Argelia Cuenca

Organisations

Researcher, National Institute of Aquatic Resources
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Research outputs:

Validation of a novel one-step reverse transcription polymerase chain reaction method for detecting viral haemorrhagic septicaemia virus
Viral haemorrhagic septicaemia (VHS) is one of the most serious viral diseases in salmonid and olive flounder farms. Various diagnostic methods for detecting VHS virus (VHSV) are described in the VHS chapter of the World Organization for Animal Health (OIE) Aquatic Diagnostic Manual. A conventional reverse transcription-PCR (cRT-PCR) targeting the viral nucleocapsid gene is recommended for the detection of VHSV and, to some extent, for genotypic classification. However, the recommended assay exhibits low sensitivity for the detection of VHSV genotype IVa isolates and often shows non-specific amplicons when the RNA template is extracted from non-infected fish cell lines. For these reasons, it is necessary to develop a new RT-PCR method for the foolproof detection of all VHSV genotypes and elimination of non-specific results. In this study, we selected five candidate primer sets that target the VHSV nucleoprotein (N) gene, and selected the most sensitive among them (3F/2R). We then established the optimal reaction conditions for these primers, and ensured that no non-specific amplification had occurred in the fish tissues, fish cell lines, or heterologous viruses. The analytical sensitivity of the novel cRT-PCR was compared to that of cell culture assays, real-time RT-PCR, and other cRT-PCR methods and was found to be as sensitive as or superior to the other methods for detecting all VHSV genotypes. Our newly developed cRT-PCR assay was tested with 80 isolates, representing a collection of all known VHSV genotypes worldwide. Clear and unique amplicons were amplified from all 80 VHSV isolates. The reproducibility, and partly the robustness, of the assay were confirmed by an inter-laboratory proficiency tests including nine laboratories. A high diagnostic sensitivity and specificity was confirmed on tissue material from affected fish. In conclusion a highly robust, sensitive and specific cRT-PCR for detection of VHSV was developed and validated.

General information
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Contributors: Kim, H. J., Cuenca, A., Olesen, N. J.
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BFI (2018): BFI-level 2
Molecular and Antigenic Characterization of Piscine orthoreovirus (PRV) from Rainbow Trout (Oncorhynchus mykiss)

Piscine orthoreovirus (PRV-1) causes heart and skeletal muscle inflammation (HSMI) in farmed Atlantic salmon (Salmo salar). Recently, a novel PRV (formerly PRV-Om, here called PRV-3), was found in rainbow trout (Oncorhynchus mykiss) with HSMI-like disease. PRV is considered to be an emerging pathogen in farmed salmonids. In this study, molecular and antigenic characterization of PRV-3 was performed. Erythrocytes are the main target cells for PRV, and blood samples that were collected from experimentally challenged fish were used as source of virus. Virus particles were purified by gradient ultracentrifugation and the complete coding sequences of PRV-3 were obtained by Illumina sequencing. When compared to PRV-1, the nucleotide identity of the coding regions was 80.1%, and the amino acid identities of the predicted PRV-3 proteins varied from 96.7% (λ1) to 79.1% (σ3). Phylogenetic analysis showed that PRV-3 belongs to a separate cluster. The region encoding σ3 were sequenced from PRV-3 isolates collected from rainbow trout in Europe. These sequences clustered together, but were distant from PRV-3 that was isolated from rainbow trout in Norway. Bioinformatic analyses of PRV-3 proteins revealed that predicted secondary structures and functional domains were conserved between PRV-3 and PRV-1. Rabbit antisera raised against purified virus or various recombinant virus proteins from PRV-1 all cross-reacted with PRV-3. Our findings indicate that despite different species preferences of the PRV subtypes, several genetic, antigenic, and structural properties are conserved between PRV-1 and-3.
Outbreak of viral haemorrhagic septicaemia (VHS) in lumpfish (Cyclopterus lumpus) in Iceland caused by VHS virus genotype IV

