Performance of several generations of winter wheat composite crosses populations with a modern cultivar for grain yield and disease resistance under organic farming

Belay Garoma Fufa

Major Thesis for Master of Science in Plant Science

(Specialization Plant Breeding and Genetic Resource)

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Abbreviations

^{0}C = degree Celsius
CCPs= Composite crossed populations
cm = centimeter
FHB = Fusarium Head Blight
g = gram
TKW= Thousand Kernel Weight
mm = millimetre
LSD = Least Significant Difference
OA = Organic Agriculture
t/ha = tonnes per hectare
VCU= Value for Cultivation and Use

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Abstract

Composite cross populations (CCPs) are being tested for their value in organic systems as they are expected to buffer against changing environments due to their inherent genetic diversity resulting in improved yield stability over the years. The experiment was conducted in organic field of Wageningen University and Research center in 2013/2014. Seven winter wheat composite crossed populations and one pure line as a check were evaluated for yield potential, resistance to disease and aphid infestation in a randomized complete block design with three replications. The result of this year showed no significant difference among genotypes for grain yield (p= 0.45), whereas a highly significant (p=0.002) difference for TKW. The highest TKW was recorded from population HU-13-YQMS (43.23 g) and the lowest for the pure line (37.43 g). Population HU-13-YQMS with the highest TKW showed a better yield potential than other CCPs and the pure line. Traits such as plant height and the distance between flag leaf to spike showed a significant difference (P <0.03), whereas spike length and the distance between spikelet did not show significant differences among genotypes. The longest genotype was recorded from population HU-11-YQMS with an average length of 91.42 cm, whereas population HU-12-YQMS was the shortest recorded with the average length of 76.28 cm. A highly significant difference (P<0.0001) was observed among wheat genotypes for the yellow rust incidence and severity across growth stages. Whereas, a non-significance (P= 0.13) for aphid infestation among genotypes. The highest yellow rust incidence (92.27 %) was recorded for the pure line and followed by population B and A at milk stage. Also, the highest yellow rust severity (6.01) based on 0 to 9 scale), or 60.64 % on second flag leaf was recorded on the pure line and followed by the population B and A. The yellow rust incidence and severity expanded across growth stages. The newly introduced populations showed very low incidence and severity across growth stages. Good estimation of phenotypic correlation coefficient was observed when excluding the pure line within several traits. Plant height revealed a significant positive association with spike length (r= 0.867), the flag leaf spike distance to spike (r= 0.750), fertile spikelet (r= 0.646) and the distance between spikelet (r= 0.683). Similarly, spike length showed a significant strong correlation with number of fertile spikelet's (r= 0.782) and the distance between spikelet (r= 0.741). These traits are significantly positively associated with each other and with yield components. Therefore, these traits should to be considered for selection criteria under organic condition.

Key words: winter wheat, composite cross populations, low input/organic, yellow rust

1. Introduction

1.1. Background and justification

Wheat (*Triticum aestivum* L.*)* is a cereal crop and belongs to the grass (Gramineae or Poaceae) family and genus Triticum (Zhnag *et al*., 2006). It is believed to originate from South-Western Asia (Acquaah, 2007). Wheat is a staple food in large part of the world and grown on 216.7 million of ha worldwide in 2012 (http://faostat.fao.org/default.aspx). It feeds about 40% of the world population and occupies a central position in maintaining world food security (Asif *et al*., 2014). Wheat plays an important role in everyday life during human consumption, since it provides a source of protein and calories. For instance, wheat alone provides 20% of the calories and protein for the world population (Baraune *et al*., 2010). It is also used as feed and as a source of various raw materials for industry in different products.

Wheat can be grown in wider range of environments from the equator to latitude of 60^0N, 27 to 40^0S and found worldwide at altitude ranging from sea level to 3000 m (Kang and Priyadarshan, 2008). The optimum growing temperature is about 25 ^{0}C, but the minimum and maximum growth temperature is 3-4 and 34-36 ^{0}C, respectively. It can be grown in most locations where annual precipitation ranges from 250 to 1750 mm (Prohens, 2008). Acquaah (2007) reported that the crop is the best adapted to cool temperate climate where the rainfall is not greater than 400-600 mm per year. As for season production, wheat can be divided into two, winter and spring wheat. Spring wheat is sown in early spring and is less tolerant to low temperature and even damaged by light frost of -2 to -1^0c whereas winter wheat is sown in the fall so that it can have some growth before onset of cold weather in winter. Winter wheat needs the vernalization to process became generative. Winter wheat growth ceases and remains dormant through winter, resuming growth in spring and harvested during summer (Acquaah, 2007).

In the last decade, the yield of wheat slightly increased globally. For instance, the average world wheat yield in 2002 was 2.68 t ha^{-1} whereas 3 t ha^{-1} in 2012 (http://faostat.fao.org/default.aspx). The slightly increase of yield in that period was due to the continuous investment of plant breeding and other multidisciplinary activities including disease and insect pest management effort made. Plant breeding for low input and organic conditions is becomes emerging and growing (Phillips and Wolfe, 2005; Löschenberger *et al*., 2008). Local based breeding program is the best opportunity to achieve a sustainable increase of agricultural production under low input conditions (Ceccarelli, 1996). Under low input conditions external inputs application such as synthetic chemicals are reduced whereas under organic conditions these chemicals inputs are prohibited. According to Murphy *et al*., (2005) genetic diversity such as composite crossed population is suited for low input and organic conditions to buffer against changing environments. It also contributes to yield stability, to induce disease resistance and adaptation to low soil fertility.

Breeding for organic agriculture can best be done as a kind of participatory research and embraces multidisciplinary stakeholders. It strives for a close interaction between researchers, farmers and processers (industry). Farmers expect to obtain high yield with resistance to disease and tolerance to abiotic stress, and processing industries are looking a good milling and baking qualities, and consumers require high nutritional food and healthy products (Lammerts van Bueren *et al*., 2002)

Organic agriculture requires breeding for robust varieties that are bred and selected under low input and organic conditions. In Austria, official organic variety trials started in 1995, which led to the establishment of an organic testing system for cultivation and use (VCU) for winter wheat and spring barley in 2001 and 2002, respectively (Löschenberger *et al*., 2008). Similarly, French agricultural research Institute (INRA) started an organic winter wheat breeding program in 2003 and tested cultivars under organic and low input conditions (Rolland *et al*., 2008). Other cereals breeding programs are also carried out in Germany, for example, Getreidezuchtungsforschung Darzau (http://www.darzau.de) and Keyserlink Institute and in UK (http://www.efrc.com) at the Elm Farm Organic Research Center in order to develop composite cross populations.

Exploitation and broadening genetic variability in the gene pool population is one strategy of breeding for organic agriculture. This enables to select for important traits and the development of a population variety that is adapted to ecological farming system (Lammerts van Bueren *et al*., 2005; Wolfe & Döring, 2010). The broadened genetic population is enriched by a number of crosses involving varieties particularly suited for organic agriculture and low input conditions (Löschenberger *et al*., 2008). Furthermore, the development of the composite cross population approach can be one option to increase genetic diversity within cultivars to promote better adaptation towards unpredicted biotic and abiotic stress factors. For instance, compost cross populations are heterogeneous crop that can show superior performance under unpredicted stress conditions (Phillips and Wolfe 2005). In addition, composite cross populations were the best performing ones under low input conditions compared to pure lines because these populations consisted of broadened genetic diversity that enabled to buffer against an harsh environment. It was demonstrated that 10 winter wheat cultivars tested under organic and conventional management conditions showed significant variation in yield and baking quality (Hilderman *et al*., 2009). Similarly, five composite cross population of barley were studied for their performance in relation to powdery mildew, and among them one of the populations having the Mla1 allele showed resistance to powdery mildew (Danquah *et al*., 2002). Multiline varieties and variety mixture can also provide a functional diversity that limits pathogen and pest expansion in crops. This approach is to reduce the risk of resistance breakdown due to wider range of mechanisms, including barriers in mixtures, frequency effect and induced resistances (Finckh *et al*., 2000). Further possible explanation, the variety mixture and multiline can provides functional diversity that limits the pathogens expansion due to diverse genetic background incorporated, each cultivar carrying different sources of resistance to disease, as barrier via crop physical structure as well as varied wax layers and encourage resistance of crop against disease. The physical and chemical characteristics of the leaf surface play an important role in governing the success or failure of fungal pathogens. For instance, leaf surface feature vary among cultivars of the same species, between upper and lower surface of the same plant and or leaf can influence the establishment of pathogens due to different composition of cuticle and waxy layers (Allen *et al*., 1991). It can be expected that similar functions appear in crossed composite population to restrict the development of pathogens.

1.2. Problem statement

Worldwide, about 1.4 billion people are dependent on traditional agriculture a system that is characterized by marginal agriculture environment and limited use of external inputs (Murphy *et al*., 2005). Genetically uniform varieties that are developed via pedigree methods are the dominant commercial breeding method to acquire high yielding and wide adaptability when high application of inputs and favorable environment conditions are available (Phillips and Wolfe, 2005). However, these varieties cannot always perform well in marginal agriculture environments with low external inputs applied. In addition, resource poor farmers particularly in developing country are unable to afford buying high levels of input such as new varieties, chemicals and synthetic fertilizer to maximize their production. According to Ceccarelli (1996) breeding is mostly conducted under high input conditions and therefore missed the opportunity to exploit genetic capacity to adapt at low level of inputs.

Since 1960s, global wheat yield roughly increased three-fold (Carver, 2009). However, the production of wheat is limited by biotic and abiotic factor stresses. Among biotic stresses, foliar diseases are the most economically important diseases on wheat crop production. Foliar diseases such as, yellow rust (strip rust) caused by *Puccinia Striiformis*, leaf rust (brown rust) caused by *Puccinia triticina*, septoria tritici bloch (STB) caused by *Mycosphaerella gramunicola*, fusarium head blight caused is caused by is caused by *fusarium graminearum* (teleomorph *Gibberella zeae*) and *fusarium culmorum* and powdery mildew caused by *Blumeria graminis* and eye spot caused by *Tapesia yallundae* are the most economical wheat diseases (Lonnet, 1997; Lucas, 1998; Marshall, 2009). In addition, common bunts caused by *Tilletia caries* and dwarf bunt caused by *Tilletia controversa* are also important seed borne disease of winter wheat because, for seed production the use of synthetic chemical application is prohibited under organic farming to control these seed diseases (Huber and Buerstmayr, 2006 ; Lammerts van Bueren *et al*., 2011). But, according to Löschenberger *et al*. (2008) powdery mildew and eyespot disease are less economical important under organic conditions because these disease incidence is influenced by cropping systems.

Foliar disease such as yellow rust, leaf rust, septoria tritici bloch and fusarium head blight are the major important diseases under organic farming. These diseases are not only causing the economic yield losses but also incurred cost of chemical used to control the disease (Pretorius *et al*., 2001). Worldwide, yield losses due to above mentioned disease can vary and considerably depend on crop developmental stage/growth condition, inoculum pressure, susceptibility of wheat cultivar and weather conditions (Agrios, 2005). Yellow rust infection occurred at early stage of plant development and can result in stunted and weakened plants, leading to yield losses. The losses were estimated to be as 50 % due to shriveled grain and damaged tillers (Roelfs *et al*., 1992). The yield loss due to yellow rust (strip rust) was 40-80% throughout the world (Mcintosh *et al*., 1995).When yellow rust was widespread, severe disease outbreak, the yield losses ranging from 50-60% in Europe (Moldenhaur *et al*., 2006) and 10-70% in China (Chen, 2005).

Septoria Tritici Bloch (SLB) is wide spread and economically important disease worldwide (Cook *et al*., 1991; Scharen 1999; Zhang *et al*., 2001). As is a typical leaf disease, when infection occurred and become severe on the flag leave or immediately below, losses in grain yield become greatest (Thomas *et al*., 1989). Like foliar diseases, fusarium head blight (scabs) or ear blight as important fungal disease affecting several gramineous hosts including wheat and barley. Fusarium head blight causes severe grain yield reduction and decrease grain quality (reduced grain size and shriveled grain). Decrease of grain quality resulted in rejection (downgrading marketing values), decrease of baking and the nutritive value qualities. Infected grain may contain harmful levels of mycotoxins that prevent its use for human consumption and or feed (Snijders, 1990; Bai and Shaner, 1994).

Exploitation and broadening of genetic variability is as one option to optimize yield and resistance to disease and insect pest under organic and low input conditions. Also, organic farming integrates biodiversity, robust variety and ecological agronomic practices. This can provide insurance with respect to the impact of biotic and abiotic stress factors rather than application of synthetic chemicals (Finckh, 2008). Therefore, organic farmers need cultivars adapted to organic and low input systems. Breeding for the organic sector requires the desired traits such as high yield, baking quality, resistance to biotic and abiotic, weed suppression, nutrient use efficiency and others parameters under taken (Löschenberger *et al*.,2008; Lammerts van Bueren *et al*., 2011). A range of existing genotypes, including traditional landraces, composite, modern varieties and relative wild wheat species are currently being crossed and the progenies are selected for optimal grain yield and baking quality, improved nutrient use efficiency and weed competitiveness under organic farming condition (Murphy *et al*., 2005 and 2007). Organic Research Center, Elm Farm in the United Kingdom developed composite cross populations (CCPs) of winter wheat from twenty parents. Their parental lines provided source for yield potential, baking quality and both. Composite cross populations made from all possible cross combinations combining yield potential with quality (YQ) are taken for further evaluation in different European countries. Wageningen University is one of the trial sites for this cycling project to evaluate the performance of composite crossed population of winter wheat over several generations for yield potential and resistance to disease and insect pest.

1.3. Hypothesis

The composite crossed populations would be expected to perform better in yield under low input and organic farming conditions than the pure line. In addition, it is expected that composite crossed population would have a better disease buffering than pure line under low input and organic conditions, because a composite crossed population is based on broadened genetic diversity that enables to buffer against varying stress environments.

1.4. Objective

General objective of the study: to evaluate the performance of several generations of a composite cross populations of winter wheat and one modern pure line cultivar for grain yield, morphological traits and resistance to foliar disease under low input organic condition.

Specific objectives

- To compare the performance of CCPs with a pure line under low input conditions.
- To study the yield stability of CCPs and their diversity evolved over years as well as which traits contribute more to diversification.
- To compare the yield performance of CCPs among each other
- To identify a better performing CCP against disease resistance under low input organic conditions.
- To identify which CCP show a better insect pest resistance and morphological traits to be considered.

1.5. Research questions

- ➢ Does the yield of composite cross populations differ from modern cultivar under low input?
- ➢ Do the composite cross populations show better disease and insect pest resistance than the pure line under low input organic conditions?
- ➢ Which CCP would show a good performance under low input organic conditions?
- ➢ Among crossed populations, which CCP would show better disease and insect pest resistance low input organic conditions?
- ➢ Is the performance of the CCPs stable across years?

2. Material and methods

2.1. Source of germplasm

Nine and eleven parents were selected based on their yielding potential and baking quality, respectively. Totally, twenty parents were selected for yield and baking quality (Table.1) and then, 190 possible cross combinations was made based on half diallel crossing scheme at UK-Elm Farm Organic Center in 2001 (Fig 1).

Table 1. Description of different parent varieties potential for yield and quality

S. No	Parental varieties	description	remarks
1	Bezostaya	Yield and quality population	Potential for yield and quality
2	Buchan	Yield population	
3	Claire	Yield population	
4	Deben	Yield population	
5	High Tiller Line	Yield population	
6	Norman	Yield population	
7	Option	Yield population	
8	Tanker	Yield population	
9	Wembley	Yield population	
10	Cadenza	Quality population	
11	Hereward	Quality population	
12	Maris Widgeon	Quality population	
13	Mercia	Quality population	
14	Monopol	Quality population	
15	Pastiche	Quality population	
16	Renan	Quality population	
17	Renesansa	Quality population	
18	Soissons	Quality population	
19	Spark	Quality population	
20	Thatcher	Quality population	

Source: The Organic Research Centre, Elm Farm, UK.

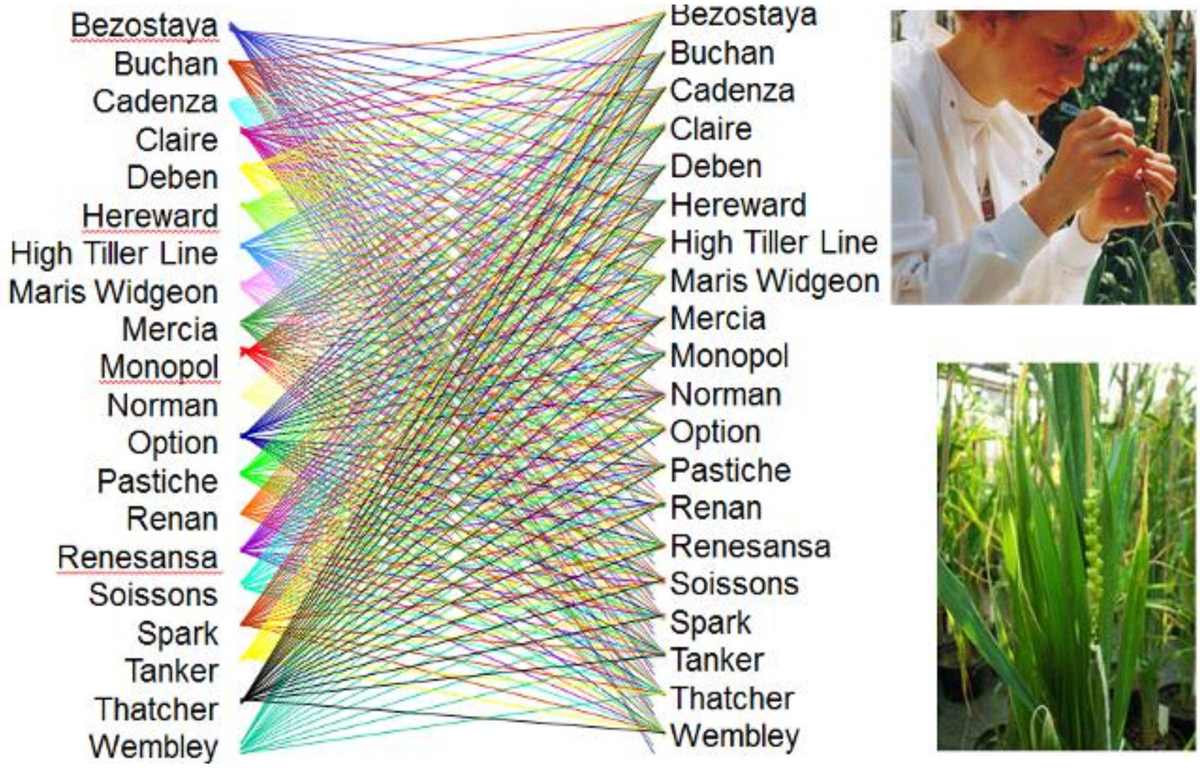
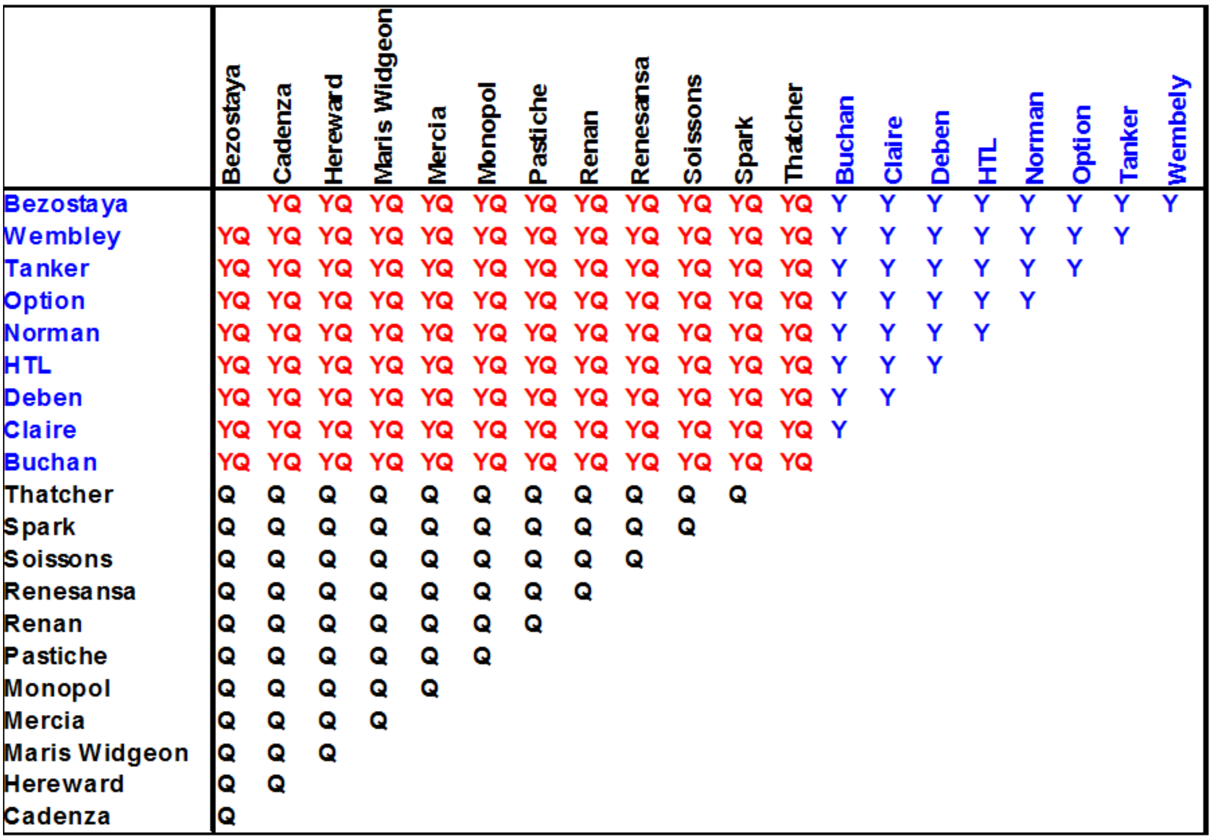


Figure 1. Twenty parental of winter wheat were crossed and 190 possible combinations made via half diallel cross at UK-Elm Farm Organic Center.

