

Supplementary Materials

Biores Comm. January 2015. 1(1), 01-10.

Corchorus L. and Hibiscus L.: Molecular Phylogeny Helps to Understand Their Relative Evolution and Dispersal Routes

Arif Mohammad Tanmoy¹, Md. Maksudul Alam^{1,2}, Mahdi Muhammad Moosa^{1,3}, Ajit Ghosh^{1,4}, Waise Quarni^{1,5}, Farzana Ahmed¹, Nazia Rifat Zaman¹, Sazia Sharmin^{1,6}, Md. Tariqul Islam¹, Md. Shahidul Islam^{1,7}, Kawsar Hossain¹, Rajib Ahmed¹ and Haseena Khan^{1*}

¹Molecular Biology Lab, Department of Biochemistry and Molecular Biology, University of Dhaka, Dhaka 1000, Bangladesh.

²Department of Molecular and Cell Biology, Center for Systems Biology, University of Texas at Dallas, Richardson, TX 75080, USA.

³Graduate Studies in Biological Sciences, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA. ⁴Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, Aruna Asaf Ali Marg, New Delhi 110067, India.

⁵Department of Pathology and Cell Biology, University of South Florida, 12901 Bruce B. Downs Blvd., Tampa, FL 33612, USA.

⁶Department of Kidney Development, Institute of Molecular Embryology and Genetics, Kumamoto University, 2-2-1 Honjo, Kumamoto 860-0811, Japan. ⁷Breeding Division, Bangladesh Jute Research Institute (BJRI), Dhaka 1207, Bangladesh.

Suppl.1: GeneBank Accessions for all species

<u>IGS1</u>		<u>IGS1</u>	
<u>Species name</u>	<u>Accessions</u>	<u>Species name</u>	<u>Accessions</u>
<i>Corchorus olitorius</i>	JQ609257.1	<i>Tarasa capitata</i>	AY187656.1
<i>Corchorus fascicularis</i>	FJ624205.1	<i>Tarasa cerratae</i>	AY187658.1
<i>Corchorus aestuans</i>	JQ609256.1	<i>Tarasa corrugata</i>	AY187660.1
<i>Corchorus capsularis</i>	JQ609258.1	<i>Tarasa geranioides</i>	AY187661.1
<i>Corchorus siliquosus</i>	FJ624202.1	<i>Tarasa heterophylla</i>	AY187662.1
<i>Corchorus tridens</i>	FJ624201.1	<i>Tarasa humilis</i>	AY187663.1
<i>Corchorus trilocularis</i>	FJ624200.1	<i>Tarasa latearistata</i>	AY187664.1
<i>Gossypioides kirkii</i>	AF403553.1	<i>Tarasa marinii</i>	AY187665.1
<i>Gossypium anomalum</i>	AF403547.1	<i>Tarasa meyeri</i>	AY187666.1
<i>Gossypium arboreum</i>	AF031433.1	<i>Tarasa nototrichoides</i>	AY187667.1
<i>Gossypium barbadense</i>	AF031435.1	<i>Tarasa odonellii</i>	AY187668.1
<i>Gossypium bickii</i>	AF403552.1	<i>Tarasa operculata</i>	AY187669.1
<i>Gossypium darwinii</i>	AF031438.1	<i>Tarasa pediculata</i>	AY187670.1
<i>Gossypium davidsonii</i>	AF520723.1	<i>Tarasa rhombifolia</i>	AY187671.1
<i>Gossypium hirsutum</i>	AF031434	<i>Tarasa tarapacana</i>	AY187672.1
<i>Gossypium longicalyx</i>	AF403551.1	<i>Tarasa tenella</i>	AY187673.1
<i>Gossypium mustelinum</i>	AF031437.1	<i>Tarasa tenuis</i>	AY187674.1
<i>Gossypium robinsonii</i>	AF403548.1	<i>Tarasa thyrsoides</i>	AY187675.1
<i>Gossypium schwendimanii</i>	AF520724.1	<i>Tarasa trisecta</i>	AY187676.1
<i>Gossypium somalense</i>	AF403550.1	<i>Tarasa urbaniana</i>	AY187677.1
<i>Gossypium trilobum</i>	AF520725.1		
<i>Gossypium turneri</i>	AF520726.1		
<i>Hibiscus acetosella</i>	JQ609260.1		
<i>Hibiscus cannabinus</i>	JQ609259.1		
<i>Hibiscus macrophyllus</i>	AY727279.1		
<i>Hibiscus radiatus</i>	JQ609261.1		
<i>Hibiscus sabdariffa</i> var. <i>altissima</i>	FJ624204.1		
<i>Hibiscus sabdariffa</i> var. <i>sabdariffa</i>	FJ624203.1		
<i>Hibiscus surattensis</i>	JQ609262.1		
<i>Sphaeralcea angustifolia</i>	AY187640.1		
<i>Sphaeralcea cordobensis</i>	AY187641.1		
<i>Sphaeralcea crispa</i>	AY187642.1		
<i>Sphaeralcea philippiana</i>	AY187644.1		
<i>Sphaeralcea wrightii</i>	AY187643.1		
<i>Tarasa albertii</i>	AY187652.1		
<i>Tarasa antofagastana</i>	AY187654.1		

