Supplementary figures

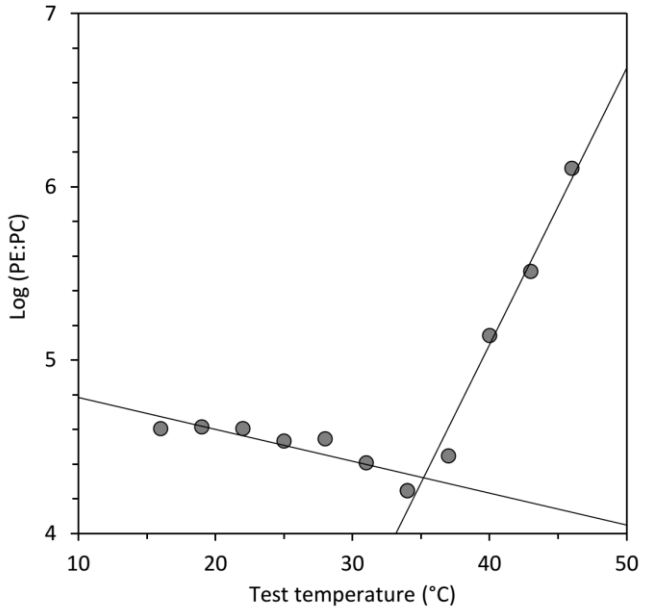

Figure S1: Example of determination of the phycobilisome (PBS) breaking temperature (T_{PBS}) of *Synechococcus* sp. MVIR-16-2 grown at 16°C. The logarithm of the phycocyanin to phycoerythrin fluorescence emission ratio (PE:PC) is related to rod phycobiliprotein coupling. The temperature at which PBS breaks down (T_{PBS}), determined in a similar way as Arrhenius calculation (Dalhoff et al. 1991, Stillman et al. 1996) constitutes a proxy for assessing phycobilisome thermostability.

References

Dahlhoff E, O'Brien J, Somero GN, & Vetter RD (1991) Temperature effects on mitochondria from hydrothermal vent invertebrates: evidence for adaptation to elevated and variable habitat temperatures. *Physiological Zoology* 64(6):1490-1508.

Stillman J & Somero G (1996) Adaptation to temperature stress and aerial exposure in congeneric species of intertidal porcelain crabs (genus Petrolisthes): correlation of physiology, biochemistry and morphology with vertical distribution. *The Journal of Expe Biol*199(8):1845-1855.

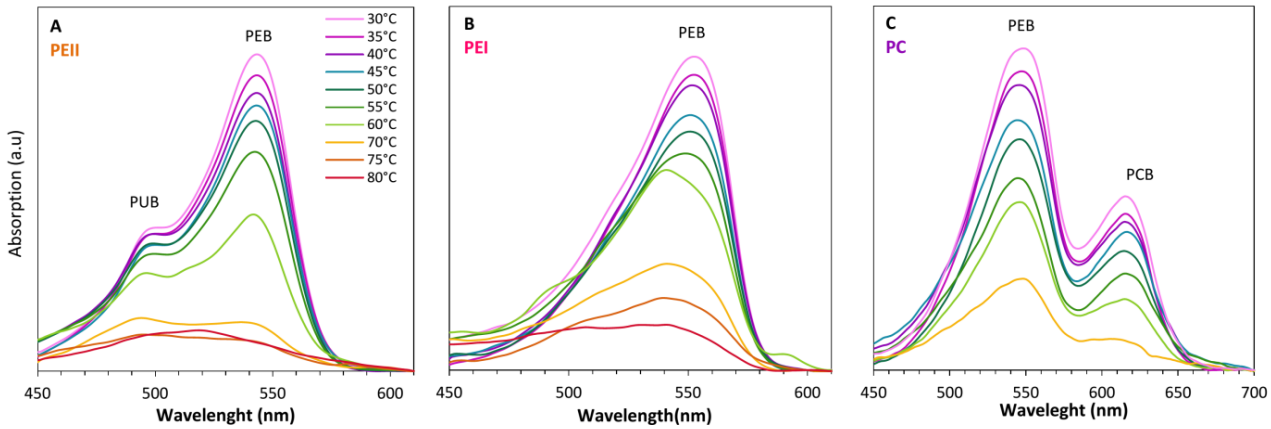

Figure S2: Absorption spectra of phycoerythrin II (PE; **A**) phycoerythrin I (**B**) and phycocyanin (PC; **C**) from the subtropical clade II *Synechococcus* sp. strain M16.1 measured over a thermal denaturation curve. PCB, Phycocyanobilin. PEB; Phycoerythrobilin; PUB: Phycourobilin.

