Dynamics of proteins, carbohydrates and global DNA methylation patterns during induction of nodular cluster cultures from seeds of *Vriesea reitzii*

Jenny Paola Corredor-Prado1*, Daniela De Conti2, Miguel Pedro Guerra2, Lirio Luiz Dal Vesco2,3 and Rosete Pescador2

1Department of Biology and Chemistry, University of Sucre, Cra 28 # 5-267, 700001, Puerta Roja, Sincelejo, Sucre, Colombia. 2Programa de Pós-Graduação em Recursos Genéticos Vegetais, Universidade Federal de Santa Catarina, Florianópolis, Santa Catarina, Brazil. 3Centro de Ciências Agrárias, Universidade Federal de Santa Catarina, Campus Curitibanos, Curitibanos, Santa Catarina, Brazil. *Author for correspondence. E-mail: jenny.corredor@unisucre.edu.co

**ABSTRACT.** Tissue culture techniques have been employed for bromeliad mass propagation by means of the morphogenetic route of nodular cluster cultures (NCs). This study aimed to assess protein, carbohydrate and global DNA methylation (GDM) level dynamics during NCs induction from *Vriesea reitzii* seeds. Seeds were inoculated into Murashige and Skoog (MS) liquid medium supplemented with 4 µM α-naphthylacetic acid (NAA) to induce NCs and in culture medium without plant growth regulators to form normal seedlings. Samples collected at 0, 5, 7, 10, 14, and 21 days of culture were analyzed. All parameters assessed showed the same variation pattern. However, seeds inducing NCs showed significantly lower starch (6.0 mg g⁻¹ FM), carbohydrate (10.7 mg g⁻¹ FM) and GDM (11.0%) levels than seeds forming normal seedlings after 21 days in culture. On the other hand, the protein content (9.1 mg g⁻¹ FM) was significantly higher during induction. NCs induction process through seeds is the result of gene reprogramming in the explant, which leads to morphological, biochemical and metabolic alterations. This involves dedifferentiation, high cell proliferation, high energy demand and protein synthesis, which is related to elevated metabolic activity.

**Keywords:** bromeliaceae; bromeliad; germination; micropropagation; seedling.

Received on April 19, 2018.
Accepted on July 15, 2018.

**Introduction**

Bromeliads are complex ecological systems that contribute to the maintenance of the forest ecosystems stability due to their high levels of specialization (Benzing, 2000). In addition to their ecological role, bromeliads have a high landscape value, which is recognized by the ornamental industry worldwide (Guerra & Dal Vesco, 2010; Negrelle, Mitchell, & Anacleto, 2012). Among the bromeliads, *Vriesea reitzii* is an epiphytic plant that occurs in southern Brazil at altitudes ranging from 750 - 1200 m (Leme & Costa, 1991). As observed in most bromeliads, the beautiful shape and colors of *Vriesea reitzii* enable its ornamental use (Negrelle et al., 2012). In recent decades, the development of tissue culture techniques has promoted new strategies for mass propagation of bromeliads (Guerra & Dal Vesco, 2010). Previous work on bromeliad micropropagation reported an *in vitro* morphogenetic pathway based on nodular cluster cultures (NCs). NCs are defined as groups or conglomerates of organogenic nodules with high regenerative efficiency (Dal Vesco & Guerra, 2010; Dal Vesco et al., 2011). Strategies for induction of NCs in bromeliads include nodal segments (Dal Vesco, Stefenon, Welter, Guerra, & Scherer, 2011), leaf segments (Alves, Dal Vesco, & Guerra, 2006; Dal Vesco & Guerra, 2010; Scherer et al., 2013; Dal Vesco, Vieira, Corredor Prado, Guerra, & Elter, 2014b) and seeds (Dal Vesco, Pescador, Corredor Prado, Welter, & Guerra, 2014a; Corredor-Prado et al., 2015). This work has established a system of NCs induction and regeneration of shoots in response to different types and combinations of plant growth regulators (PGRs). Other studies regarding NCs multiplication and differentiation to microshoots are related to GDM levels (Scherer, Fraga, Klabunde, Silva, & Guerra, 2015) and genetic analysis using amplified fragment length polymorphism (AFLP) markers (Dal Vesco, Stefenon, Welter, Steiner, & Guerra, 2012; Scherer et al., 2015). On the other hand, characterization
of the NCs induction process has been focused on morphological and anatomical alterations (Corredor-Prado et al., 2015). Biochemical and epigenetic alterations have not been evaluated.

