Experiment 5 - Data S6

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Experiment 5 – BX-feedbacks on wheat pathogen resistance

We examined wheat resistance against Zymoseptoria tritici in a fifth experiment, again with a fully randomized design testing the factor conditioning (BX+ or BX-). A greenhouse-conditioned batch of Changins soil was employed for this climate chamber experiment (Table S1). With the goal to prepare a control soil we sterilized BX+ and BX- soil variants with x-rays. The BX+ and BX- soils were prepared by re-inoculating to them with microbial washes (Hartman et al., 2017) extracted from non-sterilized BX+ and BX- soils. A 1:1 mixture of sterile BX+ and BX- soils without microbial wash was finally used as control soil. The experiment was set in three blocks (so that plants could be sampled at three timepoints) and ten replicates resulting in 90 experimental units (3 soil variants * 3 timepoints * 10 replicates; Data S5). These soils were filled into 200 mL pots and planted with four Drifter seeds per pot, and then cultivated at 18°C, 70% relative humidity for 3 weeks until starting the pathogen assay.

Table 1: Number of replicates

BX+	BX-	Sterilized_control
10	10	10

Feedback experiment with wheat (Drifter) growing on Changins soil conditioned by maize B73 (BX+ soil), by maize B73(*bx1*) (BX- soil) and a sterilized control (*BX_condition* variable).

Wheat *Z. tritici* assay: pycnidia counts

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	3.984	0.2677	14.88	1.564e-14
BX_conditionBX-	-0.6697	0.4601	-1.455	0.1571
BX_conditionSterilized_control	-1.381	0.5975	-2.312	0.02866

(Dispersion parameter for quasipoisson family taken to be 38.5129)

Null deviance:	1216.0 on 29 degrees of freedom
Residual deviance:	950.3 on 27 degrees of freedom

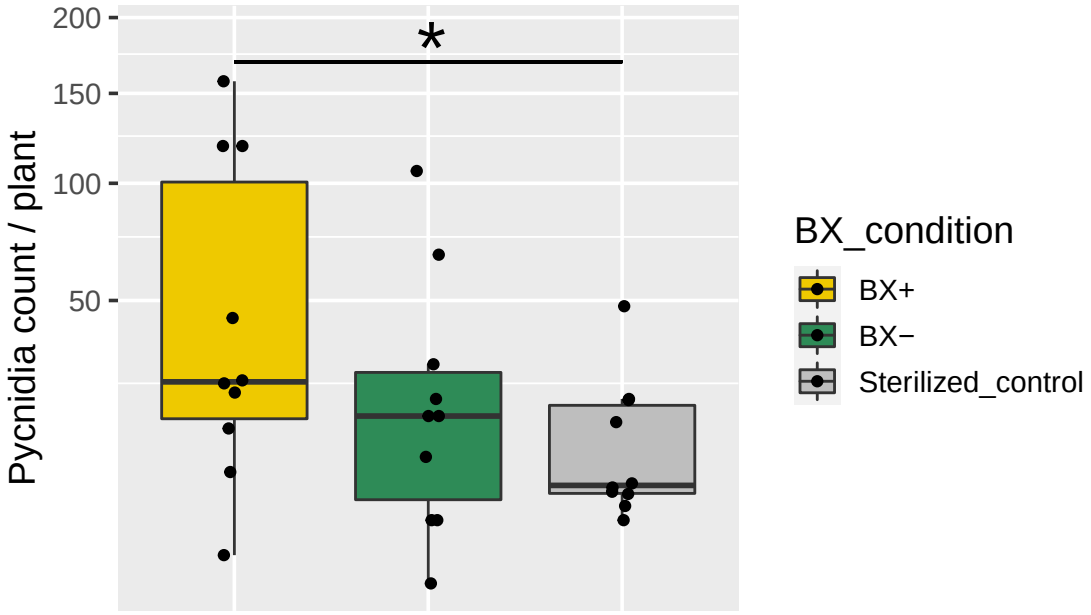
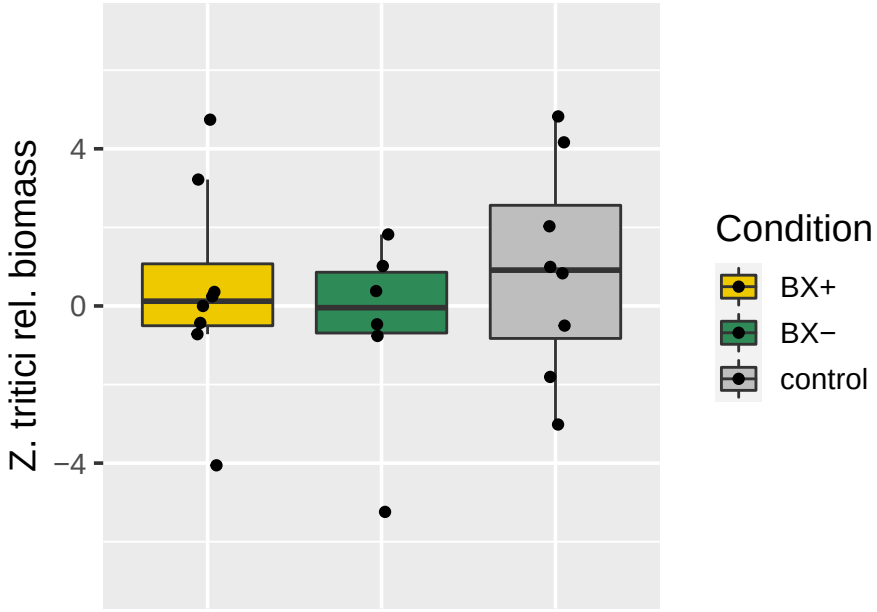


Figure S4 | BX-effect on wheat pathogen resistance
Wheat plants from cultivar Drifter were grown on soils that were X-ray sterilized and re-inoculated with initial BX-conditioned bacterial microbiomes ('BX+' and 'BX-' soil variants), and on mixture of x-ray sterilized BX+ and BX- soil ('control' soil variants). Success of pathogen Zymoseptoria tritici colonization was measured as pycnidia counts (mean per pot), counted on the infected leaf. Stars reported on the graph correspond to significant difference with glm on square root data for (A) (significance code: $P < 0.001$ ***; $P < 0.01$ **, $P < 0.05$ *).

Wheat *Z. tritici* assay: qPCr

Table 4: ANOVA on relative fungal biomass quantified by qPCr, at 6 weeks. Model = rel biomass ~ BX_condition

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
BX_condition	2	7.599	3.799	0.5481	0.5869
Residuals	19	131.7	6.932	NA	NA



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Descriptive statistics

Table 5: Quantiles pycnidia counts for each treatments

	BX+ group	BX- group	control group
0%	0.5	0	2.5
25%	16.94	4.375	5.062
50%	25.38	17.5	6
75%	100.6	27.81	19.81
100%	157.5	106.2	48