A novel viral haemorrhagic septicaemia virus (VHSV) of genotype IV was isolated from wild lumpfish (Cyclopterus lumpus), brought to a land-based farm in Iceland, to serve as broodfish. Two groups of lumpfish juveniles, kept in tanks in the same facility, got infected. The virus isolated was identified as VHSV by ELISA and real-time RT-PCR. Phylogenetic analysis, based on the glycoprotein (G) gene sequences, may indicate a novel subgroup of VHSV genotype IV. In controlled laboratory exposure studies with this new isolate, there was 3% survival in the I.P. injection challenged group while there was 90% survival in the immersion group. VHSV was not re-isolated from fish challenged by immersion. In a cohabitation trial, lumpfish infected I.P. (shedders) were placed in tanks with naïve lumpfish as well as naïve Atlantic salmon (Salmo salar L.). 10% of the lumpfish shedders and 43%-50% of the cohabiting lumpfish survived after 4 weeks. 80%-92% of the Atlantic salmon survived, but no viral RNA was detected by real-time RT-PCR nor VHSV was isolated from Atlantic salmon. This is the first isolation of a notifiable virus in Iceland and the first report of VHSV of genotype IV in European waters.

General information
State: Accepted/In press
Organisations: National Institute of Aquatic Resources, Public Sector Consultancy, Fish Diseases, University of Iceland
Contributors: Guðmundsdóttir, S., Vendramin, N., Cuenca, A., Sigurðardóttir, H., Kristmundsson, A., Moesgaard Iburg, T., Olesen, N. J.
Publication date: 2018
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Publication information
Journal: Journal of Fish Diseases
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Impact factor 2.004
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Impact factor 2.138
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Impact factor 2.053
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Mitochondrial genome evolution in Alismatales: Size reduction and extensive loss of ribosomal protein genes

The order Alismatales is a hotspot for evolution of plant mitochondrial genomes characterized by remarkable differences in genome size, substitution rates, RNA editing, retrotranscription, gene loss and intron loss. Here we have sequenced the complete mitogenomes of Zostera marina and Stratiotes aloides, which together with previously sequenced mitogenomes from Butomus and Spirodela, provide new evolutionary evidence of genome size reduction, gene loss and transfer to the nucleus. The Zostera mitogenome includes a large portion of DNA transferred from the plastome, yet it is the smallest known mitogenome from a non-parasitic plant. Using a broad sample of the Alismatales, the evolutionary history of ribosomal protein gene loss is analyzed. In Zostera almost all ribosomal protein genes are lost from the mitogenome, but only some can be found in the nucleus.

General information
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Organisations: National Veterinary Institute, Fish Diseases, University of Copenhagen, University of British Columbia, Cornell University
Contributors: Petersen, G., Cuenca, A., Zervas, A., Ross, G. T., Graham, S. W., Barrett, C. F., Davis, J. I., Seberg, O.
Number of pages: 21
Publication date: 2017
Peer-reviewed: Yes
Localized Retroprocessing as a Model of Intron Loss in the Plant Mitochondrial Genome

Loss of introns in plant mitochondrial genes is commonly explained by retroprocessing. Under this model, an mRNA is reverse transcribed and integrated back into the genome, simultaneously affecting the contents of introns and edited sites. To evaluate the extent to which retroprocessing explains intron loss, we analyzed patterns of intron content and predicted RNA editing for whole mitochondrial genomes of 30 species in the monocot order Alismatales. In this group, we found an unusually high degree of variation in the intron content, even expanding the hitherto known variation among angiosperms. Some species have lost some two-third of the cis-spliced introns. We found a strong correlation between intron content and editing frequency, and detected 27 events in which intron loss is consistent with the presence of nucleotides in an edited state, supporting retroprocessing. However, we also detected seven cases of intron loss not readily being explained by retroprocessing. Our analyses are also not consistent with the entire length of a fully processed cDNA copy being integrated into the genome, but instead indicate that retroprocessing usually occurs for only part of the gene. In some cases, several rounds of retroprocessing may explain intron loss in genes completely devoid of introns. A number of taxa retroprocessing seem to be very common and a possibly ongoing process. It affects the entire mitochondrial genome.
Phylogeny of the Alismatales (Monocotyledons) and the relationship of Acorus (Acorales?)

