

Supplementary Material

The effect of hypoxia on *Daphnia magna* performance and its associated microbial and bacterioplankton community: a scope for phenotypic plasticity and microbiome community interactions upon environmental stress.

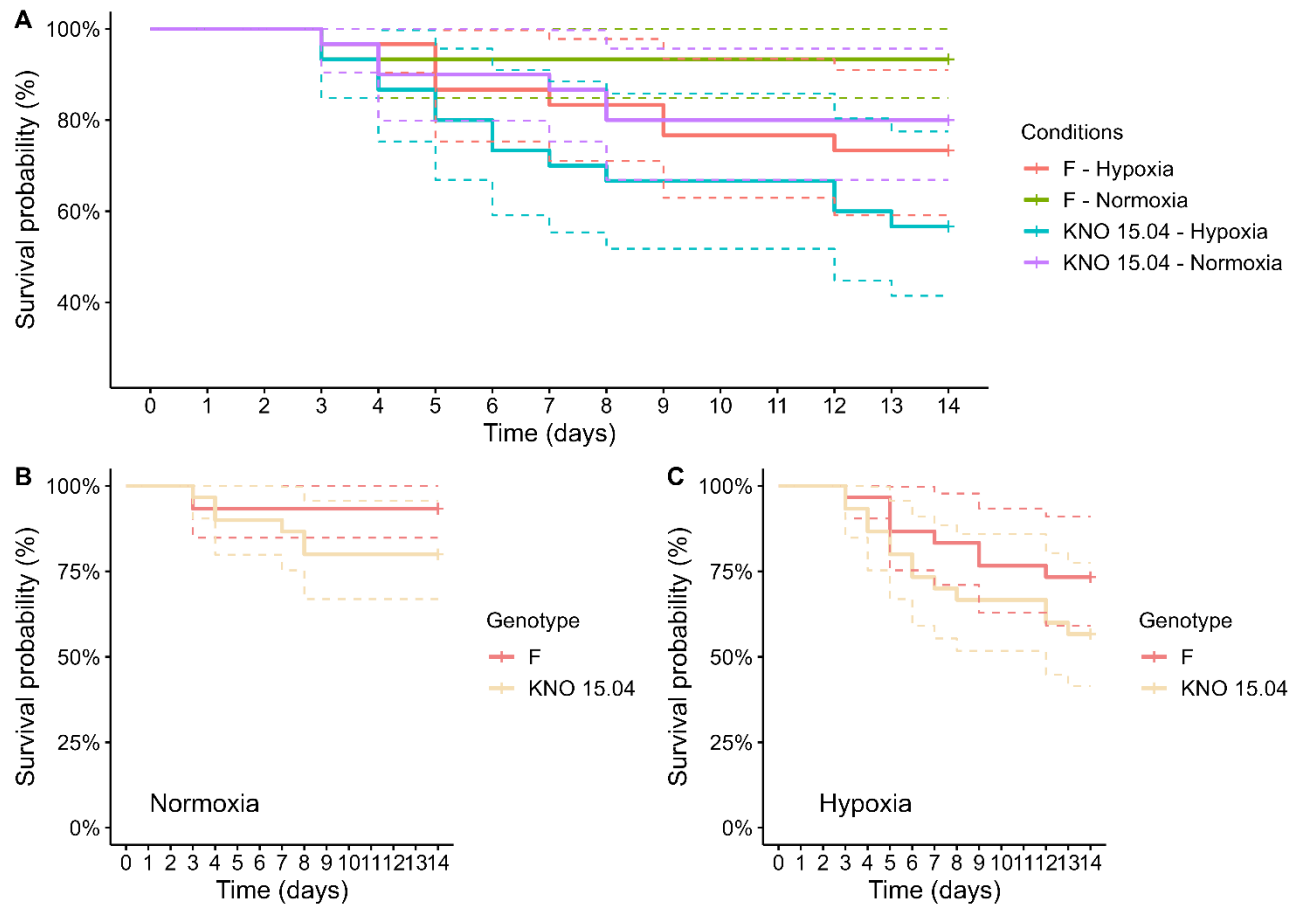
