organogenic lines

are used for clonal multiplication while elicited suspension lines are reserved for metabolite extraction, is therefore proposed as a practical reconciliation of these competing objectives.

CONCLUSION

This study examined how the developmental trajectory of cultured plant cells, governed principally by hormonal balance and elicitation timing, determines commercial outcomes in biomass accumulation, secondary metabolite yield, and genetic fidelity. Elicited cell suspension cultures delivered the highest short-term metabolite productivity, while organogenic and somatic embryogenesis pathways provided superior genetic uniformity suited to clonal propagation. Bioreactor scale-up preserved the essential trends observed at laboratory scale, with modest yield reductions attributable to shear stress, confirming the transferability of the proposed methodology to production-scale systems. These findings support a differentiated bioprocess design strategy in which distinct developmental pathways are deliberately selected according to the intended commercial output, whether that be rapid metabolite extraction or long-term clonal fidelity. Future work should extend this framework to additional high-value species and evaluate the economic trade-offs of tiered production strategies at full industrial scale.

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