<u>IGS2</u>	
<u>Species name</u>	<u>Accessions</u>
<i>Adansonia digitata</i>	AY328150.1
<i>Adansonia grandidieri</i>	HQ696739.1
<i>Adansonia gregorii</i>	HQ696740.1
<i>Adansonia za</i>	HQ696741.1
<i>Alcea aucheri</i>	EF679754.1
<i>Alcea excubita</i>	EF679755.1
<i>Alcea kurdica</i>	EF679757.1
<i>Alcea longipedicellata</i>	EF679758.1
<i>Alcea pallida</i>	EF419767.1
<i>Alcea rechingeri</i>	EF679760.1
<i>Alcea rhyticarpa</i>	EF679761.1
<i>Alcea rosea</i>	EF419766.1

<u>IGS2</u>		<u>IGS2</u>	
<u>Species name</u>	<u>Accessions</u>	<u>Species name</u>	<u>Accessions</u>
<i>Alcea rugosa</i>	EF679763.1	<i>Corchorus siliquosus</i>	JQ625349.1
<i>Alcea sachsachanica</i>	EF679764.1	<i>Corchorus tridens</i>	JQ625346.1
<i>Alcea schirazana</i>	EF679766.1	<i>Corchorus trilocularis</i>	JQ625347.1
<i>Alcea setosa</i>	EF679765.1	<i>Eriotheca candolleana</i>	HQ696772.1
<i>Alcea sulphurea</i>	EF679767.1	<i>Eriotheca discolor</i>	HQ696775.1
<i>Alcea tabrisiana</i>	EF679768.1	<i>Eriotheca dolichopoda</i>	HQ696773.1
<i>Alcea wilhelminae</i>	EF679769.1	<i>Eriotheca gracilipes</i>	HQ696762.1
<i>Althaea armeniaca</i>	EF679771.1	<i>Eriotheca longitubulosa</i>	HQ696771.1
<i>Althaea hirsuta</i>	EF419717.1	<i>Eriotheca obcordata</i>	HQ696774.1
<i>Althaea ludwigii</i>	EF419723.1	<i>Eriotheca pentaphylla</i>	HQ696768.1
<i>Althaea officinalis</i>	EF419727.1	<i>Eriotheca roseorum</i>	HQ696765.1
<i>Ayenia fruticosa</i>	HM488376.1	<i>Eriotheca ruizii</i>	HQ696777.1
<i>Ayenia magna</i>	HM488372.1	<i>Eriotheca squamigera</i>	HQ696776.1
<i>Ayenia microphylla</i>	HM488377.1	<i>Firmiana platanifolia</i>	AY328156.1
<i>Ayenia palmeri</i>	HM488373.1	<i>Gossypium arboreum</i>	AF031439.1
<i>Ayenia praeclara</i>	HM488371.1	<i>Gossypium hirsutum</i>	AF031440.1
<i>Bombax buonopozense</i>	HQ696742.1	<i>Gossypium mustelinum</i>	AF031443.1
<i>Bombax ceiba</i>	HQ696743.1	<i>Gossypium tomentosum</i>	AF031442.1
<i>Bombax malabaricum</i>	AY328149.1	<i>Heritiera angustata</i>	AY328155.1
<i>Byttneria biloba</i>	HM488392.1	<i>Heritiera littoralis</i>	AY328154.1
<i>Byttneria catalpifolia</i> subsp. <i>africana</i>	HM488393.1	<i>Heritiera parvifolia</i>	AY328153.1
<i>Byttneria cordifolia</i>	HM488395.1	<i>Hibiscus acetosella</i>	JQ625357.1