The composite crossed populations were grouped into three groups based on their parent potential for yield (Y), quality (Q) and best combination both yield and quality (YQ) (Fig 2). The trail in Wageningen consists of the combination of parents YQ that includes 93 cross combinations. The seeds were bulked over the years by sowing, re-sowing and allowing natural selection.



	Bezostaya	Cadenza	Hereward	Maris Widgeon	Mercia	Monopol	Pastiche	Renan	Renesansa	Soissons	Spark	Thatcher	Buchan	Claire	Deben	HTL	Norman	Option	Tanker	Wembely
Bezostaya		YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y	Y	Y	Y	Y	Y
Wembley	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y	Y	Y	Y	Y	
Tanker	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y	Y	Y	Y		
Option	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y	Y	Y			
Norman	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y	Y				
HTL	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y	Y					
Deben	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y	Y						
Claire	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	Y							
Buchan	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ	YQ								
Thatcher	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q									
Spark	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q										
Soissons	Q	Q	Q	Q	Q	Q	Q	Q	Q											
Renesansa	Q	Q	Q	Q	Q	Q	Q	Q												
Renan	Q	Q	Q	Q	Q	Q	Q													
Pastiche	Q	Q	Q	Q	Q	Q														
Monopol	Q	Q	Q	Q	Q															
Mercia	Q	Q	Q	Q																
Maris Widgeon	Q	Q	Q																	
Hereward	Q	Q																		
Cadenza	Q																			

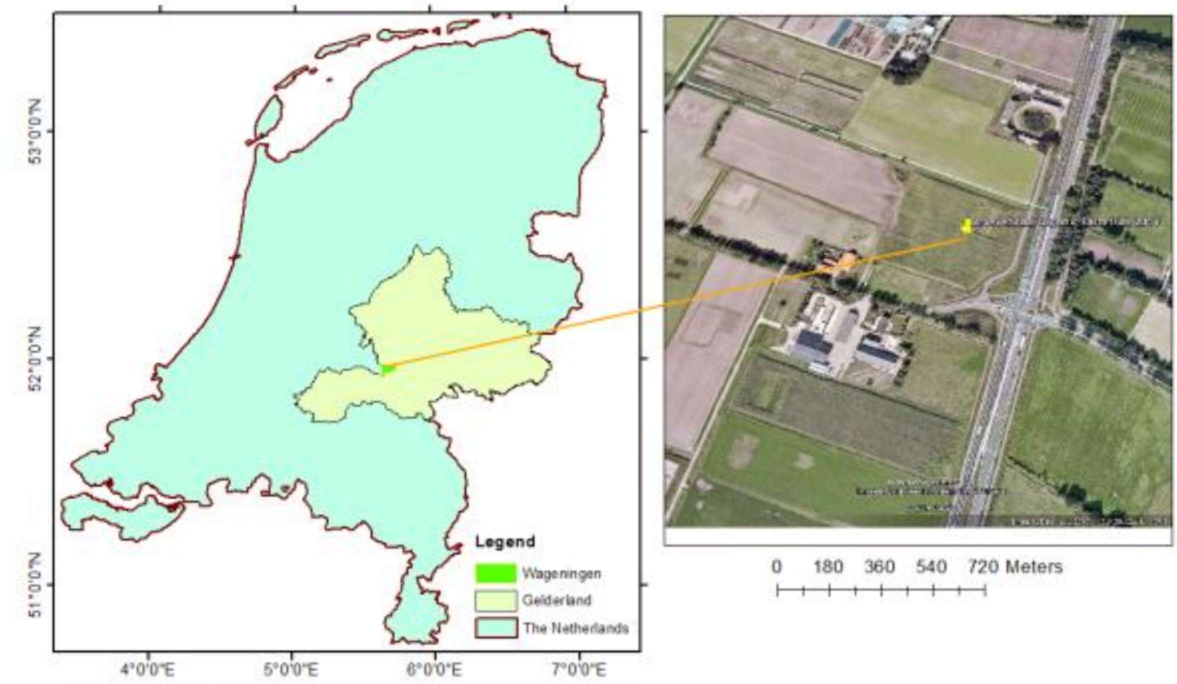
Y - 33 crosses; Q – 63 crosses; YQ –93 crosses

Figure 2. Parental varieties and their possible combination for grain yield and quality(Y= yield, Q= quality, and YQ= yield and quality.

Some CCP included naturally derived male sterility (MS) to stimulate cross fertilization. For instance, YQMS. These composite cross populations were distributed every year to different European countries where the project is cycling. Therefore, Wageningen University and Research Center is one of the collaborating organic trials, receiving composite cross population seed every year from cycling project partners (Hungary and Witzenhausen /Kassel University, Germany) and after conducting the trial at Droevendaal, organic trial field, the seed send to Witzenhausen /Kassel University, Germany. The European cycling of composite cross population for yield and quality started in 2008.

2.2. Experimental set up

The experiment was conducted at the organic farm trial, Droevendaal (Fig 3) of Wageningen University and Research Center during 2013/2014. The area is located at $51^0$57’57’’N, $5^0$38’37’’E Wageningen, the Netherlands. Seven CCPs and one pure line as check, totally eight genotypes were used as treatment in a randomized complete block design (RCBD) with three replications (Fig 4). The plot size for each genotype was 6 m x 7.5 m = 45 m^2. Each plot consists of four beds of 1.5m width and 7.5m row length and each bed consists of 10 rows. Barley was planted on 3 m x 7.5 m to prevent cross pollination among the CCP winter wheat population. The experiment was conducted on sandy soil and synthetic fertilizer and pesticides were not applied during experiment conducted. The seed was treated with Tillecur (based on organic mustard powder).The experimental plot sown on the 24th of October 2013, the seed rate was 200 kg/ha (20 g m^{-2}) or 900 g per 45 $m^{2)}$ and harvested on the 24th of July, 2014.



Source of Netherlands boundary:DIVA-GIS (http://www.diva-gis.org/gdata)

Figure 3. Map of Wageningen at location of Droevendaal organic trial of composite cross population in 2014, Wageningen UR, The Netherlands.

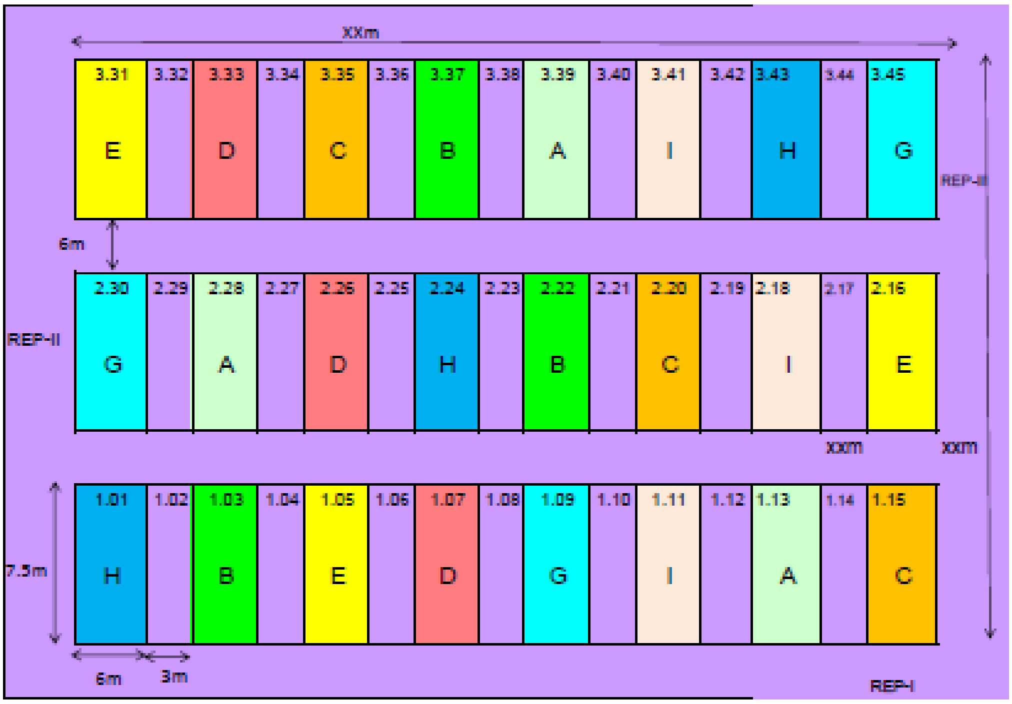


Figure 4. CC Population- experimental design 2013/2014 at Organic experimental Farm Droevendaal in Wageningen.

Table 2. Description of the tested composite cross populations and number of seasons grown at the organic experimental farm Droevendaal of Wageningen University and Research Center (WUR).

Genotype code	Description	Number of year/season grown in Wageningen
A	YQMS cycling experiments	6th season
B	UK CCP Organic	6th season
C	Pure line	3rd season
D	YQMS cycling experiment	4th season
E	YQMS cycling experiment	3rd season
G	YQMS cycling experiment	5th season
H	YQMS cycling experiment	2nd season
I	YQMS cycling project	1st season

Remark: F= intercrop (barley) to prevent cross pollination among CCP

2.3. Collected data

2.3.1. Foliar disease and insect pest data

Yellow rust (strip rust), fusarium head blight (FHB) and septoria tritici blotch (STB) were assessed visually for disease incidence and severity at different growth stage**.**

Disease assessment:

Every plot was assessed visually at growth stage of the main shoot with two up to three tillers (21), pseudo-stem erection with first node detectable (31), flag leaf sheath extending up (39), flowering (61) and dough development (83) according to Zadoks *et al.,* (1974) and Lancashire *et al.,* (1991), BBCH, growth scale (Fig 5).

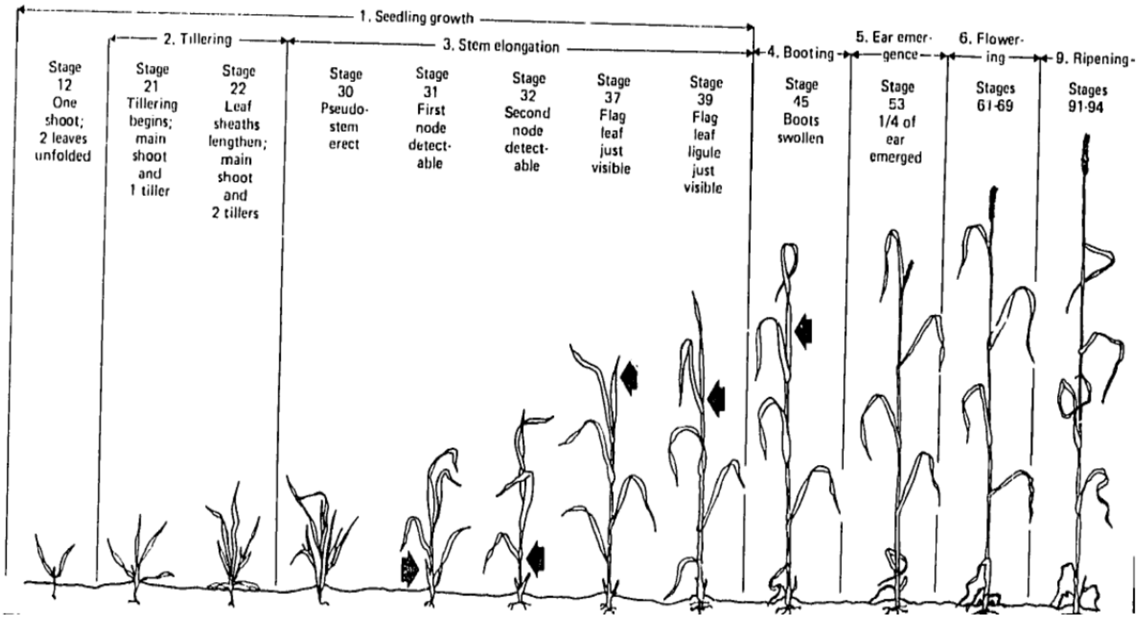


Figure 5. Zadoks scale of cereals growth stages

Remark: Lancashire *et al.,* (1991), BBCH (Base, Bayer, Ciba-Geigy and Hoechst) also described based on Zadoks scale.

2.3.1.1. Yellow rust (strip rust)

Preliminary disease incidence was assessed at (21) early tillering growth stage because yellow rust can infect at early seedling growth (Fig 6). In addition, yellow rust was assessed at pseudo-stem erection with fist node detectable (31 growth stage), flag leaf sheath extending up (39 growth stage), flowering (61 growth stage) and milk growth stages (83 growth stage). Further see for the methodology under a-d as follow.

Figure 6. Yellow rust symptoms at seedling growth stage. Picture taken at Organic experimental Farm, Droevendaal, Wageningen, April 2, 2014.

Yellow rust disease incidence and severity evaluation methods:

a) Preliminary observation for yellow rust incidence at 21 and 31 growth stages

30 cm ruler length was thrown randomly four times in a diagonally way to count disease incidence for each treatment at main shoot with two up to three tillers (21) and pseudo-stem erection with fist node detectable (31) growth stages, respectively. In each 30 cm ruler length, total number of leaves and infected leaves was counted for preliminary incidence observation.

According to Cooke (2006) disease incidence (%) = $\left(\frac{Number\ of\ infected\ plant\ units}{total\ number\ of\ plant\ units\ assesed} * 100\right)$

% incidence = $\left(\frac{Number\ of\ infected\ leave}{total\ number\ leave}\right)$ = average infected leaves * 100

b) Yellow rust incidence assessment at 39, 61 and 83 growth stages

20 plants were tagged from each plot randomly. Yellow rust disease incidence for each plot was assessed at 39, 61 and 83 growth stages. From each tagged plant, number of leaves and infected leaves was counted for disease incidence at these growth stages.

c) Yellow rust disease severity evaluation at 39, 61 and 83 growth stages

Visual scales range from no symptoms score, 0 and or 1 as few isolated lesion, very severe symptoms score 9 and other categories in various disease symptoms at corresponding fallen number was scored. Disease severity evaluated at flag leaf sheath extending growth stage (39), flowering stage (61) and grain filling (83) growth stages. Severity of disease was scored visually per tagged plant and its average taken.

Based on 0-9 scale, according to (Saari and Prescott, 1975; Couture, 1980; Stubbs *et al*,. 1986; ICARDA report 1995-1998; Donner *et al*., 2006; Cook, 2006) shown (Fig 7) for disease severity evaluation.

Where, severity evaluation explained at these growth stages

0= no infection or free from infection

1= resistant: a few isolated lesions on only the lowest leaves

2 = resistant: Scattered lesions on the second set of leaves with first leaves slightly infected.

3= resistant: Light to moderate infection at lower the leaf plant

4= moderately resistant: Moderate infection of lower leaves with scattered and light infection below the middle of the plant.

5= severe infection on the lower leaves of the plant; moderate, scattered light infection which extended to the middle of the plant

6= moderately susceptible to disease: higher infection of the lower as well as middle leaves and scattered lesions onwards part of the plant

7= susceptible: Lesions very high on lower and middle leaves with high infection and extended to the leaf below the flag leaf.

8= susceptible: Lesions severe on lower and middle leaves; moderate to severe infection of upper third of plant; flag leaf infected in amounts more

9= highly susceptible: Severe infection on all leaves; spike also infected to some degree; Spike infection is scored on a modified scale based on the percentage of the total area covered; the percentage figure follows the numerical leaf infection score

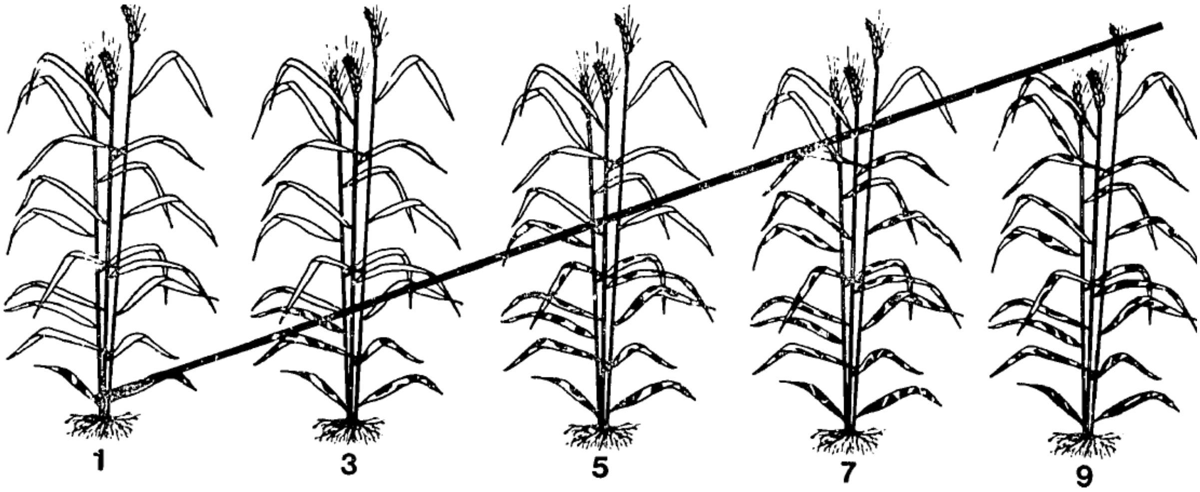


Figure 7. Scale for appraising the intensity of foliar disease in wheat and barley

(Saari and Prescott, 1975; Couture, 1980; Stubbs *et al*,. 1986; ICARDA report 1995-1998; Cook, 2006).

d) Yellow rust disease severity evaluation 61 and 83 growth stages

In addition to above yellow rust severity evaluation, 0-100 % scaling method was assessed from tagged plant on first leaf and the penultimate leaf at flowering and milk stages, respectively.