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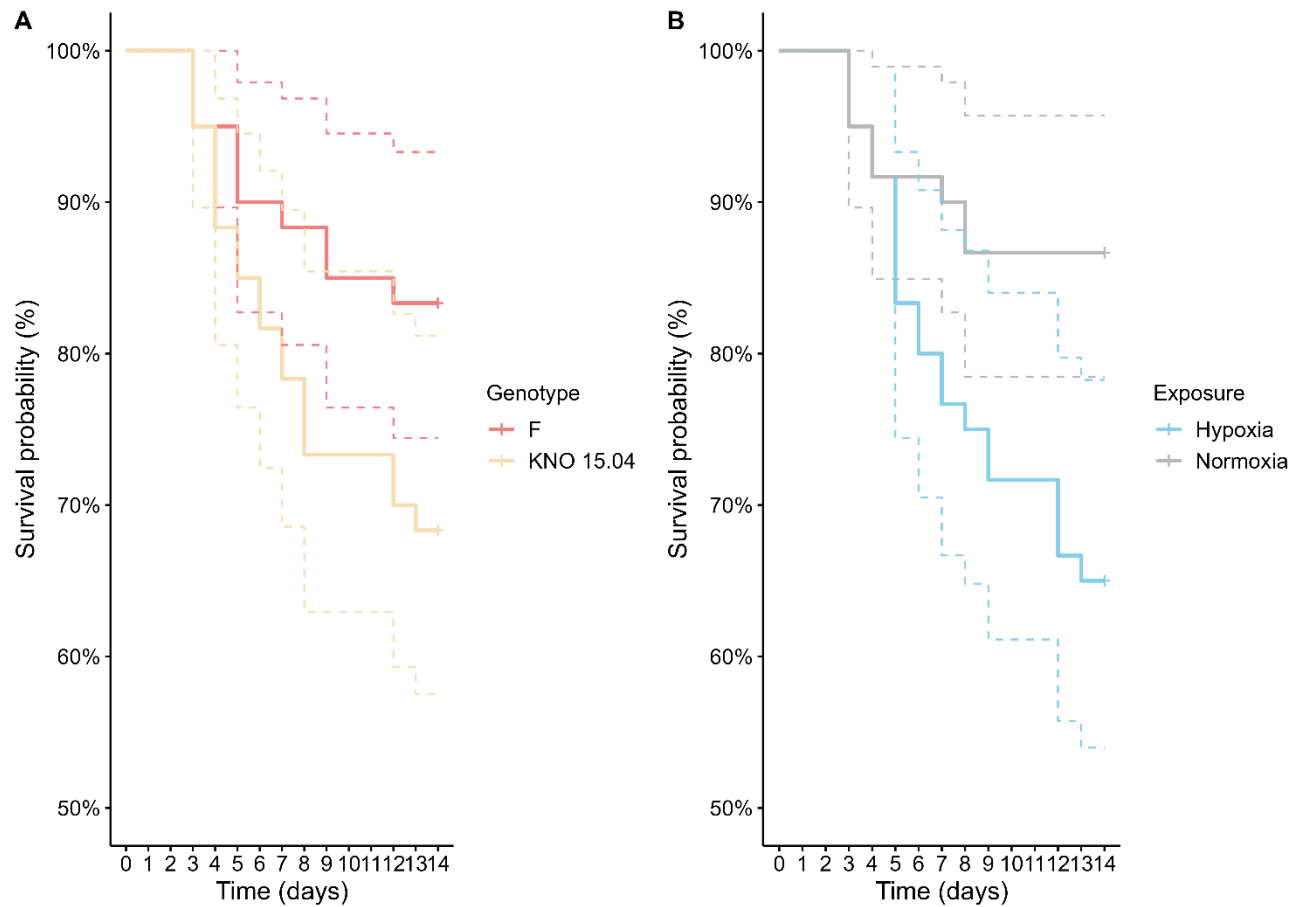
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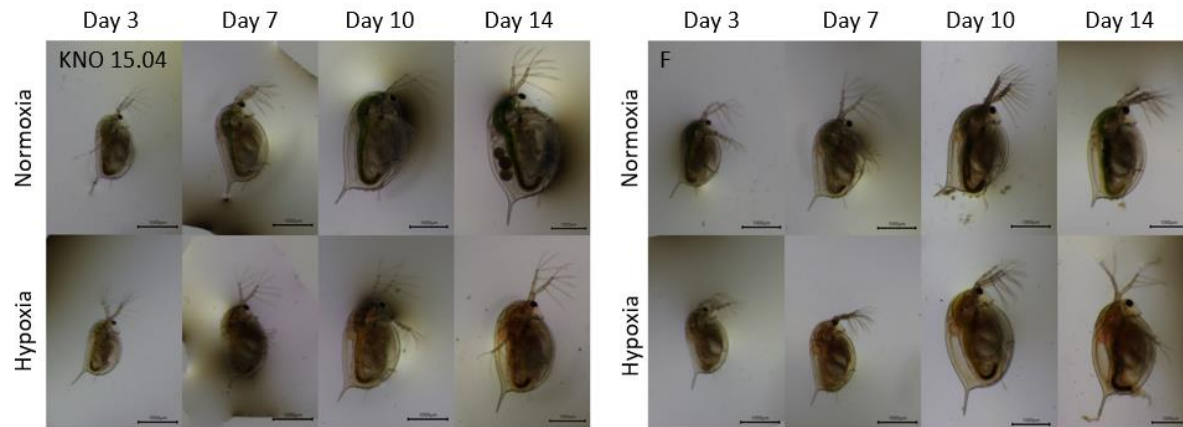
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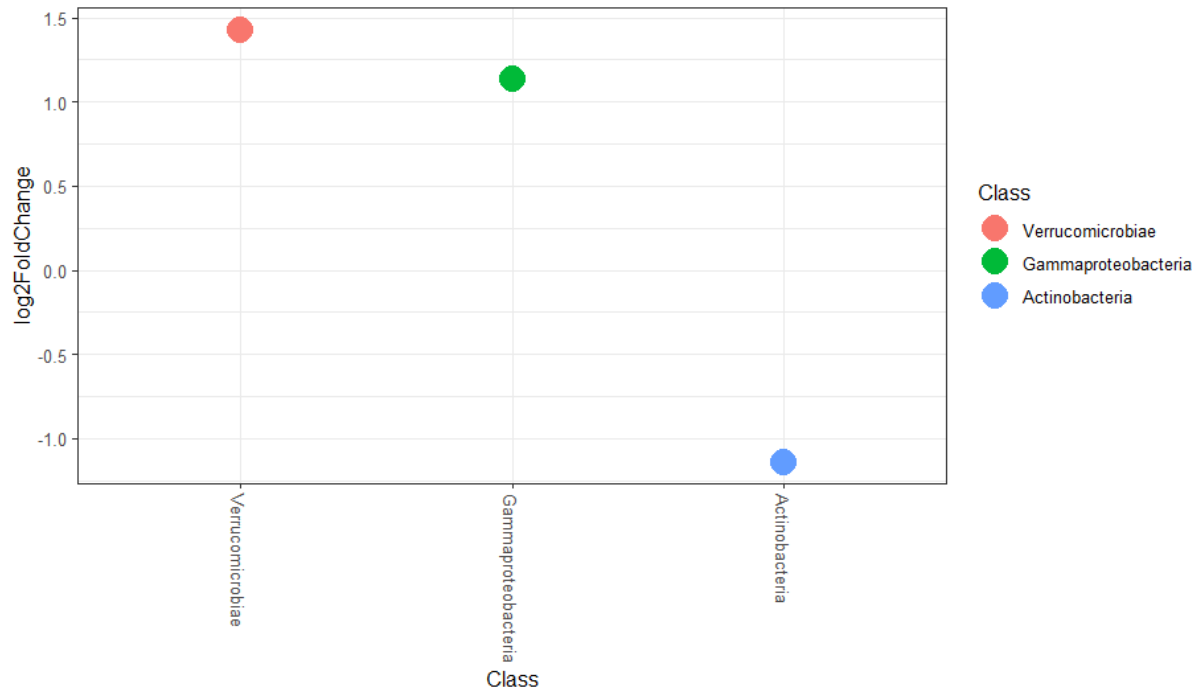
Supplementary Figure 1. Comparison of survival of KNO 15.04 and F genotypes in a hypoxia or normoxia environment. (A) Full comparison of the two genotypes and two exposures. Comparison of the F and KNO 15.04 genotypes in (B) normoxia and (C) hypoxia, respectively. Dashed lines represent the 95% confidence intervals. Sample size was $n=30$ (10 individuals * 3 replicates) for each genotype * exposure combination.