A phylogenetic analysis of the early branching lineages of the monocotyledons is performed using data from two plastid genes (rbcL and matK), five mitochondrial genes (atp1, ccmB, cob, mttB and nad5) and morphology. The complete matrix includes 93 terminals representing Acorus, the 14 families currently recognized within Alismatales, and numerous lineages of monocotyledons and other angiosperms. Total evidence analysis results in an almost completely resolved strict consensus tree, but all data partitions, genomic as well as morphological, are incongruent. The effects of RNA editing and potentially processed paralogous sequences are explored and discussed. Despite a decrease in incongruence length differences after exclusion of edited sites, the major data partitions remain significantly incongruent. The 14 families of Alismatales are all found to be monophyletic, but Acorus is found to be included in Alismatales rather than being the sister group to all other monocotyledons. The placement is strongly supported by the mitochondrial data, atp1 in particular, but it cannot be explained as an artifact caused by patterns of editing or by sampling of processed paralogues.

General information
State: Published
Organisations: University of Copenhagen
Contributors: Petersen, G., Seberg, O., Cuenca Navarro, A., Stevenson, D. W., Thadeo, M., Davis, J. I., Graham, S., Ross, T. G.
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Publication information
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Scopus rating (2017): CiteScore 4.15 SJR 1.962 SNIP 3.146
Web of Science (2017): Impact factor 5.877
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 3.26 SJR 1.943 SNIP 2.398
Web of Science (2016): Impact factor 4.309
Scopus rating (2015): CiteScore 3.31 SJR 2.654 SNIP 2.839
Web of Science (2015): Impact factor 4.952
Scopus rating (2014): CiteScore 3.45 SJR 2.248 SNIP 2.61
Scopus rating (2013): CiteScore 3.9 SJR 2.237 SNIP 2.387
Web of Science (2013): Impact factor 6.091
Scopus rating (2012): CiteScore 3.55 SJR 2.506 SNIP 2.097
Web of Science (2012): Impact factor 5.043
Scopus rating (2011): CiteScore 5.13 SJR 3.351 SNIP 3.156
Web of Science (2011): Impact factor 5.25
Scopus rating (2010): SJR 2.887 SNIP 2.945
Web of Science (2010): Impact factor 6.74
Scopus rating (2009): SJR 2.682 SNIP 2.573
Scopus rating (2008): SJR 2.135 SNIP 2.469
Scopus rating (2007): SJR 2.538 SNIP 1.869
Plastid phylogenomics and molecular evolution of Alismatales

Past phylogenetic studies of the monocot order Alismatales left several higher-order relationships unresolved. We addressed these uncertainties using a nearly complete genus-level sampling of whole plastid genomes (gene sets representing 83 protein-coding and ribosomal genes) from members of the core alismatid families, Tofieldiaceae and additional taxa (Araceae and other angiosperms). Parsimony and likelihood analyses inferred generally highly congruent phylogenetic relationships within the order, and several alternative likelihood partitioning schemes had little impact on patterns of clade support. All families with multiple genera were resolved as monophyletic, and we inferred strong bootstrap support for most inter- and intrafamilial relationships. The precise placement of Tofieldiaceae in the order was not well supported. Although most analyses inferred Tofieldiaceae to be the sister-group of the rest of the order, one likelihood analysis indicated a contrasting Araceae-sister arrangement. Acorus (Acorales) was not supported as a member of the order. We also investigated the molecular evolution of plastid NADH dehydrogenase, a large enzymatic complex that may play a role in photooxidative stress responses. Ancestral-state reconstructions support four convergent losses of a functional NADH dehydrogenase complex in Alismatales, including a single loss in Tofieldiaceae.

