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Assessment of spatial distribution of enset plant diversity and enset bacteria wilt using geostatistical techniques in Yem special district, Southern Ethiopia

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Abstract

Background: Ensete plant (Enset ventricosum) is a monocarpic perennial crop, found under genus Ensete. It is mainly known and planted by farmers as a drought resistant crop and staple food in the rural community of southern Ethiopia. Large numbers of enset clones are growing in a wide range of altitude. Currently, enset plant diversity and production has been endangered by devastated enset bacterial wilt disease (EBW) which is caused by *Xanthomonas campestris* pv. musacearum. The study aimed at to assess the spatial distribution of enset clone richness and diversity, and enset bacterial wilt disease in Yem special district of southern Ethiopia using ArcGIS geostatistical (Kriging) techniques.

Results: The highest diversity was recorded in Semu Awash kebele with Shannon index of 3.38 and the lowest was in Nuba kebele an index of 2.56. The Sorenson similarity/variation indices showed that Gurmina Hangeri/Meleka and Ediya/Gurmina Hangeri each pairs of kebeles share 18 clones with index value of 0.81 and 0.67, respectively. While lowest share recorded between Laignaw (upper) Kesheli and Tachignaw (lower) Kesheli kebeles with Sorenson indices of 0.16 (only five clones in common recorded). Enset bacterial wilt disease is distributed in all sampled kebeles in varying ranges. The rate of disease prevalence, incidence and severity lies between ranges of 75–100%, 46.8–88.9%, and 36.1–81.4%, respectively. Semu Awasho and Laignaw Kesheli kebeles scored 100% prevalence while in Shemona Metelo kebele it is scored 75%.

Conclusions: Therefore, the analyzed results indicate that it is necessary to compact EBW distribution and to conserve enset richness and diversity in the district for the sake of enhancing food security of farmers at household level in Yem special district. Otherwise, in the longer run the food security and enset plant species would be endanger and it may have significant impact on socio-economic development of the rural community. This study considered limited bio-physical factors for EBW analysis, we recommend in further research in the future should be conducted including other socio-biophysical factors.

Keywords: Enset, Diversity, Enset bacteria wilt (EBW), Kriging, Yem district

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Introduction

Ensete ventricosum (false banana) is a monocarpic perennial crop, found under the same genus ensete and have close similarity with the domesticated banana. It has the ability to withstand drought condition and use as a substantial food item for many millions of people in Ethiopia. (Brandt et al. 1997). South and southwestern parts of Ethiopia are among the potential producers of enset (Spring et al. 1996). It is a crop upon which over twenty million people in the southern part of Ethiopia rely on as a staple and co- staple source of food (Dereje 2012). Enset plant has also other many benefits, as a fiber, animal forage, medicine and for cultural practices (Fekadu and Ledin 1997). Enset is widely accepted and adopted by rural community, due to many reasons like enset is rich in carbohydrate and mineral substances like calcium and iron. In addition, enset plant help to prevent soil erosion and conserves soil, which contributes to the sustainability of the farming system particularly in steep land (Shigeta 1990). Central statistics agency of Ethiopia has reported that, 302,000 ha of land are covered by enset plant in Ethiopia. Out of the total enset plant production, 211,000 ha of land covered by enset plant is found in South Nations and Nationalities of People Regional State(SNNPR). In general, around 75% of enset plant production is located in southern part of the country (MOA 2006).

Even if enset plays a vital role in food security and economy of the country, abiotic and biotic factors strongly constrained its production. Among the biotic factors, enset diseases are caused by bacteria, fungi, viruses and nematodes (Mekuria et al. 2016). The presence of the bacterial wilt disease which is caused by *Xanthomonas campestris* pv. musacearum is threatening cultivation of enset in country-wide scale and enset production is at risk. This disease is first reported in 1960's in Keffa zone of Ethiopia. Currently, it is distributed in all enset growing area of the country causing serious loss of enset crop productivity (Dagnachew and Bradbury 1968).

According to several reports, the productivity of enset is declining continuously from time to time in several parts of the country due to enset bacterial wilt (Addis et al. 2010). Once the disease established in an area, the disease spreads rapidly and results in total yield loss (Mekuria et al. 2016). Desalegn and Addis (2015) stated that bacterial wilt disease was the major problem which has been reported in Borena and in other potential enset producing area. Normally, once the plant is attacked by the disease, it affects the whole system and usually causing a maximum yield loss. Bacterial wilt disease is one of the most common widely distributed diseases at a destructive level with high incidence and it is a great concern of farmers living in the southern part of the country. Earlier, a few studies have reported about the spread of bacteria wilt disease in Tikur inchini and Jibat districts of west Shewa. However, there is limited study that shows—the spatial distribution of the disease in some major enset growing districts of Ethiopia (Mengistu et al. 2014; Aregahegn et al. 2013).

Different, wild species of enset plant is broadly distributed in a number of countries in the central and eastern Africa including Congo, Mozambique, Uganda, Tanzania and Zambia (Brandt 1996). It is important to conserve genetic resources, and use of agro-biodiversity to enhance farming systems (FAO 2012). Recently, study has been reported that landraces of enset declining from time to time. Diversity studies acquire current information on the occurrence, extent, abundance and spatial dynamics of the available diversity which is instrumental for planning and implementation of effective in situ and ex situ conservation strategies (Altieri and Merrick 1987). Enset landraces diversity was studied by different investigators in different enset cultivating areas. Alemu and Sandford (1991) reported that names of 99 enset clones in North Omo area, while Shigeta (1990) listed 78 vernacular names of cultivated enset clones in arid area of southern Ethiopia. Awole et al. (2014) identified 312 enset clones from eight zones in southern Ethiopia. Zerihun et al. (2014) described 218 different enset cultivars from seven zones in SNNPRS. Bizuayehu and Ludders (2003) reported 86 enset clones, Bizuayehu (2008) also again reported 119, Amare and Daniel (2016) recorded 61, and Tesfaye (2002) reported 79 enset clones in Sidama Zone, Southern Ethiopia. Furthermore another author Temesgen et al. (2014) recorded 67 landraces from Wolaita zone. Almaz (2001) also described 146 enset clones in five different regions in southern and southwestern Ethiopia. Normally, farmers cultivate a variety number of landraces, because of the polyclonal nature of enset tree knowledge or traditions associated with enset cultivation (Temesgen et al. 2014). Since Yem special district of South West Ethiopia is among the major enset growing areas, however there has been limited studies have been conducted about enset plant diversity and spatial enset bacteria wilt (*Xanthomonas campestris* pv. Musacearum) disease distribution and incidence. It is very important to study and asses the spatial distribution using geostatistical analysis tool for quick enset plant bio-diversity conservation and enset bacteria wilt diseases distribution (Bouwmeester et al. 2015). In order to conserve the biodiversity and enhance the food security of the rural community, it is important to clearly understand and investigate the available enset species diversity and the distribution of the chronic enset disease for sustainable agricultural

management. Therefore, this study aimed-to assess the spatial distribution of enset clones wealth and enset bacteria wilt disease status using kriging techniques in Yem special district of Southern Ethiopia. The study report would help in providing direction for the concerned stakeholders to take critical action measurement on farm land level to improve the socio-economic development of the country in particularly to Yem special district.

