

**TITLE: EVOLUTION OF TRYPTOPHAN BIOSYNTHETIC PATHWAY IN MICROBIAL GENOMES: A COMPARATIVE GENETIC STUDY**

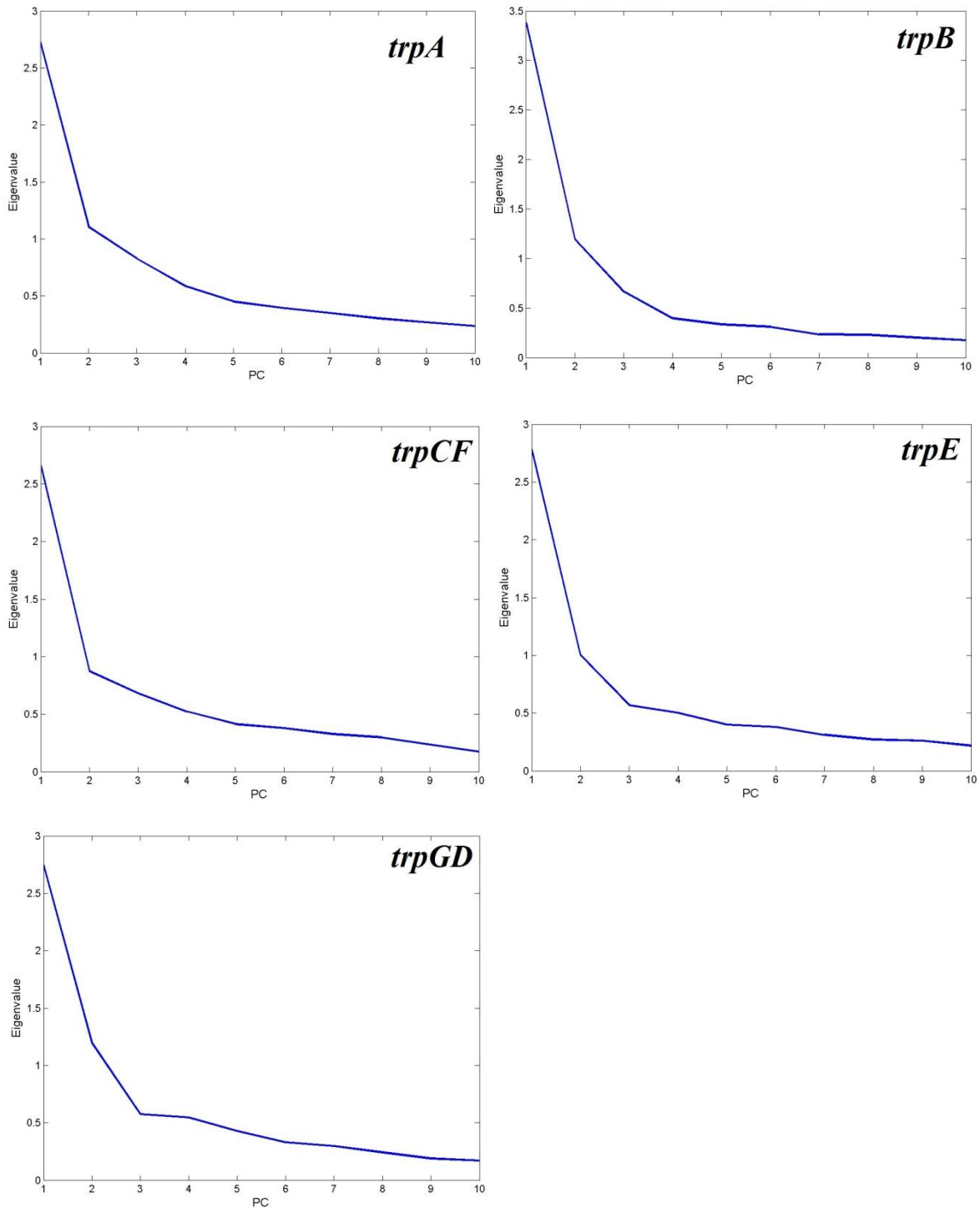
Journal: Systems and Synthetic Biology

AUTHORS: PRIYA V K<sup>1</sup>, SUSMITA SARKAR<sup>1</sup> AND SOMDATTA SINHA<sup>2</sup>

AFFILIATION: <sup>1</sup> Csir-Centre For Cellular And Molecular Biology, Uppal Road, Hyderabad, India.

<sup>2</sup> Indian Institute Of Science Education & Research Mohali, Punjab, India

Email: [ssinha@iisermohali.ac.in](mailto:ssinha@iisermohali.ac.in); [somdattasinha@gmail.com](mailto:somdattasinha@gmail.com)



**Fig 1.** Scree plots of Principal Component Analysis of the normalized RSCU values of Tryptophan biosynthesis pathway genes

