

Supplementary material

Influence of germination on the protein content, total phenolic content, and antioxidant capacity of quinoa (*Chenopodium quinoa* Willd.): a systematic review and meta-analysis

3.5 Publication bias

3.5.1. Egger's test

Protein content

Test for Funnel Plot Asymmetry: $z = 0.2437$, $p = 0.8074$

Limit Estimate (as sei $\rightarrow 0$): $b = 0.0814$ (CI: 0.0148, 0.1481)

Total phenolics compounds

Test for Funnel Plot Asymmetry: $z = 0.4712$, $p = 0.6375$

Limit Estimate (as sei $\rightarrow 0$): $b = 0.3364$ (CI: 0.1717, 0.5011)

Antioxidant capacity

Test for Funnel Plot Asymmetry: $z = 1.8952$, $p = 0.0581$

Limit Estimate (as sei $\rightarrow 0$): $b = 0.1549$ (CI: 0.0215, 0.2883)

3.5.2. Begg's test

Protein content

Rank Correlation Test for Funnel Plot Asymmetry

Kendall's tau = -0.2080, $p = 0.1343$

Total phenolics compounds

Rank Correlation Test for Funnel Plot Asymmetry

Kendall's tau = 0.1000, $p = 0.5022$

Antioxidant capacity

Rank Correlation Test for Funnel Plot Asymmetry

Kendall's tau = 0.1238, $p = 0.5590$

3.5.3. Trim and fill

Estimated number of missing studies on the left side: 3 (SE = 2.8284)

Test of H0: no missing studies on the left side: p-val = 0.0625

Equal-Effects Model (k = 18)

I² (total heterogeneity / total variability): 99.80%

H² (total variability / sampling variability): 497.08

Test for Heterogeneity:

Q(df = 17) = 8450.3292, p-val < .0001

Model Results:

Estimate	se	zval	pval	ci.lb	ci.ub
0.1523	0.0015	102.8301	<.0001	0.1494	0.1552 ***

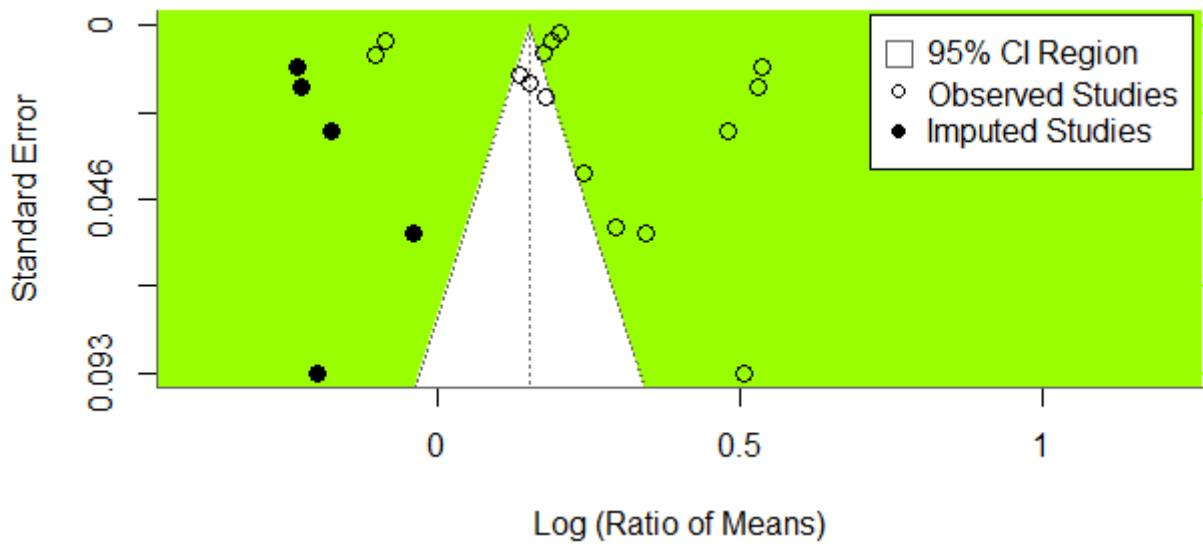
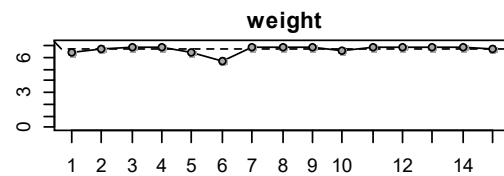
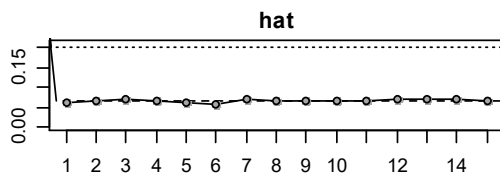
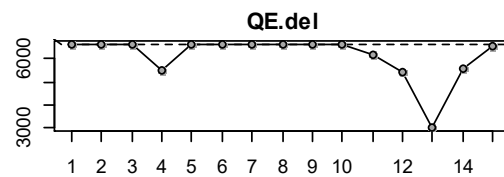
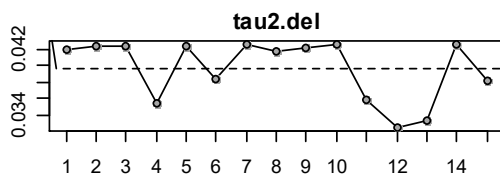
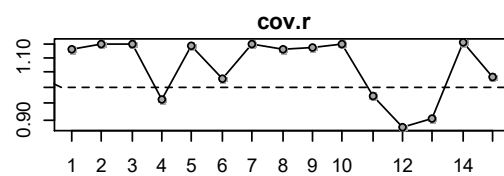
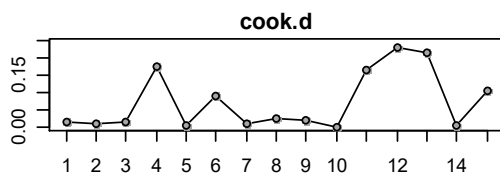
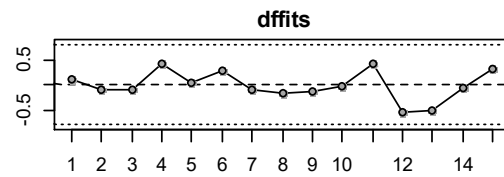
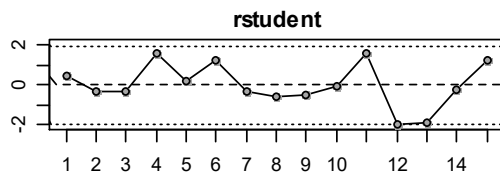