Materials and methods

Study area description

The study was conducted in Yem special district, elevation ranges from 1967 to 2859 m.a.s.l. Yem special district is one of the districts in the Southern Nations, Nationalities, and Peoples' Regions (SNNPR) of Ethiopia. Yem special district is situated in the northwestern apex of SNNPR and is located between 7° 57′N to 8° 02′N latitude and 37° 40′E to 37° 61′E longitude. The topography of the district is characterized by rolling mountains, long gorgeous land, steeply sloppy areas and flat to undulating plateaus. In general, the physiographic features of the district are framed by Laba peaks in central part and by Gibe river in the east part of the district (Figs. 1, 2 and Table 1) (Kassahun 2011).

Sample size and sampling techniques

In order to collect the necessary data, basic information about Yem special district was collected during reconnaissance survey before selecting sampled kebeles. Yem special district has 35 kebeles, four urban and 31 rural kebeles. To select sample kebeles, group discussion had been done with agricultural experts, farmers and elders. It was concluded that except few kebeles almost all potential enset producer kebeles had different ranges of enset bacteria wilt disease distribution. Then after, based on potential enset productivity and prevalence of enset bacteria wilt, different of agro ecological conditions and geographical adjacency of kebeles were identified to select sampled kebeles. In addition, a field visit was made prior to the actual sampled kebeles selection. Finally ten kebeles were purposively sampled (Table 2).

Out of the total population 5800 farm holders in all kebeles in the district, 200 households of sample size were selected for survey, using Eq. (1) Yemane and Fassil (2006), 20 households per kebele were determined and considered for the study. In Yem special district, each kebele has its own clustered developmental groups, developmental groups in each kebele ranges from 4 to 10. Based on household developmental group lists, representative households from each kebele were selected randomly. Data collected from each farm land accordingly.

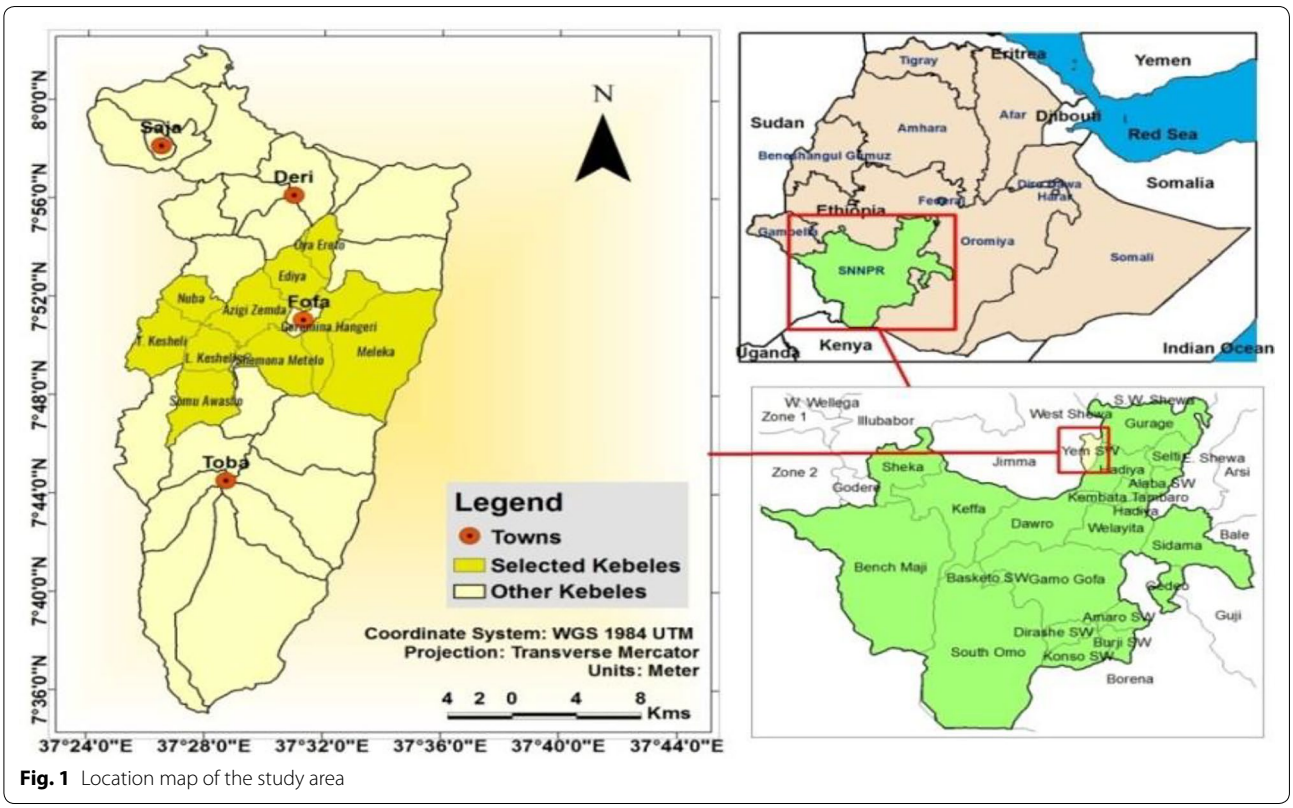

Fig. 1 Location map of the study area

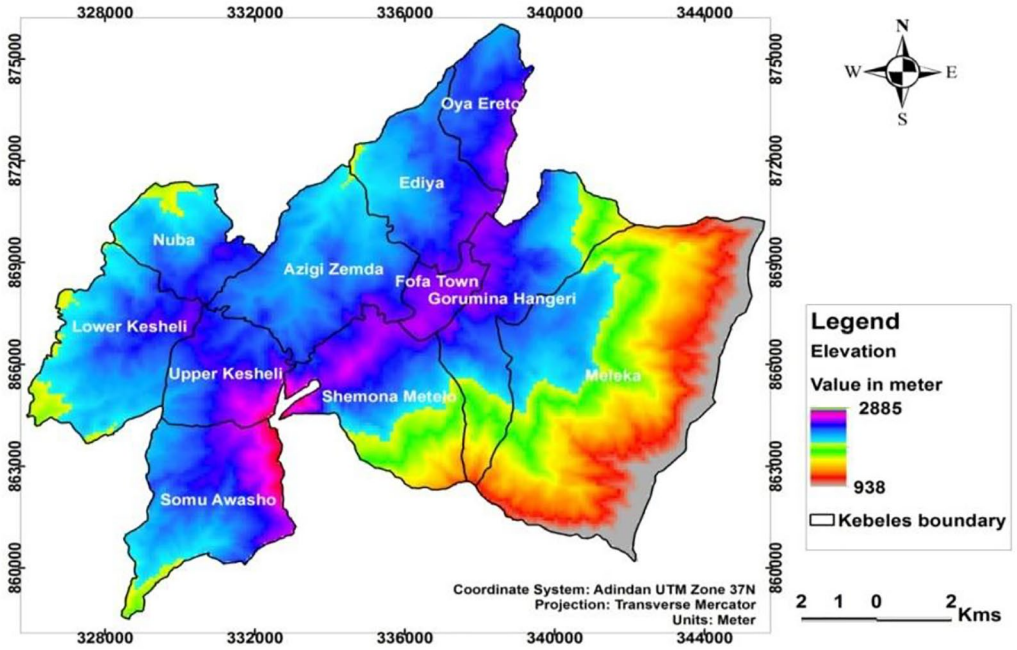

Fig. 2 Digital elevation model (DEM) of the study area

Table 1 Agro ecology, temperature, rain fall, and altitude of Yem special district

