

Supplementary Information

Defining the Environmental Adaptations of Genus *Devosia*: Insights into its Expansive Short Peptide Transport System and Positively Selected Genes

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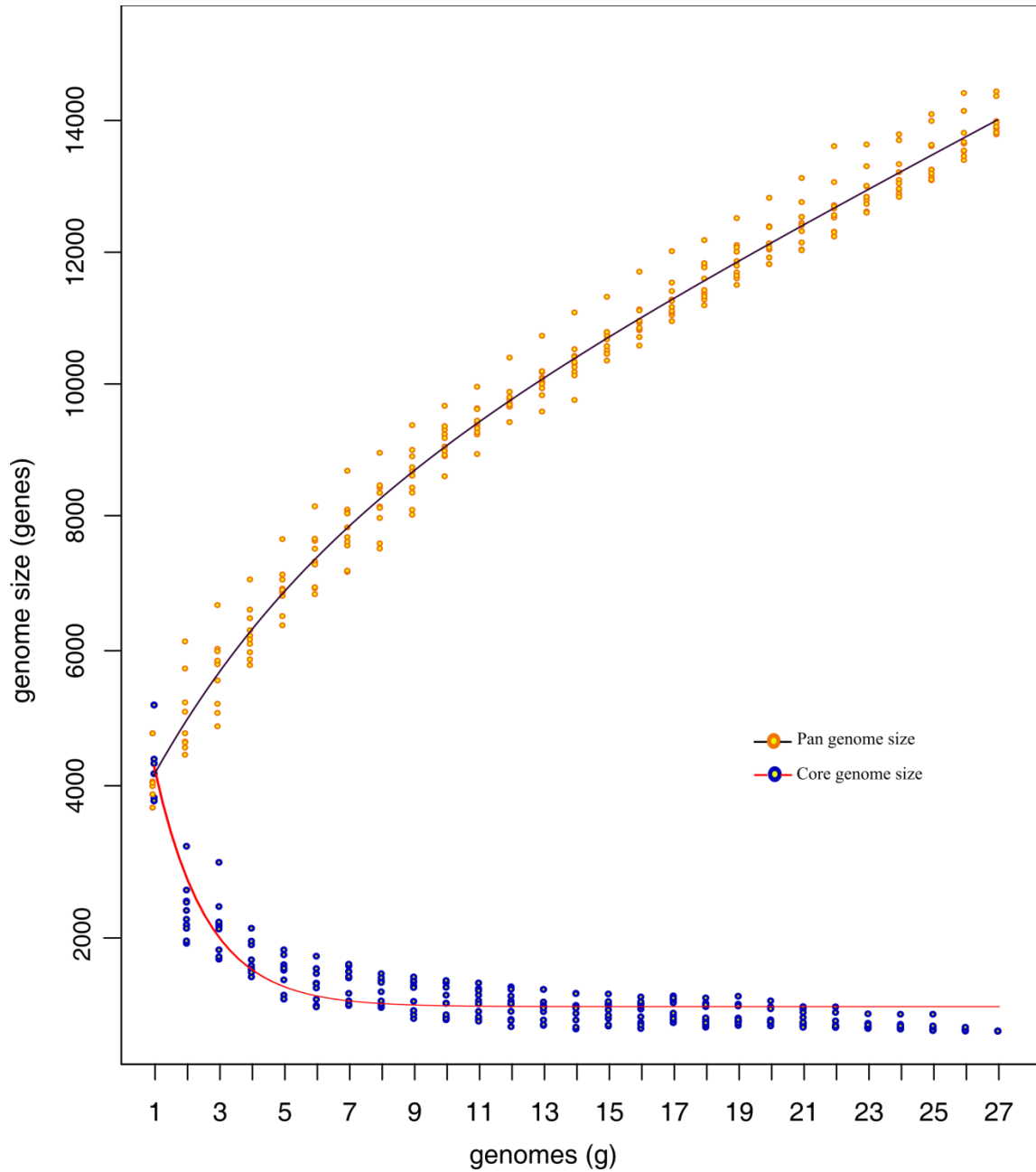
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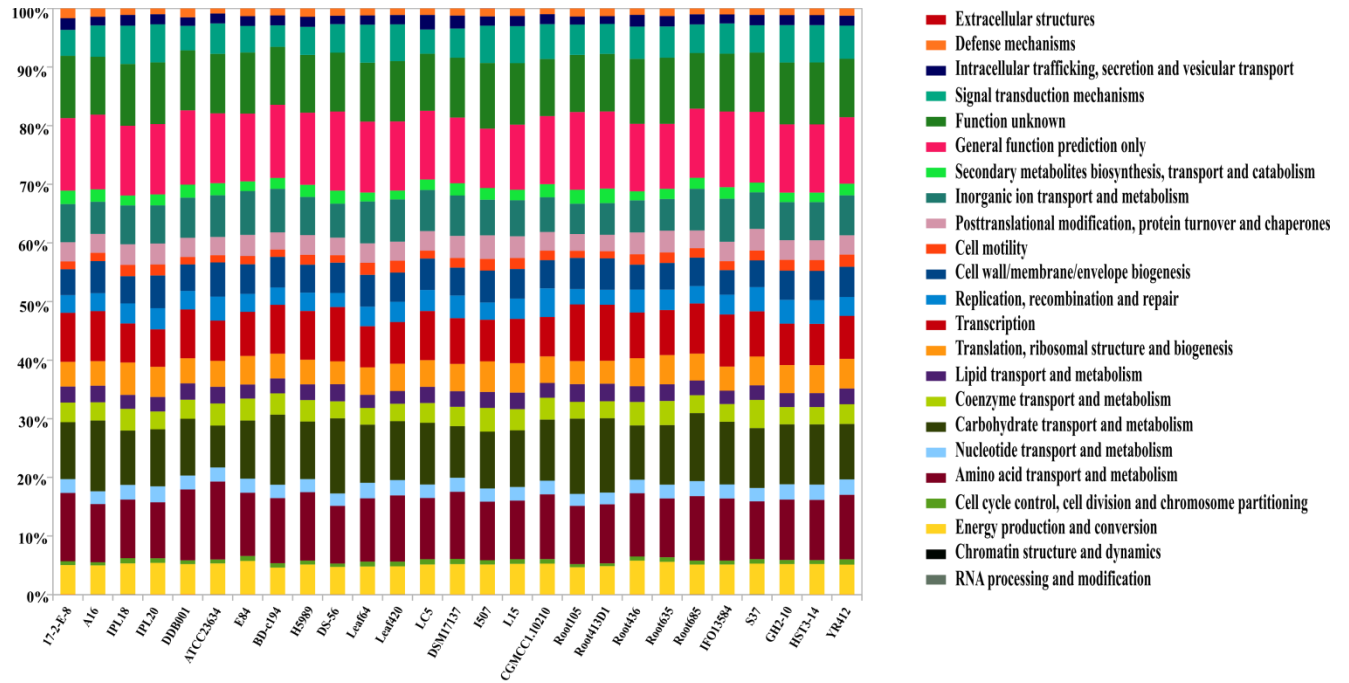
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Figure S1



