Variations in seed and post-harvest residue yields and residues quality of common bean (Phaseolus vulgaris L.) as a ruminant feedstuff

Variations in seed and post-harvest residue yields and residues quality of common bean (*Phaseolus vulgaris* L.) as a ruminant feedstuff

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ABSTRACT

Common bean is widely grown as a food legume and the post-harvest crop residues (CR) (i.e. haulm + pod wall (HPW)) are valuable as ruminant feedstuffs. The yields and constituents indicative of nutritive value for ruminants of the HPW from a wide range of common bean genotypes (G) were examined at 4 trial sites in Ethiopia during the 2013 main cropping season to assess the extent of genetic variation among G for simultaneous improvement of both HPW attributes and seed yield. Attributes measured were seed and HPW yields and the amounts of the morphological components, their concentrations of total nitrogen (N), neutral detergent fibre (aNDFom) and acid detergent fibre (ADFom), and the dry matter digestibility (DMD). The constituents were measured using near infrared

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spectroscopy (NIRS) and calibrations based on a large set of reference tropical forages and CR (including common bean), and were validated against other CR reference samples. These CR quality attributes were very well predicted with R^2v and RPDv ranging from 0.90 to 0.98 and 3.13-7.36, respectively. There was considerable variation in yields of HPW and seed, and in the proportions and attributes of the HPW fractions among the common bean G. Trial site means for yields of HPW and seed ranged from 0.74-2.54 t/ha and 0.79 - 2.62 t/ha, respectively while for N, aNDFom and ADFom concentrations and DMD of HPW ranged from 7.7-11.4 g/kg DM, 648-739 g/kg DM, 502-585 g/kg DM, and 467-570 g/kg DM, respectively. Environment (E), as represented by site, generally affected the yields of HPW and seed ($P<0.001$) and nutritive value of the HPW fractions ($P<0.05$) as feedstuffs. Seed yield was positively correlated with HPW yield both within and across trial sites ($r=0.92$; $P<0.0001$), but in general seed yield was not related to the N concentration. Across all sites, seed yield was positively correlated ($r=0.68$; $P<0.0001$) with haulm DMD. Although this correlation may be due to variation associated with E rather than G, it is nevertheless important in that selection for higher seed yield is likely to also increase metabolisable energy (ME) content of the HPW. There were G x E interaction effects on yields of HPW ($P<0.0001$) and seed ($P=0.011$), but these were generally less important than E effects which explained 52-58% of the variation. In conclusion the study demonstrated that it is possible to identify genotypes such as ECAB0081 which combine high yields of both seed and HPW, and with HPW attributes which improve their quality as ruminant feedstuffs.

Keywords: Common bean, Grain legumes, Haulm, Ruminants, East Africa

Abbreviations: ADFom, Acid detergent fibre corrected for the ash concentration of the residue; aNDFom, Neutral detergent fibre assayed with α–amylase and corrected for the ash concentration of the residue; CR, crop residues; CV, Coefficient of variation; DDM, Digestible dry matter; DM, Dry matter; DMD, dry matter digestibility; E, environment; G,

genotypes; HI, Harvest index; HPW, Haulm + pod wall (whole CR); IVOMD, In-vitro organic matter digestibility; LSD, Least significant difference (P=0.05); ME, Metabolisable energy; N, Concentrations of total nitrogen; NA, North Australian; NIRS , Near infrared spectroscopy; R^2, The coefficient of determination in calibration; R^2v, the coefficient of determination in validation values; RPDv, the relative predictive determinant = standard deviation of validation data set/ SEP(C); PUI, Potential utility index; SECV, Standard error of cross validation; SEP, Standard error of performance; SEP(C), the SEP corrected for bias.

1. Introduction

Phaseolus vulgaris L., often known as bean, common bean, haricot bean, kidney bean or field beans is a very important grain legume crop in eastern and southern Africa (Beebe et al., 2011), and also globally. Since common bean is usually consumed as the mature seed, the primary objective of genetic improvement programs is usually increasing seed yield. The amount and quality of post-harvest residues from common bean crops, although important in many smallholder crop-livestock systems as ruminant feedstuffs (Asfaw and Blair, 2014), are rarely considered (Beebe et al., 2013; Blümmel et al., 2012; Mekbib, 2002; Tullu et al., 2001). Crop residues (CR) from common bean crops are, as for other grain legume CR, usually retained after harvest and used as livestock feedstuffs during the dry season, and usually for ruminants (Yoseph et al., 2014). They are particularly important due to their generally higher N and metabolisable energy (ME) concentrations than cereal CR (Capper, 1990; López et al., 2005; Mekbib, 1997). Although use of common bean CR (haulm + pod wall (HPW)) during the dry season as ruminant feedstuffs is routine in crop-livestock systems, little quantitative information is available on their nutritive value compared to that for cereal CR (Capper, 1990; Nigam and Blummel, 2010). Objective information on the feeding value of common bean HPW is limited to a few reports involving goats (Ayoade et al., 1983; Pieltain et al., 1996) and cattle (Aredo and Musimba, 2003; Ebro et al., 2005). However, each of these studies was limited to a single

78 batch of HPW and usually without description of the genotype, environment, or the
79 morphological components.
80
81 Exploiting plant genetic variability and selection of more appropriate dual-purpose crop
82 genotypes that combine good food grain yields with high yield and quality of the CR as
83 feedstuffs (Blümmel et al., 2013; Lenné et al., 2003; Sharma et al., 2010) are likely to be
84 particularly appropriate for smallholder farmers.(De Groote et al., 2013). There appears to
85 be considerable potential for selecting improved genotypes of the CR of maize (Blümmel
86 et al., 2013; Lenné and Thomas, 2006), sorghum and pearl millet (Blümmel et al., 2003;
87 Sharma et al., 2010) and some grain legumes (Kafilzadeh and Maleki, 2012; Nigam and
88 Blummel, 2010; Prasad et al., 2010; Singh et al., 2003) without compromising grain yield.
89
90 The present study was designed to: (1) assess the extent of genetic variation in yields
91 of seed and HPW, and HPW quality attributes, among current popular common bean
92 genotypes (G) in East Africa, (2) examine the main and interaction effects of G and E, (the
93 latter was represented by site) on yields of seed and HPW, and on HPW quality attributes,
94 and (3) investigate the associations among HPW attributes and seed yield to evaluate the
95 consequences of such interrelationship for simultaneous improvement.
96
97 **2. Materials and methods**

98 *2.1. Trial site descriptions*

99 The study was undertaken during the 2013 cropping season at four trial sites in the
100 south (at *Shalla Wereda* (local administrative unit)), West (at *Bako-Tibe Wereda)*, South-
101 west (at *Boricha Wereda)* and North-west (at *Mandura Wereda)* regions of Ethiopia. The
102 trial sites and genotypes tested are summarized in Table 1. Sites were selected to
103 represent smallholder crop-livestock systems where common bean is an important grain

104 legume crop (Farrow, 2014). The genotypes were chosen to represent those well-adapted
105 and often grown by smallholder farmers in each of the regions, and for which seed was
106 readily obtainable. Not all genotypes were available at each site except at Boricha and
107 Mandura (Table 1).
108 TABLE 1 NEAR HERE
109
110 *Shalla* site located in the central Rift valley, represented an erratic and unreliable rainfall
111 characterized by a short rainy season from February/March through to April followed by a
112 main rainy season from June through to September, and with the remaining months
113 generally dry (Dinka et al., 2010). The mean annual minimum and maximum temperatures
114 were 14.0^{o}C and 28.7^{o}C, respectively. During the 2012 and 2013 cropping seasons the
115 annual rainfalls were 925 mm and 920 mm, respectively (MARC, 2014).
116
117 *Bako-Tibe* site was characterized by bimodal rainfall, with a short rainy season
118 beginning in March and continuing intermittently until the main rainy season from June to
119 October (Hassen et al., 2006). The minimum, maximum and mean monthly temperatures
120 recorded during the 2013 cropping season were 12.9, 29.1 and 21.0^{o}C respectively.
121 During the 2012 and 2013 cropping seasons the area received annual rainfall of 887 mm
122 and 1431 mm, respectively (Abebe and Feyisa, 2017).
123
124 *Boricha* site was characterized by a bimodal rainfall pattern, with a short rainy season
125 from February/March to April and a main rainy season from June/July to October (Asfaw et
126 al., 2013). Annual temperature varies from 20–33^{o}C (Quinlan et al., 2015).
127
128 The minimum, maximum, and annual mean temperatures at *Mandura* site were 16.8,
129 27.4 and 24.5^{o}C respectively (Emiru, 2014).