Agro ecology	Temperature (°C)	Rain fall (mm)	Altitude (m.a.s.l)
Dega	12–16	1200–2200	2300–2500
Woyina Dega	16–20	900–1200	1500–2300
Kolla	20–30	> 900	1500–2300

$$n = N/(1 + Ne^2) \quad (1)$$

where n = corrected sample size, N = population size, and e = Margin of error (Moe).

Table 2 Climate data of selected Kebeles

Kebele	Altitude range	Mean annual temp (°C)		Annual precip (mm)	
		Min	Max	Min	Max
Meleka	2174–2351	16.94	23.33	1039	1235
Nuba	2066–2502	16.33	18.28	1265	1304
Shemona Metelo	1967–2654	15.09	20.16	1216	1317
Tachignaw Kesheli	2035–2512	16.09	19	1286	1332
Laignaw Kesheli	2289–2712	14.83	17.63	1263	1337
Azgi Zemeda	2244–2471	15.76	18.05	1230	1270
Semu Awasho	2159–2859	14.63	18.43	1268	1346
Oya Ereto	2419–2556	15.35	16.74	1207	1265
Edyia	2211–2566	15.5	17.99	1212	1263
Gurmina Hangeri	2169–2584	15.61	20.53	1170	1254

N = 5800, e = 0.07 (93% confidence interval), n = 5800/(1 + 5800(0.0049)), n = 5800/29 = 200

Individual interview of farmers, development agents (DAs) and FGD (focus group discussion) were carried out for each kebeles.

Data collection

Field survey for both enset clonal diversity and bacterial wilt disease assessment was carried out in the rainy season from mid of March—June, 2017 in which typical symptoms of enset bacterial wilt expressed clearly and vividly. The wilt symptoms seem to progress faster during the wet season than dry season. The time taken to reach different stages of symptom expression may differ with cultivar and environmental conditions (Tripathi et al. 2009).

Enset bacterial wilt prevalence, incidence, and severity

All target households selected from each kebeles were involved in EBW disease data collection. It was carried out together with experienced trained enumerators (development agents) who could easily identify enset bacterial wilt disease symptoms. Moreover, enset plants measurement was made on each of selected household's farm plots with semi-structured questionnaires interviews.

The assessment was made along the two diagonal (in an "X" fashion) of the field at three points 10 m by 10 m area. Pythagoras theorem (3-4-5) was followed by leaving 1 m space from all direction to control border effects (Mengistu et al. 2014). In each field, plants within the area were counted and recorded as disease affected and healthy clones, and prevalence, incidence, and severity of enset bacterial wilt were calculated accordingly.

The prevalence, incidence, and severity data collected on enset bacterial wilt from all sampled farm plots were analyzed by using the descriptive statistical analysis (frequencies, percentages, and average).

Prevalence

Prevalence of the disease was calculated using the number of fields affected divided by the total number of fields assessed and expressed in percentage.

$$\text{Prevalence } \% = \frac{\text{Number of farms affected}}{\text{Total number of farms assessed}} * 100 \quad (2)$$

Disease incidence

Disease incidence was calculated by counting the number of infected plants and expressed as percentage of total number of plants assessed (Bhopal, 2002).

$$\text{Disease incidence } \% = \frac{\text{Number of infected plants}}{\text{Total number of plants assessed}} * 100 \quad (3)$$

Disease severity

Disease severity was done by counting the number of wilted leafs within the sampled area with respect to name of the clone for each plant and by using the formula below (Bhopal, 2002).

$$\text{Disease severity } (\%) = \frac{\text{Sum of all disease rating}}{\text{Total no. of rating} \times \text{Maximum disease grade}} * 100 \quad (4)$$

The severity scale was customized accordingly (Table 3).

Table 3 Customized disease-scaling (Bhopal, 2002)

Disease scaling	Level of damage
0	No disease
1	1–25%
2	26–50%
3	51–75%
4	76–100

Enset bacterial wilt (*X. campestris* pv. Musacearum) character evaluation

Leaf petioles pieces of 20 cm long with active bacterial wilt symptom after observing the presence of ooze in the dissected section of the tissue were collected. A total of 366 plant tissues (2 plants per field) were taken from the sampled 200 farmers' field. Character evaluation of the bacteria was done by purifying the sampled tissues on yeast peptone sucrose agar: 5 g yeast extract, 10 g of peptone, 20 g of sucrose, and 15 g of agar per liter of distilled water then incubating at a temperature of 28 °C for 48–72 h (Schaad et al. 2001). Bacterial isolate identification was conducted in plant pathology laboratory of Jimma University College of Agriculture and Veterinary Medicine, Jimma University, Ethiopia (Fig. 3).

Previously, bacterial wilt (*Xanthomonas campestris* pv. musacearum) was commonly known in Ethiopia, but recently it has been also reported in Uganda, and the Republic of Congo, So far there are no reliable reports of other vascular diseases of banana or enset in Africa which is caused by bacteria other than bacteria wilt (Tripath et al. 2009). Gram reaction is tested by using potassium hydro oxide (KOH) solubility test to determine the gram reaction whether it is(positive or negative) of the isolates (Fahy and Hayward 1983). Besides, the isolated samples were streaked on nutrient agar medium (23 g nutrient agar, 5% glucose per liter of distilled water) to differentiate campestris from other Xanthomonas species based on color appearance after incubating at 28 °C for 48–72 h (Fig. 4) (Bradbury 1986).

Enset clonal diversity

Enset clonal diversity assessment was conducted for all 200 randomly selected households through structured questionnaires. Total landrace composition was determined by making a presence-or-absence record of clones in farms of each sampled household. Farmers were asked to report verbally names of landraces that are grown in their home garden. Identification of clones found in each kebeles based on physical/morphological features, particular uses of clones, and farmers' perception on disease tolerance was made by focus group discussions (FGD) Temesgen et al. (2014). Farmers were asked to name and evaluate each of the different landraces they grew in their respective kebeles gardens. Farmers distinguish one enset clone from the other by looking at the colors of petiole, midrib, leaf sheath, leaf orientation, size, and colors of leaves and circumference and length of pseudostem (Abreham et al. 2012). Finally, field elevation and coordinates were taken using handheld GPS (geographical positioning system).