2.3.1.2. Other disease and insect:

e) Fusarium head blight (FHB) and Septoria tritici blotch (STB): a STB disease was assessed at flag leaf and flowering growth stages. However, Fusarium head blight (FHB) disease assessment was taken at anthesis (flowering stage) and grain filling because FHB symptoms can appeared and crucial at these stages.

f) Percent of aphid infestation

In each plot, four samples were taken randomly and these plants in quadrant of 0.5m x 0.5m were assessed and the number of heads infested by aphid counted. Data was taken at heading (anthesis) and grain filling stages.

% of aphid infested = $(\frac{\text{Number of heads infested by aphid}}{\text{total number heads in quadrant}} * 100)$

2.3.2. Yield and other agronomic traits data

a) The distance between spikelet's

40 plants per plot were taken from tagged and neighbouring plants. Spike length was measured from these sampled plants. The number of spikelets per spike was calculated based on the following formula.

Distance between spikelets (cm) = $\frac{Length\ of\ spike}{number\ of\ spiklets\ per\ spike}$

b) Plant height: 40 plants per plot were taken from tagged and neighbouring plants. Plant height was measured in cm from these sampled plants and their average was considered as plant height.

d) **The distance between the flag leaf and spike**: 40 plants per plot were taken from tagged and neighbouring plants. The distance between the flag leaf and spike was measured in cm from these sampled plants and their average was taken.

c) Grain yield: after physiological maturation, each genotype was harvested and grain yield per plot weighted and recorded.

d) **Thousand kernel weight (TKW)**: TKW weighted for each bed

2.4. Environmental condition /weather data

The amount of rain fall were measured in mm, monthly temperature in ^{0}C, relative humidity in % and other weather data of experimental area was recorded in the metrological weather station of university. The summary of weather data presented from Fig 14-16 under appendix.

2.5. Statistical analysis

Statistical analysis was conducted by using Genstat 16th edition software. Analysis of variance through REML program was performed to test genotypes as treatment and replication as block structure. I used criterion for declaring significant $P < 0.05$ and mean separation comparison significant for treatments separated by Fisher protected LSD-test at 5%. The association within morphological traits, between agronomic triats and disease was analyzed by using correlation coefficient. Normality and equal variance of raw data was tested by using residual and graphing methods (Appendix)

3. Literature review

3.1. Cytogenetic of wheat

Wheat is one of the largest gene pool among the cereal crops and noteworthy for its diversity. It is a predominately self-pollinating crop and up to 4% natural cross pollination occurs. The species of Triticum are grouped into three ploidy classes, these are: diploid (2n= 2x= 14), tetraploid (2n=4x=28) and hexaploid (2n=6x=42). Genetically, bread wheat (*Triticum aestivum. L*) is an allohexaploid with AABBDD genomes and possesses 21 pair of chromosomes, while durum wheat (*Triticum durum L)*, a tetraploid with AABB genomes and possesses 14 pair of chromosomes (Acquaah, 2007; Kang and Priyadarshan, 2008).

3.2. Evolutionary breeding

Darwin proposed the theory of natural selection for the processes of evolution. This theory recognized that the evolutionary change is based upon interaction between the environment and population containing individual representing heritable variation for traits (Phillips and Wolfe, 2005). It recalls that genetic recombination is a source of variation. Genetic variation is the source that drives breeding to meet future crop improvement (Phillips and Wolfe, 2005), because the highest genetic distance between parents will result in higher heterosis in the progeny.

Evolutionary breeding is based on a mass selection technique for crop improvement used by farmers over 10,000 years ago (Murphy *et al*., 2005). The main of evolutionary plant breeding is suggested to broaden the gene pool of germplasm and continued subjection of mass progeny to competitive natural selection in the area of expected use. i.e. thus, evolving crop populations have the capability of adapting to the conditions under which they are grown. The rate of evolution in composite cross populations depends upon the strength and longevity of the selection pressure in a particular environment and the relative heritability of traits (Danquah and Barrett, 2002). In evolutionary plant breeding, landraces and or genetic diversity or CCPs are subjected to selection under natural conditions. Döring *et al*. (2011) stated that an evolutionary breeding strategy is similar to classical or conventional breeding which involves four stages to create genetic diversity or CCPs, being 1) genetic diversity created via crossing parents, 2 recycle of multiplication seed from each crosses and equal mixed to process first generation of cross composite population, 3) increasing number of populations and or maintenance and 4) finally output as well as recycle breeding processes.

3.3. Breeding for organic and low input conditions: The concept of composite cross population development

Genetically heterogeneous populations, landraces, modern populations and variety mixture enable to buffer the impacts of environmental stress. Genetic diversity can contribute more to the resilience of ecosystem rather than specific functions under changing conditions (Hughes and Stachowicz, 2004). The great genetic variation within varieties can contribute to stabilize the yield and defence against stress environment in organic farming system. Robust varieties are required under organic and low input conditions because these varieties contribute to resilience in these heterogeneous conditions (Lammerts van Bueren *et al*., 2002; Goldringer *et al.*, 2010). In addition, these robust varieties developed from broadened genetic diversity enable to buffer against heterogonous environments.

Composite cross populations are developed by assembling seed stocks with diverse parent origins and by recombination of these stocks by large number of crossings (Phillips and Wolfe, 2005). Four methods of composite cross population development were initiated in the evolutionary plant breeding (Murphy *et al*., 2005), among these, crossing 4-10 parents that are subsequently bulked and or composite cross consisting of 11 or more parents could be a better concept for development of composite cross population. Composite crossed populations are likely more capable to withstand abiotic and biotic stresses than pure line cultivars at low input and under organic conditions. Ceccarelli (1996) suggested that locally based breeding program is a good opportunity to achieve a sustainable increase of agricultural production under low input condition. For instance, composite cross populations performed better under low input condition than pure lines. Low input environments can be very valuable for some trait selection characteristics which are favorable for organic agriculture (Löschenberger *et al*., 2008). Conventional low input trials can be regarded as an indirect selection environment for organic agriculture (Wolfe *et al*., 2008). But, the relative efficiency of indirect selection at high input levels did not appeared more efficient than direct selection at low input (Ceccarelli *et al*., 1992; Brancourt-Hulmet *et al*., 2005). For instance, thirty five winter wheat genotypes tested under organic and conventional systems showed that high significant variation was in the genotypes x farming system interaction at four locations (Murphy *et al*., 2007). Also, the highest yielding winter wheat genotypes in the high input conventional system were not the highest yielding genotypes in organic systems because most traits are highly correlated between organic agriculture and low inputs. The other possible reason is that in organic plant breeding program steps of selection, propagation and maintenance are carried out under organic conditions (Lammerts van Bueren et al., 2002). Two breeding schemes were proposed for organic winter wheat breeding (Löschenberger *et al*., 2008). First scheme, crossing and pedigree selection under low-input conditions and later testing trials under organic conditions. The second approach includes the crossing and bulk reproduction of populations with individual ear selection under organic conditions followed by ear- to-row selection in a low input nursery. Yield trials are conducted parallel under low input and organic agriculture for further selection in these conditions.

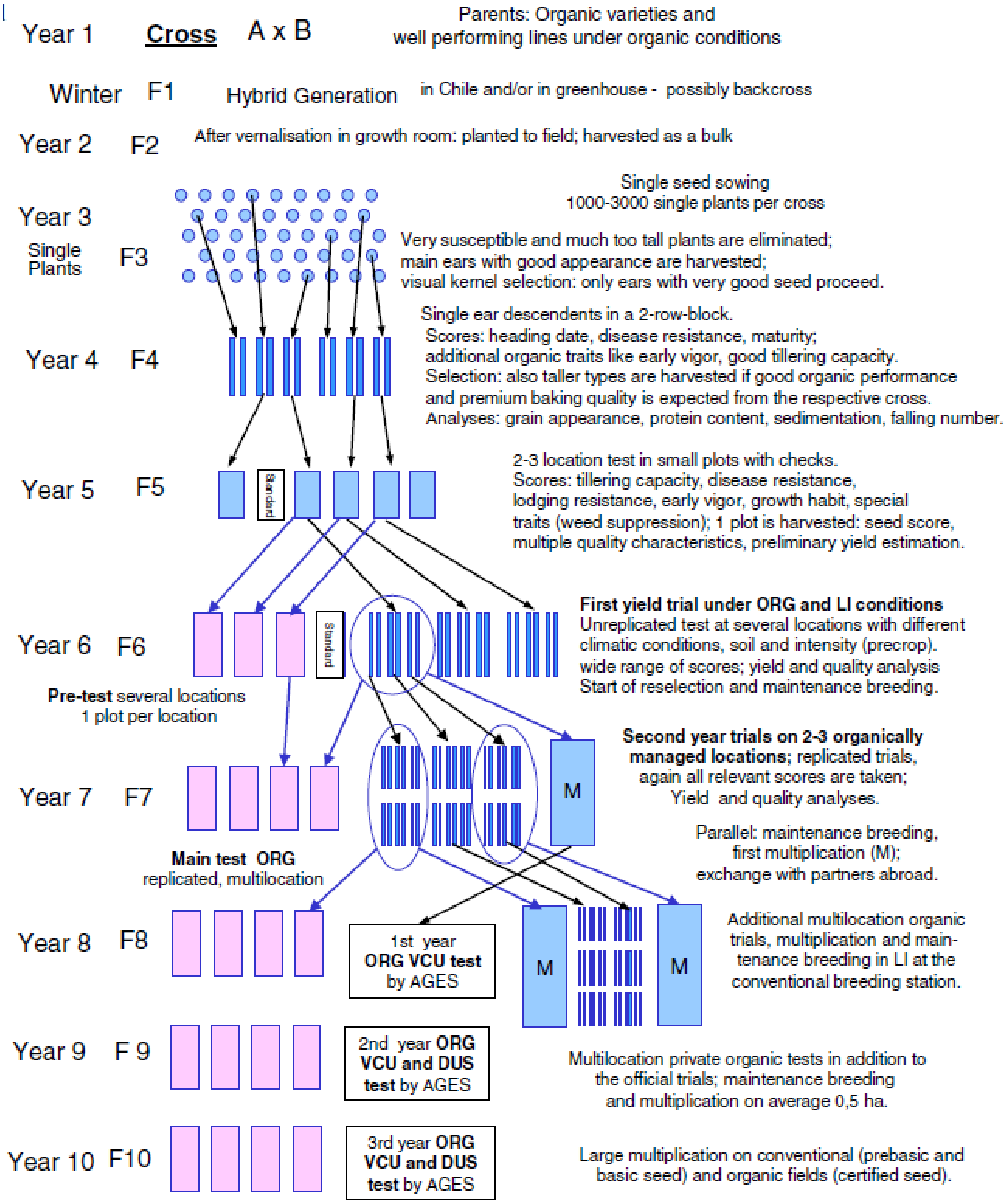


Figure 8. Breeding scheme for organic winter wheat as mainly performed by Saatzucht Donau (modified after Löschenberger *et al*., 2008)

Remark: OA= Organic Agriculture, VCU= Value of Cultivation and Use, DUS= Distinctness, Uniform and Stability, AGES=National Austria cultivar catalogue, LI= Low input

3.3.1 Desirable traits under organic agriculture

The common wheat breeding goal is high yielding, biotic resistance and abiotic tolerance, and good baking quality. In addition, relevant traits are predominately important under organic farming; these are tillering capacity, leaf area index, ground cover, early vigor and nutrient uptake efficiency (Löschenberger *et al.,* 2008). Also, traits such as better root systems, weed suppression ability and others are required under organic and low input conditions.

Cereal cultivars should have a good degree of crop competitive ability, especially to suppress weeds. This competitive ability against weed is also an important trait preference under organic farming systems that aim to limit the use of herbicides and harrowing costs (Osman and Lammerts van Bueren, 2003). The morphological and physiological traits of competitive ability and tolerance to weeds in cereals were studied. Morphological traits associated with wheat competitiveness are tillering capacity, canopy height, ground cover and early crop vigorous (Lemerle *et al*., 2001; Acciaresi *et al*., 2001; Bertholdsson, 2005). Competitive ability is attributed by various desirable traits and correlated to strengthen each other. For instance, tillering capacity and leaf area inclination are primarily affecting photosynthetic active as well as light interception (Eisele and Kopke, 1997). In barley and wheat, Bertholdsson (2005) found that early crop biomass and potential allelopathic activity were the traits that significantly contributed to competitiveness. Similarly, total leaf area index are often correlated with crop ground cover, shading ability, and associated with a relatively high fractional light interception against weed suppression (Neuhof *et al*., 2005). Also, initial root and shoot growth rate are the most important morphological traits in the organic farming (De-Lucas Bueno and Froud-Williams, 1994), because root growth rate is in competition for nutrients, water and space as well as allelopathy to suppress weeds. Therefore, desirable and correlated traits should be considered for organic breeding while selection and evaluation among cultivars carried out.

3.4. Perspectives of marker assisted selection (MAS) for organic breeding

Parallel to exploitation genetic variability under organic farming, application of biotechnological techniques will aid to search out the novel genes which are associated to desired traits as well as to speed up breeding programs. To identify such quantitative trait loci (QTL) by using segregating population from parents with contrasting phenotypes has proven to be difficult due to the complex hexaploid genetics of wheat (Messmer *et al*., 1999; Paillard *et al*., 2003). Currently, the implementation of marker assisted selection into commercial wheat breeding programs is still restricted to marker assisted backcross breeding for the introgression of major genes from un-adapted materials. But, QTL for resistance to wheat disease (for example, leaf rust, fusarium head blight, septoria) have been identified in hexaploid in wheat (Jahoor *et al*., 2005). With advanced marker techniques such as association mapping analysis, it was found that the candidate gene association analysis can be efficient in estimating of glutenin trait for wheat quality (Zheng *et al*., 2009). In addition, other technology such as TILLING (Targeting Induced Local Lesion In Genetics) can be useful for MAS (Parry *et al*., 2009). Incorporating genetic resistance led to resistance variety development. For instance, Mlo is a recessive allele in barley mediates a race-nonspecific resistance to powdery mildew. Mlo was originally developed via mutagenesis from barley landrace collected (Johnson and Jellis, 1992). In future, not only suitability of cultivars under organic conditions but also application techniques in breeding programs such as marker assisted selection to support efficient introgression of new resistance genes from relative wild species and testing their pyramided genes should be considered for organic and low input systems.

3.5. Major winter wheat disease and insect pest

3.5.1. Foliar disease

Before considering the major wheat disease, it is important to remember the key elements of plant disease epidemic their occurrence and severity. Briefly, the three key elements, which are commonly named as the disease triangle, are: a susceptible host, virulent pathogen and environment conducive to disease development (Agrios, 2005).

Foliar diseases have the most important economic impact on wheat production. Among foliar diseases, yellow rust (strip rust), leaf rust (brown rust), septoria tritici bloch (STB), fusarium head blight (FHB), powdery mildew and eye spot cause significant yield losses on wheat production (Lonnet, 1997; Lucas,1998; Marshall, 2009). In addition, common bunt and dwarf are also important seed borne diseases of winter wheat that significantly influence seed production because synthetic chemical application is prohibited under organic farming (Huber and Buerstmayr, 2006; Lammerts van Bueren *et al*., 2011). But powdery mildew and eyespot disease are less of economic importance under organic agriculture because the disease incidence is often influenced by high input cropping system.

3.5.1.1. Yellow rust (Strip rust)

Yellow rust (strip rust) is caused by *Puccinia Striiformis,* and is foliar disease with the most economical impact on wheat production (Chen, 2005; Moldenhaur *et al*., 2006). Yellow rust develops at lower temperature, optimally between 10-15 ^{0}C and normally occurs in regions that have predominately cooler climates, moist and near to coast growing areas (Chen, 2005). The disease is characterized by yellow tiny spotting and yellow to orange pustules arranged between the veins in strip. Strips of uredia or necrosis are not formed on seedling leaves whereas the narrow strips on the leaves are formed after stem elongation (Prescott *et al*, 1986; Chen, 2005*)*. The urediaspore contains a lot of uredia or spore which tends to oval shape (personal observation under microscope, 2014). Yellow rust infection at early stage (one leaf stage) of plant development resulted in stunted and weakened crop, damaged tillers, leading to yield losses (Roelfs, *et al*., 1992). When yellow rust was widespread through a severe disease outbreak, the yield losses ranged from 50-60% in Europe

(Moldenhaur *et al*., 2006) and 10-70% in China (Chen, 2005). Wheat rust disease decreases photosynthesis and translocation, and increase respiration at the seedling stages (Agrios, 2005).

Crop diversification is one of the strategies to reduce disease pressure, e.g. when it is grown as crop mixtures that differ in their reaction to pathogens. Also within a crop species, variety and multiline mixtures can provide functional diversity that limits pathogen and pest expansion (Mundt, 2002), because plant-plant interactions may interfere and make choices more complicated to plant-pathogen interaction. In addition, cultivar mixtures can more stabilise yields and can buffer stresses than pure stands (Finckh *et al*., 2000). Susceptible rice varieties planted with a resistance mixture showed higher yield and very dramatically reduced disease than its component (Zhu *et al*., 2000). Cultivar mixture showed a delayed disease development and the number of necrosis on leaves were reduced for example, for strip rust, powdery mildew and leaf rust compared with stands in wheat (Manthey and Fehrmann, 1993). Different studies were conducted on germplasm of wheat and barley resistance to yellow rust. An experiment conducted with five winter cultivars alone, six cultivars consisting of two different way mixtures and one four way mixture grown in the presence of yellow rust and eye spot, showed that the four component mixture provided better yellow rust resistance than single cultivar and two way mixtures (Mundt *et al*., 1995). Cultivar mixtures showed a reduction of more than 50% in the severity of barley powdery mildew in the UK (Wolfe and Barrett, 1980). Similarly, Dübin and Wolfe (1994) conducted an experiment on three component wheat mixture with that of its component. The experiment showed that the mixture restricted yellow and leaf rust relative to its component. Finckh and Mundt (1992) reported that as the number of varieties in a mixture increase, the severity of yellow rust was reduced compared to the component. The possible further explanation is that the variety mixture can provide functional diversity that limits the pathogens expansion due to diverse gene background, resistance genes incorporated into cultivar mixture, each cultivar carrying different sources of resistance to disease, different adaptations within races to different host plant and a barrier via crop resistant by restriction of spread pathogen.

3.5.1.2. Fusarium Head Blight

Fusarium head blight (FHB) or ear blight is caused by two fusarium species, *Fusarium graminearum* Schwabe (teleomorph: Gibberella zeae) and *Fusarium culmorum,* is an important diseases in most wheat growing region of the world (Snijders, 1990). High humidity, relative warm, heavy dew and temperature between 16-31^{0}C favor spore germination (Sutton, 1982). The ear infections are usually most severe when flowering coincides with warm and wet conditions. The disease initial infection on wheat spikes is during flowering (Bai and Shaner, 1994). An infected spikelet first show light brown, water soaked spot on glumes, on the rachis, and then spreads in all direction from the point of infection and subsequently color of ripe heads. FHB is characterized by bleaching spikelet’s in the green spikes before physiological discolored maturity. The infected seed often shrunken and of lighter weight than healthy seeds (Parry *et al*., 1995). The disease does not only cause yield losses but also produces toxic substance such as deoxynivaleno (DON) accumulation in the grain, which leads consequently to unsuitability for human consumption and animal feeding (Foroud and Eudes, 2009).