<i>Byttneria divaricata</i>	HM488383.1	<i>Hibiscus cannabinus</i>	JQ625353.1
<i>Byttneria implacabilis</i>	HM488390.1	<i>Hibiscus macrophyllus</i>	AY727226.1
<i>Byttneria maingayi</i>	HM488396.1	<i>Hibiscus radiatus</i>	JQ625354.1
<i>Byttneria melleri</i>	HM488398.1	<i>Hibiscus sabdariffa</i> var. <i>altissima</i>	JQ625355.1
<i>Byttneria microphylla</i>	HM488386.1	<i>Hibiscus sabdariffa</i> var. <i>sabdariffa</i>	JQ625356.1
<i>Byttneria morii</i>	HM488387.1	<i>Hibiscus surattensis</i>	JQ625358.1
<i>Byttneria oligantha</i>	HM488399.1	<i>Malva aegyptia</i>	EF419742.1
<i>Byttneria pedersenii</i>	HM488379.1	<i>Malva canariensis</i>	EF419687.1
<i>Byttneria scabra</i>	HM488380.1	<i>Malva cretica</i> subsp. <i>althaeoides</i>	EF419744.1
<i>Byttneria</i> sp. <i>C Ambriansyah</i>	HM488402.1	<i>Malva dendromorpha</i>	EF419707.1
<i>Byttneria</i> sp. <i>E Sidiyasa</i>	HM488404.1	<i>Malva linnaei</i>	EF419690.1
<i>Byttneria stenophylla</i>	HM488381.1	<i>Malva neglecta</i>	EF419702.1
<i>Byttneria uaupensis</i>	HM488400.1	<i>Malva nicaeensis</i>	EF419701.1
<i>Byttneria voulily</i>	HM488401.1	<i>Malva parviflora</i>	EF419694.1
<i>Ceiba acuminata</i>	HQ696752.1	<i>Malva sylvestris</i>	EF419698.1
<i>Ceiba aesculifolia</i>	HQ696751.1	<i>Malva trifida</i>	EF419739.1
<i>Ceiba crispiflora</i>	HQ696754.1	<i>Malva verticillata</i>	EF419703.1
<i>Ceiba pentandra</i>	HQ696753.1	<i>Microcos paniculata</i>	JN676067.1
<i>Ceiba schottii</i>	HQ696756.1	<i>Pachira aquatica</i>	AY328147.1
<i>Ceiba speciosa</i>	HQ696755.1	<i>Pachira insignis</i>	HQ696757.1
<i>Commersonia</i> aff. <i>gaudichaudii</i>	HQ656691.1	<i>Pachira macrocarpa</i>	AY328146.1
<i>Commersonia crispa</i>	HQ656703.1	<i>Pachira minor</i>	HQ696758.1
<i>Commersonia pulchella</i>	HQ656716.1	<i>Pachira quinata</i>	HQ696745.1
<i>Corchorus aestuans</i>	JQ625348.1	<i>Rulingia</i> aff. <i>dasyphylla</i>	HQ656729.1
<i>Corchorus capsularis</i>	JQ625350.1	<i>Rulingia craurophylla</i>	HQ656742.1
<i>Corchorus fascicularis</i>	JQ625345.1	<i>Rulingia cuneata</i>	HQ656744.1
<i>Corchorus olitorius</i>	JQ625351.1	<i>Rulingia hermannifolia</i>	HQ656750.1
<i>Corchorus pseudo-olitorius</i>	JQ625352.1	<i>Rulingia magniflora</i>	HQ656760.1