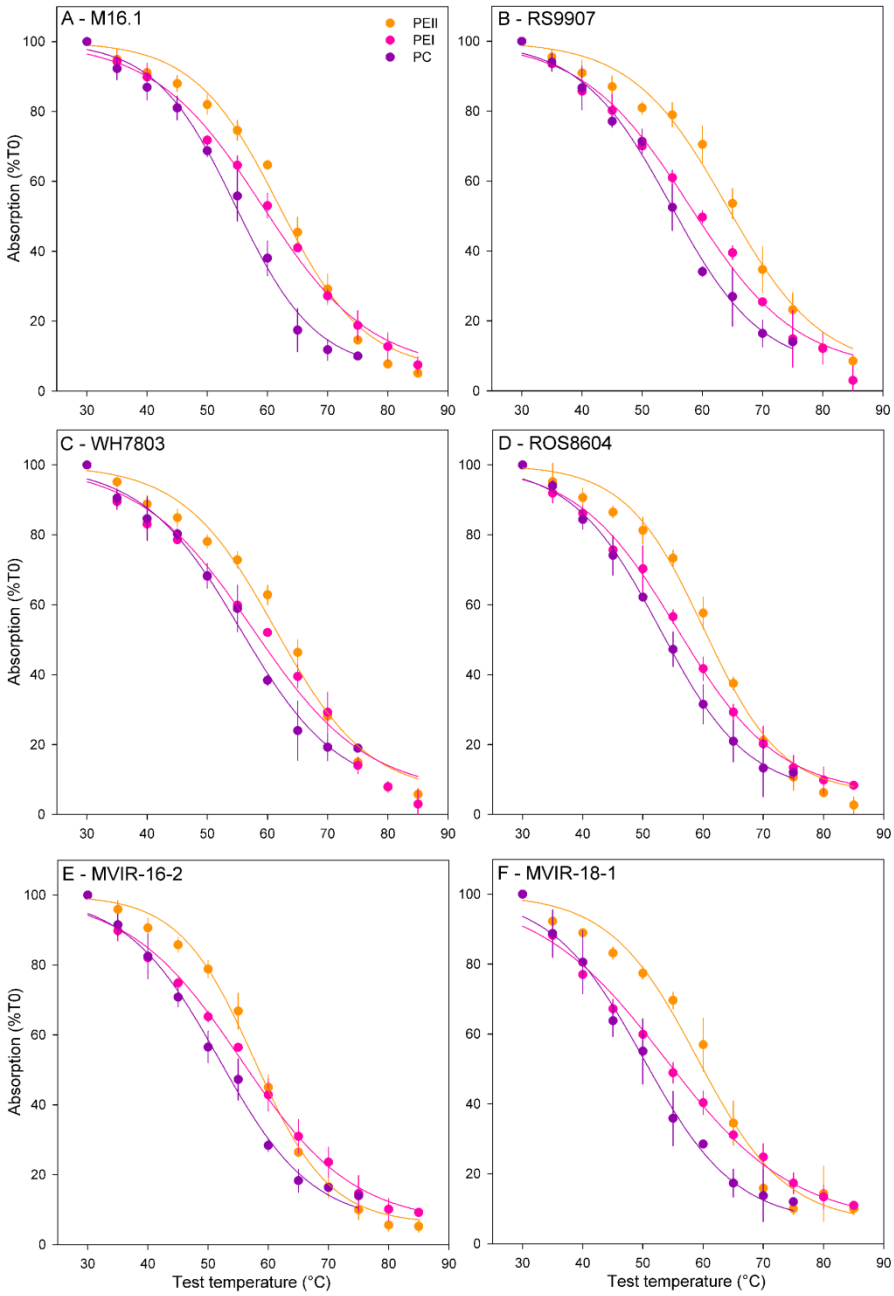

Figure S3: Temperature-induced decay of phycobiliprotein absorbance for six marine *Synechococcus* strains. Phycoerythrin II (orange), phycoerythrin I (pink) and phycocyanin (purple) absorption at 545 nm for the phycoerythrins and 620 nm for phycocyanin along thermal denaturation curves in marine *Synechococcus* spp. M16.1 (**A**), RS9907 (**B**), WH7803 (**C**), ROS8604 (**D**), MVIR-16-2 (**E**) and MVIR-18-1 (**F**). Unfolding curves allowed the calculation of $T_{50\%}$, defined as the temperature at which the phycobiliprotein has lost half of its absorption capacities. Standard deviations are calculated from the mean of three replicates.

