



Natural Occurrence of Mycotoxin-Producing Fusaria in Market-Bought Peruvian Crops: a Food Safety Threat for Andean Populations

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1. Supplementary Methods: Tri5-TCTA and Tri5-TCTB primer design

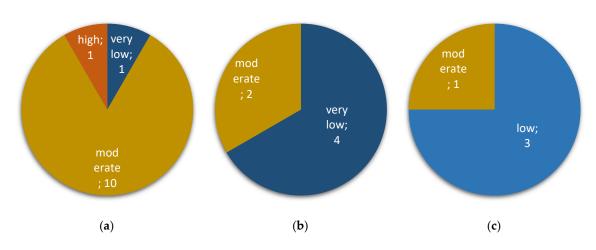
Multiple sequence alignment was performed using nucleotide sequences of *Tri5* gene extracted from *Fusarium* species that can produce either type A trichothecens (TCTA) or type B trichothecens (TCTB). Species and accession numbers are provided in Supplementary Table S1. Primers for Sybr Green-based qPCR assay were subsequently designed in discerning regions using Primer3 [1,2].

Table S1. Fusarium species and NCBI sequence accession numbers used to design TCTA and TCTB-discerning primers.

Toxins Produced	Species and Strain	NCBI Accession Number of Tri5 Sequence
TCTA	F. camptoceras NRRL3381	GQ915545.1
	F. sporotrichioides	AY130293.1
	F. langsethiae IBT 9956	AF449792.1
	F. kyushuense NRRL 25349	GQ915548.1
	F. incarnatum NRRL 31160	GQ915550.1
	F. armeniacum FRC R-0933	GQ915543.1
	G. publicaris FRC_R 07843	GQ915552.1
ТСТВ	F. graminearum NRRL9394	AY102605.1
	F. austroamericanum NRRL 2903	AY102596.1
	F. asiaticum NRRL 28720	AY102590.1
	F. graminearum GZ3639	AF359361.3
	F. graminearum PH-1	supercont3.2 -3376420-3377787 ¹
	F. cortaderiae NRRL 29306	AY102601.1
	F. culmorum NRRL 25475	AY102571.1
	F. acaciae-mearnsii NRRL 26754	AY102577.1
	F. cerealis NRRL 25491	AY102572.1

¹ Sequence source from [3].

2. Supplementary Figures



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Figure S1. Fusarium risk assessment in collected amaranth, barley and oat grain samples. Risk is ranked as *very low*, *low*, *moderate*, *high*, or *very high*. Number after semicolon indicates corresponding sample size. (a) amaranth seeds; (b) barley; (c) oat.

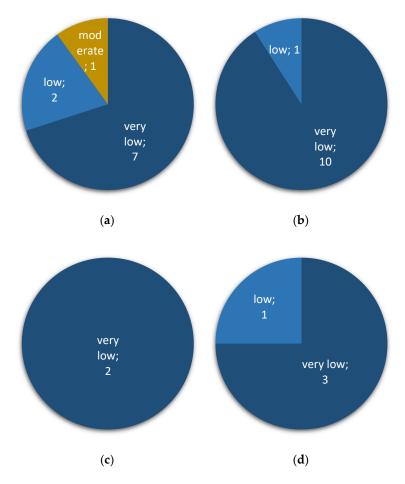


Figure S2. Assessment of the risk associated with the presence of fumonisin producers in cereal and pseudo-cereal grains contaminated with *Fusarium* species. Risk is ranked as *very low, low, moderate, high,* or *very high*. Number after semicolon indicates corresponding sample size. (a) rice; (b) amaranth seeds; (c) barley; (d) oat.

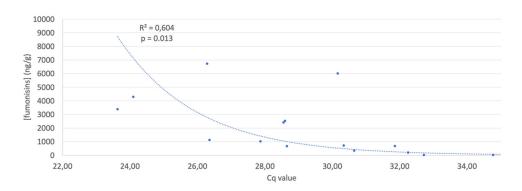
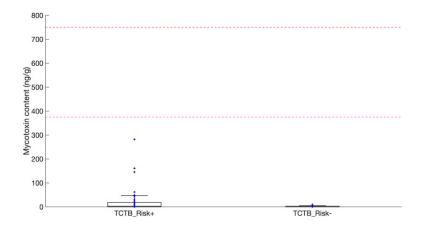
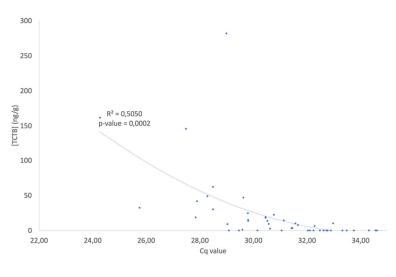


Figure S3. Fumonisin content as a function of the relative abundance of *Fum1*-containing DNA measured by qPCR in cereal samples. Pearson product-moment correlation coefficient (R^2) and associated p-value were computed with Matlab 2020b (MathWorks) and used to estimate the goodness of fit of the monotonic non-linear relationship.