The collected data was analyzed by excel and using SPSS version 20 (statistical package for social sciences). A descriptive statistical method was employed

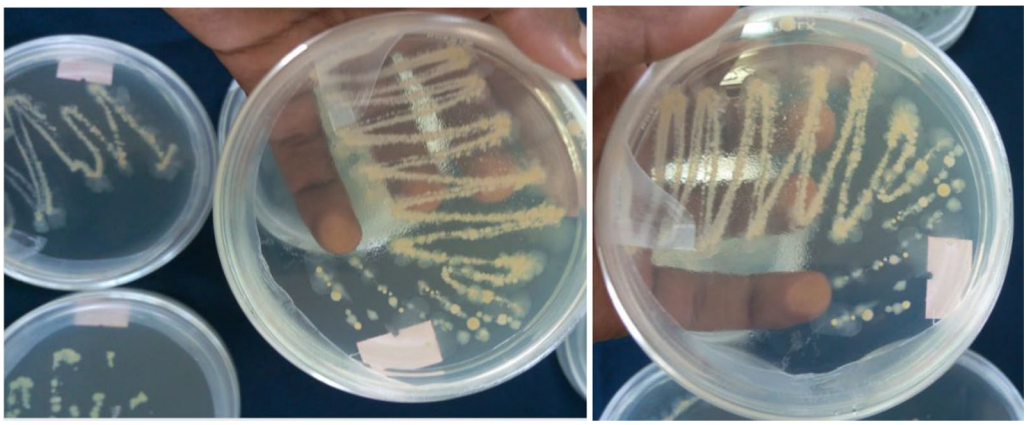

Fig. 3 Slimy mucoid to mucoidal yellow colonies appearance on nutrient agar with glucose

Fig. 4 Grain staining test

to analyze and summarize the data and to calculate percentages, means and other measures of central tendencies. Enset clones diversity analysis (Shannon and Weaver 1949) including (Shannon–Wiener Index, H') and richness and evenness (E = H′/H′max) of each study kebele were analyzed (Whittaker 1972). On the other hand, variation in landraces composition that occurred between kebeles was analyzed using Sorenson's similarity coefficient (Cs)(Kent and Coker 1992).

Mapping of spatial distribution of enset clones and enset bacterial wilt

Visiting every location in a study area to measure the concentration, or magnitude of enset clones and enset bacterial wilt disease is difficult. Instead, they were measured at collected or observed sample locations, and predicted values were assigned to all other locations. The continuous surface representation of a raster dataset represents patterns or magnitude of enset bacterial wilt disease and enset clones. Surface interpolation tools make predictions from sample measurements for all locations in an output raster dataset, whether or not a measurement has been taken at the location.

The geostatistical interpolation methods are based on statistical models that include autocorrelation (the statistical relationship among the measured points). Because of this, geostatistical techniques (particularly, kriging) not only have the capability of producing a prediction surface but also provide some measure of the certainty or accuracy of the predictions. Kriging assumes that the distance or direction between sample points reflects a spatial correlation that can be used to explain variation in the surface. The Kriging tool fits a mathematical function to a specified number of points, or all points within a specified radius, to determine the output value for each location. Therefore, to represent the pattern of enset clone and the magnitude of enset bacterial wilt disease in the study area, the geostatistical method (kriging) was used. The models were derived from 200-point data, which was collected during field survey by using ArcGIS Geostatistical Analysis (Kriging) tool. When modeling enset clone, the value of total number of enset clones counted within a farm fields was assigned for 200-point features. Similarly, to model the enset bacterial wilt incidence and severity, the values of rate of enset bacterial wilt incidence and severity recorded at a farm plots were assigned for 200-point features, respectively. Kriging interpolator is formed as a weighted sum of the data (Borga and Vizzaccaro 1996).

$$\hat{Z}(S_0) = \sum_{i=1}^{n} \lambda_i Z_i(S_i) \tag{5}$$

where: $\hat{Z}(S_0)$ = prediction value for prediction location $Z(s_i)$ = the measured value at the *i*th location, λ_i = an unknown weight for the measured value at the *i*th location, s_0 = the prediction location, n = the number of measured values, i = count number start from ith number.

Results and discussions

Analysis of enset clones richness in Yem special district

In this study, about ninety-three *enset* clones were recorded based on farmers' indigenous knowledge of identification from the sampled ten kebeles. Farmers distinguish one *enset* clone from the other by looking the colors of petiole, midrib, leaf sheath, leaf orientation, size, and colors of leaves and circumference and length of pseudostem (Abreham et al. 2012). The presence of this much vernacularly distinct clones in 1/3 of potential enset producing kebeles of the special district witnessed the area is center for diversified cultivation of enset plants. Similarly, Bizuayehu and Ludders (2003) and Amare and Daniel (2016) identified 86 and 56 landraces from Sidama Zone peasant association, respectively. Another author Temesgen et al. (2014) recorded 67 clones in Wolaita Zone.

The number of clones varies per farm within a kebele. It ranges from 1 up to 18 clones with a mean clone per farm is 9.9. The maximum number of clones per farm scored in Ediya, Semu Awasho, and Oya Ereto kebeles (>15 clones per farm), whereas minimum number of clones per farm (<6 clones per farm) mostly recorded in Nuba and Meleka kebeles. Spatial distribution of enset clones abundance for each kebeles is represented (Fig. 5).

Analysis of enset diversity in Yem special district

In most ecological studies, Shannon diversity indices typical values ranges between 1.5 and 3.5 and the index is rarely greater than 4 (Magurran 2004). In this study, the Shannon diversity indices ranges from 2.56 to 3.38 and Simpson diversity indices ranges from 0.91 to 0.96 and evenness indices ranges between 0.87 and 0.92. There are some enset clones uniquely cultivated in each kebele which ranges from 2 to 11 enset clones (Table 4). The result of this study is also in line with the study report of Gizachew (2000) and Wolde et al. (2016).

In Semu Awasho kebele, the highest numbers of enset clones diversity is recorded which accounts about 14.8% of all the landraces found in the study district. The Shannon, Simpson and Evenness diversity indices for Edyia, Oya Ereto, and Azgi zemeda kebeles are more or less comparable. This could be due to similarity in altitude among kebeles. This finding is in agreement with Bizuayehu and Ludders (2003) who reported that the number of landraces is smaller at lower altitude and larger at higher altitude.