Supplementary Figure 2. Comparison of survival of KNO 15.04 and F genotypes in a hypoxia or normoxia environment. (A) Comparison of F and KNO 15.04 genotypes in both exposures. Red lines correspond to survival of the F genotype and orange lines to survival of the KNO 15.04 genotype. (B) Comparison of hypoxia and normoxia exposure over both genotypes. Grey lines correspond to survival in a normoxia exposure and blue lines to survival in a hypoxia exposure. Dashed lines represent the 95% confidence intervals. Sample size was $n=30$ (10 individuals * 3 replicates) for each genotype * exposure combination.

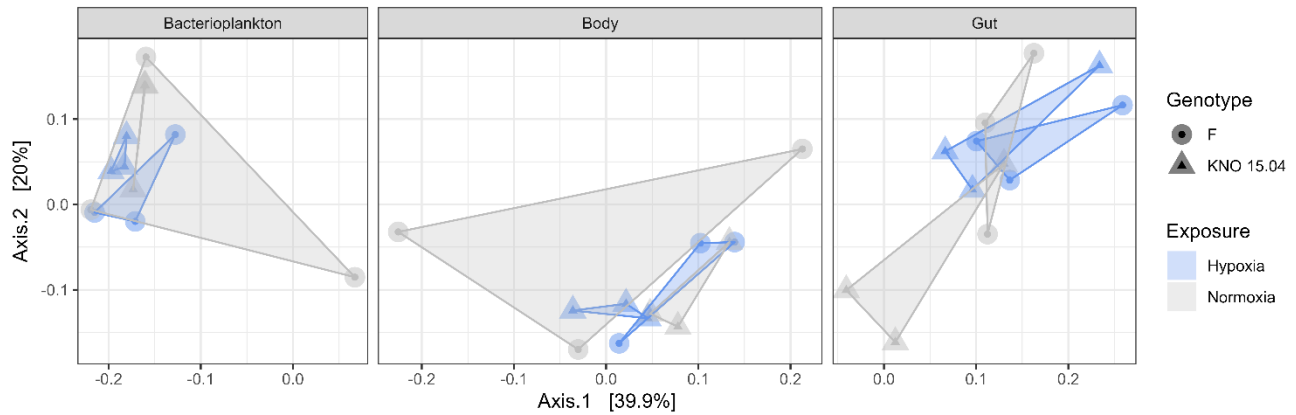


Supplementary Figure 3. Phenotypic appearance over time of normoxia (upper panels) and hypoxia (bottom panels) exposed *D. magna* of the KNO 15.04 (left figures) and F (right figures) genotype.