130 *2.2. Experimental design, field data collection and sampling*

131 At each trial site common bean genotypes were examined in a randomized complete-
132 block design with three replicates. The plot size was 3 x 4 m with 8 rows of plants (40 cm
133 between rows and 10 cm between plants within rows). Seeds were hand planted from the
134 27 June to the 24 August 2013 during the main rainy season (Table 1). Fertilizer urea
135 (46.0% w/w N, 4.5 kg N/ha), phosphorus pentoxide (43.6% w/w P, 11.5 kg P/ha) and
136 inoculant (HB-429) were applied. This rhizobium strain had been developed nationally
137 (National Soil Testing Centre, Addis Ababa, Ethiopia) and was that recommended and
138 commonly used by farmers in the area for common bean. Additional information about the
139 sites is available at a project website (N2Africa, 2014). At all sites the crop during the
140 previous season had been common bean.
141
142 At seed maturity plants were harvested from the middle 2m x 2m area of each plot. Two
143 rows were selected for each genotype for total biomass sampling. The number of plants
144 per harvest area was counted, harvested at the soil surface, and then carefully separated
145 avoiding leaf loss into haulms (stems and leaves) and pods. The pods were then
146 separated into the seed and pod wall. The haulm was separated to determine the
147 proportions of leaf and stem components. Following measurement of fresh weight the leaf,
148 stem, pod wall and seed samples were placed into cotton bags, sun-dried and later oven-
149 dried (60^{o}C for 48 h) to determine dry matter (DM). The remaining plants in each plot were
150 harvested to determine seed yield. The yields of HPW fractions, seed and total biomass
151 per unit area were calculated and the seed and HPW yields are reported on a dry weight
152 basis. Harvest index (HI) was calculated as the ratio of seed DM yield to total above
153 ground biomass DM yield at harvest. The potential utility index (PUI), a measure that
154 integrates seed yield with HPW digestible DM (DDM) yield, was calculated (Fleischer et
155 al., 1989) as:

156 $$\text{PUI} = \frac{\text{Seed DM yield} + \text{DDM HPW yield}}{\text{Total above ground biomass DM yield}}$$

157

158 *2.3. Haulm and pod wall quality analyses*

159 *2.3.1. Haulm and pod wall sample processing*

160 The leaf and stem fractions were recombined to provide haulm. Haulm and pod wall
161 samples were ground through a 1 mm screen using laboratory hammer mill (Christy and
162 Norris Limited, Chelmsford, UK) and stored at ambient temperature. Forage samples were
163 air-freighted to Australia and to meet quarantine requirements were gamma irradiated (25k
164 Gray) before transport to laboratories in Central Queensland University (CQU) and The
165 University of Queensland.

166

167 *2.3.2. Measurement of near infrared spectroscopy (NIRS) spectra*

168 All forage samples were scanned using a Foss 6500 monochromator (Silver Springs,
169 Maryland, USA) fitted with a spinning cup module. This instrument measured spectra at 2
170 nm intervals over the range 400 – 2500nm. Duplicate subsamples (~ 3 g air-dry) were
171 packed into the spinning cup cells and scanned as described by Coates and Dixon (2011).
172 Spectral data were collected with ISI-Scan (Infrasoft International version 4.6.11) software.
173 Full diagnostic tests on the Foss 6500 NIR Systems monochromator were performed daily
174 and in addition, the stability of the instrument was monitored by scanning a laboratory
175 standard sample [Buffel grass (*Cenchrus ciliaris*)] 1-4 times daily.

176

177 Chemometric analyses were conducted with WinISI software version 1.5 and the
178 spectral data were examined to relate infrared spectra to reference values (Shenk and
179 Westerhaus, 1991a). Since the samples of the present study were scanned on a different
180 instrument (the CQU instrument) of the same model to that used to develop the original
181 North Australian (NA) forage calibration data set (CSIRO instrument), the former spectra

were corrected for differences between the instruments. A set of ten sealed standards were scanned a number of times with each monochromator and the ISI software 'Instrument Standardisation' procedure used to correct the differences. The CSIRO instrument was considered as the 'primary' instrument and the CQU instrument as the 'secondary' instrument.

2.3.3. Prediction of sample constituents from the NIRS spectra and NIRS calibration

Calibrations were developed in two stages. First, the concentrations of total N, neutral detergent fibre (NDF) and acid detergent fibre (ADF), and dry matter digestibility (DMD), in the forages were predicted using the established in-house northern Australian (NA) forage calibrations which had been developed for grasses and legumes in the tropical northern Australian rangelands (NA calibration: D. B. Coates and R. M. Dixon, unpublished results). Most of the samples (n = 409 – 1688 depending on the attribute) were C_4 native and naturalized grasses such as the genera *Heteropogon, Chrysoponon, Urochloa, Astrebla, Bothriochloa, Dichanthium, Cynodon, Brachiaria, Aristida spp*., and the introduced grasses *Cenchrus, Chloris, Panicum spp*. There were also legumes comprising *Stylosanthes scabra* and *S. hamata* and other common introduced tropical and temperate legumes. In a second stage these NA forage calibrations were expanded with additional reference samples comprising a subset of the CR samples (representing species, various morphological fractions, genotypes, year, sites and grain legume crop growth stages at harvest) derived from the present and similar experiments with CR of grain legumes and maize stover from Ethiopia. These additional reference samples were identified on the basis of high standardized global H values (Mahalanobis distance)^2/f, where f is the number of factors in the model (Shenk and Westerhaus, 1991b) with stratification so that each of the morphological fractions of maize and grain legume species, genotypes, year, sites and grain legume crop growth stages at harvest was represented. Of the CR samples

208 from Ethiopia (maize 1306, common bean 652, chickpea 482, faba bean 351 and soybean
209 60) a subset of 470 samples (maize n=203; common bean n=97, chickpea n=80, faba
210 bean n=65 and soybean n=25; 15-42% of each subclass) were selected as reference
211 samples. These reference samples were analysed for DMD, and concentrations of total N,
212 NDF assayed with α–amylase and corrected for the ash concentration of the residue
213 (aNDFom) and ADF corrected for the ash concentration of the residue (ADFom), by
214 conventional wet chemistry laboratory procedures as described below. These reference
215 samples were then included with the calibration data from NA and the combined data used
216 to calculate and validate improved calibration equations.
217
218 The calibration for each attribute was developed from the reference samples and the
219 NIR spectra using modified partial least squares (Shenk and Westerhaus, 1991b) and
220 WinISI II (version 1.5) software (Infrasoft International, Port Matilda, PA, USA). Critical 'T'
221 and 'H' outlier values were set at 4 and 10, respectively; and where these critical values
222 were exceeded the sample was eliminated as an outlier. Spectra with standardized global
223 H values > 3.0 were also removed as spectral outliers. Calibration development used two
224 outlier elimination passes, a maximum of 16 terms and four cross-validation groups with
225 principal component analysis and 2,4,4,1 math treatment over the 1100-2500 nm
226 wavelength band. The revised calibrations were then used to predict the attributes in the
227 common bean CR samples for the present experiment.
228
229 *2.3.4. NIRS validation*
230 The robustness of the calibrations was evaluated using established validation
231 procedures. The samples within each species of CR from Ethiopia were randomly divided
232 into two subsets A and B. The NA data were combined with the A and B subsets data (i.e.
233 data set NA+A and NA+B) to develop calibration equations. These were then validated by

examining the errors associated with the prediction of the B and A data sets, respectively in terms of the standard error of performance (SEP), the SEP corrected for bias [SEP(C)] and the coefficient of determination in validation values (R^2_v). The relative predictive determinant (RPDv = Standard deviation of validation set data/ SEP(C)) was also calculated (Williams, 2001). In the current study, R^2v and RPDv were used to classify the performance of a given NIRS equation according to Williams (2001). Since the RPDv was greater than 3 the NIRS equation was considered to be successful for the present analytical purposes as for most NIRS applications for agricultural products (Williams, 2001).