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Scopus rating (2016): CiteScore 3.26 SJR 1.943 SNIP 2.398
Web of Science (2016): Impact factor 4.309
Scopus rating (2015): CiteScore 3.31 SJR 2.654 SNIP 2.839
Web of Science (2015): Impact factor 4.952
Scopus rating (2014): CiteScore 3.45 SJR 2.248 SNIP 2.61
Scopus rating (2013): CiteScore 3.9 SJR 2.237 SNIP 2.387
Web of Science (2013): Impact factor 6.091
Scopus rating (2012): CiteScore 3.55 SJR 2.506 SNIP 2.097
Web of Science (2012): Impact factor 5.043
Massive gene loss in mistletoe (Viscum, Viscaceae) mitochondria

Parasitism is a successful survival strategy across all kingdoms and has evolved repeatedly in angiosperms. Parasitic plants obtain nutrients from other plants and some are agricultural pests. Obligate parasites, which cannot complete their lifecycle without a host, may lack functional photosystems (holoparasites), or have retained photosynthesis (hemiparasites). Plastid genomes are often reduced in parasites, but complete mitochondrial genomes have not been sequenced and their mitochondrial respiratory capacities are largely unknown. The hemiparasitic European mistletoe (Viscum album), known from folklore and postulated therapeutic properties, is a pest in plantations and forestry. We compare the mitochondrial genomes of three Viscum species based on the complete mitochondrial genome of V. album, the first from a parasitic plant. We show that mitochondrial genes encoding proteins of all respiratory complexes are lacking or pseudogenized raising several questions relevant to all parasitic plants: Are any mitochondrial gene functions essential? Do any genes need to be located in the mitochondrial genome or can they all be transferred to the nucleus? Can parasitic plants survive without oxidative phosphorylation by using alternative respiratory pathways? More generally, our study is a step towards understanding how host-and self-perception, host integration and nucleic acid transfer has modified ancestral mitochondrial genomes.

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Contributors: Petersen, G., Cuenca Navarro, A., Møller, I. M., Seberg, O.
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Journal: Scientific Reports
Volume: 5
Article number: 17588
ISSN (Print): 2045-2322
Ratings:
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Impact factor 4.122
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Plastome Evolution in Hemiparasitic Mistletoes

Santalales is an order of plants consisting almost entirely of parasites. Some, such as Osyris, are facultative root parasites whereas others, such as Viscum, are obligate stem parasitic mistletoes. Here, we report the complete plastome sequences of one species of Osyris and three species of Viscum, and we investigate the evolutionary aspects of structural changes and changes in gene content in relation to parasitism. Compared with typical angiosperms plastomes, the four Santalales plastomes are all reduced in size (10-22% compared with Vitis), and they have experienced rearrangements, mostly but not exclusively in the border areas of the inverted repeats. Additionally, a number of protein-coding genes (matK, infA, ccsA, rpl33, and all 11 ndh genes) as well as two transfer RNA genes (trnG-UCC and trnV-UAC) have been pseudogenized or completely lost. Most of the remaining plastid genes have a significantly changed selection pattern compared with other dicots, and the relaxed selection of photosynthesis genes is noteworthy. Although gene loss obviously reduces plastome size, intergenic regions were also shortened. As plastome modifications are generally most prominent in Viscum, they are most likely correlated with the increased nutritional dependence on the host compared with Osyris.

General information
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Contributors: Petersen, G., Cuenca Navarro, A., Seberg, O.
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Volume: 7
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ISSN (Print): 1759-6653
Ratings:
The Complete Sequence of the Mitochondrial Genome of Butomus umbellatus - A Member of an Early Branching Lineage of Monocotyledons

