

Supporting Information

Microorganisms Associated with the Marine Sponge *Scopalina hapalia*: a Reservoir of Bioactive Molecules to Slow Down the Aging Process

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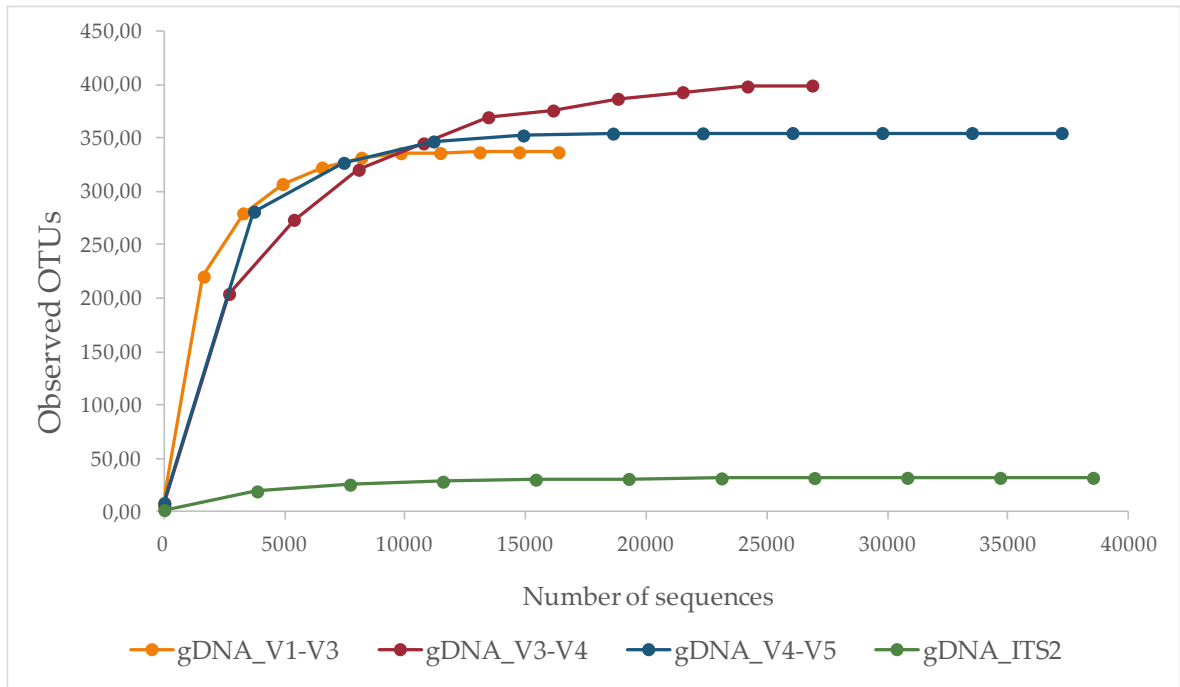


Figure S1. Rarefaction curves of observed Operational Taxonomic Units (OTUs) for each targeted genomic DNA region.