The development of morphogenetic pathways is accompanied by changes in cellular components such as proteins and polysaccharides (Martin et al., 2000; Cangahuala-Inocente, Silveira, Caprestano, Floh, & Guerra, 2014; Morel et al., 2014). These changes require the expression of genes necessary for synthesis or mobilization of those compounds. Therefore, epigenetic mechanisms play an important role in plant development (Valledor et al., 2007). One of the epigenetic changes is the methylation of cytosine in DNA, which refers to post-synthesis methylation of deoxycytosines at the 5’ position of the pyrimidine ring of cytosine, forming 5-methylcytosine, which interferes with gene translation and expression (Finnegan, 2010). Previous findings have shown that methylation in coding or regulatory regions prevents the expression of target genes, while demethylation events are accompanied with gene activation (Meng et al., 2012; Shan et al., 2013). Furthermore, the action of sugars as signaling molecules affects the expression of genes and the activity of enzymes in many metabolic pathways (Halford, 2010).

Considering that biochemical and epigenetic changes must be accomplished in order to induce NCs, the present work aimed to evaluate the dynamic changes in proteins, carbohydrates, and global DNA methylation (GDM) levels from seeds during NCs induction.

**Material and methods**

**Plant materials**

Seeds from mature fruits of *V. reitzii* were collected from plants kept in Curitibanos, at an altitude of 990 m (Santa Catarina State, Brazil, 27º16’58”S - 50º35’04”W). Sterilization was carried out according to the procedures described by Alves et al. (2006). For NCs induction, seeds were inoculated into Murashige and Skoog (MS) liquid medium supplemented with 4 μM NAA, previously established by Dal Vesco et al. (2014a) (hereinafter termed MS-NAA). Seeds inoculated in PGR-free MS medium (hereinafter termed MS) were considered controls. All explants were inoculated over filter paper bridges, into test tubes (22 × 150 mm) containing 12 mL of culture medium. Cultures were maintained in a growth room at 25 ± 2°C and 16h photoperiod, with a light intensity of 50-60 μmol m⁻² s⁻¹. Samples were collected at 0, 3, 7, 10, 14, and 21 days of culture.

**Protein content**

Each replicate (500 mg) was prepared from approximately 350 seeds. The extraction of proteins was performed following the method of Carpentier et al. (2005) with modifications. In brief, tissue collected was ground to powder with the aid of liquid nitrogen. The macerated material was homogenized with 5.0 mL of extraction buffer (50 mM Tris-HCl pH 8.5, 5 mM EDTA, 100 mM KCl, 1% w/v DTT, 30% w/v sucrose, and 1 mM PMSF) and 5.0 mL of buffer-saturated phenol (pH 8.0) by vortexing for 30 min. The homogenates were centrifuged for 30 min. at 10,000 × g at 4ºC. The phenolic phase was recovered, homogenized with 5.0 mL of extraction buffer, vortexed, and centrifuged again. The phenol phase was collected and precipitated with 100 mL of ammonium acetate in methanol (1:5 v/v) for 12h at -20°C. After centrifugation, the pellet was washed with pure methanol and acetone. The proteins were solubilized in 0.3 mL of solubilization buffer (7 M urea, 2 M thiourea, 3% CHAPS, 2% IPG-buffer, 1.5% DTT). Protein quantification was determined by means of the copper-based method 2-D Quant Kit® (GE Healthcare, Bio-Sciences AB, Uppsala, Sweden). The data were submitted to analysis of variance (ANOVA) and presented as the means of three biological replicates.

**Total soluble carbohydrates**

Samples of 500 mg were ground to powder with the aid of liquid nitrogen and subsequently submitted to an 80% ethanol extraction at 70°C for 5 min. The extracts were centrifuged at 3,000 rpm at 20°C for 10 min. and filtered through fiberglass. The extraction was repeated three times and the final volume adjusted to 5 mL with ethanol (80%). The total soluble carbohydrate content was determined using the phenol-sulfuric method (Dubois, Gilles, Hamilton, Rebers, & Smith, 1956) using glucose as a standard. The absorbance was measured at 490 nm. The data were submitted to ANOVA and presented as the means of three biological replicates.
Thin layer chromatography

Analysis for the qualitative detection of carbohydrates was carried out on the extracts described previously. Chromatographic conditions: stationary phase: Silica Gel 60 TLC aluminum plate (Alugram®); mobile phase: 2-propanol: ethyl acetate: nitroethane: acetic acid: water (45:25:10:1:19); detection reagent: orcinol-sulfuric acid- ethanol reagent; volume of sample: 2 µL. Rf values were calculated for samples and compared with standards (fructose, glucose, xylose, maltose, and sucrose).