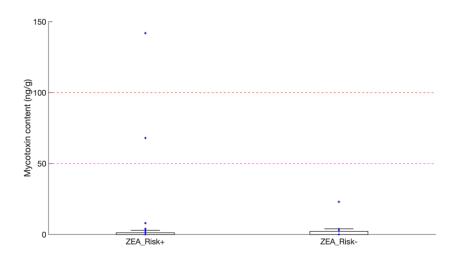
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(a)



(b)



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(c)

Figure S4. Toxin contamination profiles in cereal and pseudo-cereal grains contaminated with *Fusarium* species that can produce TCTB and zearalenone. (a) Boxplot representation of TCTB contents. "TCTB-Risk+" refers to samples with *moderate* to *very high* TCTB-associated risk, and "TCTB-Risk-" refers to 10 randomly selected samples with risk ranked as *very low* to *low*. The pink and red dashed lines indicates the 375 and 750 ng.g-1 thresholds, respectively; (b) TCTB content as a function of the relative abundance of *Tri5*-containing DNA measured by qPCR in cereal samples. Pearson product-moment correlation coefficient (R²) and associated *p*-value were computed with Matlab 2020b (MathWorks) and used to estimate the goodness of fit of the monotonic non-linear relationship; (c) Boxplot representation of zearalenone contents. "ZEA-Risk+" refers to samples with *moderate* to *very high* ZEA-associated risk, and "ZEA-Risk-" refers to samples with risk ranked as *very low* to *low*. The pink and red dashed lines indicates the 50 and 100 ng.g-1 thresholds, respectively.

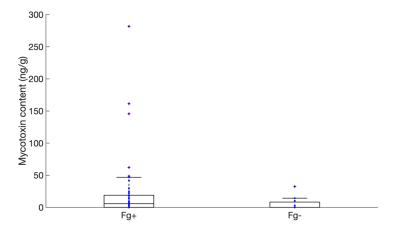
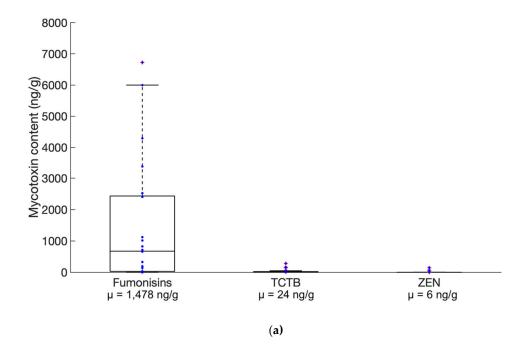


Figure S5. Boxplot representation of TCTB contents of *Tri5*-positive samples that tested positive for *F. graminearum* ("Fg+") or negative ("Fg-").



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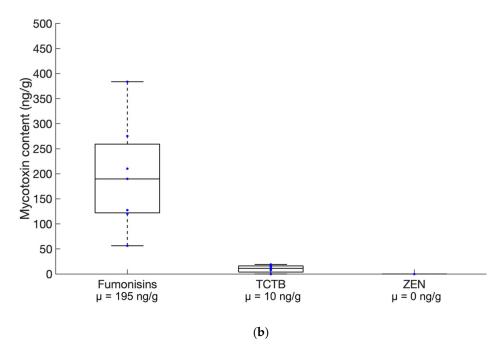


Figure S6. Boxplot representation of mycotoxin content in corn and wheat measured in samples with *moderate* to *very high* mycotoxin-associated risk. The values μ indicate mean values for the corresponding toxins. μ = 0 means no mycotoxin could be detected. (a) Corn. (b) Wheat. Boxplots and means were not computed for other cereals for which only three samples or less were at *moderate* to *very high* mycotoxin-associated risk and showing very low or no detectable levels of mycotoxins.

3. Additional references

- 1. Untergasser, A.; Cutcutache, I.; Koressaar, T.; Ye, J.; Faircloth, B.C.; Remm, M.; Rozen, S.G. Primer3—New Capabilities and Interfaces. Nucleic Acids Res **2012**, 40, e115, doi:10.1093/nar/gks596.
- 2. Koressaar, T.; Remm, M. Enhancements and Modifications of Primer Design Program Primer3. Bioinformatics **2007**, 23, 1289–1291, doi:10.1093/bioinformatics/btm091.
- 3. Wong, P.; Walter, M.; Lee, W.; Mannhaupt, G.; Münsterkötter, M.; Mewes, H.-W.; Adam, G.; Güldener, U. FGDB: Revisiting the Genome Annotation of the Plant Pathogen Fusarium Graminearum. Nucleic Acids Res **2011**, 39, D637-639, doi:10.1093/nar/gkq1016.