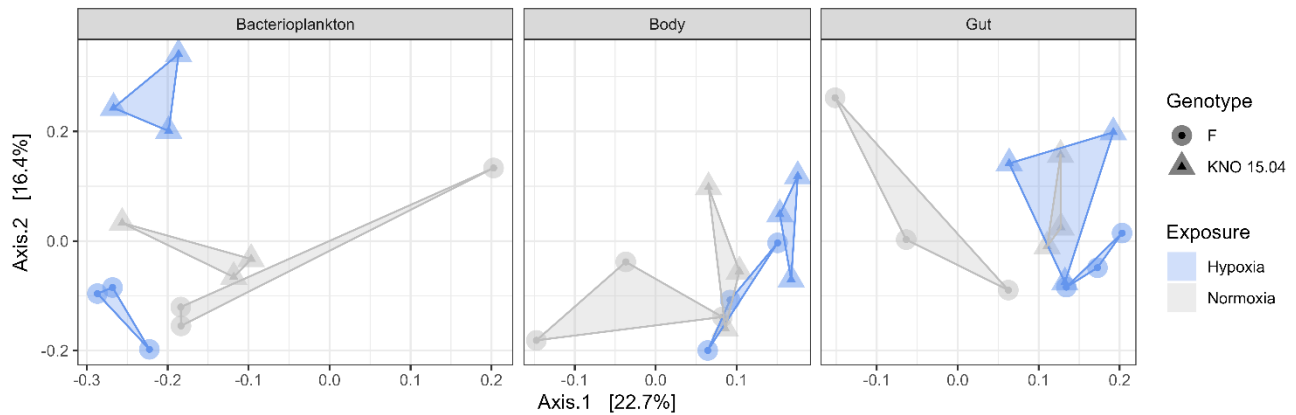


Supplementary Figure 4. Deseq2 comparison of classes between normoxia and hypoxia in the bacterioplankton samples with negative log2FoldChange values of bacterial classes being less represented in normoxia.

A Bacterial communities: Weighted Unifrac Distance



B Bacterial communities: Unweighted Unifrac Distance



Supplementary Figure 5. Beta diversity: (A) Weighted and (B) Unweighted Unifrac distance of the bacterial communities within the different sample types (left panel: bacterioplankton, middle panel: body, right panel: gut). Circles correspond to the F genotype, triangles to the KNO 15.04 genotype. Hypoxia exposure is depicted in blue, normoxia exposure in grey.

Supplementary Table 1. Relative mean class counts per sample type x exposure combination. Grey marked and bold numbers are significant different numbers, bold numbers without marking are not significant but interesting numbers.

Class	Bacterioplankton		Body		Gut	
	Hypoxia	Normoxia	Hypoxia	Normoxia	Hypoxia	Normoxia
Bacteroidia	49,007452	48,15794703	58,47184908	55,96729321	27,54841169	44,77306509
Gammaproteobacteria	12,80593703	16,24254468	35,56615448	25,7845279	48,67385049	38,42611634
Actinobacteria	24,59862856	10,08552273	0,654258523	3,120085215	6,699315313	3,28761547
Verrucomicrobiae	10,91930858	23,46311698	0,456096548	2,045449712	2,824877433	2,367270962
Alphaproteobacteria	1,650147826	1,573801194	3,274537082	12,09568286	10,74472269	10,64480521
Bdellovibrionia	0,537753415	0,131309996	1,50338234	0,457449245	3,389427019	0,235581352
Polyangia	0,038998456	0,098920028	0	0,336156013	0	0,102064544
Gracilibacteria	0,076225725	0,031985075	0,073721944	0,186336822	0,073772256	0,036903402
Planctomycetes	0,141413974	0,170917705	0	0,007019025	0,007019211	0,063235743
Bacilli	0,090206328	0	0	0	0,026322444	0,005266484
Desulfitobacteriia	0,065214918	0	0	0	0,012281441	0,00351395
Acidimicrobiia	0,05989578	0,008780248	0	0	0	0,001753463
Armatimonadia	0	0	0	0	0	0,049294039
Kapabacteria	0	0,035154327	0	0	0	0,00351395
Oligoflexia	0,008817409	0	0	0	0	0