Different germplasms were evaluated against FHB to observe the performance of cultivars. Seven parental winter wheat consisting of diverse genotypes via possible combination showed that the heterosis of F_1 crossed significant variation in resistance to FHB (Buerstmayr *et al.*, 1999). 258 winter and spring wheat genotypes were evaluated for resistance to FHB through artificial inoculation and results showed large genetic variation for resistance to FHB (Snijders, 1990). Similarly, 295 European winter wheat cultivars studied for their genetic diversity in relation to FHB resistance by using SSR marker and showed that selection of parental lines is possible in order to increase the efficiency of breeding efforts for FHB resistance (Zwart *et al.*, 2008). Five wheats were conducted to screen against FHB over years and among them, one genotype showed resistance to FHB and stem rust (Costa *et al.*, 2010).

3.5.2. Insect pest: aphid

The Russian wheat aphid *Diuraphis noxia,* (Mordvilko) is an economical important of pest on wheat and barley production. An environment such as dry, high temperature and warm humidity favor the aphid infestation, but is able to survive at high rain fall (Araya 1991). They are three aphides species, *Sitobion avenae* (Fabricius), *Rhopalosiphum padi* (Linnaeus) and *Metopolophium dirhodum* studied in the Netherlands on winter wheat and their effect on yield. Among these, *Sitobion avenae* is multiplied at a higher rate than two species and the most injurious (Vereijken, 1979). Losses in host wheat yield of between 21 up to 92% were reported in south Africa, where about 40 % of the wheat crop has been threated annually (Hewitt, 1988).

Incorporation of insect resistance/tolerance of crop variety has a great role in reducing insect pest damage. Different germplasms of spring barley were studied under field experimental conditions against Russian aphid and result showed significant variation among germplasm resistance and susceptible to aphid (Mornhinweg *et al*., 2006). Similarly, two hundred wheat lines were conducted at five locations over two years and, it was shown that except two lines most lines were susceptibility to aphid (Zhou *et al*., 2013).

Secondary plant substances and epidermal trichomes concentration in leave play an important role in resistance to cereal aphids. Leszczynski *et al*., (1989) reported that winter wheat cultivar with more content of hydroxamic acid and trichome density in the leaves showed that moderately resistant to aphid.

3.5.3. Genetic resistance to disease

Disease resistance should be targeted for organic breeding because application of synthetic chemicals is prohibited under organic agriculture. Genetic resistance to disease in plant breeding is a cost effective and environmental sound means to control diseases (Singh *et al*., 2001). Genetic resistance to disease can be classified as race specific (vertical) or race non-specific resistance (horizontal). The qualitative resistance is typically race specific and has a simple monogenic inheritance whereas the quantitative type of resistance is race non-specific, within the host the resistance genes show additively and are governed by polygenic inheritance (Parlevliet and Zadoks, 1977; Welz and Geiger, 2000).

Based on phenotypic characteristics, the polygenic (quantitative) type has a partial nature of resistance which is characterized by less infection and chlorosis. It is also associated with the slow formation of chlorotic lesions which reduces the rate of disease formation and increases the latency period (Niks *et al*., 2011). This type of resistance is controlled by many genes (polygenic nature) which have a partially dominant to additive effect. It is often characterized by its durability, effectiveness against a wide range of pathogen races, partial resistance phenotype and optimal expression at the adult plant stage (McIntosh *et al*., 1995). The resistance is often conditioned by a few to several genes with partial or additive effects. For instance, resistance to FHB is additive and the accumulation of resistance genes from different source increase resistance (Snijders, 1990; Zhuang and Li, 1993; Bai and Shaner, 1994; Buerstmayr *et al*., 2002), i.e. resistance to FHB is race non-specific. Wheat breeders are focusing on the identification and incorporation of race non-specific resistance genes that provide for partial resistance but when used in combination with other genes can highly effective resistance. (Johnson, 1988) found that leaf and yellow rusts of several cultivars is based on the slow rusting genes having additive effects. Singh *et al*. (2005) reported that durable resistance to leaf and yellow rusts can be achieved by pyramiding 4 to 5 genes.

In contrast, race-specific genes can provide effective resistance, but they can with specific races with the corresponding virulence result in cultivars losing effective resistance within a short period of time, and then the resistance can easily be overcome by new virulent races (McIntosh *et al*. 1995).

3.5.4. Disease and insect pest management

Host resistance is efficient, relativity low cost, easy to use and eco-friendly. Incorporating genetic resistance for breeding resistances led to resistant variety development. Many varieties were released with that resistance to disease. For instance, winter wheat variety was released for resistance to fusarium head blight and stem rust in USA (Costa *et al.,* 2010). Similarly, winter wheat cultivar for example, Claire is resistant to yellow rust and effective in UK and Europe since it’s release 1999 (Powell *et al*, 2013). Similarly, winter wheat resistance genes, Bt12 and Bt13 were conferred resistance to two seed borne diseases, *Tilletia caries and Tilletia controversa* under organic farming condition (Huber and Buerstmayr, 2006). It was of great importance to use genetically based resistance for protection against common bunt and dwarf bunt where chemical application is prohibited under organic farming.

Integrated pest management (IPM) is one of disease and insect pest management strategies in crop protection. Integrated pest control is a pest management system in the context of the associated environment and population dynamics of pest species, and utilizes all suitable techniques and methods in a compatible manner as possible and maintains the pest population at levels below those causing economic injury (Kogan, 1998). This definition might be applicable for high input conventional agriculture. However, application of synthetic pesticides and use of GMO is prohibited under organic agriculture. Organic agriculture system is characterized by use of ecological farming systems, functional biodiversity and cropping system (Lampkin, 1999; Lammerts van Bueren *et al*., 2002.). For instance, crop rotation is an effective technique for controlling plant disease that causes a decline in pathogen population due to reduced inoculum pressure, interruption of disease cycle, mortality and the antagonistic activities of co-existing organisms (Cook, 1986). Organic farming is believed to increase soil suppressiveness towards soil-borne disease as well as aerial diseases. For instance, high microbial biomass can reduce the severity of attack by soil born plant pathogens via means of disease suppression and or antagonistic micro-organism (Workneh and Bruggen, 1994; Tamm *et al.*, 2006).

Resistance varieties combined with diversified strategies like crop rotation, intercropping and soil amendment are basic components of organic agriculture systems for disease and pest management.

4. Results

The winter wheat genotypes were studied for diseases resistance, yield and other agronomic traits under organic condition in 2014. Result and discussion are presented following paragraphs.

4.1. Foliar diseases

4.1.1. Yellow rust

For YRInc21 and YRInc31 growth stages, the incidence data were taken from infected samples counted over a length of 30 cm. For YRIncFL39, YRIncFW61 and YRIncMS83 growth stages, the data were taken from tagged sample plants.

Analysis of variance showed highly significant differences ($P < 0.001$) for all involved winter wheat genotypes for yellow rust incidence (%) at 21 stage, 31 stage, flag leave stage, flowering stage and milk stage (Table 3). However, there were no significant differences among composite cross populations for yellow rust incidence (%) at 21 and 31 growth stages. For flag leave stage, flowering stage and milk stage significant differences were observed among composite crossed population for yellow rust incidence (%). The yellow rust incidence increases across the growth stages from 21 stage to milk stages (Table 3 and Fig 9). At YRIncMS stage, the highest yellow rust incidence (92.27%) was observed on the pure line at milk stage, followed by composite cross populations B (HU-08-UK-Comp) and A (HU-08-YQMS) and H (HU-12-YGMS).

Table 3. Comparison of mean for the yellow rust incidence (%) at different growth stages for the winter wheat trial in 2014 at Droevendaal organic experimental farm, Wageningen.

	Mean for yellow rust incidence per 30 cm sample		Mean for yellow rust incidence of tagged samples		
Genotype	YR_Inc 21S	YR_Inc 31S	YR_IncFL	YR_IncFW	YR_Inc MS
C (Naturastar/ pure line)	21.31^{b}	40.05^{b}	54.41^{c}	81.85^{d}	92.27^{c}
B (HU-08-UK composite)	1.67^{a}	2.03^{a}	33.73^{b}	41.68^{c}	43.56^{b}
A (HU-08-YQMS	2.62^{a}	5.25^{a}	10.83^{a}	27.33^{b}	30.17^{ab}
G (HU-09-YQMS)	2.32^{a}	6.33^{a}	11.08^{a}	17.53^{ab}	18.33^{a}
D (HU-10-YQMS)	0.81^{a}	4.20^{a}	9.28^{a}	17.10^{ab}	18.04^{a}
E (HU-11-YQMS)	2.46^{a}	6.90^{a}	7.91^{a}	17.13^{ab}	23.04^{a}
H (HU-12-YQMS)	0.98^{a}	2.23^{a}	7.08^{a}	17.42^{ab}	27.5^{ab}
I (HU-13-YQMS)	1.17^{a}	3.20^{a}	9.72^{a}	12.43^{a}	24.17^{a}
CV (%)	55.70	34.40	14.60	20.70	25.50
LSD at 0.05	4.22	5.57	4.86	20.20	16.34
P-value	0.001(***)	0.001(***)	0.001(***)	0.001(***)	0.001(***)

Genotypes having the same letter did not show a significant difference (P=0.05), CV%= coefficient of variation.

*** = Very highly significant difference among genotypes

**= Highly significant difference among genotypes

* = Significant difference among genotypes

YR_Inc 21S= Yellow Rust Incidence at 21 growth stage, YR_Inc 31S= Yellow Rust Incidence at 31 growth stage, YR_IncFL= Yellow Rust Incidence at flag leave appeared stage, YR_IncFW= Yellow Rust Incidence at flowering stage, YR_Inc MS= Yellow Rust Incidence at milk stage.

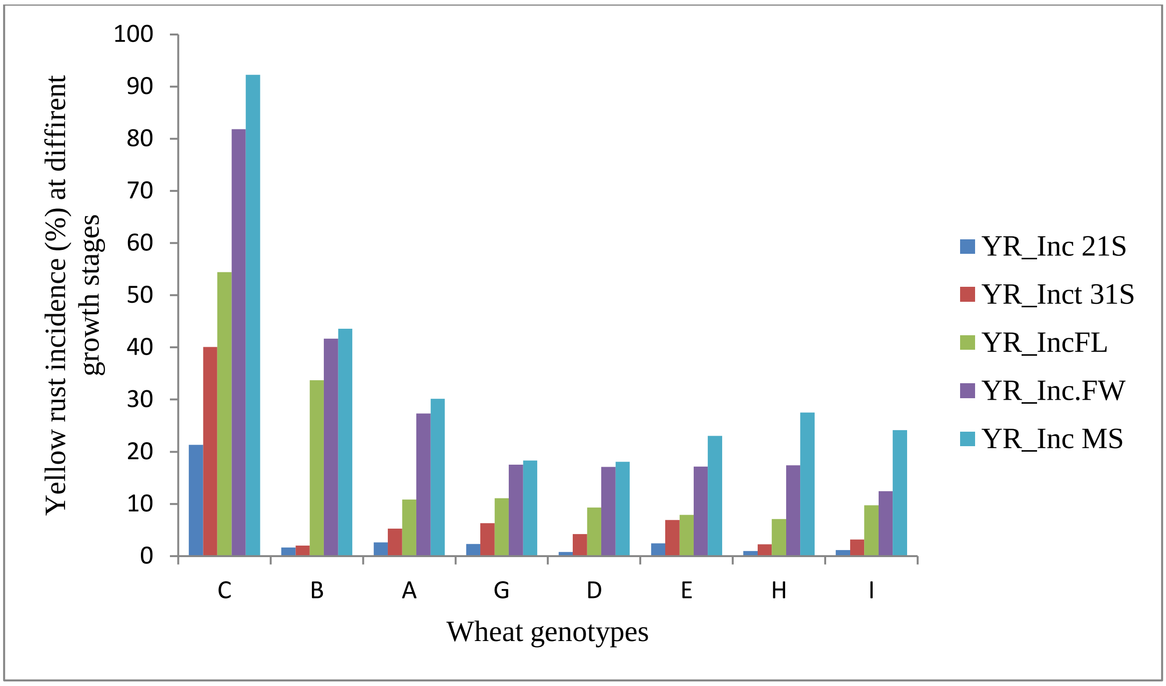


Figure 9. Trend of yellow rust incidence (%) expansion for each genotype across growth stages

Key: YRIncS21= yellow rust incidence at 21 growth stage, YRIncS31= yellow rust incidence at 31 growth stage, YRIncFL=yellow rust incidence at flag leaf appeared growth stage, YRIncFW=yellow rust incidence at flowering growth stage, YRIncMS= yellow rust incidence at milk stage.

The yellow rust frequency and disease pressure was larger in rep-I than rep-II and III. The red colour in rep-I showed more disease severity than in rep-II (indicated in blue colour). But it was vary among wheat genotypes for red colour. For instance, the yellow rust severity ranges 40-60 % for C cultivar and 10 % estimated for A and B at milk stage in rep I per plot. Whereas, 2-5% severity level per plot for the other genotypes that indicated yellow colour in rep I. It seems plausible that the higher levels of severity in rep-I is the result of the dominant wind direction. The disease pressure in rep-III was even less than in rep-II (Fig 10). The yellow colour in rep-I and II showed a more or less similar disease severity. It is not likely to conclude that the disease severity in rep-III compared to the other replications was due to flooding factor which caused some plots to have less plant densities per plot.

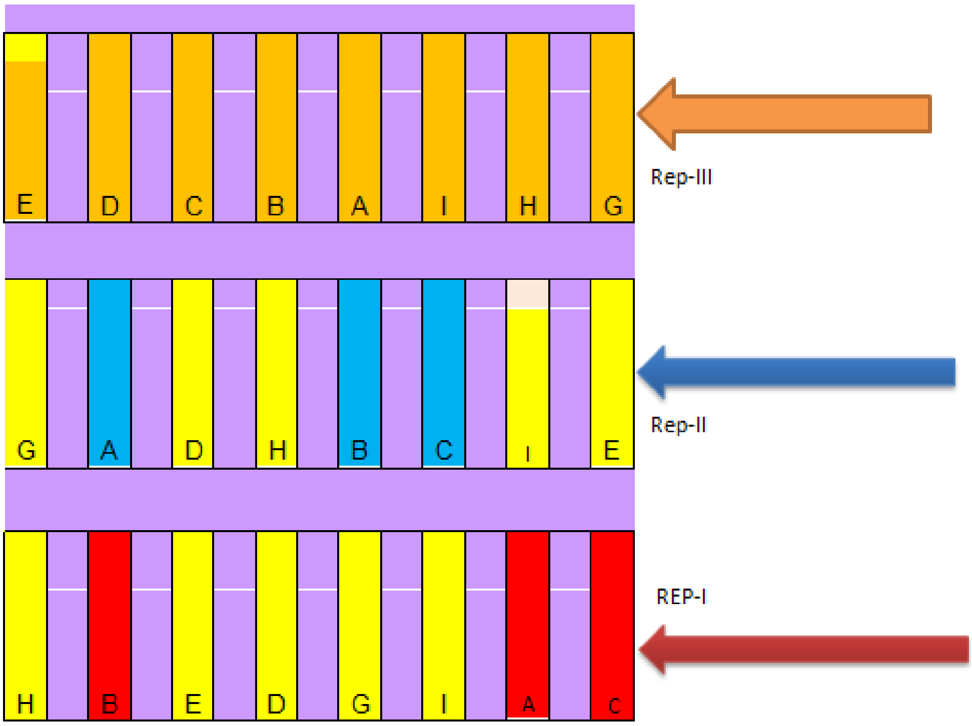


Figure 10. The degree of yellow rust severity pressure among replications

There were significant differences (*P*<0.001) among all winter wheat genotypes for yellow rust severity (0-9 scale method) at flag leaf sheath extended stage, flowering stage and milk stages (Table 4). Also significant difference was observed among composite crossed population for yellow rust severity (0-9 scale) at these stages. At milk stage, the highest severity was recorded on the pure line (6.01), followed by CCP B and A (3.10 and 2.32) respectively.

Highly significant differences (*P* <0.001) were observed among all involved winter wheat genotypes for yellow rust severity (0-100% scaling methods) on the first flag leaf and the penultimate leaf at flowering and milk stages (Table 4). Also, significant differences were found among composite crossed population for yellow rust severity at these stages. The highest yellow rust severity (60.64%) was observed at the penultimate leaf at milk stage for the pure line, followed by populations A and B (15.44 and 15.50%), respectively.

Table 4. Comparison of mean for the yellow rust severity based on 0-9 scale and 0-100 % scoring methods at different growth stages for the wheat trial in 2014 at Droevendaal organic experimental farm, Wageningen.

	Mean for Yellow rust severity based on (0-9 scale)			Mean for Yellow rust severity based on (0-100 % scale)			
Genotype	YSVFL	YSVFW	YSVM	YSV1sfLFW	YSV2ndfLFW	YSV1sfLMS	YSV2nfLMS
C	4.25^{d}	4.10^{c}	6.10^{c}	16.63^{b}	30.49^{c}	35.76^{d}	60.64^{c}
B	2.70^{c}	2.78^{b}	3.10^{b}	11.93^{b}	17.91^{b}	11.63^{c}	15.44^{b}
A	1.67^{b}	1.77^{a}	2.32^{ab}	3.59^{a}	5.45^{a}	10.44^{bc}	15.50^{b}
G	1.28^{ab}	1.36^{a}	1.68^{a}	1.15^{a}	2.03^{a}	1.88^{a}	3.25^{a}
D	1.25^{a}	1.52^{a}	1.67^{a}	1.70^{a}	3.37^{a}	3.12^{abc}	3.50^{a}
E	1.14^{a}	1.64^{a}	1.89^{a}	2.43^{a}	3.67^{a}	3.25^{abc}	4.88^{a}
H	1.22^{a}	1.42^{a}	1.92^{a}	2.12^{a}	3.63^{a}	2.62^{ab}	4.13^{a}
I	1.29^{ab}	1.37^{a}	1.93^{a}	2.36^{a}	2.42^{a}	3.75^{abc}	7.13^{ab}
CV (%)	11.8	17.50	20.10	54.50	39.00	39.80	28.40
LSD, 0.05	0.41	0.64	0.95	5.27	6.21	8.52	9.62
P-value	0.001	0.001	0.001	0.001	0.001	0.001	0.001

Genotypes having the same letter did not show significant difference (P=0.05) in per column, NS= No significant difference.

***** *(0.001) there is very highly significant difference among genotypes.*

*** Highly significant difference among genotypes, * significant difference among genotypes*

YSVFL (0-9 scale method)= Yellow Rust severity at flag leaf appeared stage, YSVFW (0-9 scale method)= Yellow Rust severity at flowering growth stage , YSVM (0-9 scale methods)= Yellow Rust severity at milk stage, YSV1sfLFW (0-100 % scaling)=Yellow Rust severity on the 1st flag leaf at flowering growth stage, YSV2ndfLFW (0-100 % scaling)= Yellow Rust severity on penultimate leaf at flowering growth stage, YSV1sfLMS (0-100 % scaling)= Yellow Rust severity on 1st flag leaf at milk stage, YSV2dfLMS (0-100 % scaling method)= Yellow Rust severity on penultimate leaf at milk stage.

4.1.2. Other minor diseases and insect

There was no significant difference (*P*= 0.31) observed among all involved winter wheat genotypes for fusarium head blight severity at flowering stage. However, a significant difference was observed among winter wheat genotypes for FHB at grain filling stage. For aphid infestation, no significant differences were found among all involved winter wheat genotypes at flowering and milk stages, respectively (Table 5). Similarly, no significant differences were found among winter wheat genotypes for septoria tritici leaf blotch incidence at flag leaf stage. But, significant differences were observed among genotypes for the septoria tritici blotch disease incidence and severity at flowering stage (Table 5). However, the level of severity was low for fusarium head blight, septoria tritici blotch and aphid infestations. These diseases and aphid were likely not of economic importance at Droevendaal organic experimental farm in this cropping season.