Figure 8. Trim and fill adjusted funnel plot

3.5.4. Leave one out

Leave one out	Estimate	se	zval	pval	ci.lb	ci.ub	Q	Qp	tau ²	I ²	H ²
-1	0.240	0.055	4.341	0.000	0.132	0.349	6648.096	0.000	0.042	99.881	837.579
-2	0.252	0.056	4.511	0.000	0.143	0.361	6657.839	0.000	0.043	99.881	837.144
-3	0.252	0.056	4.518	0.000	0.143	0.362	6656.279	0.000	0.042	99.870	768.443
-4	0.225	0.051	4.400	0.000	0.125	0.325	5486.741	0.000	0.035	99.852	676.985
-5	0.244	0.056	4.372	0.000	0.134	0.353	6652.524	0.000	0.043	99.882	848.272
-6	0.231	0.053	4.373	0.000	0.128	0.335	6645.009	0.000	0.039	99.870	769.601
-7	0.251	0.056	4.491	0.000	0.142	0.361	6615.382	0.000	0.043	99.834	602.782
-8	0.255	0.055	4.599	0.000	0.146	0.364	6654.154	0.000	0.042	99.877	811.764
-9	0.254	0.056	4.561	0.000	0.145	0.363	6658.031	0.000	0.042	99.879	824.053
-10	0.247	0.056	4.420	0.000	0.138	0.357	6654.624	0.000	0.043	99.883	852.539
-11	0.226	0.051	4.389	0.000	0.125	0.326	6166.043	0.000	0.036	99.858	702.556
-12	0.272	0.049	5.548	0.000	0.176	0.368	5439.878	0.000	0.032	99.831	592.150
-13	0.271	0.050	5.449	0.000	0.173	0.368	3017.125	0.000	0.033	99.797	492.355
-14	0.250	0.056	4.467	0.000	0.140	0.360	5563.280	0.000	0.043	99.768	431.055
-15	0.230	0.053	4.335	0.000	0.126	0.334	6531.622	0.000	0.038	99.868	759.480



3.6. Meta-regression

Protein content

Test for Residual Heterogeneity:

QE(df = 24) = 108933.7819, p-val < .0001

Test of Moderators (coefficients 1:3):

QM(df = 3) = 16.9769, p-val = 0.0007

Variety	estimate	se	zval	pval	ci.lb	ci.ub	
GroupBlack	0.041	0.049	0.853	0.394	-0.054	0.136	
GroupRed	0.050	0.053	0.944	0.345	-0.054	0.154	
GroupWhite	0.117	0.030	3.919	0.000	0.058	0.175	***

Total phenolics compounds

Test for Residual Heterogeneity:

QE(df = 22) = 26390.4548, p-val < .0001

Test of Moderators (coefficients 1:3):

QM(df = 3) = 43.6283, p-val < .0001

Variety	estimate	se	zval	pval	ci.lb	ci.ub	
GroupBlack	0.375	0.125	3.005	0.003	0.130	0.619	**
GroupRed	0.409	0.114	3.600	0.000	0.186	0.632	***
GroupWhite	0.346	0.074	4.651	0.000	0.200	0.491	***

Antioxidant capacity

Test for Residual Heterogeneity:

QE(df = 12) = 6177.2472, p-val < .0001

Test of Moderators (coefficients 1:3):

QM(df = 3) = 20.6222, p-val = 0.0001

Variety	estimate	se	zval	pval	ci.lb	ci.ub
GroupWhite	0.208	0.087	2.409	0.016	0.039	0.378
GroupBlack	0.307	0.106	2.886	0.004	0.099	0.516
GroupRed	0.246	0.097	2.548	0.011	0.057	0.435