<u>IGS2</u>		<u>MatK</u>	
<u>Species name</u>	<u>Accessions</u>	<u>Species name</u>	<u>Accessions</u>
<i>Rulingia rugosa</i>	HQ656767.1	<i>Hibiscus sabdariffa</i> var.	JQ693596.1
<i>Sparrmannia</i> sp.	AM159158.1	<i>sabdariffa</i>	
<i>Tilia hupehensis</i>	AY328158.1	<i>Hibiscus surattensis</i>	JQ693598.1
<i>Tilia kiusiana</i>	AB006420.1	<i>Hibiscus tiliaceus</i>	AB233271.1
<i>Tilia paucicostata</i>	AY328159.1	<i>Pachira aquatica</i>	AY321170.1
<i>Triumfetta</i> cf.	AM159143.1	<i>Pachira brevipes</i>	HQ696694.1
		<i>Pachira flaviflora</i>	HQ696693.1
		<i>Pachira glabra</i>	HQ696706.1
		<i>Pachira insignis</i>	HQ696704.1
		<i>Pachira quinata</i>	HQ696692.1
		<i>Pseudobombax croizatii</i>	HQ696697.1
		<i>Pseudobombax grandiflorum</i>	HQ696698.1
		<i>Pseudobombax marginatum</i>	HQ696696.1
		<i>Sparrmannia africana</i>	AY321194.1
		<i>Tilia americana</i>	AY321191.1
<u>MatK</u>		<u>XTH</u>	
<u>Species name</u>	<u>Accessions</u>	<u>Species name</u>	<u>Accessions</u>
<i>Adansonia digitata</i>	AY321168.1	<i>Corchorus olitorius</i>	JQ693581.1
<i>Adansonia grandidieri</i>	HQ696687.1	<i>Corchorus fascicularis</i>	JQ693579.1
<i>Adansonia gregorii</i>	HQ696688.1	<i>Corchorus aestuans</i>	JQ693576.1
<i>Adansonia za</i>	HQ696689.1	<i>Corchorus siliquosus</i>	JQ693577.1
<i>Ceiba acuminata</i>	HQ696700.1	<i>Corchorus tridens</i>	JQ693580.1
<i>Ceiba aesculifolia</i>	HQ696699.1	<i>Corchorus trilocularis</i>	JQ693582.1
<i>Ceiba pentandra</i>	HQ696701.1	<i>Corchorus capsularis</i>	JQ693578.1
<i>Ceiba schottii</i>	HQ696703.1	<i>Hibiscus sabdariffa</i> var.	JQ693585.1
<i>Ceiba speciosa</i>	HQ696702.1	<i>sabdariffa</i>	
<i>Corchorus aestuans</i>	JQ693590.1	<i>Hibiscus cannabinus</i>	JQ693584.1
<i>Corchorus capsularis</i>	JQ693595.1	<i>Hibiscus acetosella</i>	JQ693583.1
<i>Corchorus fascicularis</i>	JQ693589.1	<i>Hibiscus radiates</i>	JQ693587.1
<i>Corchorus olitorius</i>	JQ693588.1	<i>Hibiscus sabdariffa</i> var. <i>altissima</i>	JQ693586.1
<i>Corchorus pseudo-olitorius</i>	JQ693591.1	<i>Gossypium hirsutum</i>	HM755452.1
<i>Corchorus siliquosus</i>	JQ693592.1	<i>Gossypium arboreum</i>	EU263006.1
<i>Corchorus tridens</i>	JQ693593.1	<i>Gossypium raimondii</i>	EU263007.1
<i>Corchorus trilocularis</i>	JQ693594.1	<i>Gossypium barbadense</i>	DQ912942.1
<i>Eriotheca candolleana</i>	HQ696718.1		
<i>Eriotheca discolor</i>	HQ696720.1		
<i>Eriotheca dolichopoda</i>	HQ696719.1		
<i>Eriotheca gracilipes</i>	HQ696708.1		
<i>Eriotheca longitubulosa</i>	HQ696717.1		
<i>Eriotheca macrophylla</i>	HQ696713.1		
<i>Eriotheca parvifolia</i>	HQ696710.1		
<i>Eriotheca pentaphylla</i>	HQ696714.1		
<i>Eriotheca pubescens</i>	HQ696709.1		
<i>Eriotheca roseorum</i>	HQ696711.1		
<i>Eriotheca ruizii</i>	HQ696721.1		
<i>Eriotheca</i> sp. Duarte	HQ696712.1		
<i>Eriotheca surinamensis</i>	HQ696715.1		
<i>Grewia biloba</i>	AY321193.1		
<i>Hibiscus acetosella</i>	JQ693599.1		
<i>Hibiscus cannabinus</i>	JQ693597.1		
<i>Hibiscus elatus</i>	AB233276.1		
<i>Hibiscus glaber</i>	AB181085.1		
<i>Hibiscus hamabo</i>	AB181099.1		
<i>Hibiscus humbertianus</i>	EF207266.1		
<i>Hibiscus pernambucensis</i>	AB233275.1		
<i>Hibiscus radiatus</i>	JQ693600.1		
<i>Hibiscus sabdariffa</i> var. <i>altissima</i>	JQ693601.1		