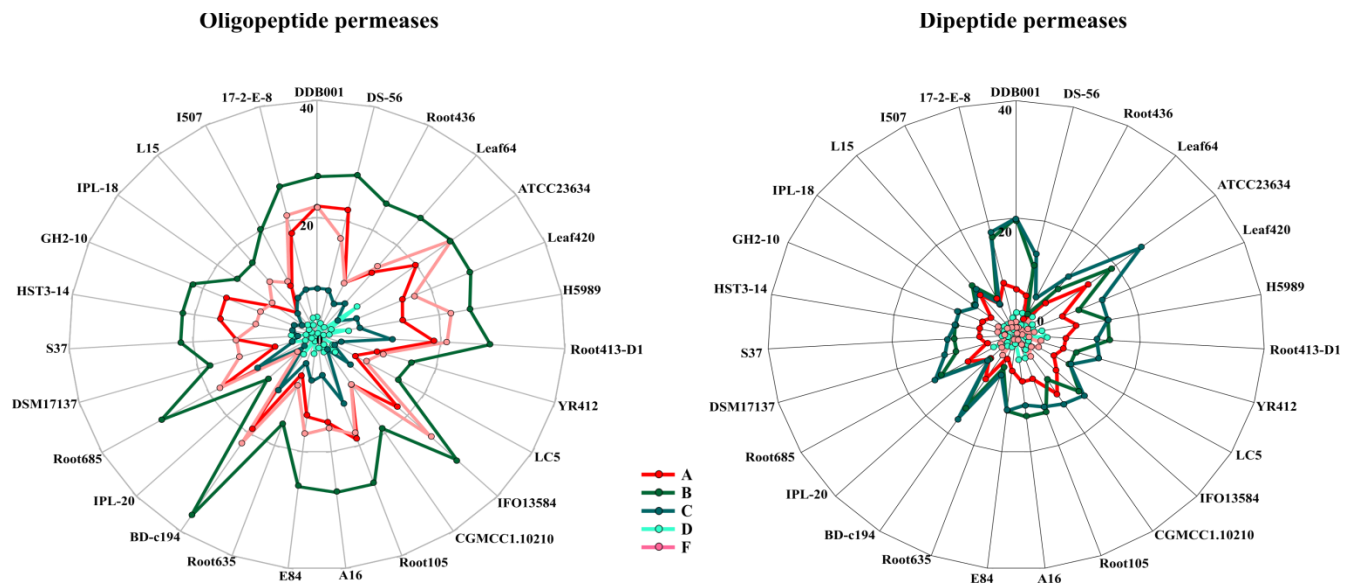
Supplementary Figure S1. Pan and core genome sizes. The numbers of pan and core genes are plotted as a function of the number of genomes (g) added sequentially. *y-axis* shows the change in core genome and pan genome sizes as a function of random addition of genomes plotted on *x-axis*. The sizes of core and pan genomes were computed using OMCL algorithm. The best fit regression represents the Tettelin curve for both core and pan genomes.