In order to study the evolution of mitochondrial genomes in the early branching lineages of the monocotyledons, i.e., the Acorales and Alismatales, we are sequencing complete genomes from a suite of key taxa. As a starting point the present paper describes the mitochondrial genome of Butomus umbellatus (Butomaceae) based on next-generation sequencing data. The genome was assembled into a circular molecule, 450,826 bp in length. Coding sequences cover only 8.2% of the genome and include 28 protein coding genes, four rRNA genes, and 12 tRNA genes. Some of the tRNA genes and a 16S rRNA gene are transferred from the plastid genome. However, the total amount of recognized plastid sequences in the mitochondrial genome is only 1.5% and the amount of DNA transferred from the nucleus is also low. RNA editing is abundant and a total of 557 edited sites are predicted in the protein coding genes. Compared to the 40 angiosperm mitochondrial genomes sequenced to date, the GC content of the Butomus genome is uniquely high (49.1%). The overall similarity between the mitochondrial genomes of Butomus and Spirodela (Araceae), the closest relative yet sequenced, is low (less than 20%), and the two genomes differ in size by a factor 2. Gene order is also largely unconserved. However, based on its phylogenetic position within the core alismatids Butomus will serve as a good reference point for subsequent studies in the early branching lineages of the monocotyledons.
Genes and Processed Paralogs Co-exist in Plant Mitochondria

RNA-mediated gene duplication has been proposed to create processed paralogs in the plant mitochondrial genome. A processed paralog may retain signatures left by the maturation process of its RNA precursor, such as intron removal and no need of RNA editing. Whereas it is well documented that an RNA intermediary is involved in the transfer of mitochondrial genes to the nucleus, no direct evidence exists for insertion of processed paralogs in the mitochondria (i.e., processed and un-processed genes have never been found simultaneously in the mitochondrial genome). In this study, we sequenced a region of the mitochondrial gene 1, and identified a number of taxa were two different copies of the region co-occur in the mitochondria. The two 1 paralogs differed in their (a) presence or absence of a group II intron, and (b) number of edited sites. Thus, this work provides the first evidence of co-existence of processed paralogs and their precursors within the plant mitochondrial genome. In addition, mapping the presence/absence of the paralogs provides indirect evidence of RNA-mediated gene duplication as an essential process shaping the mitochondrial genome in plants.

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Contributors: Cuenca Navarro, A., Petersen, G., Seberg, O., Jahren, A. H.
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Scopus rating (2017): CiteScore 1.91 SJR 0.911 SNIP 0.634
Web of Science (2017): Impact factor 1.957
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.79 SJR 1.182 SNIP 0.627
Web of Science (2016): Impact factor 2.434
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.5 SJR 0.977 SNIP 0.475
Web of Science (2015): Impact factor 1.847
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.57 SJR 0.956 SNIP 0.571
Web of Science (2014): Impact factor 1.68
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.85 SJR 1.088 SNIP 0.56
Web of Science (2013): Impact factor 1.863
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.32 SJR 1.384 SNIP 0.746
Web of Science (2012): Impact factor 2.145
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.43 SJR 1.321 SNIP 0.738
Web of Science (2011): Impact factor 2.274
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
DNA Damage in Plant Herbarium Tissue

Dried plant herbarium specimens are potentially a valuable source of DNA. Efforts to obtain genetic information from this source are often hindered by an inability to obtain amplifiable DNA as herbarium DNA is typically highly degraded. DNA post-mortem damage may not only reduce the number of amplifiable template molecules, but may also lead to the generation of erroneous sequence information. A qualitative and quantitative assessment of DNA post-mortem damage is essential to determine the accuracy of molecular data from herbarium specimens. In this study we present an assessment of DNA damage as miscoding lesions in herbarium specimens using 454-sequencing of amplicons derived from plastid, mitochondrial, and nuclear DNA. In addition, we assess DNA degradation as a result of strand breaks and other types of polymerase non-bypassable damage by quantitative real-time PCR. Comparing four pairs of fresh and herbarium specimens of the same individuals we quantitatively assess post-mortem DNA damage, directly after specimen preparation, as well as after long-term herbarium storage. After specimen preparation we estimate the proportion of gene copy numbers of plastid, mitochondrial, and nuclear DNA to be 2.4-3.8% of fresh control DNA and 1.0-1.3% after long-term herbarium storage, indicating that nearly all DNA damage occurs on specimen preparation. In addition, there is no evidence of preferential degradation of organelle versus nuclear genomes. Increased levels of C -> T/G -> A transitions were observed in old herbarium plastid DNA, representing 21.8% of observed miscoding lesions. We interpret this type of post-mortem DNA damage-derived modification to have arisen from the hydrolytic deamination of cytosine during long-term herbarium storage. Our results suggest that reliable sequence data can be obtained from herbarium specimens.