Starch content

The pellets used in the total soluble carbohydrates extraction received the addition of 1 mL of cold distilled water and 1.5 mL of 52% perchloric acid and was maintained in an ice bath with occasional agitation. Subsequently, 2.0 mL of water was added, and the material was centrifuged at 3,000 rpm for 15 min. The extraction was repeated, and the final volume adjusted to 10 mL with distilled water. The starch content was estimated by the phenol-sulfuric method (Dubois et al., 1956), using glucose as a standard, according to the method proposed by McCready, Guggolz, Siliviera, and Owen (1950). The absorbance was measured at 490 nm. The data were submitted to ANOVA and presented as the means of three biological replicates.

Global DNA methylation (GDM)

DNA isolation was based on CTAB methodology (Doyle & Doyle 1990). Digestion procedures, purification, and analysis by high-performance liquid chromatography (HPLC) were based on the method described by Fraga et al. (2012). Samples of seeds germinated containing nucleosides, including 5-methyl-2’-deoxycytidine (5mdC) and deoxycytidine (dC), were filtered (0.22 µm pore size) and injected into HPLC. A Hyperclone 5 µm C18 column (250 x 4.6 mm) (Phenomenex®), Torrance, CA, USA), a precolumn (4.0 x 5.0 mm) (Phenomenex®), and UV detector at 280 nm were used. Two eluents were used: A (0.5% v/v methanol in 10 mM KH$_2$PO$_4$ buffer, pH adjusted to 3.7 with H$_2$PO$_4$) and B (10% v/v methanol in 10 mM KH$_2$PO$_4$ buffer, pH adjusted to 3.7 with H$_2$PO$_4$). The column was eluted with 100% eluent A for 3 min., followed by a linear gradient of 0 – 100% eluent B over 17 min. and then with 100% eluent B for 5 min. Nucleoside separation was performed at flow rate of 1 mL min.$^{-1}$, with 20 µL of each sample injected. Deoxynucleotides, dNTPs (Fermentas®, Vilnius, Lithuania), were digested for 2h with alkaline phosphatase (10 U mL$^{-1}$) and Tris–HCl (0.5 M, pH 8.3) to form the nucleoside standards (dA, dT, dC, 5mdC, and dG) (5 – 50 mM). The identification of each nucleoside was made by comparison with the external standards according to the peak area formed. 5mdC quantification (%) was calculated according to 5mdC concentration divided by 5mdC concentration plus dC concentration and multiplied by 100. The data were submitted to ANOVA and presented as the means of three biological replicates.

Histological analysis

Samples of seeds germinated were fixed in 2.5% paraformaldehyde in 0.2 M (pH 7.2) sodium phosphate buffer overnight. The samples were then dehydrated in increasing series of ethanol aqueous solutions. After dehydration, the samples were infiltrated with Historesin (Leica® Historesin, Heidelberg, Germany). Sections (5 µm) were obtained using a manual rotation microtome (Slee Technik®) and were stained with Periodic Acid-Schiff (PAS) to identify neutral polysaccharides and Coomassie Brilliant Blue (CBB) 0.4% in Clarke’s solution to identify proteins. Sections were analyzed with a camera (Olympus® DP71) attached to a microscope (Olympus® BX-40).