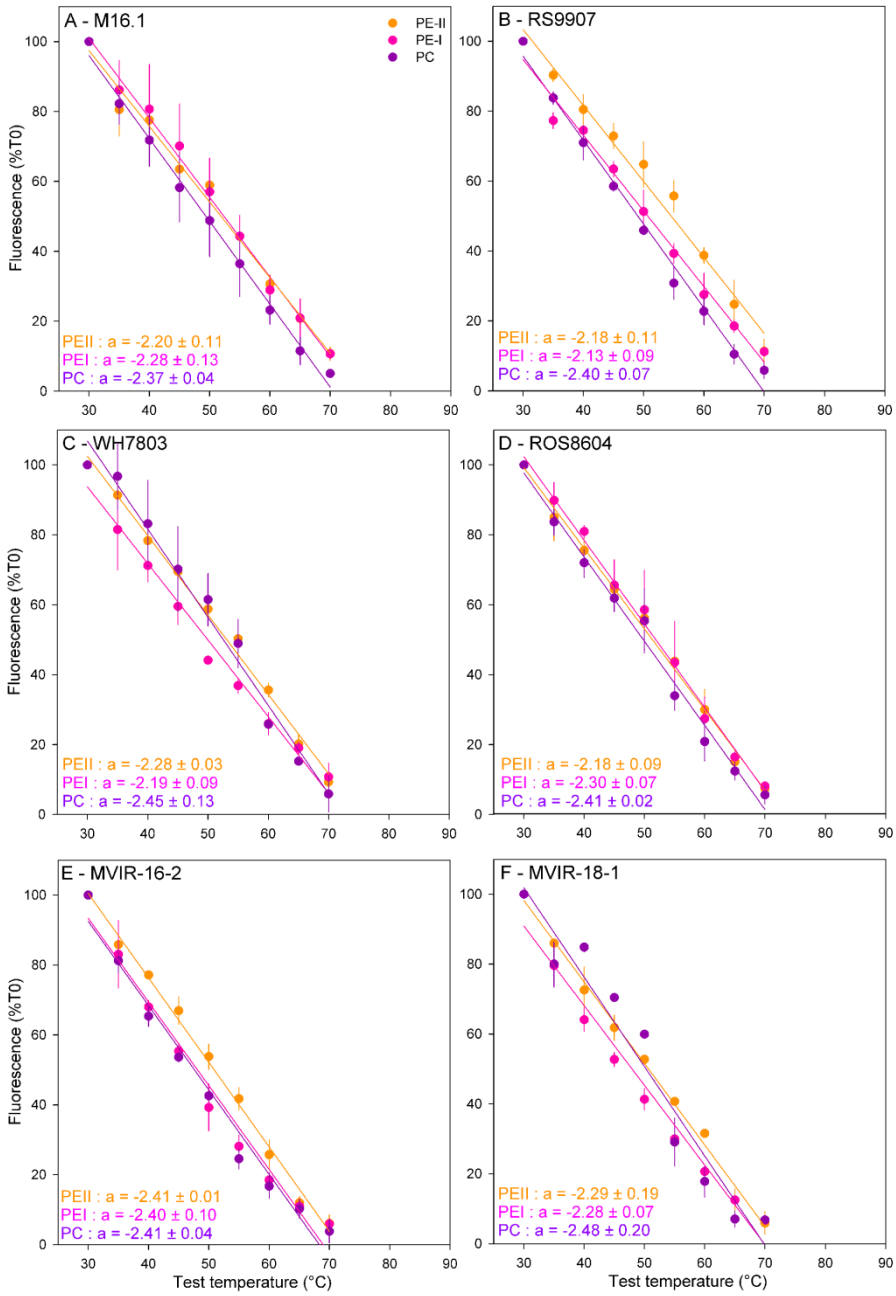

Figure S4: Variation of phycoerythrin II (orange) and I (pink) and phycocyanin (purple) fluorescence emission properties, upon excitation at 545 nm for phycoerythrins and 620 nm for phycocyanin, along thermal denaturation curves in marine *Synechococcus* spp. M16.1 (**A**), RS9907 (**B**), WH7803 (**C**), ROS8604 (**D**), MVIR-16-2 (**E**) and MVIR-18-1 (**F**). The extinction fluorescence slope for each phycobiliprotein is mentioned in inserts. Standard deviations are calculated from the mean of three replicates.

