Low cytomolecular diversification in the genus *Stylosanthes* Sw. (Papilionoideae, Leguminosae)

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Abstract

Stylosanthes (Papilionoideae, Leguminosae) is a predominantly neotropical genus with ~ 48 species that includes worldwide important forage species. This study presents the chromosome number and morphology of eight species of the genus Stylosanthes (S. acuminata, S. gracilis, S. grandifolia, S. guianensis, S. hippocampoides, S. pilosa, S. macrocephala and S. ruellioides). In addition, staining with CMA and DAPI, in situ hybridization with 5S and 35S rDNA probes, and estimation of DNA content were performed. The interpretation of Stylosanthes chromosome diversification was anchored by a comparison with the sister genus Arachis and a dated molecular phylogeny based on nuclear and plastid loci. Stylosanthes species showed 2n = 20, with low cytomolecular diversification regarding 5S rDNA, 35S rDNA and genome size. Arachis has a more ancient diversification (~ 7 Mya in the Pliocene) than the relatively recent Stylosanthes (~ 2 Mya in the Pleistocene), and it seems more diverse than its sister lineage. Our data support the idea that the cytomolecular stability of Stylosanthes in relation to Arachis could be a result of its recent origin. The recent diversification of Stylosanthes could also be related to the low morphological differentiation among species, and to the recurrent formation of allopolyploid complexes.

Keywords: Arachis; cytogenetics; evolution; Leguminosae; Stylosanthes.

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Introduction

Chromosomal evolution, including polyploidization (auto or allopolyploidy), chromosomal rearrangements and heterochromatin polymorphisms are known to be important mechanisms promoting speciation in plants (Raskina et al., 2008; Soltis and Soltis, 2009; Reis et al., 2014; Pinto et al., 2016). However, chromosome changes may be neutral, with no direct impact on the adaptability or reproductive viability of the individuals carrying the polymorphism (Levin, 2002), and will not necessarily result in speciation. For example, Pimentel et al. (2017) investigated patterns of diversification and chromosomal evolution in Pooidae (Poaceae) in the light of past environmental changes. In this group, the haploid basic chromosome number has remained stable, with no direct association of chromosome transitions with diversification shifts.

One aspect that would influence the accumulation of cytomolecular diversity in plant lineages over time is the age of the group (Levin, 2002; Soltis and Soltis, 2009; Susek et al., 2016). Therefore, it would be expected that groups of recent diversification would have more stable and uniform
karyotypes, while those with older divergences would have time to accumulate more cytomolecular differences, resulting in higher karyotypical diversity. However, it is not clear if the timing of diversification of a given lineage reflects variation at the cytogenetic level. For example, there are cases of recently evolved lineages with highly variable karyotypes (eg. genus Nothoscordum [Amaryllidaceae] Souza et al., 2012), and ancient groups showing high karyotype stability (eg. subfamily Bombacoideae [Malvaceae] Costa et al., 2017).

In recent years, different studies reported new insights on the phylogeny and karyotype evolution of legumes, making this group an interesting model to investigate diversification and karyotype evolution. The period between the origin and diversification of Leguminosae was estimated to be short, with the divergence of the main lineages around 60 Million years ago (Mya) (Lavin et al., 2005). Within the Leguminosae, subfamily Papilionoideae comprises one of the most diverse and ecologically successful plant radiations, presenting a diversification history stemming from the Early Cenozoic (Lavin et al., 2005; Cardoso et al., 2012; LPWG, 2017). Wong et al. (2017) suggested that a single Whole Genome Duplication (WGD) event near to the base of Fabales was associated with the onset of Leguminosae diversification and that subsequent chromosome number reductions contributed to the success and diversification of Papilionoideae.

Within the papilionoid Pterocarpus clade (Cardoso et al., 2013), the sister genera Arachis and Stylosanthes represent a useful model for analyzing the evolution of karyotypic diversity in closely related lineages of similar size. The South American genus Arachis comprises approximately 82 species arranged in nine sections that were grouped according to the geographic distribution, morphology and cross-compatibility (Krapovickas and Gregory 1994; Valls and Simpson, 2005), and includes widely cultivated crops (peanut) and forages. Stylosanthes is a predominantly neotropical genus with nearly 48 species with low inter and intraspecific morphological variation (Stace and Cameron, 1984; Costa, 2006), including important species cultivated as forage in Africa and Australia (Costa, 2006). Due to their adaptability to low fertility soils and nitrogen fixing capacity, some species of the genus are grown to recover degraded soils (Shelton et al., 2005; Starr et al., 2013; Liu et al., 2016).