Comparison of enset clones diversity among Kebeles in Yem special district

The Sorenson similarity indices revealed that kebeles or farmers had a long-lasting practice of enset clones sharing to each other (Table 5). The indices range from 0.16 to 0.81 with clones in common lies between ranges of

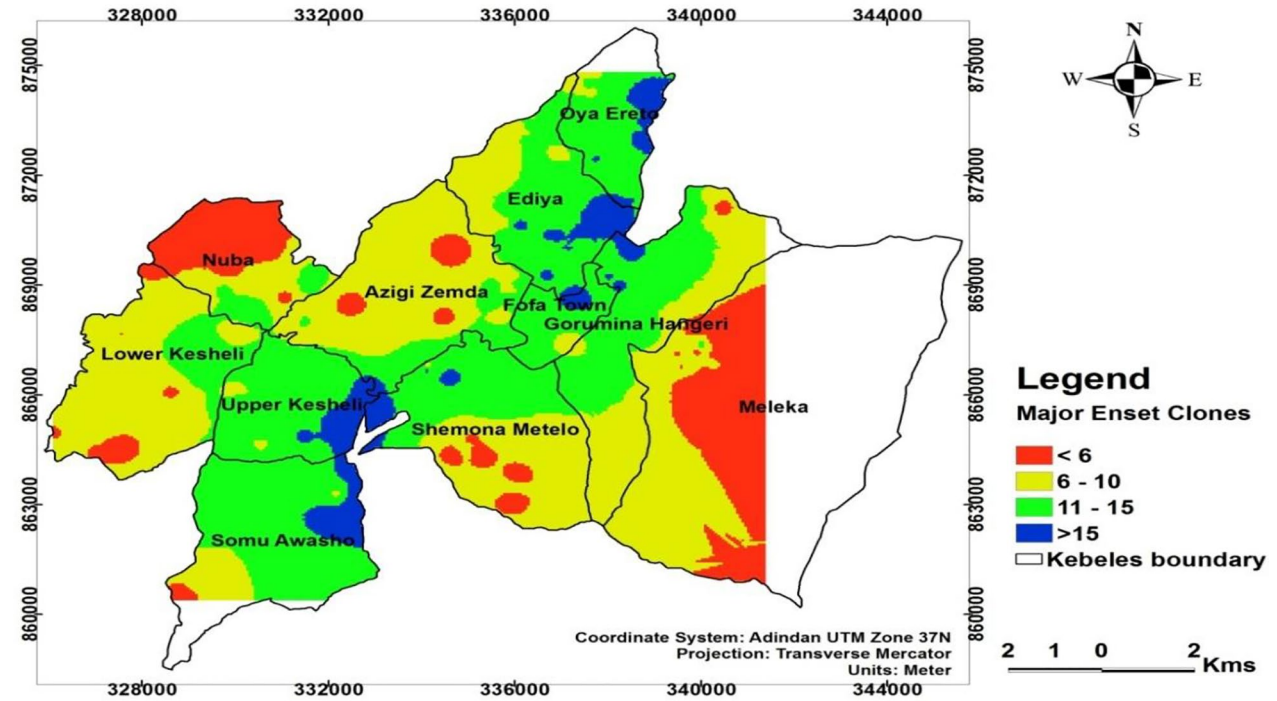

Fig. 5 Distribution of enset clones in Yem special district

Table 4 Enset clones diversity in the sampled kebeles, richness, simpson (1 − D) and shannon (H′) diversity indices, and evenness

Kebeles	Richness (%)	Unique clones	Simpson	Shannon	Evenness
Laigna	41 (14.8)	11	0.95	3.26	0.88
Semu/Awa	39 (14.0)	5	0.96	3.38	0.92
Edyia	31 (11.1)	6	0.94	3.07	0.89
Oya Ereto	33 (11.2)	5	0.95	3.14	0.89
Gurmina/Ha	23 (8.3)	2	0.92	2.75	0.88
Azgi/Zem	27 (9.7)	6	0.94	2.94	0.89
Tachi	19 (6.9)	4	0.92	2.61	0.89
Shem/Met	24 (8.9)	7	0.92	2.79	0.88
Nuba	19 (6.9)	5	0.91	2.56	0.87
Meleka	21 (7.5)	4	0.93	2.70	0.89

Laign Laignaw Kesheli, *Semu* Semu Awasho, *Edya* Ediya, *Oya* Oya Erato, *Gur* Gurmina Hangeri; *Azgi/Ze* Azgi Zemeda, *Tachi* Tachignaw Kesheli, *Shem* Shemona Metelo, *Nub* Nuba, *Mele* Meleka

5—18. The highest number of clones shared was registered in pairs of kebeles between, Gurmina Hangeri and Meleka, and Ediya and Gurmina Hangeri where each kebeles cultivate 18 clones in common and Sorenson similarity/variation coefficient of 0.81 and 0.67 were recorded for each pair, respectively. This might be due to the geographical location of these pairs of kebeles. Normally, they use common marketing place called "Fofa" for buying and selling of agricultural goods could facilitate sharing of different enset clones. Moreover, linguistic and cultural similarity plays a significant role for the existed similarities. The lowest share of clones scored in a pair of kebeles; Laignaw Kesheli and Tachignaw Kesheli was five clones with Sorenson similarity indices of 0.16. This could be because of the existing altitudinal variation between pair of kebeles. This finding is in line with Zerihun et al. (2014) who reported the presence of a large number of similar clones in pair of Zones in southern Ethiopia, namely: Hadiya/Kembata, Gurage/Silte, and Dawero/Wolaita. Another report by Amare and Daniel (2016) in Sidama zone Aleta Chiko district of five kebeles reported that the highest share of clones recorded between kebeles found under close altitudinal variation, while the lowest share scored between kebeles found in higher altitudinal variation. In the same manner, Melesse et al. (2014) stated that highest enset clone diversity recorded at high altitude than compared to low altitudinal area. This could be, the agro-ecology of high land areas are very suitable for presence of enset variety and productivity (Awole et al. 2014).

Relation between altitude and number of clones and farm size

There is strong variation in enset clone diversity across various altitudinal ranges. In each sampled Kebeles, it ranges from 1 to 18 clones per farm. The presence of clones per farm increased as the elevation increases. The linear regression between these two variables showed a

Table 5 Enset clones in common (underline) and sorensen similarity indices between pairs of Kebeles (italics)

Kebeles	Laign	Semu	Edya	Gurmi	Azgi/ze	Tachi	Shem	Nuba	Meleka
Laign	24	14	10	13	6 5	9	9	13	
Semu	*0.6*	22	13	18	10	13	18	15	16
Edya	*0.39*	*0.57*	13	18	10	13	15	13	17
Oya	*0.27*	*0.36*	*0.4*	13	8	7	13	10	12
Gur	*0.4*	*0.58*	*0.67*	*0.46*	11	13	18	13	18
Azgi/ze	*0.17*	*0.3*	*0.34*	*0.27*	*0.44*	8	10	7	11
Tachi	*0.16*	*0.45*	*0.52*	*0.27*	*0.62*	*0.35*	11	8	12
Shem	*0.28*	*0.57*	*0.54*	*0.46*	*0.38*	*0.39*	*0.5*	10	13
Nub	*0.3*	*0.51*	*0.52*	*0.38*	*0.62*	*0.3*	*0.42*	*0.48*	12
Mele	*0.41*	*0.53*	*0.65*	*0.55*	*0.81*	*0.46*	*0.6*	*0.58*	*0.6*

