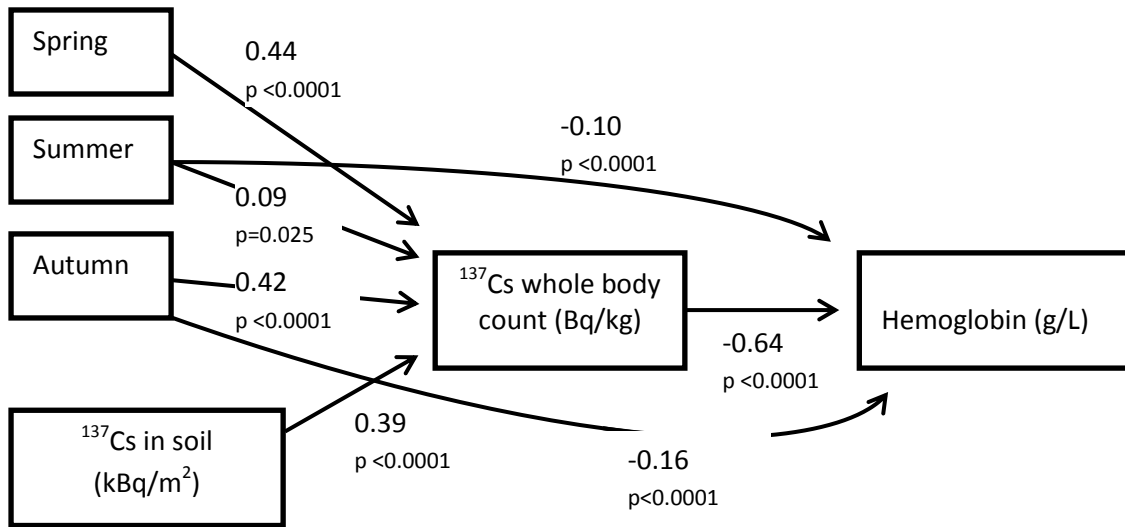
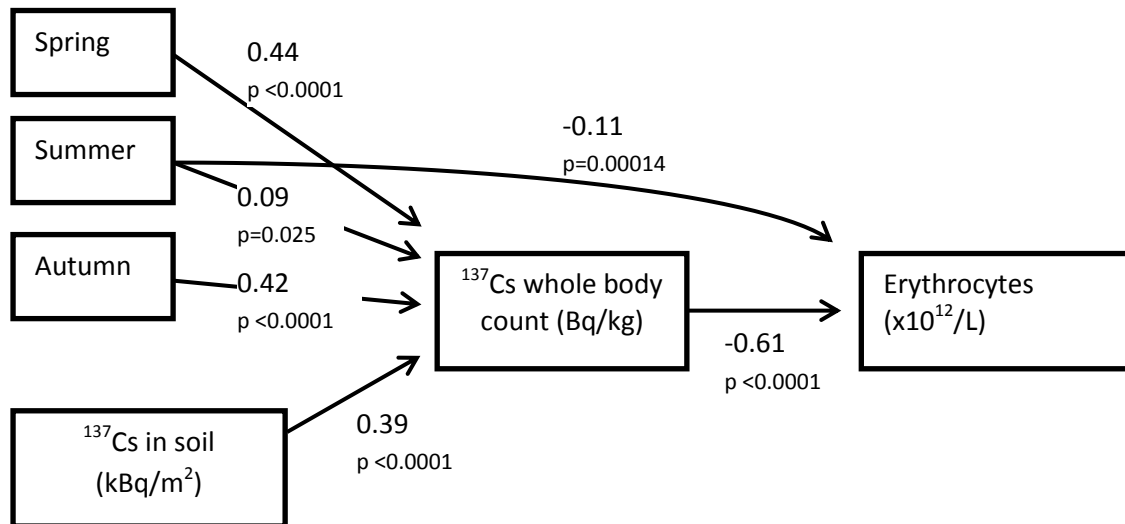