Results and discussion

Vriesea reitzii bromeliad seeds were germinated on the 5th day of in vitro culture. Subsequently, seeds on MS culture medium resulted in the development of normal seedlings (Figure 1a and c), while seeds inoculated on MS-NAA-supplemented culture medium showed enhanced cell division and proliferation of cells with meristematic characteristics (Figure 1d and f). In this context, NAA in the culture medium altered the seedling development for NCs induction. Other studies have reported the effect of auxins combined with cytokinins, which also caused NCs induction from Vriesea seeds but at lower percentages (Dal Vesco et al., 2014a; Corredor-Prado et al., 2015). In morphogenetic routes, such as somatic embryogenesis, several steps including dedifferentiation and somatic cells reprogramming, are necessary for the initiation and
progression of development programs (Zhang & Ogas, 2009). In this respect, auxins are important signaling molecules related to division, elongation and differentiation regulation in plants (Perrot-Rechenmann, 2010). In the present study, carbohydrate, starch, protein, and GDM levels showed significant differences between V. reitzii seeds on MS and those cultured on MS-NAA medium.

A gradual decrease in protein and starch levels was observed until the last measurement time (Figure 2a and b). Previous studies have shown that Vriesea genus seeds store starch and protein in the endosperm (Magalhaes & Mariath, 2012; Corredor-Prado et al., 2014). According to Bewley (1997), reserves stored in seeds are predominantly mobilized during and after radicle protrusion. Hydrolyzed amino acids release large ammonium amounts during protein degradation, which are assimilated again, synthesizing new nitrogenous molecules (Cantón, Suárez, & Cánovas, 2005), while starch degradation is related to triglyceride release and subsequent carbohydrate metabolism (Stone & Gifford, 1999).

In the present work, dry seeds (0 days of culture) with the highest protein and starch content (35.4 and 17.8 mg g\(^{-1}\) FM, respectively) showed a marked decrease on the 3\(^{rd}\) day of culture, when seeds germinated. In barley seeds, Sreenivasulu et al. (2008) demonstrated that genes involved in reserve catabolism are expressed much earlier during seed germination, i.e., already 24 hours after imbibition. According to the authors, reserve mobilization activation is one of the first events that occur before radicle protrusion.

Reduction in the protein and starch content continued until the last days were evaluated. However, cultures on MS-NAA medium that developed NCs had higher protein (9.1 mg g\(^{-1}\) FM) and lower starch (6.0 mg g\(^{-1}\) FM) levels than seedlings after 21 days in culture (Figure 2a and b). Proteomic studies carried out in
leaves and seeds explants in the induction phase of NCs in the bromeliad *V. reitzii* showed an increase in protein content and number of spots detected in two-dimensional electrophoresis. Proteins identified were related to the regulation of effects of stress conditions in the culture medium, the adjustment of metabolism, and the increase in cell division (Corredor-Prado et al., 2016). Silveira, Floh, Handro, and Guerra (2004) also related protein level increases with high mitotic activity during exponential growth stages in *in vitro* cultures of *Pinus taeda*.

In histological sections with double staining (PAS-CBB), starch granules were observed in lower amount in NCs-inducing seeds (Figure 1f) than in seedlings (Figure 1c). This event may be related to increased metabolism of sugars, during the induction of NCs, generating a higher consumption of starch. Figure 1f, shows cells with starch, close to others with high mitotic activity, forming a cambial and provascular tissue. Thus, cortex with starch and cambial tissue surrounding the bundle would be the beginning of the NCs. Early starch presence in plant cells has been reported during *in vitro* development, acting as an energy source or as an osmotic agent that is essential for development (Martin et al., 2000). It has been suggested that starch accumulation might be a prerequisite of morphogenesis. For instance, in tobacco, starch acts as a direct cellular reserve of the energy and is rapidly converted to hexoses for the development of meristemoids (Thorpe et al., 2008).

![Figure 2](image.png)

**Figure 2.** Content of proteins (a), starch (b), carbohydrates (c), and global DNA methylation (d) in *Vriesea reitzii* seeds cultivated on NCs induction medium (MS-NAA) and PGR-free MS medium (MS). Data are means ± standard errors.

**Total soluble carbohydrates**

Quantification of the carbohydrates (mono- and disaccharides), revealed the lowest value (10.4 mg g⁻¹ FM) for dry seed (0 days of culture). Carbohydrates reached the highest level on the 10th day of culture in seeds inducing NCs (15.8 mg g⁻¹ FM) (Figure 2c). Through qualitative thin layer chromatography, glucose monosaccharide (RF: 0.58) and sucrose disaccharide (RF: 0.50) were identified in seeds on MS and MS-NAA.
medium (Figure 3, Table 1). Fructose, xylose, and maltose were not identified using this technique. However, at later stages of rice seed germination, Howell et al. (2009) detected several carbohydrate types, with increases primarily in fructose, glucose, and maltose. Before radicle protrusion in germination of barley seeds, activation of transcription factors for mobilization of starch reserves supplies sucrose and hexoses, which provide energy for development (Sreenivasulu et al., 2008).