2.3.5. Wet chemistry analysis of selected reference samples for NIRS

Wet chemistry of the CR samples from Ethiopia was conducted to generate reference samples to expand NA forage calibrations and then develop new calibrations for each attribute which were then used to predict the attributes in the common bean CR samples for the present experiment. The lab analyses were done in duplicate. Total N (0.15-0.18 g samples) was determined using a LECO combustion system (TruMac® CN analyser 2013 version1.3x) (LECO Corporation, St. Joseph, MI, USA) which complies with AOAC (2005) analysis #990.03. aNDFom concentration was analysed using heat stable α-amylase and sodium sulphite followed by incineration of the fibre residue to correct for ash (aNDFom) (Mertens, 2002; Mertens, 2011). ADFom concentration was determined according to Van Soest et al. (1991). Both the aNDFom and ADFom were analysed using anANKOM^{200} Fibre Analyser (Model200, ANKOM Technology, Macedon, NY, USA) with F57 filter bags (ANKOM 57 micron pore size-ANKOM Technology, NY). In-vitro DMD was determined with the filter bag method in DAISY^{II} incubator (ANKOM Technology, Macedon, Fairport, NY, USA). A laboratory standard sample *(Astrebla* spp C_4 grass) and empty blank bags were included in each batch. Laboratory errors in the current study were controlled at an

acceptable level, with a coefficient of variation between duplicate analyses of less than 5%.

2.4. Statistical analysis

Analysis of variance was undertaken using the General Linear Model procedure in Statistical Analysis System (SAS, 2009) software. The model $Y_{ij}= \mu + t_i + e_{ij}$ was used for each of the trial site, where Y_{ij} represents the j^{th} observation ($j = 1, 2,\ldots..., n_i$) on the i^{th} genotype($i = 1, 2, \ldots, k$). μ represents overall mean effect, t_i represents the i^{th} genotype effect and e_{ij} represents the random error present in the j^{th} observation on the i^{th} genotype.

The data were not analysed across trial sites *Shalla* and *Bako-Tibe*, or across all sites, due to the differences in the genotypes tested at *Shalla*, *Bako-Tibe* and *Boricha*. However, because the same genotypes were used at *Boricha* and *Mandura* the model $Y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ij}$ was used to analyse site (i.e. environment (E)) effects across these two sites, where Y_{ij} was the mean of genotype (G) *i* in environment *j*, μ was the overall mean, α_i and β_j were the main genotype and environment effects, $(\alpha\beta)_{ij}$ was the G x E interaction effect, and ε_{ij} was the residual associated with genotype *i* in environment *j*. Linear relationships between yield, composition and residue digestibility were analysed by SAS Proc Corr. The comparison of means between genotypes and environments was carried out using the least significant difference (LSD) test where the F-tests indicated significant difference ($P<0.05$).

3. Results

3.1. Development of the modified NIRS calibrations and the expected errors in the NIRS measurement of attributes of the samples

The frequent measurements (n = 91) of the laboratory standard indicated stability of the instrument with coefficients of variation of 0.687, 0.290, 0.323 and 0.449% for total N concentration, DMD, aNDFom and ADFom, respectively. There was a wide range in the reference values for each of the constituents (n=2068, range 2.2-54.5 g/kg DM for N; n=1320, range 253-891 g/kg DM for DMD; n= 877, range 222-886 g/kg DM for aNDF and n= 855, range 181-704 g/kg DM for ADFom) in both the NA and the Ethiopian CR data sets. The coefficients of determination in calibration (R^2) of known forage quality values on NIRS values were ≥ 0.93 for the four constituents, with that for total N being highest at 0.98. Inclusion of the Ethiopian CR data set into the NA forage data set resulted in improvement in calibration R^2 values for DMD (0.88 vs 0.93). The SECV was reduced slightly for each attribute but there were no changes in the R^2 values for total N and the fibre fractions.

The validation statistics of the NIRS calibration (NA +A) from predicting half of the common bean CR samples (validation set B) showed that N (n=48) and aNDFom (n=49) concentrations and DMD (n=46) were successfully predicted by NIRS with $R^2v > 0.90$ (range 0.91-0.97) and RPDv >3 (range 3.07-5.06). The ADFom (n=49) concentration was predicted less successfully, with $R^2v = 0.76$ and RPDv = 2.02. The validation statistics of the NIRS calibration (NA +B) from predicting half of the common bean CR samples (validation set A) showed that N (n=49), aNDFom (n=48) and ADFom (n=48) concentrations were successfully predicted with $R^2v > 0.91$ (range 0.92-0.99) and RPD_v >2.9 (range 2.95-8.57). However, HPW DMD was not well predicted ($R^2v = 0.44$ and RPDv = 1.19). The final calibration used, which was calculated from the NA+A+B data set,

would be expected to further improve R^2v and RPDv values and reduce the prediction error as SEP or SEP(C). The R^2v and RPDv for prediction of common bean HPW (n=97) from the NA+A+B calibration in the present experiment were ≥0.90 and >3, respectively. Also the SEP was less than 45.2 g/kg for DMD, and less than 1.6, 41.6 and 33.4 g/kg for the total N, aNDFom and ADFom concentration, respectively. Generally common bean HPW (n=97) quality attributes as total N, DMD, aNDFom and ADFom were very well predicted by NIRS using the NA+A+B with R^2v and RPDv ranging from 0.90 to 0.98 and 3.13-7.36, respectively.

3.2. Variations in seed and post-harvest residue yields and residue yield components among common bean genotypes

3.2.1. Seed and post-harvest residue yields and harvest index

Seed yield varied among genotypes at *Shalla* and *Mandura* ($P < 0.001$), but not at sites *Bako-Tibe* and *Boricha* ($P>0.05$) (Tables 2 and 3). Similarly, HPW yield and HI generally varied among genotypes, the exceptions being at *Bako-Tibe* for HPW and at *Boricha* for HI. There were genotype differences ($P<0.01$) in PUI only at *Shalla*. The highest seed (3.47 t/ha) and HPW (3.36 t/ha) yields were observed for genotypes Nasir and ECAB0081 at *Shalla*, and the lowest for Argene and Loko were 0.46 t/ha for seed at *Mandura* and 0.52 t/ha for HPW at *Bako-Tibe* (Tables 2 and 3).

There were wide ranges across all sites in yields of seed (mean 1.42, range 2.05 - 3.47 t/ha) and HPW (mean 1.77, range 1.59-3.36 t/ha), and in HI (mean 0.51, range 0.47-0.56), and the greatest ranges were observed at *Shalla*. Genotype ECAB0081 at *Shalla* gave the highest seed and HPW yields but did not consistently provide higher HI (Table 2). Similarly higher yielding genotypes at *Mandura* did not consistently provide higher HI (Table 3). The lowest yielding genotype Awash-1 at *Shalla* and *Mandura* (Tables 2 and 3) also tended to

have a higher HI. When data were combined across *Boricha* and *Mandura* (Table 3) the differences among genotypes were substantial (P <0.05 and P< 0.001) for seed and HPW yields. Also site (i.e. E) affected yields of seed (P=0.0007) and HPW (P<0.001). Genotype x E also affected yields of seed (P=0.011) and HPW (P<0.0001). In general, the variation observed among genotypes at each trial site was higher for HPW yield than seed yield.