The species of Arachis are mostly autogamous and have the basic chromosome number $x = 10$ (except $x = 9$ in A. porphyrocalyx Valls & C.E.Simpson, A. palustris Krapov., W.C.Greg. & Valls, and A. praecox Krapov., W.C.Greg. & Valls). There are diploid ($2n = 2x = 20$ or $2n = 2x = 18$) and tetraploids species ($2n = 4x = 40$) with six different genomes (A, B, D, F, G and K) (Fernández and Krapovickas 1994; Peñaloza and Valls 2005; Silvestri et al., 2015; Ortiz, 2017). DNA contents are known for 23 species of Arachis, with an average of $2C = 2.83$ pg (http://data.kew.org/cvalues). On the other hand, Stylosanthes karyotype data are extremely scarce, with most data coming from chromosome counting and few species with genome size and molecular cytogenetics were
investigated (Vieira et al., 1993; Chandra and Kaushal, 2009; Lira, 2015; Marques et al., 2018). Most of the species of the genus are diploids (2n = 20) but few polyploid species (2n = 40, 60) were also reported (Cameron, 1967; Karia, 2008). Their chromosomes are small and with similar morphology, making it difficult to recognize chromosome pairs and to interpret the karyotype evolution (Vieira et al., 1993). A recent study based on cytogenetic and genomic data of the allopolyploidy S. scabra (2n = 40) revealed its origin from two diploid progenitors (Marques et al., 2018).

Phylogenetic and cytogenetic analyses are useful to investigate the time and mode of genome evolution, as well as to examine the impact of chromosome changes in plant diversification (e.g., Escudero et al., 2012). The combination of fluorescent in situ hybridization (FISH) and/or fluorochrome banding with phylogenetic comparative methods is a powerful tool for reconstructing detailed karyotype evolution (Guerra, 2012; Van-Lume et al., 2017). These techniques are useful to display chromosome morphological features, heterochromatin distribution and physical locations of repetitive DNA in plants. Such combination of methods is particularly interesting in revealing relationships among species and their genomic organizations, helping to understand the evolutionary history of plant groups (Reis et al., 2014; Ortiz et al., 2017; Samoluk et al., 2017). Here we analysed chromosome numbers and morphology of eight species of Stylosanthes, including chromomycin A3 (CMA) and 4′-6-diamidino-2-phenylindole (DAPI) chromosome banding, FISH for 5S and 35S ribosomal DNA (rDNA), as well as genome size estimate by flow cytometry. These data were used to investigate the relationship between timing of diversification and karyotypic diversity, using for comparison the sister genus Arachis, which has been extensively characterized in terms of cytology. The interpretation of chromosome variation within genera was anchored by a dated molecular phylogeny based on nuclear and plastid sequences.

Material and Methods

Plant material

The present study was based on material obtained from seeds of 12 accessions of eight Stylosanthes species [S. acuminata, S. gracilis, S. grandifolia, S. guianensis, S. hippocampoides, S. macrocephala, S. pilosa, and S. ruelliioides]. Five accessions of S. guianensis (1480, 4171, 1463, LC2538 and cv. Mineirão) were also investigated (See Table S1 in supplementary material for additional information).

For cytogenetic analysis, root tips obtained from seeds or seedlings were pretreated with 8-hydroxyquinoline (0.003 M) for 7 h at room temperature, fixed in ethanol:acetic acid (3:1; v/v) for 24 h at room temperature, and then stored at −20 °C. Fixed root tips were washed in distilled water
and digested in a solution of 2 % (w/v) cellulase /20 % (v/v) pectinase (Onozuka) at 37 °C for 5 h. The slides were prepared according to Carvalho and Saraiva (1993, 1997).

