Supplementary Table S1. Percentage inhibition of DPPH free radical by *Eugenia* extracts. Data are represented as Mean±SD of triplicate determinations (n=3). Values in same row or column with different letters are significantly different (P<0.05).

Eugenia species	Solvent systems / % inhibition / 100 μL crude extract						
	DCM only	DCM:MeOH	MeOH only				
<i>E</i> .spp (big leaves)	$19.73\pm0.16_{\rm f}$	$91.88\pm0.02_d$	$93.49\pm0.01_c$				
E.crassipetala	$91.50\pm0.05_d$	$95.28\pm0.02_{ab}$	$95.02\pm0.02_{ab}$				
E. kanakana	$7.85\pm0.23_h$	$93.69 \pm 0.04_{c}$	$94.06 \pm 0.02_{bc}$				
<i>E</i> .spp(small leaves)	$12.96\pm0.11_g$	$95.50 \pm 0.02_{a}$	$94.56 \pm 0.02_{abc}$				
E. tinifolia	$77.29\pm0.02_e$	$95.02\pm0.02_{ab}$	$95.11 \pm 0.02_{ab}$				

Supplementary Table S2. MIC values for *Eugenia* species extracts against *Escherichia coli*, *Proteus mirabilis* and *Staphylococcus aureus*.

	MIC (mg/mL)								
Bacteria	Escherichia coli		Proteus mirabilis			Staphylococcus aureus			
Extracts	DCM	Н	Μ	DCM	Η	Μ	DCM	Н	Μ
<i>E</i> . spp (big leaves)	2.53	3.14	3.13	2.53	3.14	6.25	0.63	1.57	1.56
E.crassipetala	2.61	3.15	1.56	2.61	3.15	3.13	1.31	1.57	1.56
E.kanakana	2.21	3.13	6.26	0.55	3.13	6.26	0.55	3.13	3.13
<i>E</i> .spp (small leaves)	3.42	3.14	3.13	0.86	6.27	6.26	0.43	1.57	3.13
E.tinifolia	2.98	3.13	1.57	5.96	6.25	6.28	0.74	0.78	0.78
Chloramphenicol	3.13		6.25		1.56				

DCM.: DCM crude extract, H: Hexane fraction, M: Methanol fraction

Primer	ner Sequence Number of			er of	%		
	5'→3'	Markers Used	Monomorphic markers	Polymorphic markers	polymorphism		
OPA-10	GTGATCGCAG	15	0	11	73.3		
OPD-02	GGACCCAACC	7	2	4	57.1		
OPD-13	GGGGTGACGA	10	0	2	20.0		
OPP-20	GACCCTAGTC	11	0	2	18.2		
OPL-05	ACGCAGGCAC	20	0	16	80.0		
OPB-11	GTAGACCCGT	6	0	3	50.0		
OPW-04	CAGAAGCGGA	11	0	1	9.1		
OPA-19	CCAACGTCGG	28	1	16	57.1		
OPA-04	AATCGGGCTG	17	1	8	47.1		
OPA-02	TGCCGAGCTG	14	1	9	64.3		
OPA-12	TCGGCGATAG	15	1	7	46.7		
OPA-11	CCATCGCCGT	26	0	15	57.7		
OPA-08	GTGACGTAGG	14	0	11	78.6		
OPH-04	GGAAGTCGCC	9	0	6	66.7		
OTH-04 ODAA01COCC 9 0 6 60.7							

Supplementary Table S3. RAPD markers and polymorphism.

Statistical Analysis	Source	Significance (P value)	Correlation coefficient, r <sub>s</sub>	R <sup>2</sup> value (Excel)
Spearman's correlation coefficient	TFC and DPPH inhibition	0.041	0.533	0.3445
	TPC and DPPH inhibition	0.026	0.570	0.6750

## Spearman's correlation coefficient for TFC and/or TFC and DPPH percentage inhibition.

Average genetic dissimilarity (estimated as genetic distance) among the five *Eugenia* species using the 9 RAPD primers and 3 ISSR primers. Range of genetic distances estimated was from 48.6 to 100% (to 3 s.f.). Maximum genetic distances (100%) were estimated between *E. kanakana* and *E. tinifolia* while 48.6% genetic distance was estimated between *E.*spp (big leaves) and *E.*spp (small leaves).

	<i>E</i> .spp (big leaves)	E. crassipetala	E. kanakana	<i>E</i> .spp (small leaves)
E. crassipetala	0.9695			
E. kanakana	0.8094	0.8540		
<i>E</i> .spp (small leaves)	0.4863	0.8240	0.6420	
E. tinifolia	0.8540	0.6774	0.999	0.9013



## Total Flavonoid Content in the Eugenia species

Supplementary Figure S1. Total flavonoid content in the *Eugenia* spp. crude extracts with respect to the different solvent systems (Data presented in QE  $\mu$ g/g FW, standard error included as Y error bars, n=3). Bar charts with different letters are significantly different (P<0.05).



Supplementary Figure S2. Total phenolics content in the *Eugenia* spp. crude extract with respect to the different solvent systems (Standard error included as Y error bars). (Data presented in GAE  $\mu$ g/g FW, standard error included as Y error bars, n=3). Bar charts with different letters are significantly different (P<0.05).



Supplementary Figure S3. Banding pattern produced from DNA amplification using RAPD primers OPD-13 and OPP-20 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S4. Banding pattern produced from DNA amplification using RAPD primers OPL-05 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S5. Banding pattern produced from DNA amplification using RAPD primers OPB-11 and OPW-04 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S6. Banding pattern produced from DNA amplification using RAPD primers OPA-19 and OPA-04 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S7. Banding pattern produced from DNA amplification using RAPD primers OPA-02 and OPA-12 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S8. Banding pattern produced from DNA amplification using RAPD primers OPA-11 and OPA-08 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S9. Banding pattern produced from DNA amplification using RAPD primers OPH-04 and OPC-08 with lanes labelling shown in the textbox beside. Hyperladder II (Bioline) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S10. Banding pattern produced from DNA amplification using ISSR primer ISSR-2 with lanes labelling shown in the textbox beside. Hyperladder (All-purpose HI-LO DNA marker) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S11. Banding pattern produced from DNA amplification using ISSR primer ISSR-3 and ISSR-4 with lanes labelling shown in the textbox beside. Hyperladder (All-purpose HI-LO DNA marker) was used and double sterilised water used as negative control (-ve control).



Supplementary Figure S12. Dendogram illustrating genetic relatedness among the five endemic *Eugenia* species of Mauritius generated by the UPGMA cluster calculated from 156 RAPD markers and 48 ISSR markers.