TABLE 2 NEAR HERE

TABLE 3 NEAR HERE

3.2.2. Leaf, stem and pod wall fractions

The stem fraction always constituted the highest proportion of HPW at harvest (means ranging from 633-692 g/kg DM) followed by pod wall (256-299 g/kg DM). Leaf comprised only 52-69 g/kg DM in HPW and was ≤ 87 g/kg DM (Tables 2 and 3). The proportion of pod wall to seed in the whole pods ranged from 191-267 g/kg DM (values not shown). There were generally large differences (P<0.01) amongst genotypes in the proportions of leaf, stem and pod wall fractions in the HPW (Tables 2 and 3), and in leaf to stem ratio (P<0.0001) (values not shown). When data were combined across *Boricha* and *Mandura* (Table 3) the leaf and stem proportions were affected by genotype (P <0.0001; P=0.035), and tended to differ for pod wall proportion (P=0.061). Environment had no effect (P>0.35) on the proportion of any of the morphological fractions but there was a G X E interaction for the proportions of leaf (P<0.0001) and stem (P=0.04).

3.3. Variations in quality attributes of post-harvest residue fractions and HPW among common bean genotypes

Trial site means for concentrations of N, aNDFom and ADFom and for DMD in HPW ranged from 7.7-11.4 g/kg DM, 648-739 g/kg DM, 502-585 g/kg DM, and 467-570 g/kg

DM, respectively (Tables 4 and 5). There were also wide differences (P<0.01) amongst the HPW and the pod wall and haulm fractions of the genotypes for each of the laboratory nutritive quality attributes measured at *Shalla* and *Bako-Tibe* (Table 4). For instance at *Shalla* the mean total N concentration in HPW varied two-fold (range 6.1-12.5 g/kg DM, mean 9.6 g/kg DM). At sites *Bako-Tibe* and *Mandura* the mean total N concentration in HPW varied from 8.6-13.2 g/kg DM and from 6.4-11.1 g/kg DM, with mean values of 11.4 g/kg DM and 8.5 g/kg DM, respectively (Tables 4 and 5). Similarly, large variations (range 139 and 132 g/kg DM units) in DMD were observed at *Shalla* and *Bako-Tibe,* respectively (Table 4). In general HPW quality attributes for genotype ECAB0081 (e.g. HPW DMD 647 g/kg DM and total N 12.5 g/kg DM) were higher than for other genotypes at *Shalla* (Table 4). This genotype also had higher PUI than the other genotypes (Table 2).

TABLE 4 NEAR HERE

TABLE 5 NEAR HERE

When data were combined across *Boricha* and *Mandura* (Table 5), site affected the DMD (P=0.020), and concentrations of N (P=0.017), aNDFom and ADFom (P<0.001) in HPW. Similarly E had significant effects on all fodder quality parameters measured for the HPW fractions but did not affect N concentration or DMD of the pod wall fraction. The G x E interaction was significant (P<0.05) for all quality parameters measured for the pod wall fraction but not for the haulm or the HPW.

3.4. Relationships between seed and HPW yields, and total biomass yield

Across all trial sites there was a positive relationship between the yields of HPW and seed both within each site and for data pooled across sites (r=0.92; P<0.0001; n=33) (Figure 1). Thus there was also a strong association (r=0.98; P<0.0001; n=33) between

384 seed yield and total biomass yield across sites (values not shown). However there was no
385 general association between seed yield and HI.
386
387 FIGURE 1 NEAR HERE
388

389 *3.5. Relationships between seed yield and HPW quality attributes*

390 There were no relationships (P>0.05) between seed yield and HPW DMD at any of the
391 trial sites considered independently, but there was a positive association (r= 0.68;
392 P<0.0001; n=33) in the pooled data between seed yield and HPW DMD (Figure 2). In the
393 pooled data there was no association (r= -0.22; P=0.22; n=33) between seed yield and
394 HPW N concentration (Figure 3), although this relationship was significant at *Mandura* (r= -
395 0.90; P<0.001; n=9).
396
397 FIGURE 2 NEAR HERE
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399

400 **4. Discussion**

401 *4.1. Variations in seed and post-harvest residue yields and residue yield components*
402 *among common bean genotypes*

403 The large genetic variation among common bean genotypes in yields of seed and HPW
404 in the present study, particularly at Shalla and *Mandura*, were comparable with the large
405 variation in seed yield often reported (Araújo and Teixeira, 2003; Tadesse et al., 2014).
406 Furthermore in the present study the variation among genotypes was generally higher for
407 HPW yield than for seed yield. The positive relationship between yields of seed and haulm
408 (Figure 1) indicated that selection of genotypes for high seed yield will on average

409 increase haulm yield almost proportionately (by 98%), although there is likely to some
410 variation in HI. Similarly Scully and Wallace (1990) and Erskine et al. (2000) reported that
411 genotypes with higher seed yields had higher haulm yields also indicating that yields of
412 seed and haulm can be increased concurrently. The observation in the present study that
413 haulm DMD generally increased considerably (up to 150 g/kg units of DMD) (Figure 3), is
414 also important since it indicates that selection for increases in seed yield are likely to
415 increase, and is not likely to decrease, the ME content of the CR for ruminants.
416
417 The importance of G and G x E differences varied among the trial sites and therefore E.
418 At *Bako-Tibe* there were no differences in seed or haulm yields due to genotype but this
419 was associated with very low yields (means 0.79 and 0.74 t/ha, respectively) (Table 2)
420 compared with those in the other three environments (mean 1.32-2.62 and 1.61-2.54 t/ha,
421 respectively). This demonstrated the importance of E effects. In addition at *Boricha* and
422 *Mandura* where the G x E interactions could be examined there were interaction effects on
423 the yields of both seed and HPW, and on the morphological proportions of leaf and stem
424 (Table 3). These yields attributes demonstrated G x E interactions were most affected by
425 site or E (52-58%) (values not shown) and did not have a stable yield performance across
426 sites. Other studies have also demonstrated G x E interactions for seed yield in common
427 bean (Gebeyehu and Assefa, 2003; Mekbib, 2002; Mekbib, 2003) also indicating that
428 selection of genotypes for yield of both seed and haulm must also consider the
429 environment.
430
431 *4.2. Variations in quality attributes of post-harvest residue fractions and HPW among*
432 *common bean genotypes*
433 As the stem component usually comprised about 630-690 g/kg of the CR the nutritive
434 value of the entire CR was highly dependent on the nutritional quality of the stem. Most of

435 the remaining CR fraction comprised pod wall which was much lower in both aNDFom and
436 ADFom, and higher in DMD (ranging from 616-660 g/kg across sites) than HPW fraction.
437 When the pods are shelled to remove the seed there may be opportunity to collect pod
438 wall and use this CR fraction separately to provide a feedstuff of higher ME concentration.
439 However the pod wall was, like haulm, low in N concentration and would require additional
440 dietary N to provide for even moderate production by ruminants. Leaf is well known to be
441 high in N and digestibility (Pieltain et al., 1996) and to be usually associated with high
442 voluntary intake, but because it comprised only a small proportion of the CR (generally
443 only 50-70 g/kg) had little effect on the nutritive value of the entire CR. The low proportion
444 of leaf in the CR was most likely associated with extensive loss of leaf during the later
445 stages of plant growth and/or at harvest and was an important factor in the low nutritive
446 value of the CR (Asfaw and Blair, 2014; Larbi et al., 1999). Selection of genotypes and
447 modification of harvest procedures (earlier harvesting of CR soon after attaining
448 physiological maturity before the quality deteriorates) to increase the proportion of leaf in
449 the CR is likely to have important effects to increase the nutritional value of the CR. The
450 proportion of leaves in forage declines and this is usually more pronounced in food
451 legumes than cereals (Batterham and Egan, 1986). The differences observed between
452 leaf-rich and stem-rich straws of legumes in general, and common bean in particular,
453 confirm the importance of morphological composition of the legume CR to its nutritive
454 value (López et al., 2005). Moreover, if genotypes that retain their leaf at crop
455 physiological maturity can be identified and this attribute selected effectively, it could be
456 included by plant breeders into genotypes selection criteria with a major impact in
457 increasing the nutritive value of the CR.
458
459 There was substantial variation among genotypes in the present study in N
460 concentration and DMD of the CR with the genotypes ECAB0081, GLP2 and Awash-1 at