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Journal: P L o S One
Volume: 6
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ISSN (Print): 1932-6203
Ratings:
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Are substitution rates and RNA editing correlated?

General information
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Organisations: University of Copenhagen
Contributors: Cuenca Navarro, A., Petersen, G., Seberg, O., davis, J. I., Stevenson, D. W.
Number of pages: 15
Publication date: 2010
Peer-reviewed: Yes
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Phylogeny and evolution of morphological characters in tribe Chamaedoreeae (Arecaceae)

Within the palm family, molecular analyses have resulted in a need to re-evaluate characters previously considered useful to establish hypotheses of relationships among groups. Recent phylogenetic analyses of tribe Chamaedoreeae have shown that characters traditionally used as strong indicators of relationships, such as presence of solitary flowers and dioecy, are homoplasious within this tribe. In the largest genus, Chamaedorea, published molecular analyses recover well-supported groups not previously proposed based on morphological characters and at the same time resolve some of the current subgenera as polyphyletic. In this study we further explore the phylogenetic relationships in Chamaedoreeae and search for morphological synapomorphies for the monophyletic groups recovered. Phylogenetic analyses of morphological, nuclear (PRK, RPB2), and plastid (matK, ndhF, trnD-trnT, rps16 intron, trnL-trnF) data are performed and morphological characters are subsequently optimized on the resulting topologies. Although most of the morphological characters included are highly homoplasious, the inclusion of morphological characters in the phylogenetic analyses improves the resolution within Chamaedoreeae, particularly among species of Chamaedorea. With the exception of Synechanthus and Wendlandiella, all the genera and subgenera in Chamaedoreeae are defined by a combination of homoplasious characters, none of which is unique within the tribe. Two of the seven subgenera of Chamaedorea included in our analyses, C. subg. Eleutheropetalum and subg. Stephanostachys, are supported as monophyletic with a number of morphological synapomorphies also used in the original descriptions of these subgenera. Some morphological characters not used in the traditional subgeneric classification of Chamaedorea, such as leaf sheath structure and pistillode, gynoecium and filament connation, though homoplasious, are resolved as synapomorphies and, therefore, potentially useful when defining subgenera within this genus.
A dated phylogeny of the palm tribe Chamaedoreeae supports Eocene dispersal between Africa, North and South America

The palm tribe Chamaedoreeae reaches its higher diversity in Central America, however, its distribution ranges from the north eastern part of Mexico to Bolivia with a disjunction to the Mascarene Islands in the Indian Ocean. The disjunct distribution of Chamaedoreeae is generally considered a result of Gondwana vicariance and extinction from Africa and/or Madagascar. However, latitudinal migrations and their role in shaping the distribution of this tribe in the Americas have been largely overlooked. In this study we used seven plastid and two nuclear DNA regions to investigate the phylogenetic relationships and biogeography of the Chamaedoreeae. The resulting phylogeny fully resolved the generic relationships within the tribe. The exact area of origin of the tribe remains uncertain, but dating analyses indicated an initial diversification of the Chamaedoreae during the Early Eocene, followed by long distance dispersion to the Mascarene Islands in the late Miocene. The radiation of Hyophorbe could have taking place on islands in the Indian Ocean now submerged, but its former presence in Africa or Madagascar cannot be ruled out. At least two independent migrations between North and South America predating the rise of the Panama isthmus need to be postulated to explain the distribution of Chamaedoreae, one during the Middle Eocene and a second during the Miocene. Whereas the traditional interpretation of distribution of Chamaedoreeeae species assumes a west Gondwana origin of the group, the findings presented in this paper make it equally possible to interpret the group as a primarily boreotropical element. (C) 2007 Elsevier Inc. All rights reserved.
Phylogeny of the palm tribe Chamaedoreeae (Arecaceae) based on plastid DNA sequences