Figure 3. Thin Layer Chromatogram of *Vriesea reitzii* seeds cultivated 21 days in PGR-free medium (MS) and in NCs induction medium (MS-NAA) against standard (fructose-Fru, glucose-Glc, xylose-Xyl, maltose-Mal, and sucrose-Suc).

Table 1. Retention factor (Rf) of detected spots in thin layer chromatography (TLC) from *Vriesea reitzii* seeds. Standards used: fructose (Fru), glucose (Glc), xylose (Xyl), maltose (Mal), and sucrose (Suc). PGR-free medium (MS) and in NCs induction medium (MS-NAA).

<table>
<thead>
<tr>
<th>Days of culture</th>
<th>Retention factor (Rf) of detected spots</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MS</td>
</tr>
<tr>
<td></td>
<td>Glc (0.58)</td>
</tr>
<tr>
<td>0</td>
<td>0.57</td>
</tr>
<tr>
<td>3</td>
<td>0.57</td>
</tr>
<tr>
<td>7</td>
<td>0.57</td>
</tr>
<tr>
<td>10</td>
<td>0.58</td>
</tr>
<tr>
<td>14</td>
<td>0.57</td>
</tr>
<tr>
<td>21</td>
<td>0.57</td>
</tr>
</tbody>
</table>

In addition to having the role of substrates for cell component synthesis, sugars also act as signaling molecules in the regulation of expression of various genes (Marsch-Martínez & Pereira, 2010). There is a strong hexose sugar increase in seeds after imbibition, followed by large changes in gene transcription (Fait et al., 2006; Howell et al., 2009). From this, a significant difference in carbohydrate content on the 10th day of culture on MS-NAA and MS medium, could be related to gene expression programming variation for NCs induction or for seedling development. According to Weber, Borisjuk, and Wobus (1997), sugars may interfere with cell cycle regulation by changing morphogenetic responses.

On the last day assessed (21 days of culture), carbohydrate content decreased in *V. reitzii* seeds. Significant differences between seeds on MS and MS-NAA medium were found (Figure 2c). Most likely, the presence of structures with different differentiation levels cause different energy levels necessary that support their metabolism. Lower values found in seeds that induced NCs (Figure 2c) indicate that this morphogenetic route has high energy demand. These results suggest that glycolytic intermediates formed by starch degradation are mainly catabolized to provide the necessary ATP for metabolism during cell proliferation that leads to NCs induction. On the other hand, higher carbohydrate content in seeds on MS medium allowed higher storage in starch (Figures 1c and 2b). In *Aechmea blanchetiana* bromeliad seedlings
cultured in vitro with different auxin concentrations, Chu et al. (2010) found that the highest starch and soluble carbohydrate content in plants were in the auxin-free medium. These results support the relation of auxin effect in carbohydrate metabolism.

**Global DNA Methylation (GDM)**

GDM levels decreased during germination until the 7th day of culture, reaching 9.2% in seeds on MS medium and 8.1% in seeds on MS-NAA medium (Figure 2d). Our results corroborate with those previously reported, in which methylation levels were higher in dry seeds than germinating seeds in *Capsicum annuum* L. (Portis, Acquadro, Comino, & Lanteri, 2004), *Brassica napus* (Lu et al., 2006), *Triticum aestivum* L. (Meng et al., 2012) and *Phelipanche ramosa* L. (Lechat et al., 2015). DNA hypomethylation during seed germination seems to be a necessary step for transcriptional activation of gene expression, contributing to the development of gene regulation (Lu et al., 2006). During wheat seed germination, Meng et al. (2012) found that the number of demethylation events was three times higher than methylation events, indicating demethylation predominance. According to Zluvova, Janousek, and Vyskot (2001), seed global hypomethylation during *Silene latifolia* germination and postgermination periods reflects transition from the metabolically quiescent seed to the actively growing and developing seedling.

