EVALUATION OF BARLEY GENOTYPES FOR THEIR RESISTANCE AGAINST BARLEY SHOOT FLY, *Delia flavibasis* Stein (DIPTERA: ANTHOMYIIDAE) IN SOUTH EASTERN ETHIOPIA

MSc THESIS

BY

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JUNE 2024

JIMMA, ETHIOPIA

Evaluation of Barley Genotypes for their Resistance against Barley Shoot Fly, *Delia flavibasis* Stein (Diptera: Anthomyiidae) in South Eastern Ethiopia

By

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MSc Thesis Research

Submitted to Department of Horticulture and Plant Sciences, College of Agriculture and Veterinary Medicine, Jimma University, In the Partial Fulfillment of the Requirements for the Award of Masters of Science (MSc) in Agricultural Entomology

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June 2024

Jimma, Ethiopia

DEDICATION

I dedicate this thesis manuscript to my mother, KIBITU WAGE, who wishes me success in every direction but passed away without seeing my success, my beloved wife, BONTU LETA, who paid a heavy price with me, and my beloved son, BEKAN MEGERSA.

STATEMENT OF THE AUTHOR

First, I hereby declare that this thesis is my work and that all sources of materials used for this thesis have been duly acknowledged. This Thesis has been submitted in partial fulfilment of the requirements for an MSc degree at Jimma University and is to be made available for end users and borrowers at the university's library under the rules and regulations of the library.

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Submission Date: _____

BIOGRAPHICAL SKETCH

The author was born on May 21, 1992, in Dandi Gudi Kebele, Kiltu Kara Woreda, in the West Wollega Zone of Oromia Regional State, to his mother, Kibitu Wage, and his father, Abdisa Jaleta. He attended his elementary, secondary, and preparatory school education at Bechara Gudi Elementary School, Kiltu Kara Secondary School, and Mene Sibu Senior Secondary School, respectively, from 1998 to 2010.

After successful completion of the Higher Educational Entrance Examination in 2010, the author joined Wollega University in 2011 and graduated with a BSc Degree in Plant Science on June 26, 2013. After his graduation, he was employed by the Oromia Bureau of Agriculture and assigned as a crop production expert in the Agricultural Development Office in the position of Pulse and Oil Crops at West Wollega Zone, Babo Gambel Woreda. He served there from December 2014 to October 2017. Then after, he was employed by the Federal Ministry of Agriculture as a crop production and marketing management instructor at Agarfa Agricultural Technical Vocational and Educational Training (ATVET), where he served from November 2017 to April 2018. After six months of stay in the Ministry of Agriculture, he joined the Oromia Agricultural Research Institute (OARI) on May 1, 2018 and was assigned to the Sinana Agricultural Research Center (SARC) as an agricultural entomology researcher under the Crop Protection Research Process. He served as Junior Researcher, Assistance Researcher-I, and Assistance Researcher-II, starting from May 2018 to April 2019, May 2019 to April 2021, and May 2021, until he joined Jimma University College of Agriculture and Veterinary Medicine (JUCAVM) in September 2022 to pursue Master of Science in Agricultural Entomology, respectively.

ACKNOWLEDGEMENTS

First of all, I give thanks to God, who helped me to finish my work. Next, I would like to thank my advisors, Dr. Wakuma Bayissa and Dr. Allo Aman for their genuine advice, constructive comments and encouragement starting from proposal writing up to the completion of this experimental study.

I would like to proudly thank the Oromia Agricultural Research Institute (OARI) and Sinana Agricultural Research Centre (SARC) for sponsoring and facilitating my thesis research work and Jimma University for offering me the study opportunity. I am also very indebted to express my appreciation to the centre director of SARC, Mr. Tamene Mideksa, for his kindness and sustained support throughout the period of my study. I am also grateful to all team leaders for their consistent encouragement and understanding.