Laign Laignaw Kesheli, *Semu* Semu Awasho, *Edya* Ediya, *Oya*:Oya Erato, *Gurmi* Gurmina Hangeri, *Azgi/Ze* Azgi Zemeda, *Tachi* Tachignaw Kesheli, *Shem* Shemona Metelo, *Nub* Nuba, *Mele* Meleka

strong positive association with a mean and standard deviation 9.7 and 4.8, respectively. This might be due to the existed variability in climatic factors such as temperature, rainfall (abundance and distribution), humidity within a close range of altitudes is similar. The variation in number of clones per farm become higher among farms found between high altitudinal range differences (Fig. 6). This finding is in conformity with Brandt et al. (1997) and Maina et al. (2006) similarly reported that enset bacterial wilt is very serious in mid and highland areas. It shows the pathogen needs high moisture, humidity and low temperature than low moisture, and high temperature. From the total surveyed household, 77.5% of household heads cultivate enset on greater than 2 ha of land. As the size of land increases, the probability of growing variable clones is higher. The maximum numbers of clone per farm (18 clones per farm) were recorded on 4 ha of land whereas the minimum numbers of clones per farm (1 clone per farm) mostly were counted in the households that posse 0.75 ha of land. On the other hand, the linear regression coefficient equation resulted in ($R^2 = 53\%$), that means 53% of the variation in the number of clone per farm size (Fig. 7). The possible reason for this might be large farm size were mostly occupied by wealthy and model farmers of the district. Large farm size holders have the highest possibility of cultivating many enset clones than small land size owners. This study is in agreement with Almaz (2001).

Spatial distribution of prevalence, incidence, and severity of enset bacterial wilt (EBW) in Yem special district

This study confirmed that EBW (Enset Bacteria Wilt) disease is distributed in all sampled kebeles of different altitudinal ranges in a variable level of damages (Fig. 8). Several authors reported that enset bacterial wilt distribute in a wide range of agro ecology (Dereje 1985; Anita et al.1996 and Spring et al. 1996). *Xanthomonas campestris* pv. musacearum is known to systemically invade

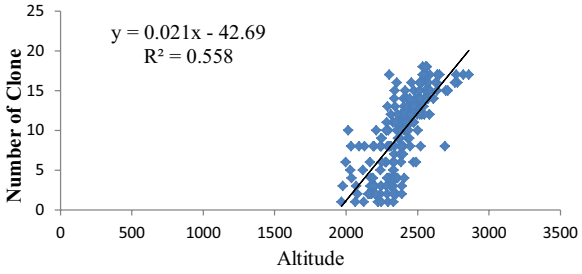

Fig. 6 Simple linear regression between altitude and number of clone per farm

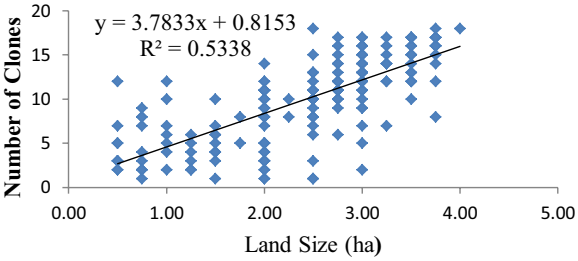

Fig. 7 Simple linear regression between number of clones per farm and size of land

all tissues of enset and banana after infection. This may involve the upward movement of bacteria through the vascular tissues if infection occurs in the lower parts of the plants (rhizome or pseudo stem) or the downward movement of bacteria if infection occurs through the inflorescence. It can be well established in the area comfortable for enset cultivation (Tripathi et al. 2009).

The present study revealed that from the total surveyed 200 fields, 91.5% (183 farms) of farms are infected with the deadly bacterial wilt of enset at different level of magnitude (Fig. 8). The rest 8.5% of households' heads cultivate only few selected (Shenea, Lobo, and Wagu) enset clones on their field than others. The disease is a major concern for all households due to the rapid spread and damage on enset production. Owners of disease-free farmers reported that their fear that once the disease introduced in a single farm, it could reach to the whole farms within a short period of time.

Laignaw Kesheli and Somu Awasho kebeles are with highest rate of enset bacteria wilt incidence. While other kebeles such as Meleka, Nuba, and Tachignaw kesheli scored minimum disease incidence and prevalence (Fig. 9). This might be because enset bacterial wilt prefers humid environment (high moisture) and low temperature for causing maximum damage than low humid and high temperate area. This finding agreed with Brandt et al. (1997) who reported that bacterial wilt is very serious in highland than lowland. In addition to this almost all sampled households confirmed that enset bacterial wilt disease is very serious in the summertime than winter season in study area. This indicates that there is low disease intensity with increasing temperature and vice versa. Therefore, low temperature might be favorable for pathogen multiplication than high temperature. Pathogens require high moisture and lower temperature (Mekuria et al. 2016). In areas where there is high moisture abundant whether in the form of rain, dew, or high humidity, is the dominant factor for the development of most epidemics diseases caused by oomycetes and fungi, bacteria, and nematodes (Agrios 2005). Agrios (2005) also