On the last days evaluated (10, 14, and 21 days of culture), an increase in methylation levels was observed, reaching up to 11.7% in seeds that formed seedlings and 11.0% in seeds that induced NCs (Figure 2d). *Quercus suber* L. somatic embryo germination coincides with a significant 5mdC content decrease. However, when somatic embryos developed in seedlings with roots and initial leaves, a strong DNA methylation increase was observed (15%) (Pérez, Viejo, LaCuesta, Toorop, & Canal, 2015). Generally, differentiation coincides with increased DNA methylation, which is associated with normal ontogenic development (for review see Valledor et al., 2007).

Results on the last days also show significant GDM differences between seeds on MS and MS-NAA medium (Figure 2d). Methylation levels in seeds on MS medium could be associated with the differentiation process during normal seedling development. Therefore, the significantly lower level found in seeds that induced NCs is associated with tissue dedifferentiation. It has been reported during in vitro morphogenetic route induction, significant GDM decreases related to cell dedifferentiation and undifferentiated state cell maintenance (Fraga et al., 2016). According to Valledor et al. (2007), demethylation normally precedes the onset of new differentiation programs. However, even if GDM remains lower in seeds inducing NCs (associated with cellular dedifferentiation), the percentage keeps rising on the last days evaluated, which may be related to three factors, as follows: 1) some cells could be continuing the differentiation process, causing GDM level increases; 2) high cell proliferation, which is associated with high methylation levels (Wang et al., 2012); and 3) new meristematic zone formation in explants, which is in accordance with Scherer et al. (2015), who observed that high methylation levels were associated with new apical meristems formation in NCs of pineapple. Neelakandan and Wang (2012) conducted studies involving *Arabidopsis thaliana* epigenetic mutant characterization and observed that WUSCHEL (WUS) gene expression and signaling derived from auxins, which are crucial for meristem formation, are regulated, in part, by DNA methylation.

It is possible to relate methylation status with specific in vitro morphogenetic competence (Noceda et al., 2009). Accordingly, during somatic embryogenesis, embryogenic cells generally display lower GDM levels than nonembryogenic cells (Miguel & Marum, 2011). Similarly, lower GDM levels have been correlated with organogenic capability increases (Valledor, Mejíón, Hasbún, Cañal, & Rodrigues, 2010). The results of this study suggest that low GDM levels are related to explant capacity for NCs induction. This indicates that NAA supplemented in induction medium results in alterations of gene expression. According to Zhang, Yuan, and Zhang (2012), there is a functional interplay between environmentally induced epigenetic modifications, response to PGRs, and phenotypic plasticity. Auxins used in PGR-supplemented treatment, have been frequently linked to compromised genomic stability through the promotion of DNA methylation deregulation coupled with gene expression modifications in embryogenic cultures of *Daucus carota* (LoSchiavo et al., 1989) and *Araucaria angustifolia* (Fraga et al., 2016).

**Conclusion**

The findings of this study suggest that NCs induction from *V. reitzii* seeds using the culture medium supplemented with NAA results in explant gene reprogramming, which leads to morphological, biochemical and metabolic changes. NCs induction is a complex process in which epigenetic control (related to GDM levels decrease) seems to play an important role in the initiation of the morphogenic response.
Concomitantly, dedifferentiation followed by cell proliferation, high energy demand given by starch degradation present in the tissues, and higher protein content is related to elevated metabolic activity.

However, more detailed studies should be conducted to determine specific relations between the different signaling networks that regulate changes associated with the acquisition of skills to develop this morphogenic route.

Acknowledgements

The authors thank Programa de Estudantes-Convênio de Pós-Graduação (PEC-PG) da Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa e Inovação do Estado de Santa Catarina (FAPESC-PRONEX 2780/2012-4) for fellowships, research grants, and financial support.

References

Alves, G., Dal Vesco, L. L., & Guerra, M. P. (2006). Micropropagation of the Brazilian endemic bromeliad Vriesea reitzii through nodule clusters culture. Scientia Horticulturae, 110(2), 204-207. DOI: 10.1016/j.scienta.2006.06.014


Dal Vesco L. L., & Guerra, M. P. (2010). In vitro morphogenesis and adventitious shoot mass regeneration of Vriesea reitzii from nodular cultures. Scientia Horticulturae, 125(4), 748-755. DOI: 10.1016/j.scienta.2010.05.030


and non-embryonic calli from *Medicago arborea* L. *Plant Science*, 154(2), 143-151. DOI: 10.1016/S0168-9452(99)00251-4