Chromosome banding

Chromosome banding was performed according to Schweizer (1976) with few modifications. Slides were stained with CMA (0.5 mg/mL) for 1h, dystamicyn (0.1mg/mL) for 30 min and DAPI (2μg/mL) for 30 min. The slides were mounted in glycerol:McIlvaine buffer pH 7.0 (1:1 v/v), and examined using an epifluorescence microscope (Olympus BX51).

Fluorescent in situ hybridization (FISH)

Fluorescent in situ hybridization (FISH) was performed using a 18S (located in a repetitive unit known as 45S rDNA, Roa and Guerra, 2015; or 35S rDNA, Garcia et al., 2017) spacer rDNA probes from *Triticum aestivum* L. (Gerlach and Bedbrook, 1979) and 5S rDNA probes from *Zea mays* L. (courtesy of Koo and J. Jiang). Each probe was labeled with digoxigenin by nick translation using DIG-Nick Translation Mix (Roche), and then hybridized according to Jiang et al. (1995) with some modifications. The hybridization mixture was denatured at 90 °C for 10 min and immediately transferred to an icebox. The slides were denatured at 85 °C for 1 min and treated with a series of alcohol washes (70% ice cold, 90% and 100% at room temperature for 5 min each). The hybridization mixture was then added to the slides and the chromosomes allowed to hybridize at 37°C for 24h. Post hybridization washes were carried out using 2 × SSC buffer (0.3 mol/L sodium citrate,0.03 mol/L sodium chloride, pH 7) and 1 × PBS buffer (0.136 mol/L sodium chloride, 0.27 mol/L potassium chloride, 0.1 mol/L dibasic sodium phosphate, 0.2 mol/L monobasic potassium phosphate, pH 7.4). Probes were detected with anti-DIG conjugate with rhodamine (Sigma) and post detection washes were performed using 1 × TNT buffer (0.1 mol/L Tris, 0.15 mol/L sodium chloride, 0.05% Tween-20) and 1X PBS at room temperature. Metaphases were counter-stained with 2μg/mL of DAPI (Sigma). The slides were mounted in Heatshield (Vector, Burlingame, California, USA), and samples were rehybridized. Images with 5S (red) and 18S (green pseudocolor) signals were merged using Adobe Photoshop CS5.

Flow cytometry

Nuclear DNA content estimation was performed according to Galbraith et al. (1983) using a FacsCanto II Flow Cytometer. Approximately 20-30 mg of young and fresh leaves and the same amount of tissue of standard references (*Pisum sativum* L. 9.09 pg) were chopped with 1mL of WPB lysis buffer (Loureiro et al., 2007). The histograms were analyzed with Flowing Software 2.5 software (http://www.uskonaskel.fi/flowingsoftware/).
DNA nuclear content (pg) of each sample was estimated by the relative fluorescence intensity of the sample and the internal reference standard. Three samples of each species/accessions were measured according to Dolezel et al. (2003):

\[
DNA \text{ content} = \frac{\text{PIFI of sample} \times \text{DNA content of standard}}{\text{PIFI of standard}}
\]

were PIFI is the fluorescence intensity of propidium iodide in G1 cells. DNA content among \( S. \ guianensis \) accessions was analyzed by ANOVA using Genes computational software (Cruz, 2013).

Phylogenetic sampling

The phylogenetic analysis of \( Styllosanthes \) and its sister genus \( Arachis \) was based on ITS nuclear region (ITS1-5.8S-ITS2) and \( matK \) plastid gene. ITS and \( matK \) sequences of 25 species of \( Arachis \) were retrieved from previous studies (see Genbank references on Table 1; Bechara et al., 2010; Lavin et al., 2001). However, only four \( matK \) sequences were available for \( Arachis \) species. New ITS and \( matK \) sequences for ten accessions of \( Styllosanthes \) were generated (Genbank accession numbers MH223599- MH223618). The related species \( Chapmannia floridana \) Torr. & A. Gray (Cardoso et al., 2013) was included as an outgroup (Genbank accession numbers KJ772648 and AF203562).