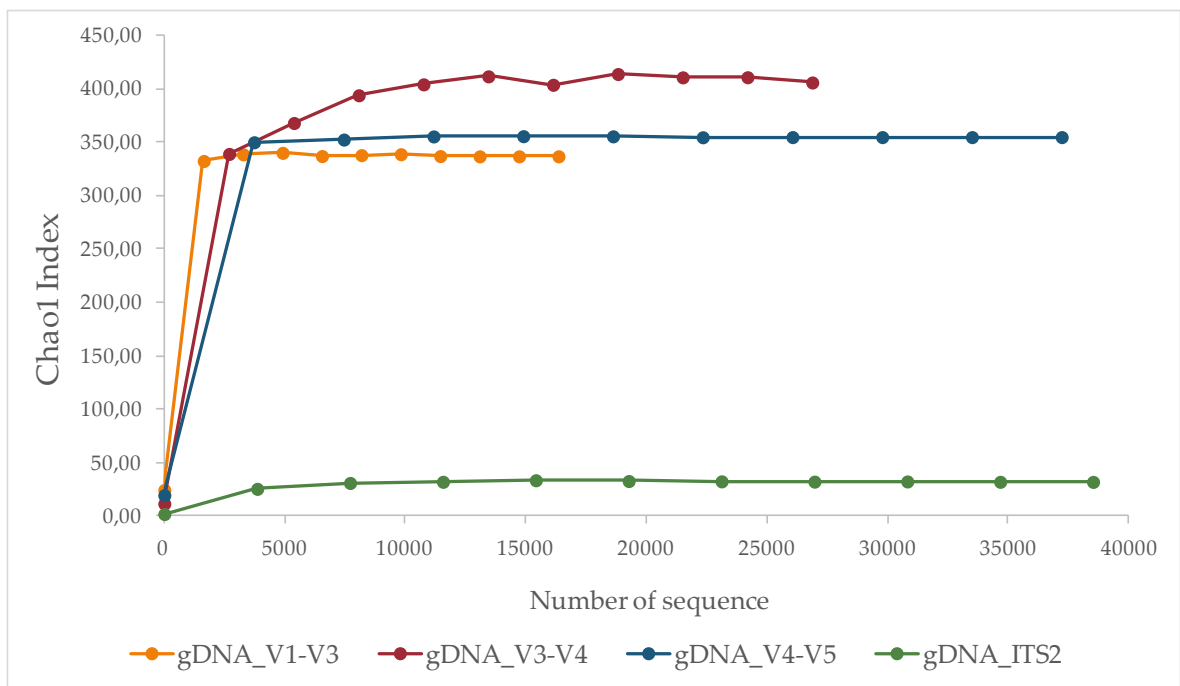


Figure S2. Rarefaction curves of Chao1 Index for each targeted genomic DNA region.

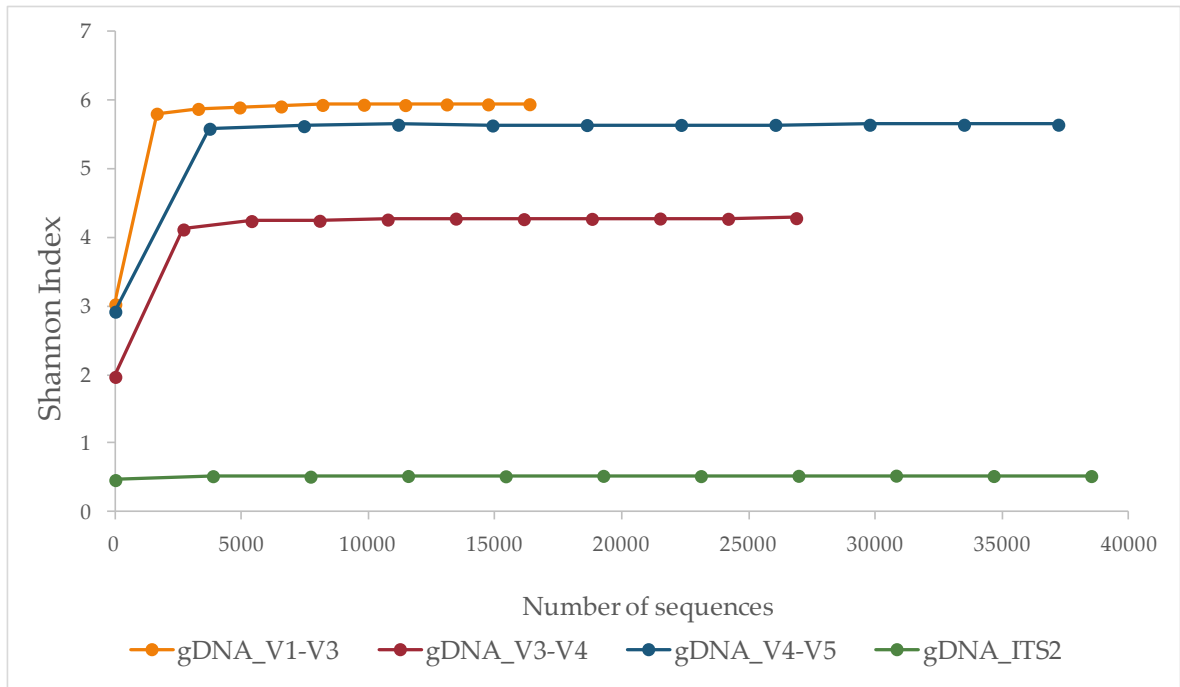


Figure S3. Rarefaction curves of Shannon Index for each targeted genomic DNA region.