461 *Shalla* and genotype H-Dume at *Bako-Tibe* being of higher value (Table 4). These higher
462 values could be partly attributed to the differences in the proportions of the morphological
463 fractions or higher leaf proportion in the HPW (Table 2). Conversely the lower mean DMD
464 of the HPW at *Bako-Tibe* than *Shalla* and *Boricha* might be attributed to the higher stem
465 (692 g/kg) and the lower leaf (52 g/kg) and pod wall (256 g/kg) in the HPW although the
466 relative importance of genotype and environment on these differences could not be
467 identified. These results indicate that there are opportunities to identify genotypes which
468 provide CR of higher value as ruminant feedstuffs in specific environments. However,
469 additional diet N will still be required to provide for the requirements for animal productivity
470 rather than maintenance, especially if the common bean CR are fed mixed with cereal CR
471 of usually even lower N concentration. It is generally accepted that forages need to
472 contain at least 10 g N/kg with a DM digestibility of 500 g/kg DM to provide for
473 maintenance or slow growth of ruminants, while a DMD of 550-600 g/kg DM is needed for
474 moderate growth or for lactating animals (Minson, 1990; Van Soest, 1994). It is clear that
475 the nutritional value as concentrations of N and ME of common bean CR is generally low
476 and when fed alone is suitable only for maintenance or moderate growth of non-lactating
477 animals.
478
479 The few studies available have reported the composition of common bean residues in
480 the range 0.8 – 1.6 g N/kg DM, 510-690 g NDF/kg DM, 373-565 g ADF/kg DM, and DMD
481 of 530-590 g/kg DM (Aredo and Musimba, 2003; Ayoade et al., 1983; Ebro et al., 2005;
482 López et al., 2005). Voluntary intake by cattle and goats has ranged from 18-30 g DM/kg
483 live weight and hence has tended to be higher than usually observed with cereal CR
484 harvested at grain maturity (Capper, 1990). For instance voluntary intake of maize stover
485 by cattle and sheep ranged from 14-19 g DM/kg live weight, respectively (Aredo and
486 Musimba, 2003; Koralagama et al., 2008; Tolera and Sundstøl, 2000). The mean values

for the nutritional attributes of common bean CR observed in the present study were generally in accord with these previous reports although both the N concentration and DMD tended to be lower in the present study. Only at *Bako-Tibe* were the concentrations of N, and at *Shalla* the DMD of the HPW, comparable with those reported in the previous studies.

There is also substantial variation in chemical composition and digestibility of haulms associated with genotype and environment of other grain legume crops such as groundnut, lentil and cowpea genotypes has also been reported (Erskine et al., 1990; Grings et al., 2012; Larbi et al., 1999; Omokanye et al., 2001). For example in a wide range of groundnut cultivars (*Arachis hypogaea*) and breeding lines (n=860), Nigam and Blummel (2010) reported that haulm N content varied almost two-fold (mean=1.7, range 12-23 g/kg DM), and IVOMD varied ($P<0.0001$) by almost 100 g/kg DM units (mean 563; range 517-611 g/kg DM). Similarly a wide range has been reported in lentil haulm DMD which varied from 400-490 g/kg DM, and CP content which varied from 58-69 g/kg DM, among cultivars (Erskine et al., 1990).

4.3. Relationships between seed and HPW yields, and feedstuff quality attributes of post-harvest residue

The relationships between seed and biomass yield and quality in food crops are important since crops tend to be bred for seed production even though the biomass is also widely used for livestock feeding in developing countries. Understanding these relationships helps to support the introduction of breeding objectives beyond simply seed yield. The positive relationships between yields of seed and both haulm and total biomass in the present study are comparable with the associations previously reported for common bean (Araújo and Teixeira, 2003; Scully and Wallace, 1990). Although seed yield has also

513 been positively related to HI (Araújo and Teixeira, 2003; Tar'an et al., 2002) it appears that
514 the biomass yield is the most important attribute for yield improvement in common bean
515 (Scully and Wallace, 1990).
516
517 Negative associations between seed yield and HPW N concentration at Mandura may
518 have been due to the translocation of N to seed during crop maturity (Araújo and Teixeira,
519 2003). However the general absence in the present study of strong inverse relationships
520 between total N concentration of haulm with seed yield and the general positive
521 association for DMD indicate that there is opportunity to select for higher seed yield
522 without adverse effects, or with an improvement, in the nutritional value of the HPW as a
523 ruminant feedstuff.
524
525 Fodder related attributes of the CR have not been considered as selection criteria for
526 new varieties of common bean in EA. However, as Schiere et al. (2004) have pointed out it
527 would be valuable for plant breeders to consider higher total biomass yield, at least
528 equivalent HI, and higher leaf to stem ratio and stem quality as selection criteria to improve
529 whole plant value rather than considering only for the value of higher seed yield. Similar
530 arguments have been made in relation to plant breeding for lentil (Kusmenoglu and
531 Muehlbauer, 1998; Tullu et al., 2001) and other grain legumes (Kafilzadeh and Maleki,
532 2012; Nigam and Blummel, 2010; Prasad et al., 2010; Singh et al., 2003). Blümmel et al.
533 (2012) also concluded that in groundnut there are strong opportunities for breeding in
534 parallel for high productivity and high fodder quality even under drought stress.
535
536
537

5. Conclusions

The CR of common bean as ruminant feedstuffs are important in many crop-livestock smallholder farming systems but the yield and nutritive value of the CR component are seldom considered during the selection of improved genotypes. The present study showed that there is considerable variability in the yield and nutritive value of the CR among genotypes which are widely grown in East Africa and that selection for these attributes need not compromise seed yield. However collaboration among plant breeders, livestock scientists and farmers is needed to achieve such outcomes.

Conflict of interest

The authors have no conflicts of interest to declare.

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777

Table 1

Trial sites description, genotypes tested and field operation for trials conducted at four sites in 2013.

	Shalla	*Bako-Tibe*[4]	*Boricha*	*Mandura*
GPS coordinates	7º281'N, 38º447'E	Comprised two sub-sites about 5 km apart at *Dambi Dima,* 9º110'N, 37º800,E and *Oda Haro,* 9º400'N, 37º190'E	6º947'N and 38º222'E	11º118'N and 36º722'E
Agro-ecology[1]	Semi-arid	Sub-humid	Sub-moist hot to warm lowland	Sub-humid hot to warm lowland
Soil type[2]	Andosols	Alfisols	Eutric fluvisols	Red laterite
Mean annual rainfall (mm)[2,3]	773	1303	963	1942
Altitude (MASL)	1696	1692	1818	1477
Genotypes	A-Melka, Awash-1, Deme, Dimtu, Dinknesh, ECAB0056, ECAB0081, GLP2 and Nasir	Anger, Dimtu, Dinknesh, H-Dume, Ibado and Loko	A-Melka, Argene, Awash-1, Dimtu, Dinknesh, H-Dume, Ibado, Nasir and SARI	A-Melka, Argene, Awash-1, Dimtu, Dinknesh, H-Dume, Ibado, Nasir and SARI
Date of sowing	03 July	27 June	07 August	24 August
Date of harvesting	23 and 29 Oct	13 and 26 Oct	07 and 11 Nov	19 and 21 Nov

GPS, Geographic positioning system; MASL, Meters Above Sea Level;
Source, [1] (Farrow, 2014) [2] (Asfaw et al., 2013; Emiru, 2014; MARC, 2014; Negassa et al., 2005); [3] Long term mean annual rainfall for the years 1978-2013,1982-2014, 1996-2012 and 1987-2013 at *Shalla, Bako-Tibe, Boricha and Mandura* sites, respectively;
[4] The measurements at the two sub-sites (each 3 replications) were averaged and considered as the *Bako-Tibe* site.