Table 5. Comparison of mean for the septoria and fusarium disease severity, and aphid infestation at different growth stages for the winter wheat trial in 2014 at Droevendaal organic experimental farm.

Genotypes	FHB_SV FWS(0-9)	FHB_SV (%)MS	STB_Inc (%)FLS	STB_Inc (%)FWS	STB_SV FWS(0-9)	Aph (%)FWS	Aph(%) MS
C	1.38	1.00^{a}	5.02	4.79^{a}	1.09^{b}	0.64	0.25
B	1.12	1.80^{ab}	11.88	12.49^{b}	1.32^{bc}	0.22	0.11
A	1.21	4.20^{d}	8.80	11.50^{b}	1.3^{b}	0.65	0.13
G	1.10	3.50^{bcd}	9.83	13.29^{bc}	1.49^{c}	1.34	0.22
D	1.13	2.00^{abc}	9.27	17.99^{c}	1.2^{ab}	0.36	0.07
E	1.23	2.40^{abcd}	8.39	14.21^{bc}	1.19^{ab}	0.25	0.39
H	1.20	2.60^{abcd}	7.28	13.28^{bc}	1.19^{ab}	0.91	0.28
I	1.33	3.60^{cd}	3.67	13.65^{bc}	1.16^{ab}	0.36	0.13
CV (%)	11.62	28.60	41.27	22.00	8.0	47.50	28.94
LSD(0.05)	NS	1.79	NS	5.13	0.18	NS	NS
P- value		0.04		0.012	0.015		

Genotypes having the same letter did not show significant difference (P=0.05), NS= No significant difference.

FHB_SV FWS (0-9) = fusarium head blight severity in 0-9 scale at flowering stag, FHB_SV (%)MS= fusarium head blight severity in % by using 0-100 scaling methods at milk stage; STB_Inc (%)FLS= septoria trictici blotch incidence in % at flag leaf appearance stage, STB_Inc (%)FWS = septoria trictici blotch incidence in % at flowering stage, STB_SV FWS (0-9) = septoria trictici blotch severity in 0-9 scale at flowering stage, Aph (%)FWS= percentage of aphid infestation at flowering stage, Aph(%) MS= percentage of aphid infestation at milk stage.

4.2. Yield and other agronomic traits

4.2.1. Grain yield and 1000 kernel weight

There was no significant difference (*P*=0.45) among the all involved wheat genotypes for grain yield. For some genotypes lower yields were observed, like for the pure line (2.86 t/ha) and population HU-08-UK-comp (2.65 t/ha) (Table 6), respectively. Highly significant differences (*P*=0.002) were found among all involved genotypes for thousand kernel weight (TKW). Also, a significant difference was observed among CCPs for TKW. The highest TKW was recorded for the population HU-13-YQMS (43.23 g) whereas the pure line (Naturastar) showed the lowest TKW (37.43 g) (Table 6).

4.2.2. Other agronomic traits

The ANOVA showed significant differences among all involved wheat genotypes for some agronomic traits; plant height ($P<0.03$), total number of spikelets ($P<0.014$) and the distance between the flag leaf and spike ($P<0.007$) (Table 6). Also, significant differences were observed among CCPs for these traits. The longest genotype was the population HU-11-YQMS with an average length of 91.42 cm, while, population HU-12-YQMS had the shortest recorded average length of 76.28 cm.

No difference were found among wheat genotypes for spike length, distance between spikelets, fertile tiller per m^2 and unfertile spikelets / spike (Table 6).

Table 6. Comparison of mean grain yield (t/ha) and other agronomic traits for wheat genotypes at Droevendaal organic experimental farm, Wageningen, The Netherlands**.**

Genotype	Grain yield (t/ha)	TKW (g)	FT/ m^2	PLHT (cm)	SL(cm)	FL(cm)	FS	UFS	TS	DS
C	2.86	37.43^{a}	421.4	80.75^{a}	8.86	14.99^{ab}	16.63^{c}	4.27	20.90^{c}	0.41
B	2.65	41.35^{bcd}	326.33	83.07^{a}	7.48	15.90^{ab}	13.79^{a}	3.92	17.71^{a}	0.42
A	3.18	41.43^{bcd}	444.33	82.89^{a}	8.16	15.53^{ab}	15.70^{ab}	3.56	19.27^{b}	0.43
G	3.26	40.96^{bc}	453.33	79.11^{a}	7.93	17.19^{b}	14.87^{ab}	3.66	18.53^{ab}	0.43
D	3.17	42.58^{cd}	500.90	82.94^{a}	7.99	16.55^{ab}	14.74^{ab}	3.28	18.02^{ab}	0.44
E	3.39	41.88^{bcd}	440.40	91.42^{b}	8.65	20.47^{c}	15.94^{bc}	3.83	19.32^{b}	0.45
H	3.15	39.80^{b}	450.33	76.28^{a}	7.66	14.08^{a}	14.71^{ab}	3.91	18.62^{ab}	0.41
I	3.39	43.23^{d}	465.00	82.54^{a}	8.00	17.11^{b}	14.44^{ab}	3.57	18.41^{ab}	0.44
CV (%)	13.90	2.90	13.85	4.60	5.70	8.20	5.60	13.85	4.10	3.52
LSD, 0.05	NS	2.12	NS	7.03	NS	2.48	1.56	NS	1.42	NS
P-value		0.002^{*}		0.03^{*}		0.007^{*}	0.05		0.014^{*}	

Genotypes having the same letter did not show significant difference (P=0.05), NS= no significant difference.

**** There is very highly significant difference among genotypes*

*** Highly significant difference among genotypes*

** Significant difference among genotypes*

TKW (g) = Thousand kernel weight, FT per m^2= number of fertile tillers m^{-2}, PLHT= plant height (cm), SL= spike length in cm, FL= the distance between Flag leaf and spike in cm, FS= number of fertile spikelet, UFS = number of unfertile spikelets, TS =total number of spikelets / spike, DS= the distance between spikelets

4.3. Correlation coefficient for some morphological traits and disease

Correlation analysis was used to study the association within the morphological traits and between the morphological traits and yellow rust disease among the CCPs and the pure line separately. A good trend of association among traits was observed among composite cross populations when excluding pure line. Correlations within morphological traits are discussed separately in the following paragraphs.

4.3.1. Correlations among morphological traits

Pearson correlation analysis showed that significant association for some characters. A good correlation within traits was observed among composite crossed population when excluding pure line based on average plot data (see Table 7 and 8). Therefore, the correlation between morphological traits among composite crossed populations based on average plot and individual plant data are described separately in following paragraph.

Based on plot average data, plant height revealed a highly significant positive association with; spike length (r=0.867), the distance between flag leaf and spike (r=0.750), fertile spikelets (r=0.646) and the distance between spikelets (r=0.683) (Table 7). Similarly, spike length showed significant positive correlation with the distance between spikelets (r= 0.741) and the number of fertile spikelets (r=0.782) (Table 7).However, plant height and spike length showed a significant negative correlation with unfertile spikes (r=-0.505) and (r= -0.552), respectively.

Based on individual plant data, the association among morphological traits showed significant positive results for the CCPs. But their association was weaker. For instance, plant height showed significant positive association with; spike length (r=0.437), fertile spikelet (r= 0.261), total spikelet (r=0.145) and the distance between spikelet (r= 0.392) (Table 13).

For the pure line, a significant positive association within the morphological traits also observed (Table 15). But plant height did not show a significant correlation with the distance between spikelets for pure line. Association within morphological traits for the pure line was found between plot average data and individual plant sample data (Table 15). Therefore, the morphological trait association was stronger on plot average than individual plant sample data for CCPs (Table 7 verses Table 13).

Table 7. Pearson correlations for some morphological traits and yellow rust incidence (%) for composite cross population based on plot average data.

	PLHT	SL	FL	FT/m2	FS	UFS	TS	%FS	DS	YRInc21	YRInc31	YRIncFL	YRIncFW	YRINCMS
PLHT	🟦	0.867**	0.750**	0.178	0.646**	-0.505*	0.369	0.587*	0.683**	0.216	0.403	0.054	0.215	0.277
SL	0.867**	🟦	0.694**	0.016	0.782**	-0.552*	0.496*	0.669**	0.741**	0.462	0.468	-0.250	-0.024	0.097
FL	0.750**	0.694**	🟦	0.160	0.444	-0.448	0.172	0.488*	0.639**	0.130	0.597*	-0.020	-0.097	-0.135
FT/m2	0.178	0.016	0.160	🟦	0.006	0.192	0.164	-0.160	-0.117	-0.541*	-0.074	-0.016	0.017	0.100
FS	0.646**	0.782**	0.444	0.006	🟦	-0.571*	0.744**	0.747**	0.306	0.414	0.406	-0.159	0.288	0.178
UFS	-0.505*	-0.552*	-0.448	..192	-0.571*	🟦	0.125	-0.972**	-0.718**	-0.457	-0.356	-0.158	-0.292	-0.131
TS	0.369	0.496*	0.172	0.164	0.744**	0.125	🟦	0.112	-0.215	0.128	0.201	-0.320	0.110	0.109
%FS	0.587*	0.669**	0.488*	-0.160	0.747**	-0.972**	0.112	🟦	0.668**	0.482	0.393	0.076	0.306	0.145
DS	0.683**	0.741**	0.639**	-0.117	0.306	-0.718**	-0.215	0.668**	🟦	0.425	0.358	-0.041	-0.122	0.021
YRInc21	0.216	0.462	0.130	-0.541*	0.414	-0.457	0.128	0.482	0.425	🟦	0.313	0.059	0.109	0.064
YRInc31	0.403	0.468	0.597*	-0.074	0.406	-0.356	0.201	0.393	0.358	0.313	🟦	-0.080	0.152	-0.166
YRIncFL	0.054	0-.250	-0.020	-0.016	-0.159	-0.158	-0.320	0.076	-0.041	0.059	-0.080	🟦	0.715**	0.489*
YRIncFW	0.215	-0.024	-0.097	0.017	0.288	-0.292	0.110	0.306	-0.122	0.109	0.152	0.715**	🟦	0.722**
YRINCMS	0.277	0.097	-0.135	0.100	0.178	-0.131	0.109	0.145	0.021	0.064	-0.166	0.489*	0.722**	🟦

** Correlation is significant at the 0.01vlevel, * correlation is significant at the 0.05 level

**The pure line was not included*

key :- PLHT= plant height in cm, SL= spike length in cm, FL= the distance between flag leaf and spike, Ft/m^2 =fertile tiller m^{-2}, FS= number of fertile spikelets, UFS= number of unfertile spikelets, TS= total spikelet, %PF= percentage of fertile spiklet, DS= distance between spikelet, YRInc21=yellow rust incidence at 21 growth stage, YRInc31=yellow rust incidence at 31 growth stage, YRIncFL= yellow rust incidence (%)at flag leaf appeared, YRIncFW= yellow rust incidence (%)at flowering stage, YRIncMS= yellow rust incidence (%) at milk stage.

Table 8. Pearson correlations for some morphological traits and yellow rust incidence (%) for all wheat genotypes based on plot average data

	PLHT	SL	FL	FT/m2	FS	UFS	TS	%FS	DS	YRInc21	YRInc31	YRIncFL	YRIncFW	YRINCMS
PLHT		0.720**	0.712**	0.203	0.515*	-0.491*	0.247	0.621**	0.660**	0.024	0.021	-0.042	0.019	0.030
SL	0.720**		0.379	0.132	0.881**	-0.206	0.734**	0.525*	0.408	0.599**	0.560*	0.334	0.413	0.446
FL	0.712**	0.379		0.122	0.140	-0.500*	-0.113	0.485*	0.667**	-0.220	-0.164	-0.247	-0.280	-.0294
FT/m2	0.203	0.132	0.122		0.141	0.193	0.228	-0.117	-0.130	-0.029	0.103	0.084	0.099	0.127
FS	0.515*	0.881**	0.140	0.141		-0.152	0.874**	0.525*	0.054	0.650**	0.617**	0.430	0.561*	0.524*
UFS	-0.491*	-0.206	-0.500*	0.193	-0.152		0.348	-0.920**	-0.754**	0.319	0.394	0.361	0.322	0.391
TS	0.247	0.734**	-0.113	0.228	0.874**	0.348		0.045	-0.320	0.773**	0.780**	0.585**	0.690**	0.689**
%FS	0.621**	0.525*	0.485*	-0.117	0.525*	-0.920**	0.045		0.671**	-0.015	-0.093	-0.139	-0.055	-0.129
DS	0.660**	0.408	0.667**	-0.130	0.054	-0.754**	-0.320	0.671**		-0.194	-0.260	-0.313	-0.348	-0.298
YRInc21	0.024	0.599**	-0.220	-0.029	0.650**	0.319	0.773**	-0.015	-0.194		0.961**	0.863**	0.879**	0.883**
YRInc31	0.021	0.560*	-0.164	0.103	0.617**	0.394	0.780**	-0.093	-0.260	0.961**		0.876**	0.904**	0.893**
YRIncFL	-0.042	0.334	-0.247	0.084	0.430	0.361	0.585**	-0.139	-0.313	0.863**	0.876**		0.948**	0.913**
YRIncFW	0.019	0.413	-0.280	0.099	0.561*	0.322	0.690**	-0.055	-0.348	0.879**	0.904**	0.948**		0.955**
YRINCMS	0.030	0.446	-0.294	0.127	0.524*	0.391	0.689**	-0.129	-0.298	0.883**	0.893**	0.913**	0.955**	

** Correlation is significant at the 0.01 level, * correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm, FL= the distance between flag leaf and spike, Ft/m^{2} =fertile tiller per m^{2}, FS=number of fertile spikelet, UFS=number of unfertile spikelet, TS= total spikelets, %PF= percentage of fertile, DS= distance between spikelet, YRInc21=yellow rust incidence at 21 growth stage, YRInc31=yellow rust incidence at 31 growth stage, ,YRIncFL= yellow rust incidence (%)at flag leaf appeared, YRIncFW= yellow rust incidence (%)at flowering stage, YRIncMS= yellow rust incidence (%) at milk stage.

* Pure line was included

4.3.2. Correlations among measurements for yellow rust incidence and severity

4.3.2.1 Yellow rust incidence

Pearson correlation analysis showed non-significant associations for the morphological traits with yellow rust incidence. Based on plot averages, some trends can be observed for the association of morphological traits with yellow rust incidence for CCPs. For instance, unfertile spikelets showed non-significant negative correlations with yellow rust incidence at all development stages (Table 7). Similarly, the distance between flag leaf and spike distance showed a non-significant negative association with yellow rust incidence at three lateral stages. Whereas, the number of tillers per area showed non-significant negative association with yellow rust incidence at three early stages. The more yellow rust infection at early stage seems to have resulted in reduced number of tillers per area. But, plant height and percentage of fertile spikelet's showed a non-significant positive correlation with yellow rust incidence for all development stages (Table 7). When including the pure line, the same trends were observed. For instance, percentage fertile spiklet and the distance between flag leaf and spike showed non-significant negative association with yellow rust incidenc at all growth stages. But, unfertile spiklet revealed non-significant correlation with yellow rust incidence (Table 8).

4.3.2.2. Yellow rust severity

Based on plot average data, the correlation analysis showed non-significant associations of morphological traits with yellow rust severity (%). However, some trends of association can be observed for CCPs. For example, there was a positive trend of association of plant height and percent of fertile spikes with yellow rust severity at all developmental stages (Table 9). But, unfertile spikelets and the distance between flag leaf and spike showed negative correlations with yellow rust incidence at all development stages on first and penultimate leaf (Table 9). On the other hand, when including the pure line, percentage fertile spiklet, the distane between flage leaf and spike show non-signifcant negative associations with yellow rust severity at all growth stages. Wheras, unfertile spiklet showed non-siginificant positive association with yellow rust severity at all growth stages (Table 10).

Also, spearman correlation analysis revealed non-significant associations of morphological traits with yellow rust severity (0-9) for CCPs (Table 11). The morphological trait association with yellow rust severity (0-9 scale) was almost similar to the trend of association of agronomic traits with yellow rust severity (%) as described in the above paragraph.

Table 9 . Pearson correlations for some morphological traits with yellow rust severity (%) for the composite cross population based on plot average data

	PLHT	SL	FL	FT/m^2	FS	UFS	TS	%FS	DS	YRSV1stfFW	YRSV2ndfFW	YRSV1stfMS	YRSV2ndfMS
PLHT	🟩	0.867**	0.750**	0.178	0.646**	-0.505*	0.369	0.587*	0.683**	0.261	0.220	0.208	0.277
SL	0.867**	🟩	0.694**	0.016	0.782**	-0.552*	0.496*	0.669**	0.741**	-0.130	-0.173	0.098	0.173
FL	0.750**	0.694**	🟩	0.160	0.444	-0.448	0.172	0.488*	0.639**	-0.024	-0.051	-0.069	-0.070
FT/m2	0.178	0.016	0.160	🟩	0.006	0.192	0.164	-0.160	-0.117	0.107	0.096	-0.164	-0.080
FS	0.646**	0.782**	0.444	0.006	🟩	-0.571*	0.744**	0.747**	0.306	0.025	-0.005	0.161	0.210
UFS	-0.505*	-0.552*	-0.448	0.192	-0.571*	🟩	0.125	-.0972**	-0.718**	-.0130	-0.115	-0.316	-0.237
TS	0.369	0.496*	0.172	0.164	0.744**	0.125	🟩	0.112	-0.215	-0.076	-0.099	-0.063	0.061
%FS	0.587*	0.669**	0.488*	-0.160	0.747**	-0.972**	0.112	🟩	0.668**	0.099	0.079	0.296	0.243
DS	0.683**	0.741**	0.639**	-0.117	0.306	-0.718**	-0.215	0.668**	🟩	-0.100	-0.131	0.160	0.149
YRSV1stfFW	0.261	-0.130	-0.024	0.107	0.025	-0.130	-0.076	0.099	-0.100	🟩	0.987**	0.649**	0.622*
YRSV2ndfFW	0.220	-0.173	-0.051	0.096	-0.005	-0.115	-0.099	0.079	-0.131	0.987**	🟩	0.590*	0.554*
YRSV1stfMS	0.208	0.098	-0.069	-0.164	0.161	-0.316	-0.063	0.296	0.160	0.649**	0.590*	🟩	0.913**
YRSV2ndfMS	0.277	0.173	-0.070	-0.080	0.210	-0.237	0.061	0.243	0.149	0.622*	0.554*	0.913**	🟩

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

Based on plot average data, pure line was not included

key :- PLHT= plant height in cm, SL= spike length in cm , FL= the distance between flag leaf and spike, Ft / m^2 *=number of fertile tillers per* m^2*, FS=number of fertile spikelets, UFS=number of unfertile spikes, TS= total number of spikelets* m^{-2}*, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YRSV1sfFW= Yellow rust severity on first flag leaf at flowering , YRSV2ndfFW= Yellow rust severity on penultimate leaf at flowering , YRSV1sfMS= yellow rust severity on first flag leaf at milk stage, YRSV2ndfMS= yellow rust severity on penultimate leaf at milk stage.*

Table 10. Pearson correlations for some morphological traits with yellow rust severity (%) for all wheat genotypes based on plot average data

	PLHT	SL	FL	FT/m2	FS	UFS	TS	%FS	DS	YRSV1stfFW	YRSV2ndfFW	YRSV1stfMS	YRSV2ndfMS
PLHT		0.720^{**}	0.712^{**}	0.203	0.515^{*}	-0.491^{*}	0.247	0.621^{**}	0.660^{**}	0.143	0.069	0.037	0.005
SL	0.720^{**}		0.379	0.132	0.881^{**}	-0.206	0.734^{**}	0.525^{*}	0.408	0.453	0.415	0.517^{*}	0.502^{*}
FL	0.712^{**}	0.379		0.122	0.140	-0.500^{*}	-0.113	0.485^{*}	0.667^{**}	-0.231	-0.258	-0.277	-0.282
FT/m2	0.203	0.132	0.122		0.141	0.193	0.228	-0.117	-0.130	0.181	0.155	0.031	0.054
FS	0.515^{*}	0.881^{**}	0.140	0.141		-0.152	0.874^{**}	0.525^{*}	0.054	0.583^{**}	0.540^{*}	0.603^{**}	0.576^{*}
UFS	$-.0491^{*}$	-0.206	-0.500^{*}	0.193	-0.152		0.348	-0.920^{**}	-0.754^{**}	0.288	0.351	0.303	0.385
TS	0.247	0.734^{**}	-0.113	0.228	0.874^{**}	0.348		0.045	-0.320	0.695^{**}	0.685^{**}	0.721^{**}	0.736^{**}
%FS	0.621^{**}	0.525^{*}	0.485^{*}	-0.117	0.525^{*}	-0.920^{**}	0.045		0.671^{**}	-0.022	-0.091	-0.021	-0.101
DS	0.660^{**}	0.408	0.667^{**}	-0.130	0.054	-0.754^{**}	-0.320	0.671^{**}		-0.297	-0.337	-0.245	-0.286
YRSV1stfFW	0.143	0.453	-0.231	0.181	0.583^{**}	0.288	0.695^{**}	-0.022	-0.297		0.983^{**}	0.909^{**}	0.881^{**}
YRSV2ndfFW	0.069	0.415	-0.258	0.155	0.540^{*}	0.351	0.685^{**}	-0.091	-0.337	0.983^{**}		0.927^{**}	0.923^{**}
YRSV1stfMS	0.037	0.517^{*}	-0.277	0.031	0.603^{**}	0.303	0.721^{**}	-0.021	-0.245	0.909^{**}	0.927^{**}		0.979^{**}
YRSV2ndfMS	0.005	0.502^{*}	-.0282	0.054	0.576^{*}	0.385	0.736^{**}	-0.101	-0.286	0.881^{**}	0.923^{**}	0.979^{**}	

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm , FL= distance between flag leaf and spike , Ft/m^2 =number of fertile tillers m^{-2}, FS=number of fertile spikelets, UFS=number of unfertile spikelets, TS= total number of spikelets m^{-2}, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YRSV1sfFW= Yellow rust severity on first flag leaf at flowering , YRSV2ndfFW= Yellow rust severity on second flag leaf at flowering , YRSV1sfMS= yellow rust severity on first flag leaf at milk stage, YRSV2ndfMS= yellow rust severity on penultimate leaf at milk stage.