Suppl.2: ITS_Distance within genera

Title: ITS
 Description
 Analysis
 Analysis ----- Distance Estimation
 Scope ----- Within group average
 Estimate Variance
 Variance Estimation Method ---- Bootstrap method
 No. of Bootstrap Replications - 1000
 Substitution Model
 Substitutions Type ----- Nucleotide
 Model/Method ----- Kimura 2-parameter model
 Substitutions to Include ----- d: Transitions + Transversions
 Rates and Patterns
 Rates among Sites ----- Gamma Distributed (G)
 Gamma Parameter ----- 1.8
 Pattern among Lineages ----- Same (Homogeneous)
 Data Subset to Use
 Gaps/Missing Data Treatment --- Pairwise deletion
 No. of Sites : 1037
 d : Estimate
 S.E : Standard error

d	S.E
Althaea	0.009 0.003
Corchorus	0.053 0.005
Hibiscus	0.101 0.009
Hoheria	0.005 0.001
Malva	0.050 0.005
Tilia	0.024 0.004
Pseudocorchorus	0.077 0.008
Triumfetta	0.070 0.008
Sparrmannia	0.008 0.003

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Kimura 2-parameter model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1.8). The analysis involved 57 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1037 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2]. The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.

1. Kimura M. (1980). A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16:111-120.

2. Tamura K., Stecher G., Peterson D., Filipowski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately (www.megasoftware.net). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.

Suppl.3: XTH_Distance within genera

Title: XTH
 Description
 Analysis
 Analysis ----- Distance Estimation
 Scope ----- Within Group average
 Estimate Variance
 Variance Estimation Method ----- Bootstrap method
 No. of Bootstrap Replications ----- 1000
 Substitution Model
 Substitutions Type ----- Nucleotide
 Model/Method ----- Tamura 3-parameter model
 Substitutions to Include ----- d: Transitions + Transversions
 Rates and Patterns
 Rates among Sites ----- Gamma Distributed (G)
 Gamma Parameter ----- 1.6
 Pattern among Lineages ----- Same (Homogeneous)
 Data Subset to Use
 Gaps/Missing Data Treatment ----- Pairwise deletion
 Codons Included ----- 1st+2nd+3rd+Non-Coding
 No. of Sites : 648
 d : Estimate
 S.E : Standard error

d	S.E
Corchorus	0.099 0.009
Hibiscus	0.031 0.005
Gossypium	0.118 0.011

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Tamura 3-parameter model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1.6). The analysis involved 16 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 648 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2].