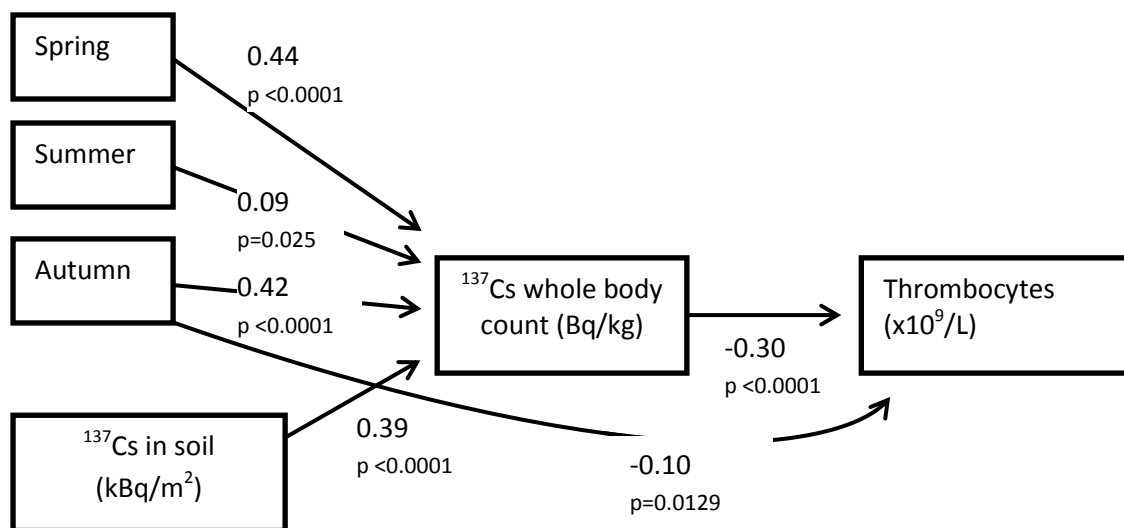
**SUPPLEMENTAL FILE S2**



**Figure S2a. Final path model for hemoglobin.** The path coefficients displayed at the arrows, are the partial correlations (correlations adjusted for other variables) between the variables, with corresponding p-values. Only significant partial correlations are displayed. Goodness of fit statistics: Chi-Square/DF= (2.4207/2) < 2. Root Mean Square Residual (RMSR)= 0.0075. Goodness of Fit Index (GFI)= 0.9986. Adjusted GFI (AGFI)=0.9851.



**Figure S2b. Final path model for erythrocyte count (RBC).** The path coefficients displayed at the arrows, are the partial correlations (correlations adjusted for other variables) between the variables, with corresponding p-values. Only significant partial correlations are displayed. Goodness of fit statistics: Chi-Square/DF = 5.0075/3. Root Mean Square Residual (RMSR)= 0.0114. Goodness of Fit Index (GFI)= 0.9971. Adjusted GFI (AGFI)= 0.9795.



**Figure S2c. Final path model for thrombocyte count (PLT).** The path coefficients displayed at the arrows, are the partial correlations (correlations adjusted for other variables) between the variables, with corresponding p-values. Only significant partial correlations are displayed. Goodness of fit statistics: Chi-Square/DF= 1.6030/3 <2. Root Mean Square Residual (RMSR)= 0.0088. Goodness of Fit Index (GFI) = 0.9991. Adjusted GFI (AGFI) = 0.9934.

### SAS code for the CALIS procedure

#### Initial model specified, which was not supported by the path analysis:

```

proc rank data=cesium.path_analysis normal = blom out = b;
var hb cs_soil log_cs_kg kids_age sex spring summer autumn;
ranks R_hb R_cs_soil R_log_cs_kg R_kids_age R_sex R_spring R_summer R_autumn;
run;

proc means data=b;
var R_hb R_cs_soil R_log_cs_kg R_kids_age R_sex R_spring R_summer R_autumn; run;

proc calis cov method=ml stderr data= b maxiter=500 mod OUTEST=pout effpart;
var R_hb R_log_cs_kg R_cs_soil r_kids_age R_sex R_spring R_summer R_autumn;
LINEQS
R_log_cs_kg= beta01 r_cs_soil + beta02 R_spring + beta03 R_summer + beta04 R_autumn
+ e_r_log_cs_kg,
R_hb =      beta11 R_log_cs_kg  + beta12 r_kids_age + beta13 R_sex + beta14
r_cs_soil + disturb;

STD
r_cs_soil = VE_r_cs_soil,
r_kids_age = VE_r_kids_age,
r_sex = VE_R_sex,
R_spring = VE_R_spring,
R_summer = VE_R_summer,
R_autumn = VE_R_autumn,
e_r_log_cs_kg = VE_e_R_log_cs_kg,
disturb = VE_disturb
;

COV