Based on plot average data, the pure line was included

Table 11. Spearman correlations for some morphological traits with yellow rust severity (0 to 9 scale) for composite crossed population based on plot average

	PLHT	SL	FL	FT/m2	FS	UFS	TS	%FS	DS	YRSVFL0-9	YRSVFF0-9	YRSVMS0-9
PLHT		0.801**	0.723**	0.049	0.529*	-0.471	0.265	0.618**	0.632**	0.007	0.308	0.416
SL	0.801**		0.699**	-0.056	0.681**	-0.490*	0.456	0.672**	0.738**	-0.214	0.064	0.239
FL	0.723**	0.699**		0.132	0.475	-0.451	0.140	0.637**	0.630**	-0.168	0.064	0.077
FT/m2	0.049	-0.056	0.132		-0.105	0.309	0.176	-0.179	-0.279	-0.190	-.0155	-0.298
FS	0.529*	0.681**	0.475	-0.105		-0.456	0.703**	0.672**	0.368	-0.068	0.151	0.004
UFS	-0.471	-0.490*	-0.451	0.309	-0.456		0.223	-0.934**	-0.765**	-0.429	-0.054	-0.401
TS	0.265	0.456	0.140	0.176	0.703**	0.223		0.054	-0.137	-0.362	0.191	-0.194
%FS	0.618**	0.672**	0.637**	-0.179	0.672**	-0.934**	0.054		0.787**	0.219	0.081	0.330
DS	0.632**	0.738**	0.630**	-0.279	0.368	-0.765**	-0.137	0.787**		-0.002	-0.129	0.367
YRSVFL0-9	0.007	-0.214	-0.168	-0.190	-0.068	-0.429	-0.362	0.219	-0.002		0.084	0.348
YRSVFF0-9	0.308	0.064	0.064	-0.155	0.151	-0.054	0.191	0.081	-0.129	0.084		0.426
YRSVMS0-9	0.416	0.239	0.077	-0.298	0.004	-0.401	-0.194	0.330	0.367	0.348	0.426	

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm , FL= distance between flag leaf and spike, Ft/m^2 =number of fertile tillers per m^2, FS=number of fertile spikelets, UFS=number of unfertile spikelets, TS= total number of spikelets m^{-2}, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YR SV FL= yellow rust severity from 0-9 scale at flag leaf stage, YR SV FW= yellow rust severity from 0-9 scale at flowering stage, YR SV MS= yellow rust severity from 0-9 scale at milk stage

Based on average plot data

The pure line was not included

Table 12. Spearman correlations for some morphological traits with yellow rust severity (0 to 9 scale) for wheat genotypes based on plot average data**.**

	PLHT	SL	FL	FT/m2	FS	UFS	TS	%FS	DS	YRSVFL0-9	YRSVFF0-9	YRSVMS0-9
PLHT		0.779**	0.639**	0.114	0.547*	-0.474*	0.235	0.679**	0.605**	-0.027	0.231	0.300
SL	0.779**		0.479*	0.053	0.718**	-286	0.523*	0.598**	0.523*	-0.016	0.201	0.353
FL	0.639**	0.479*		0.042	0.288	-0.568*	-0.072	0.628**	0.695**	-0.247	-0.111	-0.083
FT/m2	0.114	0.053	0.042		0.032	0.304	0.244	-0.112	-0.307	-0.068	-0.069	-.0184
FS	0.547*	0.718**	0.288	0.032		-0.256	0.737**	0.618**	0.191	0.088	0.255	0.130
UFS	-0.474*	-0.286	-0.568*	0.304	-0.256		0.370	-0.875**	-0.826**	-0.063	0.192	-0.066
TS	0.235	0.523*	-0.072	0.244	0.737**	0.370		0.016	-0.304	-0.029	0.383	0.094
%FS	0.679**	0.598**	0.628**	-0.112	0.618**	-0.875**	0.016		0.761**	0.065	-0.029	0.165
DS	0.605**	0.523*	0.695**	-0.307	0.191	-0.826**	-0.304	0.761**		-0.209	-0.274	0.099
YRSVFL0-9	-0.027	-0.016	-0.247	-0.068	0.088	-0.063	-0.029	0.065	-0.209		0.345	0.534*
YRSVFF0-9	0.231	0.201	-0.111	-0.069	0.255	0.192	0.383	-0.029	-0.274	0.345		0.590**
YRSVMS0-9	0.300	0.353	-0.083	-0.184	0.130	-0.066	0.094	0.165	0.099	0.534*	0.590**	

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm , FL= distance between flag leaf and spike , Ft/m^{2} =number of fertile tillers per m^{2}, FS=number of fertile spikelets, UFS=number of unfertile spikelets, TS= total number of spikes m^{-2}, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YR SV FL= yellow rust severity from 0-9 scale at flag leaf stage, YR SV FW= yellow rust severity from 0-9 scale at flowering stage, YR SV MS= yellow rust severity from 0-9 scale at milk stage

Based on average plot data

The pure line was included

4.3.3. Correlation for agronomic traits with disease based on individual plant sample data

Pearson correlation analysis also showed associations of agronomic traits with yellow rust severity from the individual sample per population. Some deviation was observed when compared to average plot data of morphological traits association with yellow rust severity for the CCPs. Based on the individual samples, some traits showed a significant and very weak positive association with yellow rust disease across growth stages (Table 13). For instance, unfertile spikelet showed significant negative association with yellow rust severity at flag leaf (r=-0.142) and milk stage development (r=-0.166). Trend of other morphological traits such as plant height, flag leaf to spike and fertile tiller showed positive association with yellow rust severity at all developmental stages (Table 13).

On other hand, spearman correlation analysis showed non-significant associations of morphological traits with yellow rust severity for pure line. However, some trends of association can be observed for the pure line. For instance, plant height, spike length, flag leaf to spike and fertile spikelet showed a non-significant and very weak positive association to yellow rust severity at all growth stages (Table 15). Unfertile spikelets and the distance between spikelets showed a non-significant negative association with yellow rust severity.

Table 13. Pearson correlation morphological trait with yellow rust severity based on 0 to 9 scale for composite cross population based on individual plant data

	PLHT	SL	FL	FS	UFS	TS	DS	YRSVFL0-9	YRSVFW0-9	YRSVMS0-9
PLHT		0.437**	0.399**	0.261**	-0.258**	0.145*	0.392**	0.107	0.046	0.131*
SL	0.437**		0.081	0.689**	-0.365**	0.570**	0.691**	0.053	-0.054	0.102
FL	0.399**	0.081		0.031	0.012	0.043	0.065	0.017	0.114	0.199**
FS	0.261**	0.689**	0.031		-0.489**	0.852**	0.082	0.106	0.014	0.208**
UFS	-0.258**	-0.365**	0.012	-0.489**		0.039	-0.475**	-0.142*	-0.053	-0.166**
TS	0.145*	0.570**	0.043	0.852**	0.039		-0.190**	0.037	-0.015	0.138*
DS	0.392**	0.691**	0.065	0.082	-0.475**	-0.190**		0.038	-0.043	0.028
YRSVFL0-9	0.107	0.053	0.017	0.106	-0.142*	0.037	0.038		0.654**	0.502**
YRSVFW0-9	0.046	-0.054	0.114	0.014	-0.053	-0.015	-0.043	0.654**		0.654**
YRSVMS0-9	0.131*	0.102	0.199**	0.208**	-0.166**	0.138*	0.028	0.502**	0.654**	

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm , FL= flag leaf to spike , FS=number of fertile spikes, UFS=number of unfertile spikelets, TS= total number of spikes m^{-2}*, %FS=percent of fertile spikelet, DS= distance between spikelet's, YR SV FL= yellow rust severity from 0-9 scale at flag leaf stage, YR SV FW= yellow rust severity from 0-9 scale at flowering stage, YR SV MS= yellow rust severity from 0-9 scale at milk stage*

Based on individual plant sample data

The pure line was not included

Table 14 .Pearson correlation morphological trait with yellow rust severity based on 0 to 9 scale for all wheat genotypes based on individual plant sample data

	PLHT	SL	FL	FS	UFS	TS	Ds	YRSVFL0-9	YRSVFW0-9	YRSVMS0-9
PLHT		0.442**	0.390**	0.279**	-0.250**	0.171**	0.387**	0.051	0.018	0.066
SL	0.442**		0.056	0.724**	-0.346**	0.614**	0.647**	0.171**	0.083	0.202**
FL	0.390**	0.056		0.003	0.014	0.011	0.066	-0.045	0.043	0.090
FS	0.279**	0.724**	0.003		-0.448**	0.865**	0.073	0.243**	0.191**	0.311**
UFS	-0.250**	-0.346**	0.014	-0.448**		0.061	-0.492**	0.013	0.022	-0.031
TS	0.171**	0.614**	0.011	0.865**	0.061		-0.195**	0.279**	0.226**	0.331**
DS	0.387**	0.647**	0.066	0.073	-0.492**	-0.195**		-0.046	-0.103	-0.041
YRSVFL0-9	0.051	0.171**	-0.045	0.243**	0.013	0.279**	-0.046		0.778**	0.730**
YRSVFW0-9	0.018	0.083	0.043	0.191**	0.022	0.226**	-0.103	0.778**		0.748**
YRSVMS0-9	0.066	0.202**	0.090	0.311**	-0.031	0.331**	-0.041	0.730**	0.748**	

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

key :- PLHT= plant height in cm, SL= spike length in cm , FL= flag leaf to spike, Ft/m^2 =number of fertile tillers per m^2, FS=number of fertile spikelets, UFS=number of unfertile spikelets, TS= total number of spikes m^{-2}, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YR SV FL= yellow rust severity from 0-9 scale at flag leaf stage, YR SV FW= yellow rust severity from 0-9 scale at flowering stage, YR SV MS= yellow rust severity from 0-9 scale at milk stage

Based on individual plant sample data

The pure line was included

Table 15: Pearson correlation morphological trait with yellow rust severity based on 0 to 9 scale for pure line based on individual plant sample data

	PLHT	SL	FL	FS	UFS	TS	DS	YRSVFL0-9	YRSVFF0-9	YRSVMS0-9
PLHT	🟩	0.602**	0.167	0.587**	-0.156	0.621**	0.240	0.054	0.079	0.017
SL	0.602**	🟩	-0.078	0.834**	-0.596**	.716**	0.689**	0.161	0.206	0.046
FL	0.167	-0.078	🟩	-0.069	0.369*	.113	-0.182	0.132	0.136	0.195
FS	0.587**	0.834**	-0.069	🟩	-0.560**	0.907**	0.320*	0.217	0.410**	0.109
UFS	-0.156	-0.596**	0.369*	-0.560**	🟩	-0.197	-0.714**	-0.202	-0.159	-0.064
TS	0.621**	0.716**	0.113	0.907**	-0.197	🟩	0.053	0.174	0.378*	0.093
DS	0.240	0.689**	-0.182	0.320*	-0.714**	0.053	🟩	0.014	-0.136	-0.082
YRSVFL0-9	0.054	0.161	0.132	0.217	-0.202	0.174	0.014	🟩	0.762**	0.607**
YRSVFF0-9	0.079	0.206	0.136	0.410**	-0.159	0.378*	-0.136	0.762**	🟩	0.604**
YRSVMS0-9	0.017	0.046	0.195	0.109	-0.064	.093	-0.082	0.607**	0.604**	🟩

** Correlation is significant at the 0.01vlevel

* Correlation is significant at the 0.05 level

Based on individual plant sample data

key :- PLHT= plant height in cm, SL= spike length in cm , FL= flag leaf to spike, Ft/m^2 =number of fertile tillers per m^2, FS=number of fertile spikelets, UFS=number of unfertile spikelets, TS= total number of spikes m^{-2}, %FS=percent of fertile spikelet's, DS= distance between spikelet's, YR SV FL= yellow rust severity from 0-9 scale at flag leaf stage, YR SV FW= yellow rust severity from 0-9 scale at flowering stage, YR SV MS= yellow rust severity from 0-9 scale at milk stage.

4.4. The trend of trait distribution over scatter plot

Scatter plot graphs showed the trend of traits distribution over the plot. Data of morphological traits were collected from individual plant samples per populations. The spike length showed the best correlation with the distance between spikelets on the scatter plot. From this scatter plot distribution, population HU-11-YQMS was more evenly distributed from mid to top whereas for population HU-12-YQMS data were more found at bottom of the scatter plot and showed variation (Fig 11 under appendix). Spike length revealed a good association with the number of fertile spikelets on the scatter plot. Each population showed a linear and even distribution over the scatter plots (Fig 12 under appendix). There was also a correlation on the scatter plot between plant height with spike length. However, their trait distribution was condensed at the central point (Fig 13 under appendix).

On the other hand, plant height did not show an association with the distance flag leaf to spike and the distance between spikelets on the scatter plot (Fig 14 under appendix). Their trait distribution showed no variation and was more condensed at the centre area.

From the scatter plot distribution and correlation coefficient analyses, my results clearly indicated that spike length showed a highly significant strong positive correlation with the distance between spikelets and the number of fertile spikelets as well as even linear distribution over the scatter plots.

5. Discussion

The current study was carried out to evaluate the performance of winter wheat composite crossed population and a pure line for disease resistance, yield and other agronomic traits. The discussion of this report is organized into two main parts. The first part concerns the foliar diseases, mainly yellow rust and other diseases. The second part focuses on yield and related agronomic traits, such as TKW, plant height, spike length, number of fertile and unfertile spikes, and the distance between spikelets. Accordingly, these will be discussed in the following paragraphs.

5.1. Foliar diseases

5.1.1. Yellow rust disease

In this study, the difference among all wheat genotypes as well as among CCPs was observed for yellow rust disease pressure across growth stages. The yellow rust disease expanded over growth stages but varied in severity among CCPs. At seedling stage, the yellow rust symptoms and frequency was quit low for CCPs. Strip line yellow rust formation was not observed at early seedling stage at Droevendaal experimental field in 2013/14. This statement was agreed with (Prescott *et al*, 1986; Chen, 2005) reported that stripes of uredia or necrosis are not formed on seedling leaves whereas narrow stripes on the leaves are only formed after stem elongation.

Environment factors such as favorable (relatively warm) winter temperature is one of the conducive factors for yellow rust disease development and severity; this was the case for the soft winter 2013/2014 without severe frost in Wageningen. From this conducted experiment, the yellow rust incidence and severity was observed to a higher extent on pure line than on the CCPs under organic conditions. This could be because the pure line is genetically uniformer compared to CCPs and the reistance of the pure line seems to have broken down. Also, its resistance breake down can explain the low tillering rate of the pure line in this season. The fact that the pure line was more severely infected by yellow rust likely has resulted in decreased photosynthesis and translocation rates during vegetative growth stages. According to Owera *et al.,* (1981) reported that barley plant infected with brown rust reduced the net photosynthesis, transport from infected leaves, and increased photo-respirations.

The newly introduced CCP and mid generations of populations showed better yellow rust resistance than the populations A and B that were grown for the longest period in Wageningen. The degree of disease pressure expansion across growth stages was more observed in these older populations.

Even though the incidence and severity of yellow rust was more observed on the old CCPs (CCPs A and B), it seams not economically important due to low severity observed. One may conclude that the diversity within a population increased the resilience of the population to restrict the spread of disease expansion across growth stages more than the pure line. This observation tends to agree with Finckh and Mundt (1992); Dübin and Wolfe (1994), Zhu *et al*. (2000) and Mundt, 2002) who argue that variety and multiline mixtures can provide functional diversity that limits pathogen and pest expansion. It is likely that due to the diversity inter-parents used to develop the population different combinations of resistance genes have been incorporated into the composite cross population and cause different barriers to restrict the spread and expansion of the pathogen.

The genetic resistance to yellow rust is polygenic in nature which is characterized by less infection and chlorosis. Johnson (1988) and Singh *et al*. (2005) found that leaf and yellow rusts of several cultivars is based on the minor genes having additive effects. In case of this experiment, it could be that the population carries different sources of induced resistance genes which reduce the lesion of disease development. The fact that the older populations A and B showed more infection speed can mean that in their history growing conditions have been negative for survival of genotypes with positive characteristics to reduce yellow rust infection. This phenomana observed partially in this first season.

5.1.2. Fusarium head blight disease and aphid insect

Difference among wheat genotypes was not observed for FHB disease at flowering and grain filling stages. But, according to Bai and Shaner (1994) FHB is usually most severe when flowering coincides with warm, wet and other favorable environmental factors. It could be that the conditions this year caused a low infection rate of FHB.

From genetic resistance point of view, FHB is polygenic in nature (Buerstmayr *et al*., 2002). Morphological traits such as the compactness and looseness of spikes are used as one option to contribute to FHB resistance (Bai and Shaner, 2004). This is due to that fact that within a compact ear the air movement between the spikelet decreases and the head of spikelet stays moist for a longer time and creates a more favourable environment for the development of disease pressure. According to this assumption, in case of our experiment, the result showed that the pure line and Population H were more compact and had a chance for more severe FHB infection. However, FHB infestation was very low and not severs among all genotypes in this year, so no conclusions can be drawn on differences in tolerance to FHB in the populations.

5.2. Grain yield and other agronomic traits

5.2.1. Grain yield and thousand kernel weight

Grain yield, quality and other desired traits are mainly considered for wheat improvement. Grain yield is a very complex trait and governed by several genes, physiological and biochemical plant processes (Mohammadi *et al*., 2012). Difference in genetic potential and environmental factors are useful determinants for interpretating the results.