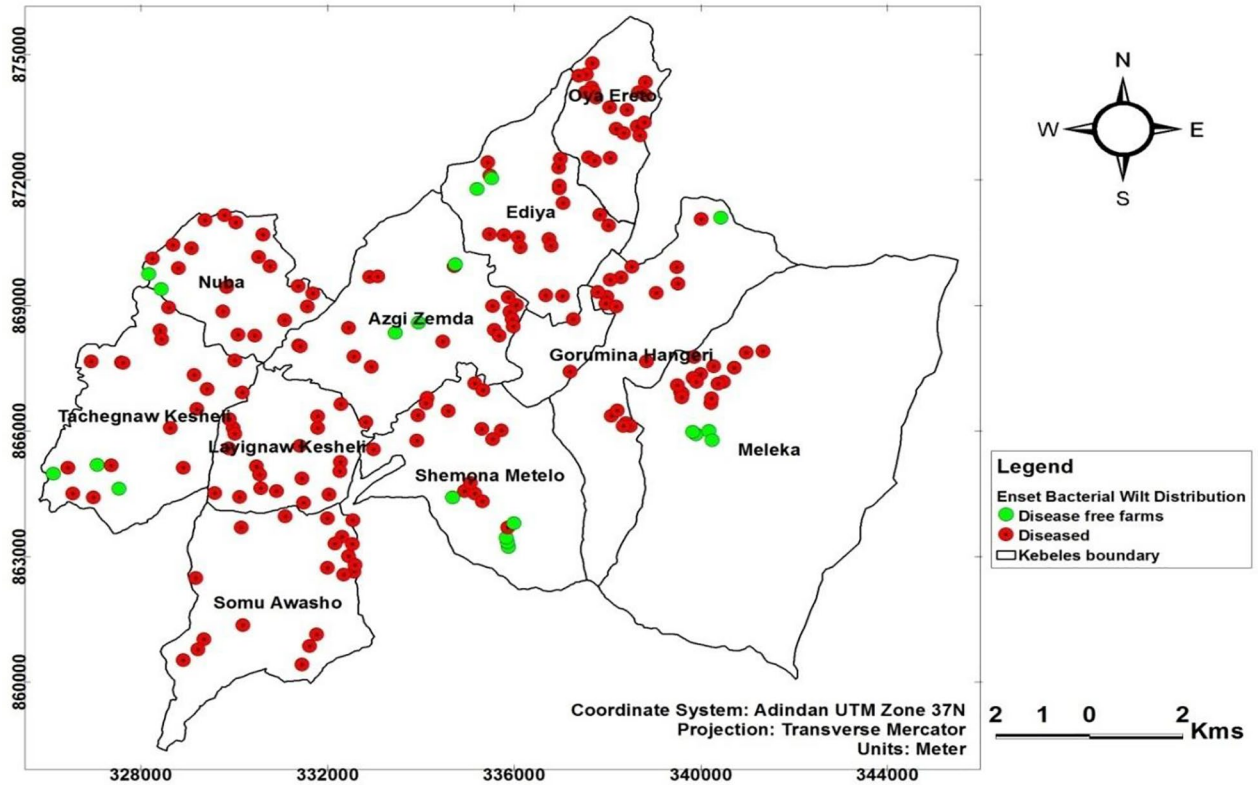

Fig. 8 Spatial distribution of enset bacterial wilt in Yem special district

explained that moisture not only promotes new succulent and susceptible growth in the host, but, more importantly, it increases multiplication of bacteria. Moreover, moisture facilitates the oozing of bacteria to the host surface, and it enables spores to germinate and zoospores, bacteria, and nematodes to move. Semu Awasho and upper kasheli or laiya gnaw kasheli kebeles severity analysis indicates that there is high level of severity of enset bacteria wilt diseases in Yem special district (Fig. 10). The linear regression analysis indicates that Enset bacterial wilt disease incidence was significantly ($p < 0.01$) influenced by altitude, the presence of leafhopper, practice of intercropping, and number of clones per farm. The combined independent variables explained 75% variation in enset bacterial wilt disease incidence. Endale et al. (1996), Tadessa and Masayoshi (2016) Ethiopian highlands are a center of genetic diversity of enset and the result of this report is in line with their findings (Table 6).

Presence of leafhopper and practice of intercropping resulted in a higher positive interaction with disease incidence. A unit increase in leafhopper and intercropping practices the disease incidence would go up by 39.5 and 16.9%, respectively. This was due to the presence of leafhoppers almost in all surveyed and infected farms and their movement within the field facilitate disease transmission from infected to the healthy plant by holding the bacteria on their entire body. Many of insects attracted by the sugars contained in the bacterial ooze and feed on it, thereby further smearing their body and mouthparts with the bacteria-containing exudates (Ing-Ming et al. 2000). The pathogen is also easily spread by any object that comes in contact with contaminated plant parts (Brandt et al. 1997).

Conclusions

This study was undertaken in Yem special district in southwestern Ethiopia with the aim of assessing the extent of enset clone wealth, figuring out its spatial distribution, and mapping of the deadly enset bacterial wilt disease distribution. A total of 200 randomly selected households from adjacent potential enset producing 10 Kebeles with 20 representatives' households per kebele were sampled.

In this study, about 93 vernacularly distinct enset clones were recorded based on farmers' indigenous knowledge of identification. The farmers differentiated by looking at the colors of the corm, corm size, maturity period, strength of the fiber, fermentation

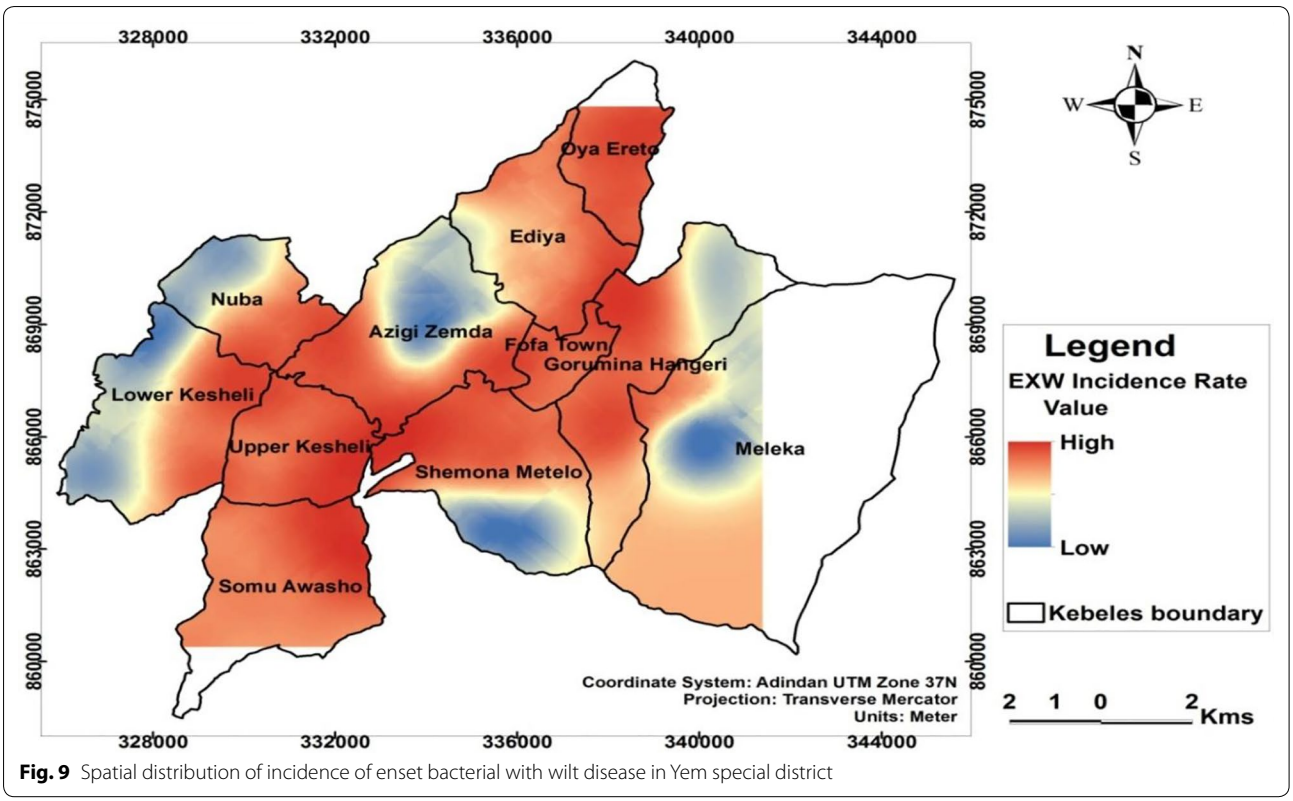

Fig. 9 Spatial distribution of incidence of enset bacterial with wilt disease in Yem special district