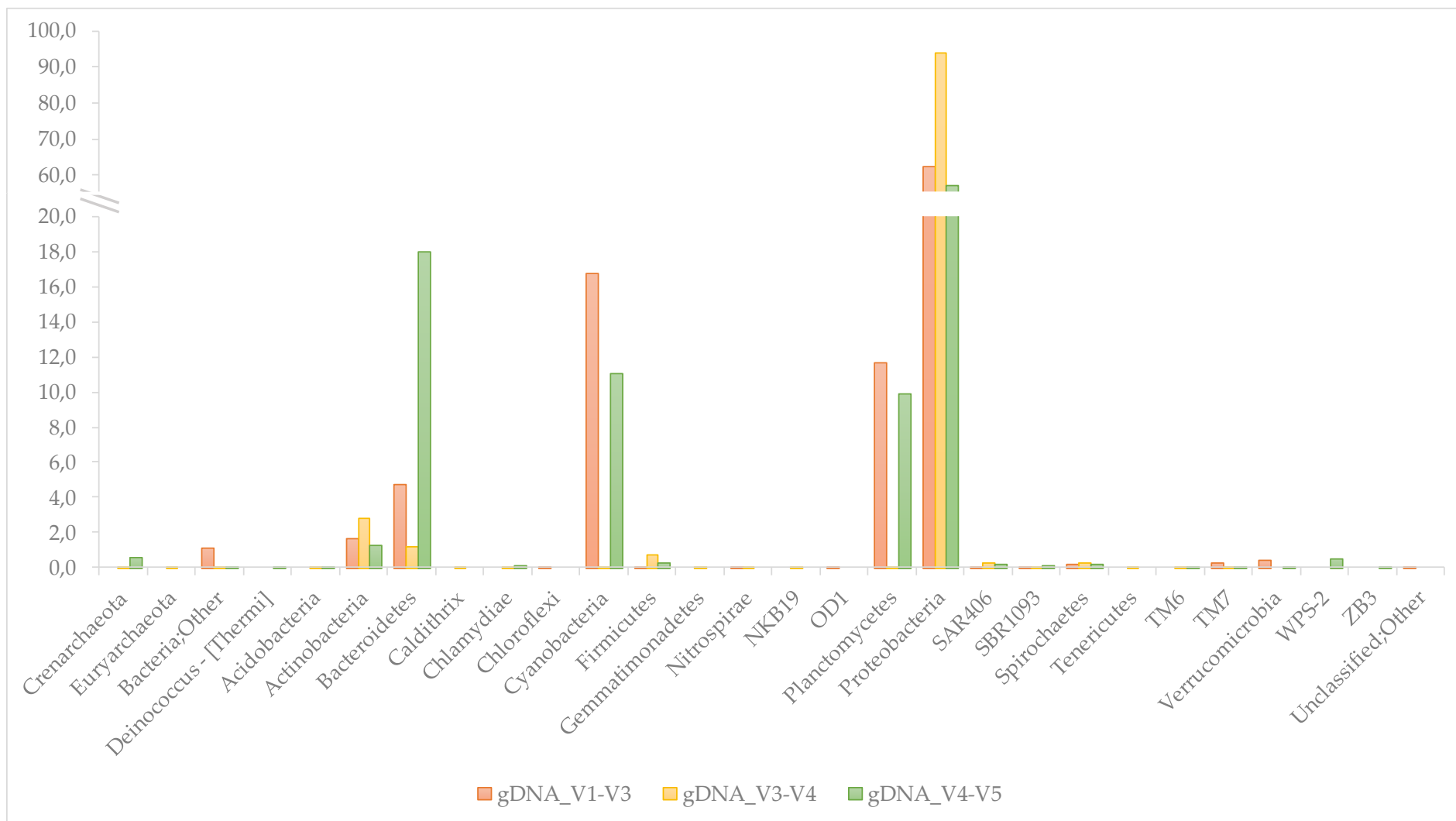


Figure S4. Phylum distribution in *Scopalina hapalia* respective with V1-V3, V3-V4 and V4-V5 data sets. The bars represent the relative abundance of 16S rRNA sequences that were assigned to a given phylum in relation to the total number of sequences in each data set.