Table 2

Yields of seed and HPW, and HI, PUI and HPW morphological fractions of common bean genotypes at *Shalla* (n = 3) and *Bako-Tibe* (n=3) in 2013.

	Yield (t/ha)				Morphological fractions (g/kg DM)		
Genotype	Seed	HPW	HI	PUI	Leaf	Stem	Pod wall
Shalla							
A-Melka	2.18^{d}	1.75^{e}	0.55^{ab}	0.79^{c}	64^{d}	692^{b}	243^{c}
Awash-1	2.05^{d}	1.59^{e}	0.56^{a}	0.81^{ab}	65^{cd}	688^{b}	247^{c}
Deme	2.83^{bc}	2.91^{bc}	0.49^{cd}	0.80^{c}	75^{b}	630^{cd}	295^{b}
Dimtu	2.53^{dc}	2.47^{d}	0.51^{cd}	0.76^{d}	48^{e}	733^{a}	220^{d}
Dinknesh	2.37^{dc}	2.30^{d}	0.51^{cd}	0.77^{d}	65^{cd}	689^{b}	245^{c}
ECAB0056	2.55^{dc}	2.83^{c}	0.47^{d}	0.77^{d}	65^{cd}	691^{b}	243^{c}
ECAB0081	3.13^{ab}	3.36^{a}	0.48^{cd}	0.82^{a}	84^{a}	614^{c}	302^{ab}
GLP2	2.52^{dc}	2.47^{d}	0.50^{cd}	0.81^{abc}	76^{b}	631^{c}	293^{b}
Nasir	3.47^{a}	3.19^{ab}	0.52^{bc}	0.79^{c}	70^{c}	620^{c}	310^{a}
Mean	**2.62**	**2.54**	**0.51**	**0.79**	**68**	**665**	**266**
Significance	0.0005	<0.0001	<0.004	<0.0001	<0.0001	<0.0001	<0.0001
CV (%)	11.3	7.5	4.7	1.2	4.3	1.4	2.9
Bako-Tibe							
Anger	0.74	0.60	0.55^{ab}	0.74	41^{d}	692^{c}	268^{c}
Dimtu	0.79	0.71	0.52^{abc}	0.74	38^{e}	712^{b}	250^{d}
Dinknesh	0.78	0.77	0.50^{bc}	0.74	45^{c}	674^{d}	281^{b}
H-Dume	0.93	0.95	0.49^{c}	0.77	77^{a}	635^{e}	288^{a}
Ibado	0.86	0.85	0.50^{bc}	0.71	46^{c}	710^{b}	243^{d}
Loko	0.67	0.52	0.57^{a}	0.76	68^{b}	726^{a}	206^{e}
Mean	**0.79**	**0.74**	**0.52**	**0.75**	**52**	**692**	**256**
Significance	0.892	0.367	0.030	0.079	<0.0001	<0.0001	<0.0001
CV (%)	34.8	33.6	4.8	3.0	2.4	0.6	1.6

Means with no superscript letters with a column of each trial site are not significantly different (P>0.05).

Table 3

Yields of seed and HPW, and HI, PUI and HPW morphological fractions of common bean genotypes at *Boricha* (n=3)*, Mandura* (n=3) and across both sites (n=6) in 2013.

	Yield (t/ha)				Morphological fractions (g/kg DM)		
Genotype	Seed	HPW	HI	PUI	Leaf	Stem	Pod wall
Boricha							
A-Melka	1.81	2.43^{a}	0.42	0.68	53^{ef}	734	213
Argene	1.28	1.98^{ab}	0.40	0.69	86^{a}	604	310
Awash-1	1.64	2.18^{ab}	0.44	0.70	77^{abc}	651	273
Dimtu	1.24	1.36^{b}	0.48	0.72	50^{f}	692	258
Dinknesh	2.09	2.55^{a}	0.44	0.71	78^{ab}	604	318
H-Dume	1.88	2.50^{a}	0.43	0.71	77^{ab}	598	324
Ibado	1.20	1.40^{b}	0.46	0.71	64de	670	266
Nasir	2.03	2.59^{a}	0.44	0.71	65^{cde}	569	366
SARI	1.82	2.55^{a}	0.42	0.69	71^{bcd}	681	249
Mean	**1.67**	**2.17**	**0.44**	**0.70**	**69**	**645**	**286**
Significance	0.188	0.033	0.895	0.961	<0.0001	0.053	0.215
CV (%)	27.9	23.0	14.9	6.7	10.2	9.1	22.7
Mandura							
A-Melka	0.92^{d}	1.08^{d}	0.46^{b}	0.73	87^{a}	651^{ab}	263^{c}
Argene	0.46^{e}	0.59^{e}	0.44^{b}	0.72	84^{ab}	668^{a}	247^{c}
Awash-1	1.14^{cd}	1.20^{d}	0.49^{a}	0.74	81^{b}	626^{bcd}	293^{b}
Dimtu	1.59^{b}	1.96^{bc}	0.45^{b}	0.70	56^{ef}	637^{bc}	307^{ab}
Dinknesh	1.55^{b}	1.88^{bc}	0.45^{b}	0.70	53^{f}	642^{bc}	306^{ab}
H-Dume	1.88^{a}	2.29^{a}	0.45^{b}	0.71	54^{ef}	624^{cd}	322^{a}
Ibado	1.61^{ab}	2.07^{ab}	0.44^{b}	0.73	74^{c}	604^{d}	322^{a}
Nasir	1.35^{bc}	1.72^{c}	0.44^{b}	0.73	64^{d}	621^{cd}	316^{ab}
SARI	1.39^{bc}	1.75^{bc}	0.44^{b}	0.72	58^{e}	626^{bcd}	316^{ab}
Mean	**1.32**	**1.61**	**0.45**	**0.72**	**68**	**633**	**299**
Significance	<0.0001	<0.0001	0.0088	0.147	<0.0001	0.0038	0.0002
CV (%)	12.3	11.2	2.9	2.3	3.9	2.4	5.4
Environment							
Boricha	1.67^{a}	2.17^{a}	0.44	0.70	69	645	286
Mandura	1.32^{b}	1.61^{b}	0.45	0.72	68	633	299
Significance							
Genotype (G)	0.0006	0.0003	0.84	0.951	<0.0001	0.035	0.061
Environment (E)	0.0007	<0.0001	0.31	0.080	0.4727	0.357	0.361
G x E	0.011	<0.0001	0.83	0.761	<0.0001	0.042	0.257
$LSD_{0.05}$	0.40	0.45	0.06	0.04	6.0	53.0	59.0

Means with no superscript letters with a column of each trial site are not significantly different (P>0.05).

Table 4

Total N concentration, dry matter digestibility and fibre fractions (g/kg DM) of pod wall, haulm (stem+ little leaf) and HPW of common bean genotypes at *Shalla* (n=3) and *Bako-Tibe* (n=3) in 2013.