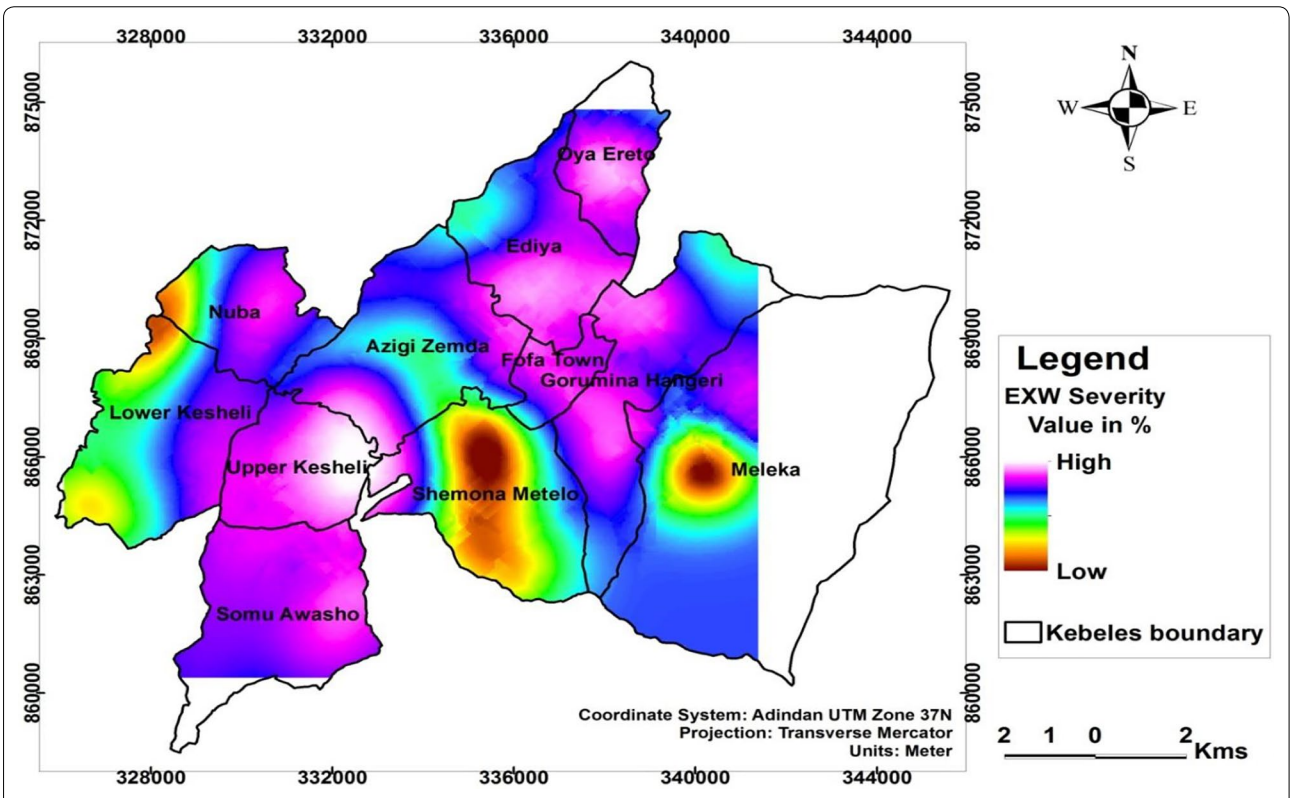

Fig. 10 Severity of enset bacterial wilt disease in Yem special district

Table 6 Multiple linear regressions

	Coefficients	Standard error	t Stat	P value	Lower 95%	Upper 95%
Intercept	− 101.19	25.28	− 4.00	0.00	− 151.04	− 51.34
Elevation	0.04	0.01	3.40	0.00	0.02	0.07
Clones	2.28	0.42	5.45	0.00	1.46	3.11
Leaf hopper	39.53	4.26	9.28	0.00	31.12	47.93
Intercropping	16.97	3.57	4.75	0.00	9.93	24.02

rate, pseudostem length, pseudostem color, leaf color, leaf length, and leaf orientation. The presence of these much vernacularly distinct enset clones has been witnessed in Yem special district. It is a place of diversified enset clones cultivation.

Different diversity indices analyses like (Shannon, Simpson, Evenness, and Richness) were computed. The highest diversity was recorded in Semu Awasho and Laignaw (upper) kesheli kebeles 3.38 and 3.26, respectively. On the other hand, the lowest diversity was scored in Nuba kebele, Shannon diversity index is 2.56. The Sorenson similarity/variation indices lies between 5 and 18 clones type cultivated in common with indices ranges from 0.16 to 0.81. There is a variation in enset clone mix across various altitudinal ranges in each sampled kebeles. The presence of clones per farm increased as the elevation increases. This research confirmed that enset bacterial wilt (EBW) is distributed in all sampled kebeles at different altitudinal variation and at variable level of damage. As the attitude increases the diseases incidence also increases proportionally. Laignaw (upper) kesheli and Semu Awasho kebeles scored with the highest level of disease prevalence, incidence, and severity as compared to other kebeles in the study area. Kebeles relatively found in mid-altitude namely, Meleka, Nuba, and Tachignaw (lower) kesheli scored minimum disease prevalence, incidence and severity. This might suggest that enset bacterial wilt may prefer humid environment (high moisture) and low temperature for causing maximum damage.

Generally, the recorded 93 vernacularly distinct enset clones need to be clearly identified by undertaking molecular genetic diversity study. In-situ and ex situ conservation for the existed enset clones should be applied. In conclusion, as enset bacterial wilt is destroying decisively enset cultivation in Yem special district, many enset clones of the area are seriously destroyed for once and for all. This research report would help to guide EXW management practices in a sustainable manner and conserve the bio diversity of enset plants. Therefore, concerned stake holders ought to take into consideration to conserve enset clones biodiversity for the sake of enhancing food security at farmer's household level in the district.

Abbreviations

EBW: enset bacterial wilt disease; ArcGIS: geographic information system; SNNPRS: South Nations and Nationalities of People Regional State; FGD: focus group discussion; GPS: geographical positioning system; DAs: development agents.

Authors' contributions

AZ collected the data and analyzed, SG, GB and KG also arranged and analyzed the data. SG prepared and edited the manuscript. All authors read and approved the final manuscript.

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Competing interests

The authors declare that they have no competing interests.

Availability of data and materials

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Consent for publication

We have agreed to submit for Environmental Systems Research Journal and approved the manuscript for submission.

Ethics approval and consent to participate

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