I am very grateful to all of my staff members at the Sinana Agricultural Research Center for all of their support during my study. My heartfelt thanks also go to the daily laborers of the Sinana Agricultural Research Center for their very ethical trial management by careful planting, data collection, weeding, applying fertilizers, harvesting, threshing, cleaning, and barley genotype management. My special thanks also go to Zerihun Ishetu, Tesfaye Legesse, Adisu Alemu, Dange Kora, Mohamed A/Zak, Bahiru Dejene, Bekele Tesfaye, Kasahun Tadesse, and Mohammed Abdulkadir for their generous assistance, starting from site selection to the harvesting activities. Finally, I would like to express my gratitude to the Bio and Emerging Technology Institute (BETin) for the kind provision of barley genotypes.

I also wish to express my deepest gratitude to my mother Kibitu Wage who nursed me with great care and affection, my father, brothers, and sisters without whose help, I would not have brought this study to completion.

Lastly, and most importantly, I am very grateful to my wife, Bontu Leta, for her great love for me, for being with me through all the ups and downs of life, long live, you are the mother of my children.

ABBREVIATIONS AND ACRONYMS

BY	Biological Yield
CR	Crop Recovery
CSA	Central Statistical Authority
CV	Coefficient of Variation
DHRT	Dead Heart
DTH	Days To 50% Heading
DTM	Days To 90% Maturity
FAO	Food and Agricultural Organization
GY	Grain Yield
INF	Infestation
L1	First Leaf Width
L2	Second Leaf Width
LG	Leaf Glossiness
LSD	Least Significant Differences
OARI	Oromia Agricultural Research Institute
OVP	Oviposition
PH	Plant Height
PT	Productive Tiller
SARC	Sinana Agricultural Research Center
BETin	Bio and Emerging Technology Institute
SC	Seedling Color
SL	Spike Length
SPS	Seed Per Spike
SSL	Seedling Stem Length
SST	Seedling Stem Thickness
SVG	Seedling Vigor
TKW	Thousand Kernel Weight
TT	Total Tiller
USDA	United States Department of Agriculture
PS	Percent survival

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ABSTRACT

Barley (Hordeum vulgare L.) is globally an important cereal crop, mainly used for food, animal feed and brewing. In Ethiopia, it is the fifth most important cereal crop after teff, wheat, maize and sorghum both in terms of area covered and production. In spite of the importance of barley, its productivity and production has remained low. Barley shoot fly (Delia flavibasis Stein) has been a major constraint to barley production at the seedling stage among other insect pests. Infestation levels of up to 100% of D. flavibasis and significant yield losses on susceptible barley cultivars were frequently reported in the highlands of Bale, Ethiopia. Host plant resistance is one of the most effective methods in managing this insect pest. Resistance to barley shoot fly is governed by complex traits that derived from biophysical or morphological and/or genetic characters of the plant. The objectives of this study were to identify resistant/tolerant barley genotypes against shoot fly, to identify key morphological and agronomic traits responsible for resistance selection, assess genetic variability among tested genotypes leading to improving resistant barley varieties, and determine resistance categories against barley shoot fly. Augmented design with six blocks was used to screen 108 landraces along with 69 exotic and 3 released varieties at Sinana Agricultural Research Center from August 2022 to December 2023. A total of 64 barley genotypes were selected to further investigate morphological and agronomic traits related to barley shoot fly damage and to evaluate genetic variability using 8 x 8 simple lattice designs with two replications. Additionally, 12 barley genotypes were selected to determine category of resistance such as antixenosis test under multi, dual and no-choice conditions, while antibiosis test was done under no-choice condition from August 2023 to December 2024. Among 180 genotypes screened, 4 entries were showed highly resistant, 37 were found resistant, 31 moderate resistance, 51 susceptible and 57 were highly susceptible to D. flavibasis, based on oviposition, infestation and dead heart percent. The landraces showed the highest resistance, followed by improved genotypes, while the least resistant was observed in exotic barley genotypes. The shoot fly showed preferences for laying eggs on T376, HB-42 and 55, than genotypes T281, T506, T524, and T575 as observed in the multi-choice test. In the no-choice test, the oviposition preference for the resistant genotypes (T281, T506, T524, and T575) was lower and had fewer dead hearts compared to the susceptible genotypes. In the dual-choice test, fewer eggs were observed on genotypes T281, T506, T524, T575, and Aruso when compared with the susceptible check (HB-42). The shoot fly completed its life cycle within a shorter period on susceptible barely genotypes based on the antibiosis and its indices test. Most of the attributes had high heritability and genetic gain suggesting a possibility for improvement directly through selection, most likely through additive gene action. Nevertheless, some traits such as days to 90% maturity and days to 50% heading exhibited high heritability, but low genetic advance indicating non-additive gene expression which may require heterosis breeding for its enhancement. In general, this study revealed the presence of sufficient variability among the tested barley genotypes that can be exploited for genotype enhancement. Furthermore, the defensive characters of accessions for shoot fly strongly influence the oviposition and feeding preference. The morphological and agronomic traits studied were used to select resistant genotypes that provide important insights into developing resistant barley varieties and have potential implications on breeding programs aimed at improving resistance against D. flavibasis in barley genotypes.