	Total N			DMD			aNDFom			ADFom		
Genotype	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW
Shalla												
A-Melka	7.5	6.8^{de}	7.0^{cd}	675^{bc}	489de	535^{ef}	564^{cd}	749^{ab}	704^{ab}	416^{b}	591^{a}	548^{ab}
Awash-1	8.7	12.5^{ab}	11.6^{a}	624^{e}	554^{c}	571^{cd}	607^{a}	641^{d}	632de	445^{a}	510^{c}	494de
Deme	8.2	10.1^{bc}	9.6^{b}	696^{ab}	557^{bc}	598^{bc}	528^{e}	650^{d}	614^{ef}	380^{c}	508^{c}	470^{e}
Dimtu	6.2	6.1^{e}	6.1^{d}	657^{cd}	466^{e}	508^{f}	582^{bcd}	761^{a}	721^{a}	418^{b}	597^{a}	558^{a}
Dinknesh	10.3	8.9^{cd}	9.3^{b}	663^{cd}	485^{e}	529^{ef}	559^{d}	730^{ab}	688^{bc}	423^{b}	585^{a}	545^{ab}
ECAB0056	7.6	10.2^{bc}	9.5^{b}	635de	533^{c}	558de	585^{abc}	681^{cd}	657^{cd}	426^{b}	533^{bc}	507^{cd}
ECAB0081	8.2	14.4^{a}	12.5^{a}	705^{a}	622^{a}	647^{a}	521^{e}	575^{e}	559^{g}	383^{c}	456^{d}	434^{f}
GLP2	6.9	14.7^{a}	12.4^{a}	634de	596^{ab}	607^{b}	587^{abc}	582^{e}	584^{fg}	409^{b}	447^{d}	436^{f}
Nasir	7.1	9.0^{cd}	8.4^{bc}	653^{cde}	530^{cd}	568^{cd}	603^{ab}	711^{bc}	677^{bc}	454^{a}	564^{ab}	529^{bc}
Mean	**7.9**	**10.3**	**0.9.6**	**660**	**537**	**569**	**571**	**675**	**648**	**417**	**532**	**502**
Significance	0.232	<0.0001	<0.0001	0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
CV (%)	21.7	13.5	11.8	2.6	4.4	3.1	2.5	4.0	2.9	2.4	4.4	3.3
Bako-Tibe												
Anger	13.8^{ab}	12.9^{ab}	13.2^{a}	573^{c}	377^{bc}	429^{cd}	615^{ab}	723^{b}	694^{bc}	450^{a}	594^{b}	556^{b}
Dimtu	7.6^{c}	13.9^{a}	12.3^{ab}	606^{b}	415^{b}	463^{bc}	548^{c}	690^{bc}	654^{cd}	395^{b}	574^{b}	530^{bc}
Dinknesh	8.8^{c}	11.4^{b}	10.7^{b}	605^{b}	441^{b}	487^{b}	640^{a}	707^{b}	688^{bc}	468^{a}	570^{b}	541^{b}
H-Dume	7.3^{c}	12.0^{ab}	10.7^{b}	610^{b}	524^{a}	549^{a}	644^{a}	640^{c}	641^{d}	469^{a}	506^{c}	495^{c}
Ibado	10.8^{bc}	7.8^{c}	8.6^{c}	629^{b}	349^{c}	417^{d}	607^{b}	782^{a}	739^{a}	449^{a}	654^{a}	604^{a}
Loko	16.2^{a}	12.5^{ab}	13.2^{a}	674^{a}	398^{bc}	455^{bcd}	549^{c}	744^{ab}	704^{ab}	411^{b}	598^{b}	560^{b}
Mean	**10.8**	**11.8**	**11.4**	**616**	**417**	**467**	**600**	**714**	**687**	**440**	**583**	**548**
Significance	0.002	0.001	0.002	0.0001	0.0012	0.0006	<0.0001	0.0025	0.0039	0.005	0.0014	0.0013
CV (%)	21.2	10.4	10.2	2.5	8.7	5.5	3.1	4.4	3.5	4.9	5.0	3.9

Means with no superscript letters with a column of each trial site are not significantly different (P>0.05).

Table 5

Total N concentration, dry matter digestibility and fibre fractions (g/kg DM) of pod wall, haulm (leaf +stem) and HPW of common bean genotypes at *Boricha* (n=3), *Mandura* (n=3) and averaged across both sites (n=6) in 2013.

	Total N			DMD			aNDFom			ADFom		
Genotype	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW	Pod wall	Haulm	HPW
Boricha												
A-Melka	8.6^{bcd}	7.5	7.8	612	401	446	618	801	762	476^{ab}	650^{a}	614
Argene	11.7^{a}	7.5	8.9	635	411	481	597	789	728	453^{bc}	634^{ab}	577
Awash-1	10.0^{abc}	7.8	8.4	622	412	469	608	772	727	464^{ab}	613^{c}	573
Dimtu	6.6^{d}	7.0	6.9	606	410	460	623	791	748	470^{ab}	633^{ab}	591
Dinknesh	7.7^{d}	7.0	7.2	617	420	482	622	790	737	485^{a}	636^{ab}	589
H-Dume	10.5^{ab}	6.9	8.1	631	415	485	605	785	727	475^{ab}	627^{bc}	578
Ibado	7.5^{d}	6.7	6.9	622	412	467	603	795	745	436^{c}	620^{bc}	571
Nasir	8.2^{cd}	6.2	6.9	619	405	483	621	790	728	484^{a}	633^{ab}	579
SARI	8.1^{cd}	8.1	8.1	614	407	458	615	788	745	476^{ab}	634^{ab}	595
Mean	**8.8**	**7.2**	**7.7**	**620**	**410**	**470**	**612**	**789**	**739**	**469**	**631**	**585**
Significance	0.0015	0.1644	0.0972	0.1253	0.863	0.3435	0.2803	0.2925	0.2809	0.0104	0.0342	0.1283
CV (%)	13.6	11.0	11.6	1.8	3.5	4.5	2.3	1.5	2.5	3.0	1.7	2.9
Mandura												
A-Melka	10.0^{b}	9.3	9.5	646^{a}	436	491	573^{e}	750	703	435^{e}	597	554
Argene	11.7^{a}	10.9	11.1	640^{ab}	452	499	577de	712	679	436^{e}	558	528
Awash-1	9.2^{bc}	8.9	9.0	612^{e}	438	489	612^{b}	747	707	463^{b}	598	558
Dimtu	9.6^{b}	8.0	8.4	616^{cde}	395	463	596^{bcd}	761	710	441^{cde}	610	558
Dinknesh	9.5^{bc}	8.0	8.5	623^{cd}	384	457	589^{cde}	775	718	435^{e}	624	566
H-Dume	7.1^{d}	6.1	6.4	606^{e}	398	465	634^{a}	798	745	481^{a}	631	582
Ibado	6.9^{d}	8.9	8.2	628^{bc}	468	520	608^{bc}	750	704	439de	596	545
Nasir	7.9^{cd}	8.9	8.6	623^{cd}	458	510	604^{bc}	739	696	455^{bc}	587	545
SARI	8.4^{bcd}	6.7	7.2	613^{cde}	439	494	603^{bc}	769	71.6	453^{bcd}	617	565
Mean	**8.9**	**8.4**	**8.5**	**623**	**430**	**488**	**600**	**756**	**709**	**449**	**602**	**556**
Significance	0.0002	0.3671	0.1722	0.0005	0.0853	0.0608	0.0002	0.4655	0.4432	<.0001	0.2815	0.2894
CV (%)	10.4	27.4	20.7	1.4	8.2	4.9	1.9	5.5	4.3	2.0	5.4	4.2
Environment												
Boricha	8.8	7.2^{b}	7.7^{b}	620	410^{b}	470^{b}	612^{a}	789^{a}	739^{a}	469^{a}	631^{a}	585^{a}
Mandura	8.9	8.4^{a}	8.5^{a}	623	430^{a}	488^{a}	600^{b}	756^{b}	709^{b}	449^{b}	602^{b}	556^{b}
Significance												
Genotype (G)	<0.0001	0.336	0.024	0.025	0.326	0.22	0.003	0.515	0.378	0.0003	0.262	0.133
Environment (E)	0.492	0.019	0.017	0.324	0.029	0.02	0.0005	0.001	0.0003	<0.0001	0.0004	<0.0001
G x E	<0.0001	0.344	0.161	0.033	0.132	0.12	0.0006	4501	0.327	0.004	0.2300	0.323
$LSD_{0.05}$	0.85	2.10	1.47	13.89	36.52	29.09	13.34	37.99	29.66	.4.02	29.85	24.58

Means with no superscript letters with a column of each trial site are not significantly different (P>0.05).