DNA extraction, polymerase chain reaction (PCR) and sequencing

DNA extraction was performed according to Doyle and Doyle (1987) using seed cotyledon/embryo tissue (30 mg per species). DNA quantification was done in a NanoDrop 2000c spectrophotometer (Thermo Scientific). The complete ITS region (ITS1-5.8S-ITS2), was amplified with universal primers ITS 4 and ITS 5 (White et al., 1990). Maturase K (\( matK \)) gene was also amplified using universal primers 1RKIM and 3FKIM (Bremer et al., 2002). Amplifications were performed in 50 µl of reaction volume containing 200 ng of genomic DNA and final concentrations of 1 × buffer, 0.3mM MgCl, 0.2 mM DNTP, 0.1 μM of each specific primers, 1.25 U Taq DNA polymerase, 1 × TBT and MiliQ water to complete the volume. ITS PCR reactions were incubated at 95 °C for 5 minutes, followed by 35 cycles of 1 minute at 95 °C, 1 minute at 55 °C, 1 minute at 72 °C and finally, 1 minute at 72 °C in an Applied Biosystems thermocycler. \( matK \) reactions were made using the same program with few adjustments: annealing temperature (56 °C) and extension time (10 minutes). After visualizing the PCR products in agarose 1% gel, the products were purified by precipitation. Purified PCR products were sequenced in a 3500 Genetic Analyzer (Applied Biosystems).
Phylogenetic analysis and character reconstruction

DNA sequences were analyzed, edited and aligned using Geneious software (version 7.1.9). An incongruence length difference test (ILD) was made in PAUP * (40.b10) (Swofford, 2002) to determine the statistical significance of incongruence between the data partitions. Bayesian Inference (BI) search was performed with the ITS1-5.8S-ITS2 + matK concatenated alignment. Since matK sequences were missing for most Arachis species (see Table 1), we also performed a phylogenetic analysis with ITS only to compare with the topology of the concatenated alignment (Figure S1). The Bayesian inference search was performed using CIPRES Science Gateway (Miller et al., 2010) using MrBayes 3.2.1 on XSEDE (Ronquist and Huelsenbeck, 2003) plugin, with 10,000,000 generations.

To interpret the evolution of cytomolecular diversification of the genus Stylosanthes a molecular clock analysis was performed using BEAST v.1.8.0 (Drummond et al., 2012a). We used the Aikake Criterion in Jmodeltest2 (Darriba et al., 2012) to select the best evolutionary model, which identified the GTR+I+G model for both partitions. Analyses were run using an uncorrelated log normal relaxed clock and a Yule Process speciation model. Two independent runs of 20,000,000 generations each were performed, sampling every 1,000 generations. In order to verify the effective sampling of all parameters and assess convergence of independent chains, we examined their posterior distributions in Tracer v.1.6. (Rambaut et al., 2014) and the MCMC sampling was considered sufficient at effective sampling sizes (ESS) higher than 200. After removing 25% of samples as burn-in, the independent runs were combined and a maximum clade credibility (MCC) tree was constructed using TreeAnnotator v.1.8.2. (Drummond et al., 2012a). Divergence time between Arachis and Stylosanthes estimated by a previous study (13.8 ± 1.7 Mya; Lavin et al., 2004) was used as a secondary calibration point using a normal prior.

The interpretation of karyotype data evolution of Stylosanthes and Arachis was done by plotting 5S rDNA, 35S rDNA, and genome size data on the dated phylogeny obtained. For this, the ancestral state reconstruction of cytomolecular characters (number of 5S and 35S rDNA) were performed in Mesquite v. 3.51 (Maddison and Maddison 2018). The trace character history function was used with the 50 % majority-rule consensus tree from the Bayesian inference analyses. The ancestral state was inferred using maximum parsimony, in which all changes are equally probable. The number of 5S and 35S rDNA sites was assumed as continuous data. Chromosome data of species were taken from the literature (Marques et al. 2018) or from this work and they were treated as an unordered, multistate character.
Results

All species of *Stylosanthes* here investigated were diploids (2n = 20) with predominantly metacentric chromosomes, measuring on average 2.7 µm (Figures 1-4). Most of the species (*S. hippocampoides, S. gracilis, S. macrocephala, S. pilosa, S. ruelliioides*, and *S. guianensis* accessions 1480, 1463, 4171, and LC2538), showed two CMA+/DAPI signals in the short arms of the smaller chromosomal pair. In addition to those bands, in *S. ruelliioides* CMA/DAPI proximal bands were also observed in all chromosomes (Figure 1h). On the other hand, *S. acuminata, S. grandifolia*, and *S. guianensis* cv. Mineirão showed four CMA+ bands, two of them in the short arms of the smaller chromosome pair and the other two in the proximal region of a large chromosome pair (Figure 1d, g, l).