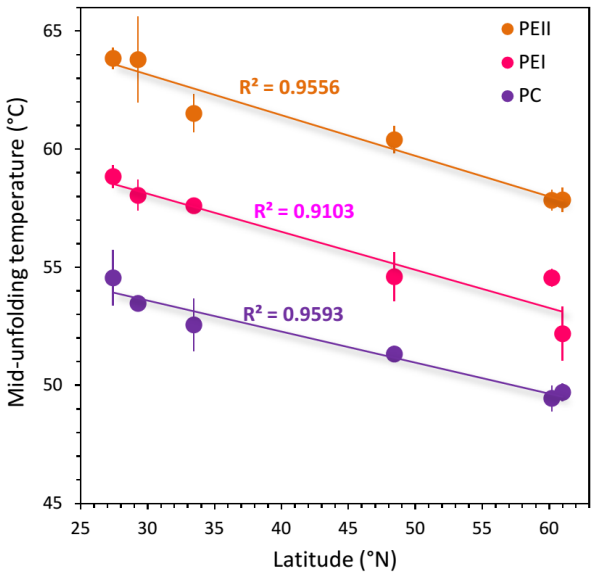

Figure S5: Mid-unfolding temperature ($T_{50\%}$) of phycoerythrin (PE) II, phycoerythrin I and phycocyanin (PC) as a function of isolation latitude of the six marine *Synechococcus* strains studied in this paper. For each phycobiliprotein and each strain, standard deviations are calculated from the mean based on three replicates.

```
RpcA
                1         10        20        30        40        50
ROS8604         MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKGLTAKADS
MVIR-18-1       MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAQASLEAAKGLTAKADS
I   WH8016      MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKGLTAKADS
WH8020          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKGLTAKADS
CC9311          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLDAAKGLTAKADA
    BL107       MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKGLTSKAEA
IV  CC9902      MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKGLTSKADA
M16.1           MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
TAK9802         MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
RS9902          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
    RS9907      MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
II  A15-44      MKTPLTEAVAAADSQGRFLSNTEIQGAFGRFNRAKAALEAAKALTTKADT
CC9605          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTGKADS
A15-62          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
WH8109          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
PROS-U-1        MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
WH8102          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
WH8103          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
III A15-28      MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADA
BOUM118         MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
RS9915          MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAKASLEAAKALTSKADS
    WH7803      MKTPLTEAVAAADSQGRFLSNTEVQAASGRFNRAAASLEAAKALTSKADS
V   BMK-MC-1    MKTPLTEAVAAADSQGRFLSNTEVQGAFGRFNRASASLEAAKALTSKADS

RpcB
                1         10        20        30        40        50
ROS8604         MFDAFTKVVAQADARGQFISSSEIDALSAMVSDSDKRLDSVSRLSSNASTB
MVIR-18-1       MFDAFTKVVAQADARGQFISANEIDALAAMVSGSNKRLDAVSRISNNASTB
I   WH8016      MFDAFTKVVAQADARGQFISSSEIDALSAMVSDSDKRLDSVSRLSSNASTB
WH8020          MFDAFTKVVAQADARGQFISTSEIDALAAMVSGSNKRLDAVSRISNNASTB
CC9311          MFDAFTKVVAQADARGQFISASEIDALAAMVSGSNKRLDAVSRISNNASTB
    BL107       MFDAFTKVVAQADARGQFISTSEIDALAAVVSDSNKRLDAVSRISSNASTB
IV  CC9902      MFDAFTKVVAQADARGQFISTSEIDALAAVVSDSNKRLDAVSRISSNASTB
M16.1           MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
TAK9802         MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
RS9902          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASSB
    RS9907      MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
II  A15-44      MFDAFTKVVAQADARGQFLNASEIDALAAMVSESNKRLDAVNRITSNASSB
CC9605          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASSB
A15-62          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASSB
WH8109          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISGNASSB
PROS-U-1        MFDAFTKVVAQADARGQFISTSEIDALASMVSDSNKRLDAVNRISSNASSB
WH8102          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
WH8103          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