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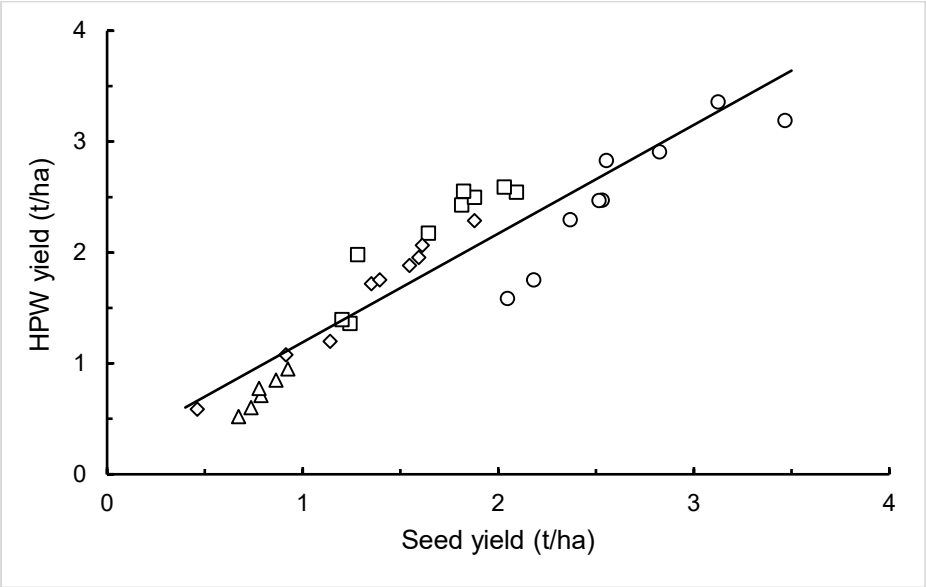


Figure 1. Relationship between the haulm + pod wall (HPW) yield (t/ha) (Y) and seed yield (t/ha) (X) in common bean genotypes at *Shalla* (o), *Bako-Tibe* (Δ), *Boricha* (□) and *Mandura* (◊) in 2013.

The regression relationships for each of the four trial sites and pooled data were:

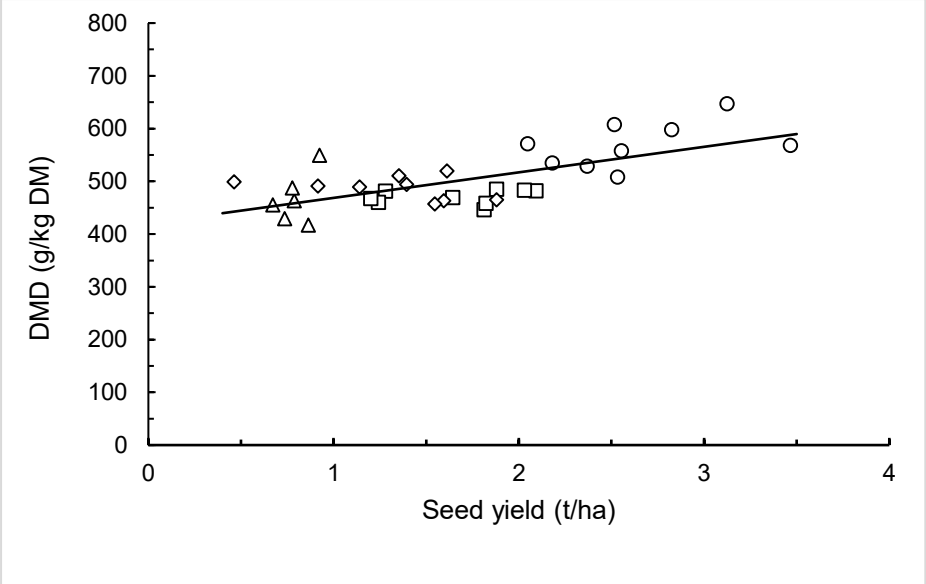
Shalla. Y = 1.23X - 0.68 (r=0.91; P<0.001; n=9);

Bako-Tibe. Y = 1.72X - 0.63 (r=0.98; P<0.001; n=6);

Boricha. Y = 1.32X - 0.03 (r=0.93; P<0.001; n=9);

Mandura. Y = 1.26X - 0.06 (r=0.99; P<0.0001; n=9);

Pooled relationship: Y = 0.98X + 0.21 (r=0.92; P<0.0001; n=33).



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831 **Figure 2.** Relationship between the haulm + pod wall (HPW) DMD (g/kg DM) (Y) and
832 seed yield (t/ha) (X) in common bean genotypes at *Shalla* (o), *Bako-Tibe* (Δ),
833 *Boricha* (□) and *Mandura* (◊) in 2013.
834 *The regression relationships for each of the four trial sites and pooled data were:*
835 *Shalla. Y = 43.62X + 454.52 (r= 0.45; P=0.221; n=9);*
836 *Bako-Tibe. Y = 262.14X + 258.50 (r= 0.50; P=0.317; n=6);*
837 *Boricha. Y = 9.36X + 454.77 (r= .0.24; P=0.538; n=9);*
838 *Mandura. Y = -18.59X + 512.20 (r= -0.37; P=0.332; n=9);*
839 *Pooled relationship: Y =48.40X + 420.21 (r= 0.68; P<0.0001; n=33).*

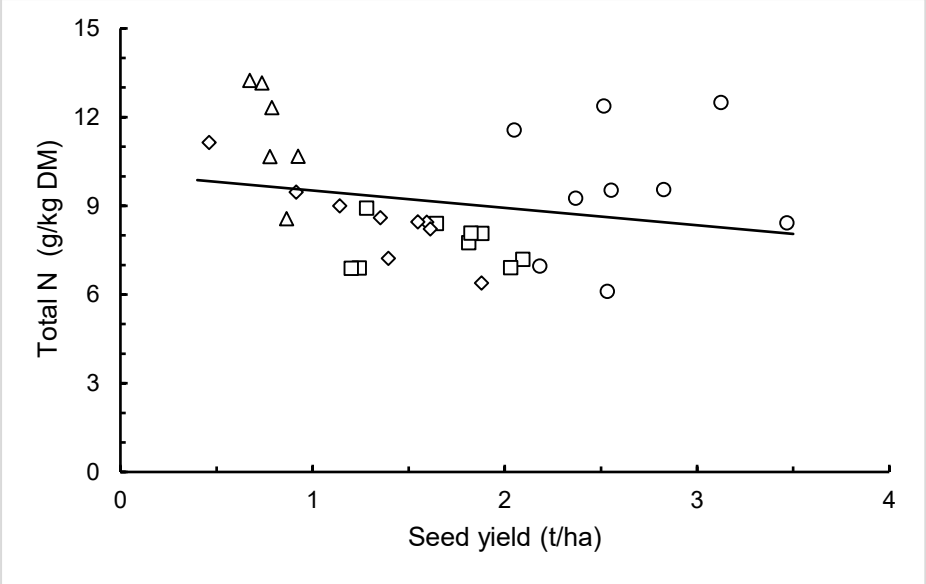

Figure 3. Relationship between the haulm + pod wall (HPW) N (g/kg DM)concentration (Y) and seed yield (t/ha) (X) in common bean genotypes at *Shalla* (o), *Bako-Tibe* (Δ), *Boricha* (□) and *Mandura* (◊) in 2013.

The regression relationships for each of the four trial sites and pooled data were:

Shalla. Y = 0.37X + 8.63 (r= 0.07; P=0.852; n=9);

Bako-Tibe. Y = -15.18X + 23.50 (r= -0.75; P=0.085; n=6);

Boricha. Y = -0.13X + 7.90 (r= -0.06; P=0.878; n=9);

Mandura. Y = -2.82X + 12.27 (r= -0.90; P<0.001; n=9);

Pooled relationship: Y = -0.59X + 10.11 (r= -0.22; P=0.22; n=33).