Figure S2



Supplementary Figure S2. Predicted oligo-peptide and di-peptide permeases in the analyzed strains.

Figure S3



Supplementary Figure S3. Phylogeny of the predicted substrate binding components of (A) oligopeptide permeases (OppA) and (B) di-peptide permease (DppA) proteins predicted in the genomes of *Devosia* (blue) and representative genomes of other genera of family *Hyphomicrobiaceae* (red) constructed using Neighbour-joining method at 100 bootstrap replications. The bootstrap confidence levels are shown with circles on the branches.

Supplementary Table S1. List of genomes of the family *Hyphomicrobiceae* with the predicted copy number of genes associated with oligo-peptide and di-peptide transporters included in the study for comparison with *Devosia*.

Genome	OppA	OppB	OppC	OppD	OppF	DppA	DppB	DppC	DppD	DppF
<i>Aquabacter</i> sp. Sn-9-2 (NZ_RWKV00000000.1)	2	3	2	2	2	3	2	2	0	0
<i>Aquabacter spiritensis</i> DSM 9035 (NZ_SMAI00000000.1)	2	3	1	2	2	2	2	2	0	0
<i>Arsenicitalea aurantiaca</i> 42-50 (NZ_RZSJ00000000.1)	8	14	3	3	9	6	10	13	2	1
<i>Blastochloris</i> sp. GI (NZ_AP018907.1)	1	2	1	0	0	0	0	0	0	0
<i>Blastochloris viridis</i> ATCC 19567 (NZ_CP012946.1)	1	2	1	0	0	0	0	0	1	0
<i>Cucumibacter marinus</i> DSM 18995 (NZ_AUCR00000000.1)	6	12	4	2	11	5	8	7	2	1
<i>Dichotomicrobium thermohalophilum</i> DSM 5002 (NZ_QXDF00000000.1)	1	2	1	0	0	0	0	0	0	0
<i>Filomicrobium insigne</i> CGMCC1.6497 (NZ_FNJC00000000.1)	1	2	1	0	0	0	0	0	0	0
<i>Filomicrobium</i> sp. MED665 (NZ_GY00000000.1)	4	6	1	0	5	2	1	6	0	0
<i>Hyphomicrobium denitrificans</i> ATCC 51888 (NC_014313.1)	1	2	1	0	0	0	0	0	0	0
<i>Hyphomicrobium facile</i> DSM 1565 (NZ_FPCH00000000.1)	1	2	1	0	0	0	0	0	0	0
<i>Hyphomicrobium</i> sp. MC1 (NC_015717.1)	1	2	1	0	0	2	0	0	0	0
<i>Hyphomicrobium sulfonivorans</i> WDL6 (NZ_LMTR00000000.1)	1	4	1	0	0	1	0	1	0	0
<i>Hyphomicrobium zavarzinii</i> ZV622 (NZ_ARTG00000000.1)	1	2	1	0	0	0	0	0	0	0
<i>Maritalea mobilis</i> CGMCC 1.7002 (NZ_SNYR00000000.1)	6	10	4	5	9	8	10	9	1	3
<i>Maritalea myrionectae</i> DSM 19524 (AUHV01)	3	7	3	3	5	8	6	7	1	3
<i>Pelagibacterium halotolerans</i> B2 (NC_016078.1)	5	17	3	0	12	9	9	10	1	0

<i>Pelagibacterium lentulum</i> B2 (NZ_RZMW00000000.1)	8	15	3	5	12	9	15	12	2	2
<i>Pelagibacterium luteolum</i> CGMCC 1.10267 (NZ_FNCS00000000.1)	3	11	3	2	8	6	5	6	1	0
<i>Pelagibacterium montanilacus</i> CCL18 (NZ_RZMX00000000.1)	1	8	3	5	7	6	3	5	0	0
<i>Prosthecomicrobium hirschii</i> 16 (LJYW01)	8	12	2	2	16	12	15	18	2	0
<i>Prosthecomicrobium</i> sp. SZUA402 (QKBQ00000000.1)	1	1	1	1	0	4	2	1	0	1
<i>Rhodomicrobium udaipurense</i> JA643 (NZ_JFZJ00000000.1)	1	2	1	0	0	0	0	0	0	0
<i>Rhodomicrobium vannielii</i> ATCC 17100 (NC_014664.1)	1	2	1	0	0	0	0	0	0	0
<i>Rhodoplanes elegans</i> DSM 11907 (NZ_NPEU00000000.1)	1	4	1	0	2	4	2	2	0	0
<i>Rhodoplanes piscinae</i> DSM 19946 (NPEW01)	1	2	1	0	0	0	0	0	0	0
<i>Rhodoplanes roseus</i> DSM 5909 (NZ_NPEX00000000.1)	1	4	1	0	2	5	2	2	0	0