Wheat genotypes did not show differences for yield this year. The different growing histories of the CCPs did not lead to grain yield differences. The mean of grain yield was poor among wheat genotypes and might be due to realtivly the low nitrogen nutrient in organic system and earlier (autumn) water logging in the field. But, some studies reported wheat gentype showed diffirence for grain yiled under organic conditions. For instance, according to Murphy *et al*., (2007) the differences observed among 35 winter wheat genotypes for grain yield and genotype × system interaction under different growing conditions (organic or conventional system). According to this author, genetic variability exists among genotypes to select under both conditions. In close agreement to this statement, I suggest that further research is advisable on genetic variability of CCPs for yield potential selection under low input and / organic conditions.

5.2.2. Other agronomic traits

Morphological traits such as plant height, the distance between flag leaf to spike and others showed difference among winter wheat genotypes. The longest plant height was observed for the mid generation, medium in height recorded for the old population and the shortest observed for the population H. Whereas the results of the pure line was in between the old and mid populations. However, except for population E (mid population) no statistical difference among wheat genotypes occurred for the plant height .i.e. in our experiments the old and the newly introduced population showed similar in plant height. This observation is in contrary with Hensleigh *et al.* (1992) who argues that the plant height of barley increased over the years of reproduction.

Plant height is one of the traits that used as criteria to select for weed suppression. Genotypes that are long and erectophile with broad leaves are good in weed suppression (see Fedrica's results). Also, genotypes with a short plant height have a negative correlation with Fusarium ear disease compared to taller wheat genotypes (Lemmens *et al*., 2005). This means that short plants have a chance to be more severely infected by FHB due to spike compactness. However, FHB was not observed and or minor observed in our experimental wheat genotypes in this year. On the other hand, in case plant height increases, a chance of plant lodging could result in crop yield penalty. But lodging is less problems in the organic and low-put agricultural, due to slow release of nutrients.

5.3. Correlation of some agronomic traits and disease

In this study, significant positive correlations were observed within morphological traits. Their association was stronger on plot average than individual plant data observed for CCPs. This implies that resilience and strength of morphological traits within population was stronger on plot average data than individual plant data. My results clearly indicated that spike length was positively correlated with the distance between spikelets and exerted positive effect through other traits like plant height because plant height also showed significant positive correlation with spike length. Akram *et al* (2008) reported that spike length had positive relationship with number of spikelet per spike. Increase in spike length is directly associated with increase in spikelet per spike as well as grain number per spike and contribute for the grain yield per plant. Therefore, plant height, spike length, grain per spike and thousand kernel weight should be considered for selection under organic conditions because these traits are directly contributing to grain yield.

On other hand, in this year trial some of the morphological traits showed non-significant positive association with yellow rust incidence and severity at various growth stages, including flag leaf and flowering stages. For example, plant height showed a non-significant positive association with yellow rust across growth stages (see correlation tables). It seems that the trend of plant height positive association with yellow rust disease. This might be the taller plant tendency to infect with rust because plant put more energy cost for its growth. The other reasons behind is that the diversity within population can support resilience of population against disease pressure.

It is not likely to conclude that there was a clear association of morphological traits with yellow rust incidence and disease severity in this cropping season at organic field trial. Therefore, I suggest that winter-wheat germplasm screening via artificial inoculation and or screening at disease pressure area is needed, and an analysis of their trait association by using correlation analysis, path coefficient, principal component analyse and QTL mapping will give more likely result of their associations for potential selection.

6. Conclusions

The curent conculusion was to answer the research questions such as the diffrence among wheat genotypes in terms of grain yield, disease resistance and assocation within morphological traits. Threfore based on research questions, the following conculsion was reported.

The composite crossed populations (CCPs) showed similar grain yield potential as the pure line Naturastar in this cropping season. The result does not support the hypothesis that the CCPs would perform better for grain yield under low-input conditions than the pure line. The overall grain yield under this year’s low input and / nutrient limited organic conditions was poor.

Significant difference was observed among wheat genotypes for thousand kernel weight. The thousand kernel weight of population HU-13-YQMS was higher but resulted in comparable grain yield than others populations. Traits like; thousand weight, fertile spikelets and number of spikes per plant contribute to grain yield and are important to consider as selection criteria.

In this study, difference in the degree of yellow rust incidence and severity was observed for all involved wheat genotypes and among the CCPs. Yellow rust incidence and severity pressure expanded strongly from young seedling to milk stages. The yellow rust was the predominant disease in the organic experimental field in the year of 2014. My results suggest that the diversity within the CCPs can improve the resilience of the population to suppress the spread of pathogens compared to the pure line. Thus, my conclusion is in close agreement with literature stating that variety and multiline mixtures can provide functional diversity that limits pathogen and pest expansion.

Significant difference was observed among wheat genotypes for plant height, the distance between the flag leaf to the spike, whereas no difference for spike length and the distance between spikelets was observed. The highest plant height and the distance between flag to spike was recorded on population HU-11-YQMS. The old and newly introduced populations showed similar plant heights.

Correlation coefficient analysis showed significant strong positive association within agronomic traits for CCPs. Plant height showed a positive correlation with spike length, the distance between flag leaf to spike, fertile spikelet and the distance between spikelets. Similarly, spike length showed a strong positive association with the distance between spikelets. The study suggested that spike length was positively correlated with the distance between spikelets and exerted positive effect through other traits like plant height because plant height also showed significant positive correlation with spike length. These triats signifcantly posetivly asscoated each other should be consider for selction criteria under organic condition.

7. Recommendation

The study showed that difference observed among wheat genotype for yellow rust disease. Whereas, no difference observed among all wheat genotypes for grain yield under organic condition. One of the objectives of organic breeding is to select better performing cultivar in yield and disease resistance, and subsequently to release that variety for farmers. Due to similar yield potential under organic condition in this year, I suggest that exploitation of additional source of genetic variation such as landraces, synthetic and cultivar wheat population will provide as source of genetic variability to develop composite crossed population. Beneficial traits from this gene pool may be combined and optimize a source of superior selection for yield, nitrogen use efficiency, quality and induced resistance under organic condition.

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9. **Appendix's; appendix-I: result of figures**

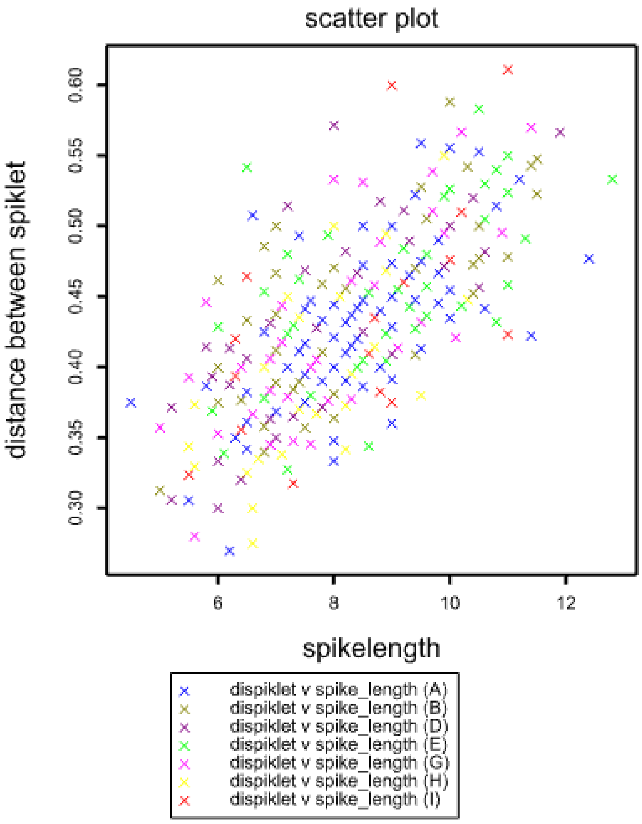

Figure 11 . Scatter plot correlation of spike length with the distance between spikelet

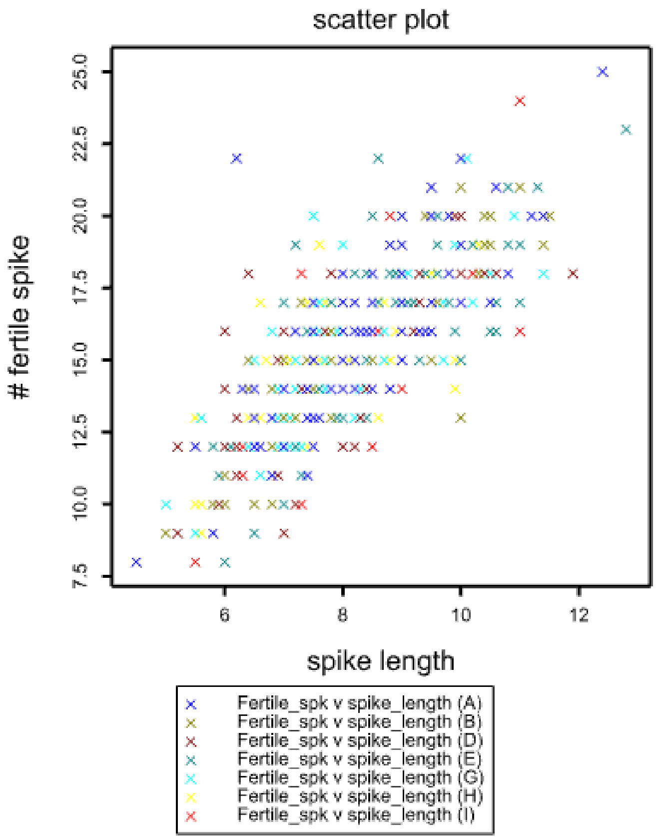

Figure 12 . Scatter plot correlation of spike length with number of fertile spike

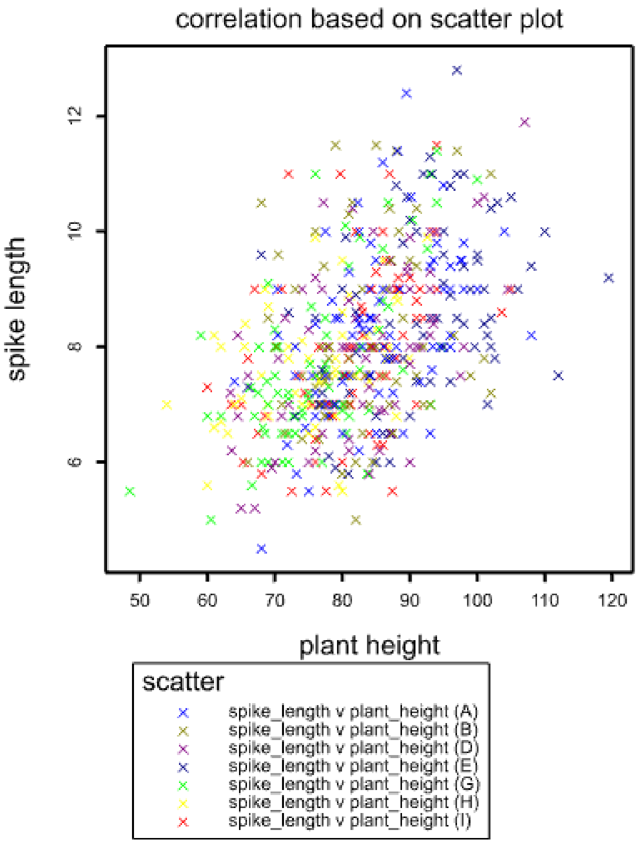

Figure 13 . Scatter plot correlation of plant height with spike length

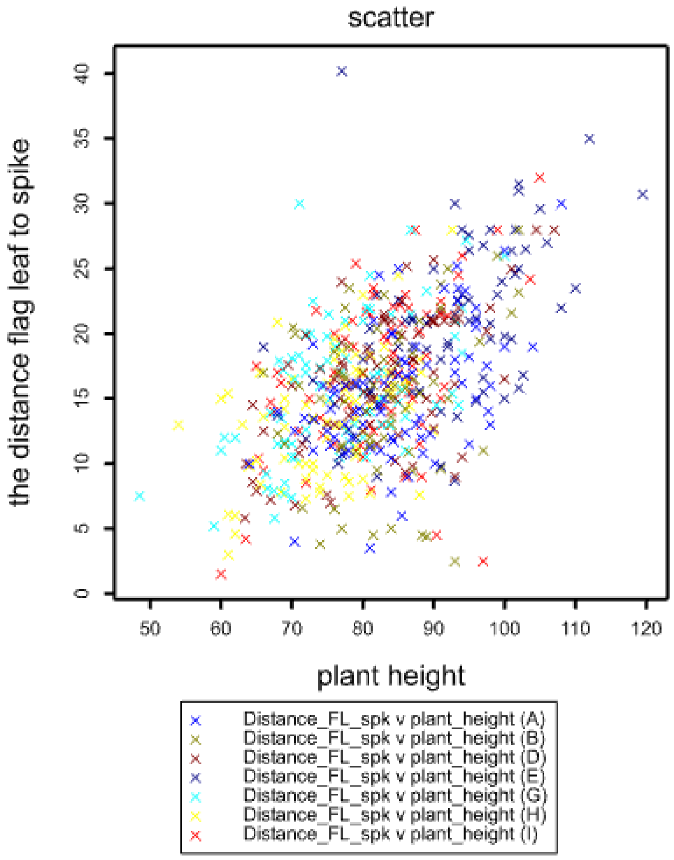

Figure 14 . Scatter plot correlation of plant height with the distance between flag leaf to spike