Table S1. 16S rRNA taxonomic affiliation of 10 of the *Scopalina hapalia* associated actinomycetes.

Isolate	Isolation Medium	Class	Closest relative in EzBioCloud (Access Number)	Identity (%) ^a
SH-36	R2A	Micromonosporales	<i>Micromonospora chokoriensis</i> (LT607409)	100.0
SH-45	SCAM	Micromonosporales	<i>Salinispora arenicola</i> (AY040619)	100.0
SH-54	MBA	Micromonosporales	<i>Salinispora arenicola</i> (AY040619)	100.0
SH-57	A1BFe+c	Micromonosporales	<i>Micromonospora echinospora</i> (LT607413)	99.6
SH-78	MBA	Micromonosporales	<i>Salinispora arenicola</i> (AY040619)	100.0
SH-82	MBA	Micromonosporales	<i>Micromonospora fluostatini</i> (LC033898)	99.2
SH-89	SCAM	Micromonosporales	<i>Micromonospora citrea</i> (FMHZ01000002)	99.5
SH-95	MBA	Micromonosporales	<i>Micromonospora tulbaghia</i> (jgi.1058868)	99.3
SH-108	R2A	Micromonosporales	<i>Micromonospora endophytica</i> (EU560726)	99.5
SH-115	SCAM	Corynebacteriales	<i>Rhodococcus nanhaiensis</i> (JN582175)	99.9

^a: indicates the percent sequence similarity shared between each isolate and its nearest type strain.

Table S2. 16S rRNA taxonomic affiliation of 17 Bacillales (order) strains isolated from *Scopalina hapalia*.

Isolate	Isolation Medium	Family	Closest relative in EzBioCloud (Access Number)	Identity (%) ^a
SH-02a	A1BFe+c	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	100.0
SH-02b	A1BFe+c	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	100.0
SH-02c	A1BFe+c	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	100.0
SH-04	A1BFe+c	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.9
SH-10	LB	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	99.9
SH-22	R2A	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	100.0
SH-42	MYA2	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	99.6
SH-46	SCAM	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.9
SH-60	LB	Bacillaceae	<i>Bacillus paralicheniformis</i> (KY694465)	100.0
SH-68a	MYA2	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.8
SH-68b	MYA2	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.8
SH-99	MBA	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.8
SH-100	MBA	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.8
SH-116a	MBA	Bacillaceae	<i>Bacillus licheniformis</i> (AE017333)	99.8
SH-137	MBA	Bacillaceae	<i>Bacillus berkeleyi</i> (JN187498)	98.8
SH-32	MBA	Thermoactinomycetaceae	DQ448769_s	100.0
SH-39 ^b	MBA	Thermoactinomycetaceae	DQ448769_s	97.1

^a: indicates the percent sequence similarity shared between each isolate and its nearest type strain, ^b: represents a potential new phylotype.

Table S3. Taxonomic affiliation of the three fungal isolates from *Scopalina hapalia* after sequencing fragments containing the Internal Transcribed Spacer (ITS) region, as well as partial beta-tubulin and calmodulin genes.

Isolate	Isolation Medium	Order	Closest Relative in the in-House Sequence Database of Westerdijk Fungal Biodiversity Institute
SH-53	A1BFe+c	Trichosphaeriales	<i>Nigrospora aurantiaca</i> Mei Wang & L. Cai
SH-122	A1BFe+c	Eurotiales	<i>Aspergillus sydowii</i> (Bainier & Sartory) Thom & Church
SH-123	LB	Sordariales	<i>Chaetomium globosum</i> Kunze