FISH analyses revealed 35S rDNA sites co-localized with the CMA+ bands in the short arms of the smaller acrocentric pair, as it was observed in *S. gracilis, S. grandifolia, S. hippocampoides, S. macrocephala* and *S. ruelliioides* (Figure 2a-d, f and Figure 3). The 5S rDNA sites were localized in the proximal region of one chromosome pair (Figure 2a-j and Figure 3). In *S. acuminata* we observed four 35S rDNA sites (Figure 2e). No variation in the number of rDNA sites was observed among *S. guianensis* accessions, being possible to map one pair of 5S rDNA and one pair of 35S rDNA (Figure 2g-j and Figure 4).

The DNA content among *Stylosanthes* species ranged from 2.05 to 3.07 pg (Table 1), with *S. macrocephala* showing the lowest value (2.05 pg) and *S. guianensis* accessions the highest (2.8 to 3.07). These values were analyzed by ANOVA and there were no significant differences between accessions (p=10.6194).

Molecular phylogenetic analysis including *Stylosanthes* (eight spp.) and *Arachis* (21 spp.) were performed. ILD test revealed no significant incongruence (p<0.05) between *matK* and ITS datasets. Thus, BI was conducted with the concatenated alignment *matK* + ITS since this alignment produced better resolved relationships. The concatenated alignment contains 1,180 base pairs, where the *matK* region seems to be more conserved (identity = 98.3%) in both groups when compared to the ITS region (identity = 91.5%). The genera *Arachis* and *Stylosanthes* were recovered as monophyletic (Figure 5), with the diversification of *Arachis* starting on the upper Miocene (7.10 Mya; Credibility Interval 7.80-4.16 Mya), followed by a more recent origin of *Stylosanthes* at (2.90 Mya; CI 3.25-2.60 Mya). The clade represented by *S. acuminata, S. gracilis, S. grandifolia, S. hippocampoides*, and the four accessions of *S. guianensis* showed more recent diversification in the Pleistocene (~3 Mya).

Available cytogenetic data and genome size were also considered to interpret the molecular phylogenetic of the genera *Stylosanthes* and *Arachis* (Table 1, Figure 5). We categorized DNA
Author's name

Discussion

Karyotype stability in *Stylosanthes*

Although most of the species of the genus *Stylosanthes* are diploids, few polyploidy species, such as *S. hamata* and *S. scabra* with 2n= 40, and *S. erecta* with 2n=60 were reported (Cameron, 1967; Karia, 2008; Polido et al., 2015). The diploid chromosome number (2n = 2x = 20) here observed is in agreement with previous report for the genus *Stylosanthes* (Vieira et al., 1993; Lira, 2015; Marques et al., 2018). Morphometric analysis of the *Stylosanthes* karyotypes revealed that the chromosomal profile was similar for all diploid species previously investigated (Vieira et al., 1993), corroborating our findings. The predominance of metacentric chromosomes suggests a symmetrical karyotype, which is generally observed in other members of Leguminosae (Bandel, 1974; Kumari and Bir, 1989; Vieira et al., 1993; Pinto et al., 2016; Van-Lume et al., 2017).

The stability or variability in legume karyotypes can be associated with the timing of diversification, reproduction strategies, and other factors related to the evolutionary history of each group (Soltis and Soltis, 2009; Gu et al., 2016). Genome comparisons have showed conserved syntenic blocks between papilionoid genomes, especially among phylogenetically closely related species (Young and Bharti, 2012). In the genus *Phaseolus* (Papilionoideae), for example, a karyotypic stability of chromosomal numbers (except for dysplody in the clade *Leptostachyus*) revealed by C-banding and fluorochrome staining (Zheng et al., 1993; Almeida and Pedrosa Harand, 2013) was observed and associated with a recent diversification over the last 5 Mya (Delgado-Salinas et al., 2006). In this genus, the use of BAC-FISH mapping indicated a high level of macro-collinearity among homeologous chromosomes (Almeida and Pedrosa-Harand, 2013; Fonsêca and Pedrosa-Harand 2017). However, other legumes with recent diversification such as *Vigna* may present polymorphic karyotypes (She et al., 2014; Delgado-Salinas et al., 2011), indicating that time alone would not be the only factor responsible for the accumulation of karyotypic variability.
**Genome size in Stylosanthes**