III A15-28      MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
BOUM118         MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
RS9915          MFDAFTKVVAQADARGQFISTSEIDALAAMVSDSNKRLDAVNRISSNASTB
    WH7803      MFDAFTKVVAQADARGQFISASEIDALAAMVSDSNKRLDAVNRISSNASTB
V   BMK-MC-1    MFDAFTKVVAQADARGQFISPSEIDALAAMVSDSNKRLDAVNRITCNASTB
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Figure S6: Amino acid sequences alignment of phycocyanin α and β-subunits showing the substitution of alanine in the warm-adapted clades II and III to glycine in the cold-adapted clades I and IV on residue 43 of RpcA (A) and asparagine to serine on residue 42 of RpcB (B). Substitutions are indicated by yellow highlighting, and clades are differently colored : clade I, light blue ; clade II, red ; clade III, orange ; clade IV, dark blue.

Table S1: Phycobiliprotein sequences used for comparative amino acid and structural analyses. The database compiled encompasses the sequences of the two subunits of 21 phycocyanin (RpcA, RpcB), 21 phycoerythrin I (CpeA, CpeB) and 20 phycoerythrin II (MpeA, MpeB). Accession numbers of the amino acid sequences are reported, and previously unpublished sequences are in bold.

Strain name	Clade	Pigment Type[1]	RCC[2] number	Iso. lat.	Iso. long.	Iso. temp.	RpcA	RpcB	CpeA	CpeB	MpeA	MpeB
CC9311	I	3dA	1086	31.9	-12.46	16.59	ABI45378	ABI47294	ABI45327	ABI46374	ABI45816	ABI45939
WH8016	I	3aA	2535	41.53	-70.67	17.83	EHA59372	EHA59373	EHA59379	EHA59378	EHA59384	EHA59385
ROS8604	I	3a	2380	48.43	-3.59	12.81	AHF23553	AHF23552	AHF23616	AHF23615	**KT955729**	**KT955719**
MVIR-18-1	I	3aA	2385	61.00	1.59	13.98	AGX70106	AHF23550	AHF23614	AHF23613	AGX70093	AGX70092
WH8020	I	3dA	2437	38.41	-69.19	16.89	AHF23549	AHF23548	AHF23612	AHF23611	AAA27333	AAA273332
M16.1	II	3a	791	27.42	-91.18	24.15	AHF23571	AHF23570	AHF23634	AHF23633	**KT955731**	**KT955721**
A15-44	II	2	2527	21.41	-17.50	22.61	AHF23587	AHF23586	AHF23650	AHF23649	n.a.	n.a.
RS9902	II	3c	2376	29.28	34.55	21.07	AHF23579	AHF23578	AHF23642	AHF23641	**KT955728**	**KT955718**
RS9907	II	3a	2382	29.28	34.55	28.99	AHF23573	AHF23572	AHF23636	AHF23635	**KT955727**	**KT955717**
TAK9802	II	3a	2528	-14.30	-145.2	29.81	AHF23575	AHF23574	AHF23638	AHF23637	**KT955725**	**KT955715**
WH8109	II	3bB	2033	39.29	-70.28	21.60	AHF62838	AHF62839	AHF62845	AHF62844	AHF62860	AHF62861
A15-62	II	3dB	2374	17.37	-20.57	26.02	AHF23577	AHF23576	AHF23640	AHF23639	**KT955733**	**KT955723**
CC9605	II	3c	753	30.41	-123.98	18.02	ABB34196	ABB34197	ABB34210	ABB34211	ABB34210	ABB34211
PROS-U-1	II	3dB	2369	30.80	-10.30	21.51	AHF23581	AHF23580	AHF23644	AHF23643	**KT955730**	**KT955720**
BOUM118	III	3c	2379	33.38	32.38	25.20	AHF23563	AHF23562	AHF23626	AHF23625	**KT955732**	**KT955722**
RS9915	III	3dB	2553	29.28	34.55	26.98	AHF23567	AHF23566	AHF23630	AHF23629	**KT955726**	**KT955716**
WH8102	III	3c	539	22.29	-65.36	25.78	CAE08538	CAE08537	CAE08531	CAE08532	CAE08524	CAE08523
WH8103	III	3cA	29	28.30	-67.23	25.45	AHF23565	AHF23564	AHF23628	AHF23627	CRY93003	CRY93002
A15-28	III	3c	2556	31.15	-20.43	25.15	AHF23569	AHF23568	AHF23632	AHF23631	**KT955734**	**KT955724**
CC9902	IV	3dA	2673	32.90	-117.25	15.56	ABB26866	ABB26865	ABB26851	ABB26850	ABB26851	ABB26850
BL107	IV	3dA	515	41.43	3.33	13.89	EAU70259	EAU70260	EAU70266	EAU70265	EAU70274	EAU70275

n.a.: not applicable (subunit not present in this strain).

[1] According to 4, 5
[2] RCC: Roscoff Culture Collection (http://roscoff-culture-collection.org/)