**Table S2.1:** Percentage variance explained

<b>PC</b>	<b><i>trpA</i></b>	<b><i>trpB</i></b>	<b><i>trpCF</i></b>	<b><i>trpE</i></b>	<b><i>trpGD</i></b>
1	35.75	45.37	38.28	39.83	39.87
2	50.26	61.4	50.87	54.16	57.2
3	61.11	70.35	60.67	62.29	65.56
4	68.79	75.66	68.2	69.46	73.48
5	74.7	80.16	74.16	75.17	79.7
6	79.9	84.33	79.63	80.6	84.5
7	84.5	87.49	84.36	85.07	88.82
8	88.48	90.57	88.66	88.95	92.34
9	92	93.28	92.08	92.68	95.09
10	95.11	95.64	94.61	95.81	97.58
11	96.89	97.4	96.4	97.41	98.87
12	98.48	98.51	98	98.69	99.54
13	99.4	99.4	99.06	99.61	100
14	100	100	100	100	100

**Table S2.2:** Loadings of *trpA* on the first three PCs. Bold numbers show loadings > 0.2.

<i>trpA</i>									
		1	2	3			1	2	3
<b>Phe</b>	<b>UUU</b>	<b>0.22213</b>	-0.1431	0.01677	<b>Ala</b>	<b>GCU</b>	<b>0.21827</b>	0.05967	-0.0831
	<b>UUC</b>	-0.164	0.13497	0.1825		<b>GCC</b>	-0.1505	-0.0592	0.01339
<b>Leu</b>	<b>UUA</b>	0.19206	-0.1769	-0.1186		<b>GCA</b>	0.11602	-0.0181	0.18508
	<b>UUG</b>	0.05697	-0.0565	0.16603	<b>GCG</b>	-0.0725	-0.1454	0.13256	
	<b>CUU</b>	0.07019	0.07409	0.14199	<b>Tyr</b>	<b>UAU</b>	0.15464	-0.1234	-0.0118
	<b>CUC</b>	-0.0395	0.17104	0.1501		<b>UAC</b>	-0.0838	0.05901	0.13511
	<b>CUA</b>	0.05131	0.00618	-0.0393	<b>His</b>	<b>CAU</b>	0.00682	-0.0815	<b>0.41502</b>
	<b>CUG</b>	-0.1737	0.04005	<b>0.21164</b>		<b>CAC</b>	-0.0016	-0.0396	<b>-0.3702</b>
<b>Ile</b>	<b>AUU</b>	0.18067	<b>-0.2225</b>	0.08065	<b>Gln</b>	<b>CAA</b>	0.16916	<b>-0.2517</b>	-0.049
	<b>AUC</b>	-0.1171	-0.012	-0.0238		<b>CAG</b>	-0.1275	0.10507	0.17366
	<b>AUA</b>	0.14585	<b>0.28193</b>	0.0205	<b>Asn</b>	<b>AAU</b>	0.13515	<b>-0.2522</b>	0.02798
<b>Val</b>	<b>GUU</b>	<b>0.22496</b>	0.03465	0.08734		<b>AAC</b>	-0.1304	0.06982	0.04603
	<b>GUC</b>	-0.07	-0.0667	-0.0617	<b>Lys</b>	<b>AAA</b>	<b>0.21101</b>	-0.0131	0.08604
	<b>GUA</b>	0.1529	-0.0292	-0.0007		<b>AAG</b>	-0.1492	0.11573	0.01259
	<b>GUG</b>	-0.0102	0.03352	0.10226	<b>Asp</b>	<b>GAU</b>	0.13783	-0.0584	0.17943
<b>Ser</b>	<b>UCU</b>	0.11034	-0.1416	0.09229		<b>GAC</b>	-0.1148	-0.0375	0.04034
	<b>UCC</b>	-0.15	-0.0041	0.14716	<b>Glu</b>	<b>GAA</b>	0.06869	-0.1571	-0.0146
	<b>UCA</b>	0.14866	-0.0089	0.16808		<b>GAG</b>	-0.0236	0.17352	0.13088
	<b>UCG</b>	-0.1288	-0.181	-0.006	<b>Cys</b>	<b>UGU</b>	0.01401	-0.1436	<b>0.28956</b>
	<b>AGU</b>	0.11594	0.02065	-0.0257		<b>UGC</b>	-0.1657	-0.0288	-0.0724
	<b>AGC</b>	-0.0114	0.04598	-0.1703	<b>Arg</b>	<b>CGU</b>	0.04393	<b>-0.2217</b>	0.06041
<b>Pro</b>	<b>CCU</b>	0.16575	-0.0631	-0.0773		<b>CGC</b>	-0.189	<b>-0.212</b>	0.02631
	<b>CCC</b>	0.07768	0.08558	-0.1069		<b>CGA</b>	0.00624	-0.0608	-0.0051
	<b>CCA</b>	0.15199	0.11107	0.11047		<b>CGG</b>	-0.0183	-0.0436	0.17306
	<b>CCG</b>	-0.1615	-0.0789	0.12147		<b>AGA</b>	0.14971	0.06334	-0.0523
<b>Thr</b>	<b>ACU</b>	0.12784	0.07075	0.0645		<b>AGG</b>	0.13245	<b>0.33138</b>	-0.0634
	<b>ACC</b>	-0.127	-0.1484	-0.0495	<b>Gly</b>	<b>GGU</b>	0.18545	0.02791	0.13921
	<b>ACA</b>	0.10641	0.16667	0.09811		<b>GGC</b>	-0.1033	-0.1414	-0.0763
	<b>ACG</b>	-0.0125	<b>-0.2064</b>	0.11789		<b>GGA</b>	0.16746	0.16491	0.03953
				<b>GGG</b>		0.03216	0.12863	0.07755	