The small variation of DNA content (1.4 fold) in the *Stylosanthes* species analysed here corroborates a scenario of karyotypic stability. Although the average of DNA estimation is in agreement with other estimations for the genus, we observed different C-values for two diploid species (*S. seabrana* B.L.Maass & ‘t Mannetje and *S. viscosa*) for which 5.45pg were reported in the literature (Chandra and Kaushal, 2009). Variation of DNA content within a genus may be due to different factors such as recombination, deletion and retrotransposition (Piegu et al., 2006; Baziz et al., 2014). Among closely related species, other mechanisms appear to have some impact on genome size variations, such as expansion of tandem repeated DNA sequences, variation in intron size and transfer of organellar DNA to the nucleus (Deutsch and Long, 1999; Morgante et al., 2002; Adams and Palmer, 2003; Baziz et al., 2014). Comparing to other Leguminosae, the amount of DNA in *Stylosanthes* seems to be relatively high. *Leucaena macrophylla* Benth. has 2C value = 0.62 pg, *Trifolium arvense* L. was described with 2C = 0.78 pg and *Lotus coimbrensis* Willd. with 2C = 0.90 pg, although, *Lathyrus latifolius* L. (2C = 21.76 pg) and *Vicia faba* L. (2C = 54.8 pg) have the highest DNA content within the family (Bennett et al., 1982; Cheng and Grant, 1973; Hartman et al., 2000; Vizintin et al., 2006). The reason why the DNA content of eukaryotic genomes vary independently remains a matter of speculation. The same is true for the questions of whether there is a general tendency for increase or decrease of genome size and whether genome size and/or chromosome number have an adaptive value. Some authors hypothesized that three strategies of genome evolution (shrinkage, expansion and equilibrium) might be involved in achieving the optimal balance between genomic stability and plasticity (Gregory, 2001; Schubert and Giang, 2016).

**Heterochromatin pattern in Stylosanthes**

The co-localization of all 35S rDNA sites with CMA\(^+\) bands as found in *Stylosanthes* species is commonly reported in plants (Siljak-Yakovlev et al., 2003). Interestingly, the colocalization of 5S rDNA with heterochromatic bands, as observed in *S. guianensis* cv. Mineirão and *S. grandifolia*, is a rare condition in other higher plants (Cabral et al., 2006; Vasconcelos et al., 2010; Bernardes et al., 2013). Karyotype variability in Papilionoideae has been characterized by comparative cytogenetic studies of heterochromatin bands and rDNA sites distribution. In the genus *Crotolaria*, different heterochromatin types were observed, suggesting the occurrence of replacement of repetitive DNA families during the genus diversification (Mondin et al., 2007; Morales et al., 2011; Mondin and Aguiar Perencin, 2011). In *Astragalus*, it was reported variation in number, intensity, and position of CMA bands along the chromosomes, likewise 5S rDNA sites (Baziz et al., 2014), while cultivated species of *Canavalia* showed variations in the rDNA positions (She et al., 2017). In *Lotus japonicus* (Regel) K. Larsen and *L. filicaulis* Durieu, for which three 35S loci have been identified, initially no
polymorphism of this type was observed (Pedrosa et al., 2002). Nevertheless, a comparative cytogenetic map built for *Lotus uliginosus* (L.) Schkuhr (2n = 12) revealed intra and interspecific chromosomal rearrangements in *L. japonicus*, *L. filicaulis*, and *L. burttii* Borsos. Changes in the number, size, and position of rDNA sites were observed, as well as an intraspecific heteromorphism of the 5S rDNA site in *L. uliginosus* (Ferreira et al., 2012). Comparative analyses have demonstrated variations in the position of 5S and 45S rDNA sites in *Medicago* L. species, giving evidence of new rearrangements throughout the evolutionary history of the genus (Yu et al., 2017). Meanwhile, the genus *Lens*, showed variations mainly in 5S sites (Fernandez et al., 2005; Balyan et al., 2002). Although wide cytogenetics variation related to the repetitive fraction of the genome (heterochromatic bands and rDNA sites) has been reported in different Papilionoid genera, there is little information on the degree of intergeneric variability of whole genomes (Schubert and Giang, 2016).