1. Tamura K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9:678-687.
2. Tamura K., Stecher G., Peterson D., Filipiński A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately (www.megasoftware.net). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.

Suppl.4: MatK_Distance within genera

Title: MatK
 Description
 Analysis
 Analysis ----- Distance Estimation
 Scope ----- Within group average
 Estimate Variance
 Variance Estimation Method ----- Bootstrap method
 No. of Bootstrap Replications ----- 1000
 Substitution Model
 Substitutions Type ----- Nucleotide
 Model/Method ----- Tamura 3-parameter model
 Substitutions to Include ----- d: Transitions + Transversions
 Rates and Patterns
 Rates among Sites ----- Gamma Distributed (G)
 Gamma Parameter ----- 0.6
 Pattern among Lineages ----- Same (Homogeneous)
 Data Subset to Use
 Gaps/Missing Data Treatment ----- Pairwise deletion
 Codons Included ----- 1st+2nd+3rd+Non-Coding
 No. of Sites : 607
 d : Estimate
 S.E : Standard error

d	S.E.
Adansonia0.002	0.001
Ceiba0.003	0.002
Corchorus0.007	0.002
Eriotheca0.005	0.001
Hibiscus	0.010 0.002
Pachira0.006	0.002
Pseudobombax0.002	0.002

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Tamura 3-parameter model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.6). The analysis involved 53 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 607 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2]. The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.

1. Tamura K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9:678-687.

2. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately (www.megasoftware.net). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.

Suppl.5: CP-Combined_Distance within genera

Title: CP-Combined

Description

Analysis

Analysis ----- Distance Estimation

Scope ----- Within group average

Estimate Variance

Variance Estimation Method ---- Bootstrap method

No. of Bootstrap Replications - 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Tamura 3-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Gamma Distributed (G)

Gamma Parameter ----- 0.6

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment --- Pairwise deletion

No. of Sites : 2893

d : Estimate

S.E : Standard error

d	S.E
Corchorus0.026	0.002
Gossypium0.035	0.003
Hibiscus 0.015	0.002
Sphaeralcea0.017	0.003
Tasara0.011	0.001
Adansonia0.002	0.001
Alcea0.005	0.002
Althaea0.012	0.004
Ayenia0.015	0.004
Bombax0.003	0.002
Byttneria0.016	0.004
Ceiba0.003	0.001
Eriotheca0.009	0.001
Heritiera0.000	0.000
Malva0.010	0.003
Pachira0.006	0.001
Rulingia0.007	0.002
Tilia0.010	0.004
Pseudobombax0.002	0.002

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Tamura 3-parameter model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.6). The analysis involved 168 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 2893 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2]. The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.

1. Tamura K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9:678-687.

2. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately (www.megasoftware.net). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.

Suppl.6: All-Combined_Distance within genera

Title: All-combined

Description

Analysis

Analysis ----- Distance Estimation

Scope ----- Within group average

Estimate Variance

Variance Estimation Method ---- Bootstrap method

No. of Bootstrap Replications - 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Tamura 3-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment --- Pairwise deletion

No. of Sites : 7791

d : Estimate

S.E : Standard error

d	S.E
Altheca	0.009 0.003
Corchorus	0.042 0.002
Hibiscus	0.027 0.002
Hoheria	0.005 0.001
Malva	0.030 0.003
Tilia	0.022 0.004
Psuedocorchorus	0.084 0.010
Triumfetta	0.076 0.009
Sparrmannia	0.008 0.003
Gossypium	0.038 0.004

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Tamura 3-parameter model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.6). The analysis involved 85 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 4578 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2]. The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.

1. Tamura K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9:678-687.

2. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately (www.megasoftware.net). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.