This study presents the first phylogenetic analysis of tribe Chamaedoreeae (Arecaceae), using parsimony and Bayesian analyses of plastid DNA sequences (matK, rps16 intron, 3' region of ndhF, and trnD-trnT). The tribe includes more than 115 species, and has a disjunct distribution with four genera in Central and South America and one genus in the Mascarene Islands. While the placement of Chamaedoreeae within Arecaceae has been controversial, the monophyly of this tribe is well supported by plastid DNA sequence data. All genera in Chamaedoreeae are resolved as monophyletic with high support, but relationships among genera are not fully resolved. The placement of Hyophorbe and the monotypic Wendlandiella as sisters to the remaining genera indicates that solitary flowers and dioecy arose at least twice within this tribe, once in Wendlandiella and once in Chamaedorea. Although a low substitution rate of palm plastic, DNA has been widely noted, the results of this study show high resolution at the species level, especially within the largest genus, Chamaedorea, indicating that plastid DNA is useful for the inference of relationships at low taxonomic levels in some groups of palms.

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Long-distance colonization, isolation by distance, and historical demography in a relictual Mexican pinyon pine (Pinus nelsonii Shaw) as revealed by paternally inherited genetic markers (cpSSRs)

Pinus nelsonii is a relictual pinyon pine distributed across a wide altitudinal range in semiarid zones in Mexico near the border between the States of Nuevo Leon and Tamaulipas. It also occurs in small patches in the State of San Luis Potosi. Pinus nelsonii is classified in the monotypic subsection Nelsoniae, separated from other pinyon pines (subsection Cembroides), because it possesses several distinctive characters including persistent fascicle sheaths, connate needles, and a distinctive wood anatomy. In the present study, chloroplast simple sequence repeats (cpSSRs) were used to estimate genetic variation in most known populations (nine) of P. nelsonii. The genetic variation (H (T) = 0.73; 27 haplotypes in 256 individuals) is moderate when compared to other pine species. Population differentiation ranged between low and moderate (F (ST) = 0.13 and R (ST) = 0.05), as did the Nei and Goldstein genetic distances between populations. However, this pattern varied depending on whether the infinite alleles or stepwise mutation model was used. In the former case a significant isolation by distance was found, but not in the latter. A significant association between geographical and genetic structure in one clade, through a nested clade analysis, was found, which suggested long-distance colonization between 125,000 and 309,000 years ago. We found weak evidence for a population expansion. A mismatch distribution suggests that P. nelsonii populations underwent an expansion 4.25 times their size between 59,000 and 146,000 years ago. On the other hand, the populations’ star-like phylogeny and a slight parabolic relationship between coalescence times and lineage number also suggest weak population expansion. Overall, this species appears to have been in demographic stasis for a large proportion of the time detected by the markers used.

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Comparative genetic structure in pines: evolutionary and conservation consequences

Pines have been the focus of several studies that estimate population genetic parameters using both allozymes and chloroplast single sequence repeats (SSRs). Also, the genus has also been recently studied using molecular systematics so that we now have a more clear understanding of their evolutionary history. With this background we studied comparatively the genetic structure in pines. Expected heterozygosity is particularly constant with a 99% confidence interval between 0.19 and 0.23 in species that have been studied until now using allozymes. There is a significant
proportion of species (9/41) that show high population differentiation estimates (F-ST = or larger than 0.15) and five of these have large and wingless seeds probably associated with low densities, bird dispersal mechanisms and resistance to water stress. These species include the North American pinyon pines. Outcrossing rates are also constant among species from both subgenus Pinus and subgenus Strobits, which probably reflects a selective limit to the amount of deleterious alleles that can be maintained in pine species and this also affects inbreeding levels. We also explored the data published using microsatellites in pines and conclude that these markers uncover a higher proportion of variation and genetic differentiation as expected and that the evolutionary models that are used to derive the population genetic structure estimators should take into account other sources of mutation (point mutations, larger insertions and or deletions and duplications) to better understand the comparative applications of these molecular markers.