Variations in heterochromatin composition was also observed in *Stylosanthes*. However, only two species showed different number and positions in CMA+ bands. Thus, comparing with *Arachis*, this variability of heterochromatin can still be considered low (Silvestri et al., 2015). Interestingly, DAPI+ proximal bands were observed only in *S. ruelliioides*. This species belongs to the same clade of *Stylosanthes scabra* complex (*S. viscosa*, *S. hamata* and *S. scabra*) (Marques et al., 2018), that also showed DAPI+ bands in a (peri)centromeric location, suggesting that these species are closely related.

**Evolutionary trends in *Stylosanthes* genome**

The knowledge about the karyotype organization in *Stylosanthes* contributes to a better understanding of its evolutionary history, which is so far exemplified by the general stability in genome size and chromosome numbers. Here we evaluated the evolution of karyotypic diversity in *Stylosanthes* by comparing the variation in the number of rDNA sites and DNA content between its sister clade. In general, cytogenetic data give evidence of cytomolecular stability of *Stylosanthes* in relation to *Arachis* (Vieira et al., 1993; Silvestri et al., 2015), suggesting that the age of the group could be an important factor to be considered in karyotype diversification. However, a more representative sampling within *Stylosanthes* and *Arachis* in the dating analysis would be required to confirm the age estimates of major lineages within these genera. Low morphological differentiation, phylogenetic similarity of plastid and nuclear DNA sequences, as well as crosses between species (allopolyplodontization) from different clades support the cytomolecular stability in the recently evolved *Stylosanthes* (Vander Stappen et al., 2003). In contrast, *Arachis* presents a high variability of the CMA/DAPI banding and rDNA sites distribution (5S and 18S), being possible to identify six genomes (A, B, D, F, G and K) (Fernández and Krapovickas, 1994; Peñaloza and Valls, 2005; Silvestri et al., 2015; Ortiz, 2017). Smartt et al. (1978) initially established the A and B genomes.
based on the two different chromosome complements in the allotetraploid *A. hypogaea* (AABB). The “A chromosomes” have a differential condensation pattern during prometaphase (Fernández and Krapovickas, 1994) and have a large heterochromatic band DAPI+ in the centromeric region (Seijo *et al*., 2004). The remaining species with symmetric karyotypes, but without “A chromosomes”, have been assigned to one single genome group named B genome or non-A genome (Seijo *et al*., 2004; Robledo and Seijo, 2010). In addition, *Arachis* presents a greater diversity of species and morphological variability compared to *Stylosanthes*.

Although rDNA occupies a large fraction of the nuclear genome, it is also an unstable genomic region and the reasons for this instability are not fully understood (Kobayashi, 2008; Totta *et al*., 2017). Recent studies have been explored the dynamics of rDNA loci under an explicit phylogenetic framework. Totta *et al*. (2017) inferred that a stasis in 45S rDNA site-number occurred during the most of the evolutionary history of *Cistus* (Cistaceae) and allied genera. The authors suggested that most of the multiple shifts involving changes in the number of the rDNA loci likely occur since the Middle Pleistocene in this group, and that rDNA stasis in site number may have been underestimated in diploids. The terminal positions of 35 rDNA loci might also facilitate higher frequencies of interlocus homogenization than is found in interstitial or pericentromeric loci (García *et al*. 2017).