http://www.met.wau.nl/haarwegdata/dayfiles/2013/2014

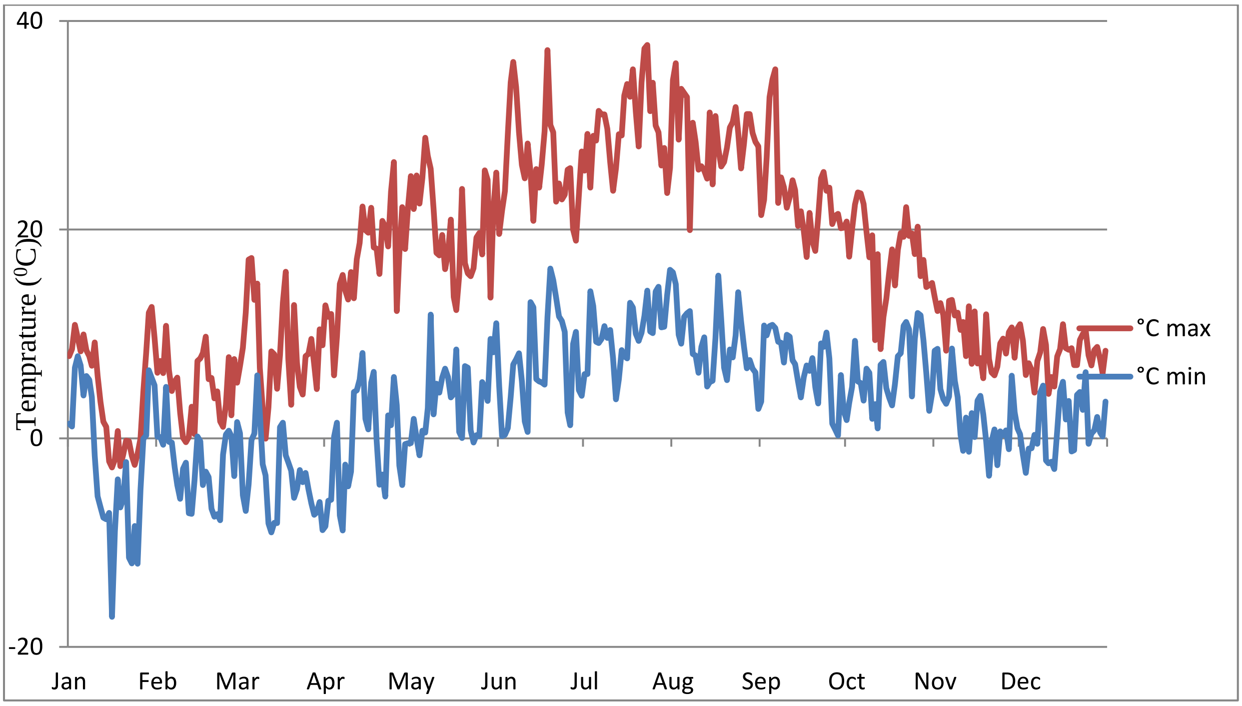

Figure 15. Minimum and maximum temperature (°C) in 2013

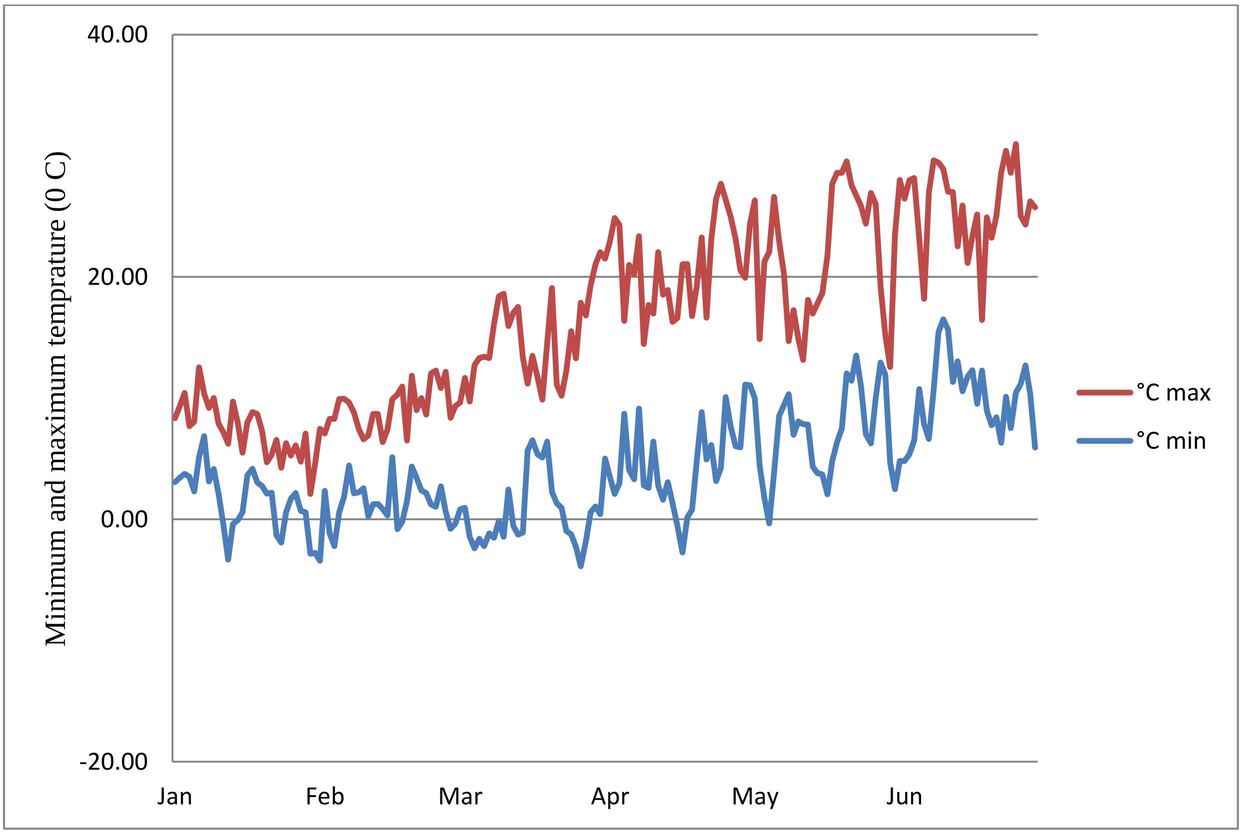

Figure 16 . Minimum and maximum temperature (°C) in 2014

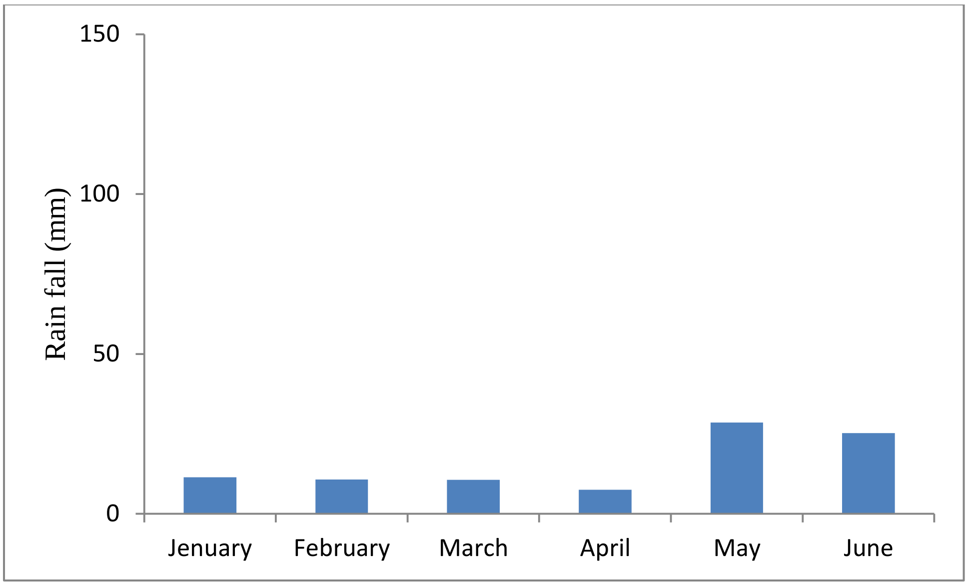

Figure 17 . Minimum and maximum rain fall (mm) in 2014

Appendix II: Normality and homogeneity output data

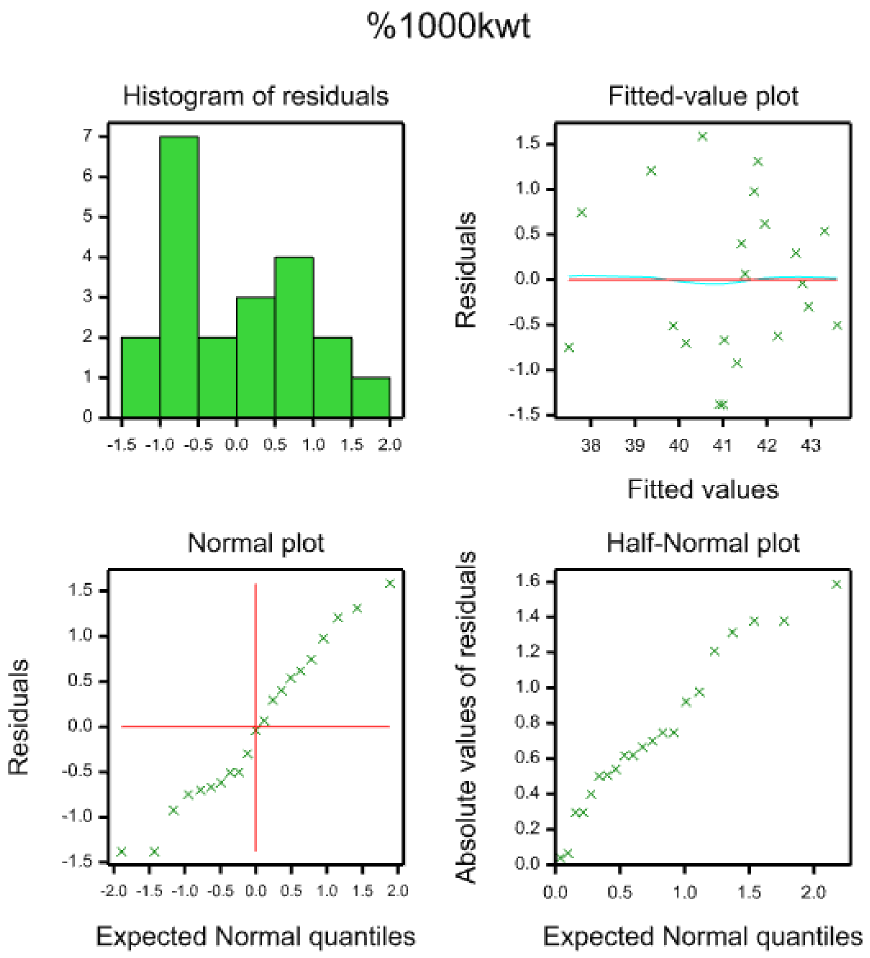

Figure 18. Normality and equal variance distribution of 1000 weight

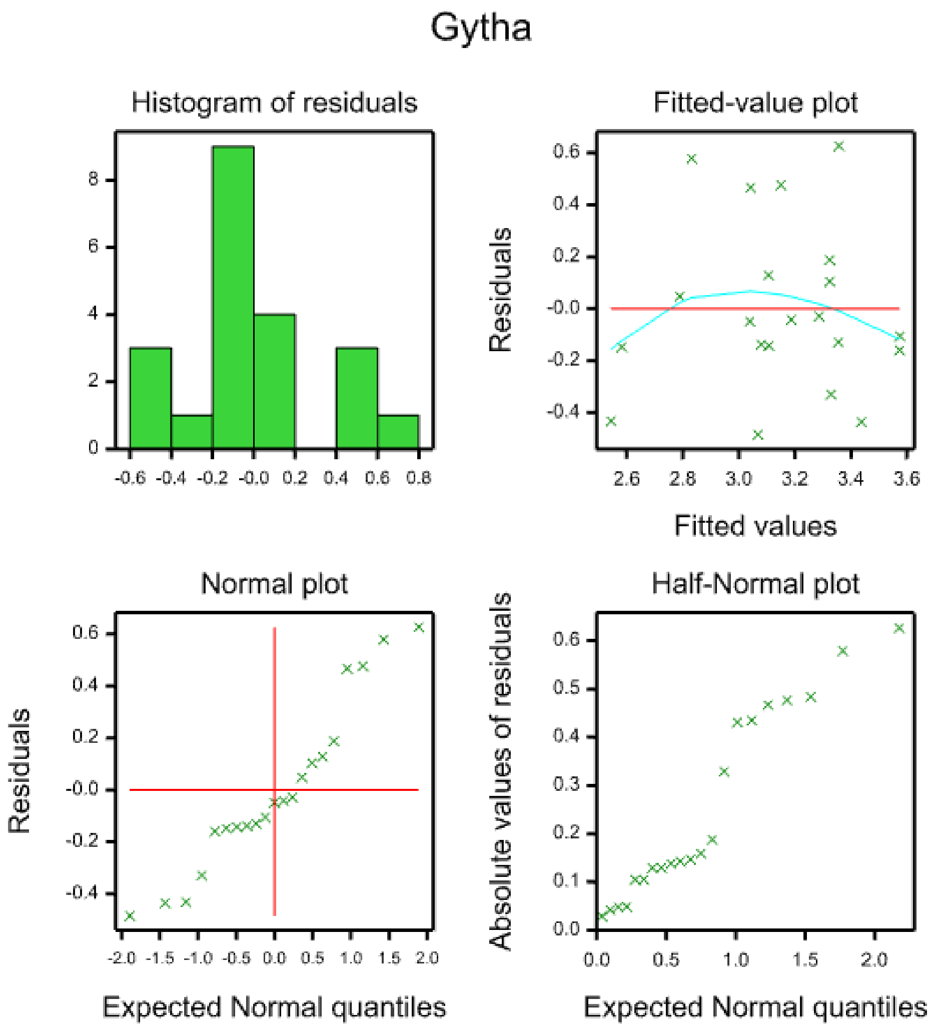

Figure 19 . Normality and equal variance distribution of grain yield data

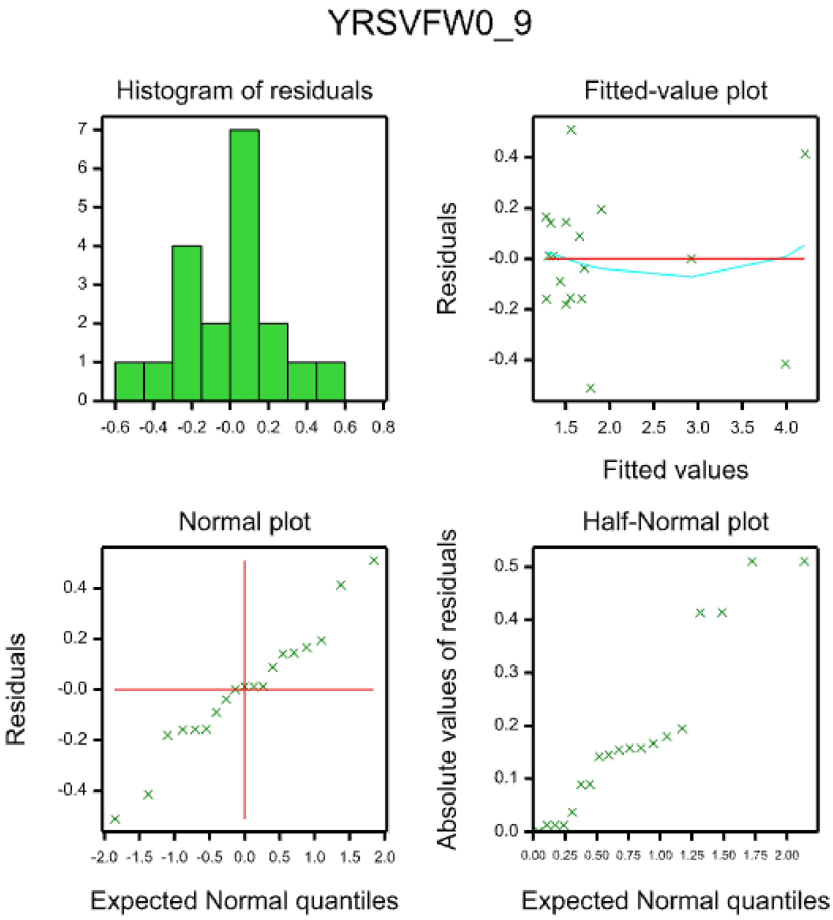

Figure 20. Normality and equal variance distribution of Yellow rust disease data at flowering based on 0-9 scaling

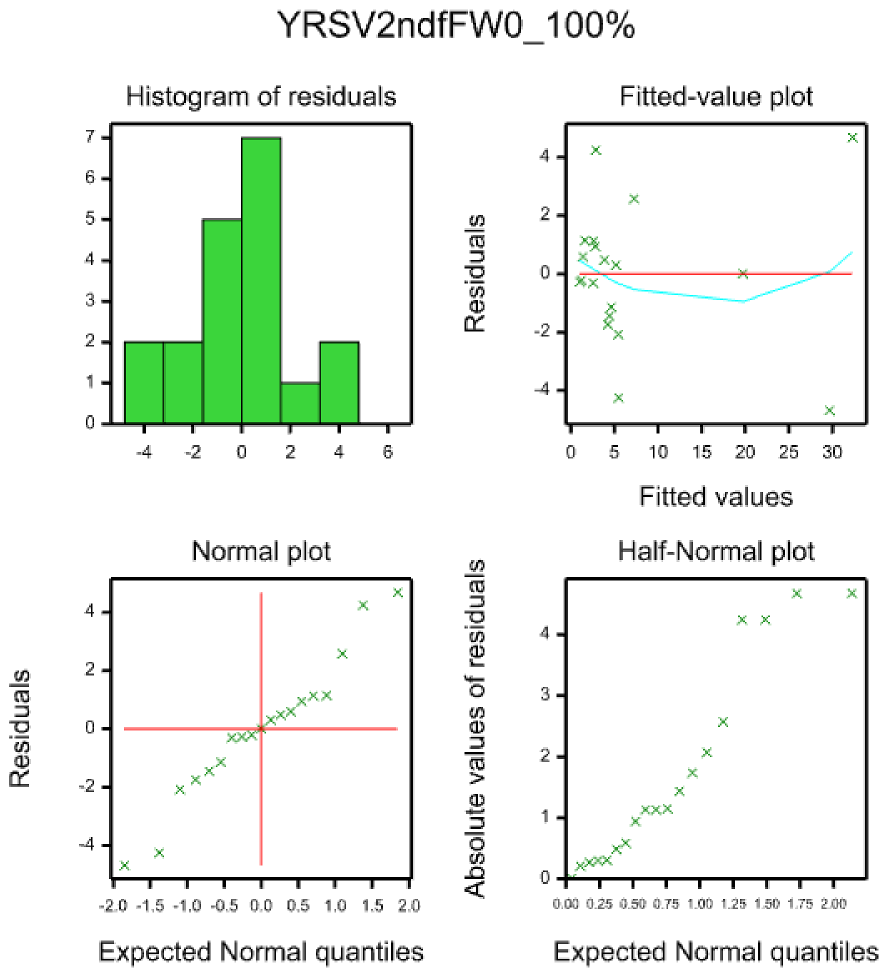

Figure 21 . Normality and equal variance distribution of Yellow rust disease data at flowering based on second flag leaf based 0-100 % scoring

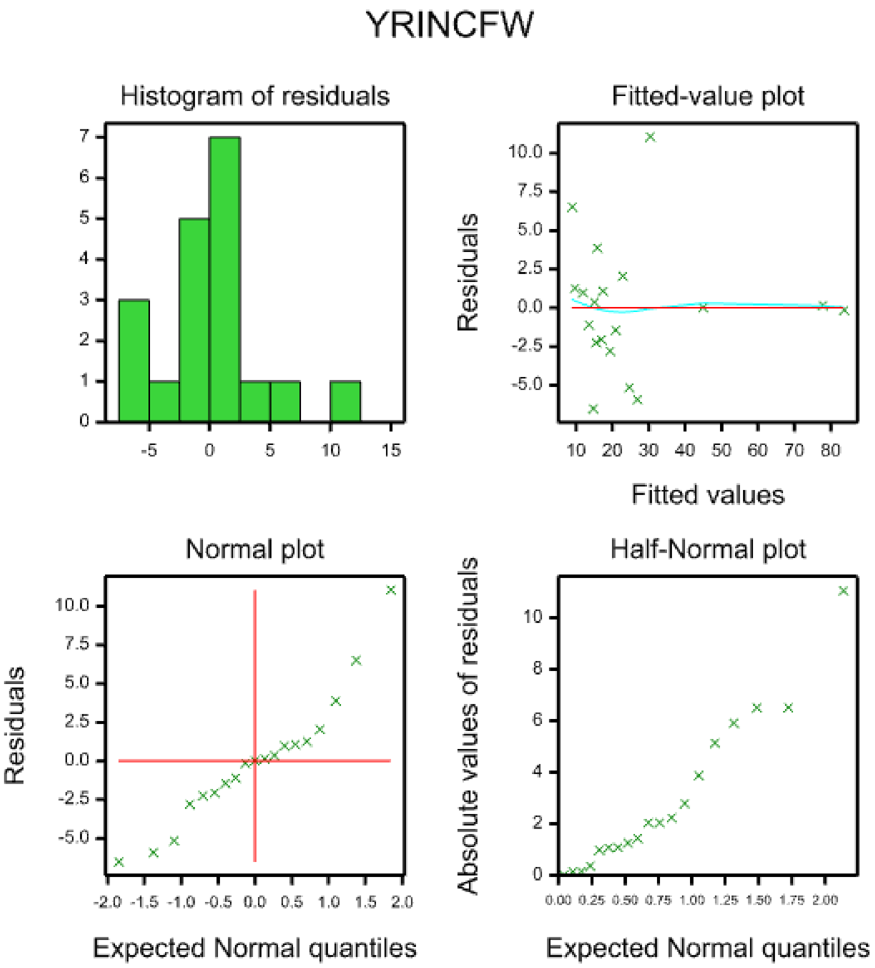

Figure 22. Normality and equal variance distribution of Yellow rust incidence at flowering

Appendix III**: disease figures**

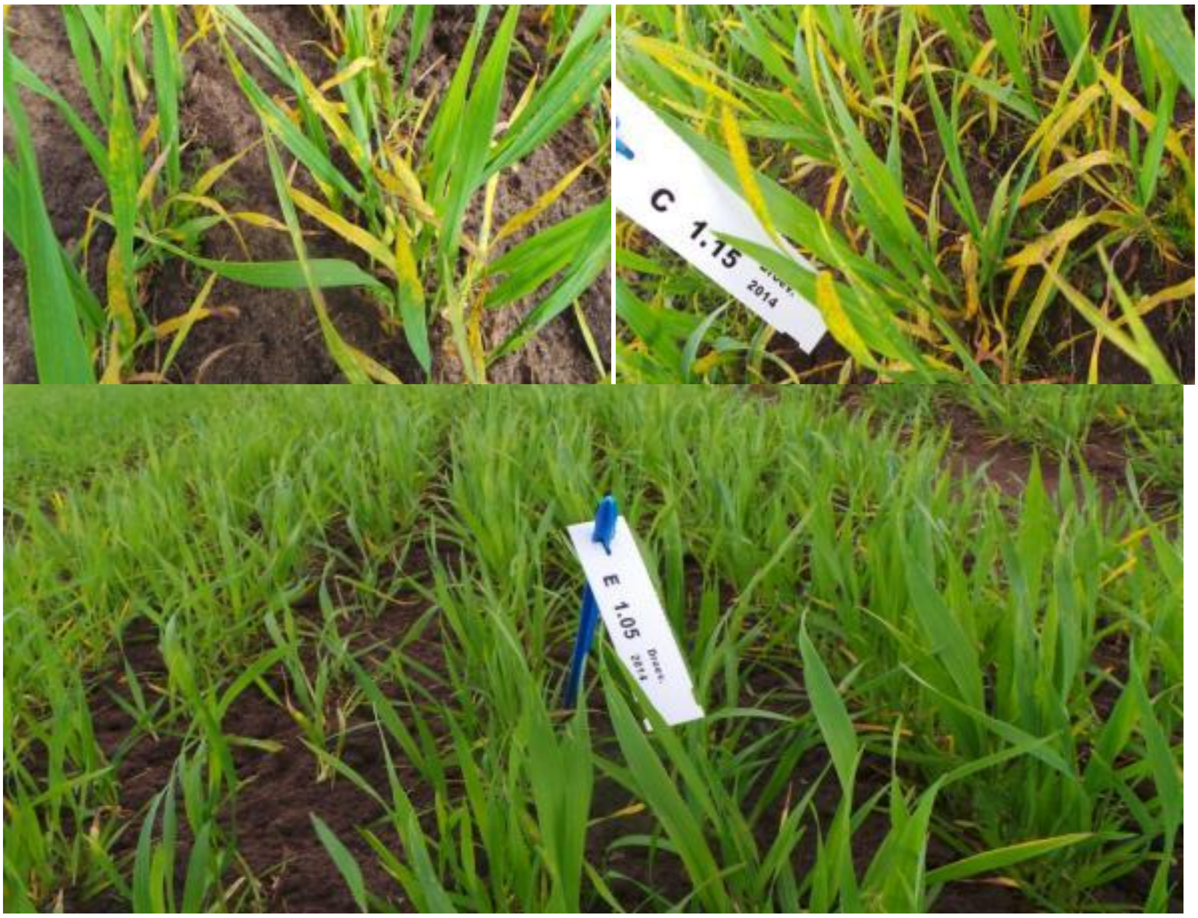

Figure 23 . Yellow rust symptoms (C) vs E (no symptoms) at early seedling (21 growth) stage

Figure 24. Yellow rust disease expansion on leaf surface

Figure 25. Yellow rust severity after heading

Figure 26. FHB observed at experimental organic field

Figure 27. Overview experimental field after heading