```

```

r_cs_soil r_kids_age = Csoilage,
r_cs_soil r_sex = Csoilsex,
r_cs_soil R_spring = Csoilspring,
r_cs_soil R_summer = Csoilsummer,
r_cs_soil R_autumn = Csoilautumn,
r_kids_age r_sex = Cagesex,
r_kids_age R_spring = Cagespring,
r_kids_age R_summer = Cagesummer,
r_kids_age R_autumn = Cageautumn,
r_sex R_spring= Csexspring,
r_sex R_summer = Csexsummer,
r_sex R_autumn = Csexautumn;
run;

```

## Final models specified, which were supported by the path analysis:

### \*Final model for hemoglobin;

```

proc calis cov method=ml stderr data= b maxiter=500 mod OUTEST=pout effpart;
var R_hb R_log_cs_kg R_cs_soil R_spring R_summer R_autumn;
LINEQS
R_log_cs_kg= BETA01 r_cs_soil + beta02 R_spring + beta03 R_summer + beta04 R_autumn
+ e_r_log_cs_kg,
R_hb = BETA11 R_log_cs_kg + beta13 R_summer + beta14
R_autumn+ disturb;

STD
r_cs_soil = VE_r_cs_soil,
R_spring = VE_R_spring,
R_summer = VE_R_summer,
R_autumn = VE_R_autumn,
e_r_log_cs_kg = VE_e_R_log_cs_kg,
disturb = VE_disturb
;

COV
r_cs_soil r_autumn = Csoilautumn,
r_cs_soil r_spring = Csoilspring,
r_summer r_autumn = Csummerautumn,
r_summer r_spring = Csummerspring,
r_autumn r_spring =Cautumnspring;
run;

```

### \*Final model for erythrocytes;

```

proc calis cov method=ml stderr data= b maxiter=500 mod OUTEST=pout effpart;
var R_rbc R_log_cs_kg R_cs_soil R_spring R_summer R_autumn;
LINEQS
R_log_cs_kg= BETA01 r_cs_soil + beta02 R_spring + beta03 R_summer + beta04 R_autumn
+ e_r_log_cs_kg,
R_rbc = BETA11 R_log_cs_kg + beta13 R_summer + disturb;

STD
r_cs_soil = VE_r_cs_soil,
R_spring = VE_R_spring,
R_summer = VE_R_summer,
R_autumn = VE_R_autumn,
e_r_log_cs_kg = VE_e_R_log_cs_kg,
disturb = VE_disturb
;

COV
r_cs_soil r_autumn = Csoilautumn,
r_cs_soil r_spring = Csoilspring,
r_summer r_autumn = Csummerautumn,

```

```
r_summer r_spring = Csummerspring,  
r_autumn r_spring =Cautumnspring;  
run;
```

### **\*Final model for thrombocytes;**

```
proc calis cov method=ml stderr data= b maxiter=500 mod OUTEST=pout effpart;  
var R_plt R_log_cs_kg R_cs_soil R_spring R_summer R_autumn;  
LINEQS  
R_log_cs_kg= BETA01 r_cs_soil + beta02 R_spring + beta03 R_summer + beta04 R_autumn  
+ e_r_log_cs_kg,  
R_plt = BETA11 R_log_cs_kg + beta14 r_autumn + disturb;  
  
STD  
r_cs_soil = VE_r_cs_soil,  
R_spring = VE_R_spring,  
R_summer = VE_R_summer,  
R_autumn = VE_R_autumn,  
e_r_log_cs_kg = VE_e_R_log_cs_kg,  
disturb = VE_disturb  
;  
  
COV  
r_cs_soil r_autumn = Csoilautumn,  
r_cs_soil r_spring = Csoilspring,  
r_summer r_autumn = Csummerautumn,  
r_summer r_spring = Csummerspring,  
r_autumn r_spring =Cautumnspring;  
run;
```