Analysis of the evolutionary rates of DNA sequence data in the rainforest tree genus *Swartzia* (Papilionoideae) indicates that it diversified rapidly after its origin, probably during the Miocene (Torke, 2006). Such information, coupled with cytogenetic features (small chromosomes, two 5S and 45S rDNA sites in metaphases as well as two positive CMA bands) are preliminary evidences of strongly conserved karyotypes in a recently evolved species-rich lineage (Pinto *et al*., 2016). The stability observed in some groups of recent divergence was also identified in other papilionid genera such as *Phaseolus* (Fonseca and Pedrosa-Harand, 2013, 2017). The lupin genus (*Lupinus*) encompasses about 270 annual and perennial species distributed in both the Old World (generally around the Mediterranean basin) and the New World (primarily North and South America) (Drummond *et al*., 2012b). The Old World lineage originated between 17-20 Mya while New World species evolved around 2-5 Mya. The Old Word lupins shows a high level of genomic diversification characterized by variation in chromosome numbers (2n = 32-52), basic chromosome numbers (x = 5-7, 9, 13), nuclear genome size, patterns of chromatin modifications at the chromosomal level, and 5S/45S rDNA sites number (Hajdera *et al*., 2003; Naganowska *et al*., 2002, 2003; Susek *et al*., 2016, 2017). On the other hand, New World lupins have more uniform karyotypes in terms of their genome structure, and have chromosome numbers of either 2n = 36 or 2n = 48 with a fixed basic chromosome number x = 6 (Naganowska *et al*., 2006; Susek *et al*., 2016). This reinforces the view that within the same group, lineages with older diversification tends to show high karyotype diversity compared to more recent lineages, as was reported here for the sister genera *Arachis* and *Stylosanthes*. 


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Torke, BM (2006) Systematics and evolutionary diversification in the species-rich neotropical tree genus *Swartzia* (Leguminosae - Papilionoideae). Thesis (PhD) Washington University, Missouri, USA.


Internet Resources

Flowing Software 2.5 software, http://www.uskonaskel.fi/flowingsoftware/


Supplementary material

The supplementary material will be available in the final version of the article.
Figure 1. DAPI/CMA banding profile in *Stylosanthes* species. (a) *S. guianensis* 1480, (b) *S. guianensis* 4171, (c) *S. guianensis* 1463, (d) *S. acuminata*, (e) *S. guianensis* LC2538, (f) *S. pilosa*, (g) *S. guianensis* cv. Mineirão, (h) *S. ruelliioides*, (i) *S. gracilis*, (j) *S. macrocephala*, (k) *S. hippocampoides*, (l) *S. grandifolia*. Bar = 10µm.
Figure 2. 5S (red) and 35S (green) probes mapped in *Stylosanthes* species by fluorescent *in situ* hybridization. (a) *S. hippocampoides*, (b) *S. gracilis*, (c) *S. grandifolia*, (d) *S. macrocephala*, (e) *S. acuminata*, (f) *S. ruellioides*, (g) *S. guianensis* LC2538, two extra points are distended satellites, (h) *S. guianensis* cv. Mineirão, (i) *S. guianensis* 4171, two extra points are distended satellites, (j) *S. guianensis* 1480 Bar = 10µm.
Figure 3. Idiograms of *Stylosanthes* species showing chromosome length (L), arm ratio (AR), 5S (red), CMA bands colocalized with 35S r DNA sites (green), and CMA bands colocalized with 5S (yellow).
Figure 4. Idiograms of *S. guianensis* accessions showing chromosome length (L), arm ratio (AR), 5S (red), CMA bands colocalized with 35S r DNA sites (green), and CMA bands colocalized with 5S (yellow).
Figure 5. Chronogram of *Arachis* and *Stylosanthes* species based on BEAST analysis using the plastid *matK* and nuclear ITS combined datasets. Blue bars indicate 95% highest posterior density intervals. 

**a**, comparative DNA content evolution, with symbols next to accessions proportional to genome size.

**b**, ancestral character estimation of number of rDNA sites along the branches and nodes of the phylogeny. The color of edges in the tree represents observed and reconstructed values for chromosome number on the tree. Red colors correspond with relatively high numbers of rDNA sites; whereas dark blue colors represent low number of observed and reconstructed rDNA sites.
Table 1. Species analyzed with their respective chromosome numbers, DNA content (average and coefficient of variation), and GenBank accession numbers.

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<th>Genus / Species</th>
<th>2n</th>
<th>2C-value (pg)</th>
<th>CV (%)</th>
<th>nº of rDNA sites</th>
<th>GenBank No.</th>
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