Key words: Antibiosis; Antixenosis; *Delia flavibasis*; Heritability; Genetic diversity; Morphological traits; Tolerance, Barley, Ethiopia.

1. INTRODUCTION

Barley (*Hordeum vulgare* L.) is the fourth most cultivated cereal crop globally, following rice, wheat, and maize (FAO, 2021). The global production of barley is approximately 145.40 million metric tons on an area of cultivation of about 49.82 million hectares, and barley is primarily grown for consumption, feed, and malting purposes. The European Union, Russia, Australia, Ukraine, Canada, Argentina, Turkey, Morocco, Iran, the United States, Kazakhstan, Ethiopia, India, and Algeria are the major barley producers in the world (USDA, 2023). The leading African barley producers are Morocco, Ethiopia, Algeria, Tunisia, and South Africa (Ephrem, 2024). In relation to barley production, Ethiopia ranks twelfth globally and second at the continental level (Daniel & Beyene, 2019). In Ethiopia, it is ranked fifth highest in terms of cereal production after teff (*Eragrostis tef*), wheat (*Triticum aestivum*), maize (*Zea mays*), and sorghum (*Sorghum bicolor*) (Yirgu *et al*., 2022).

The country cultivates two types of barley, which are food barley and malt barley. Hence, around 90% of Ethiopian barley production is accounted for by food barley, while the remaining 10% goes to malted production (Daniel and Beyene, 2019). On the other hand, injera is mostly made from barley, and other recipes like porridge or bread may also contain it (USAD, 2023). At the same time, the beer brewing industry needs malted barley, which plays an important role in it as one of the vital components in malting (Mesay, 2020; Alemayehu, 2024). On top of that, barley is mainly used for animal feed, making malt, and human consumption. It is also traditionally used in the preparation of local recipes and beverages like Dabo, Kolo, Ganfo, Kinche, Baso, Tela, Borde, etc., among many others. Straw can be equally used as a good source of animal feed besides being thatch material for roofing (Bedada *et al*., 2014).

In Ethiopia, barley is the major cereal crop with its production level being 2.53 tons per hectare and it can be grown in a wide range of agro-ecological zones from 1500 to 3500 meters above sea level particularly in the highlands of Ethiopia (Shiferaw and Tadele, 2022). In Ethiopia, the regions which produce barley most include Oromia, Amhara, Southern Nations Nationalities and Peoples as well as Tigray who are responsible for 52.7%, 31.2%, 7.86% and 6.87%, respectively. Oromia is the highest barley producer in Ethiopia.

Specifically, Arsi, West Arsi, West Shewa, North Shewa, South West Shewa, and Bale zones contribute around 78.94% towards barley production within Oromia region (CSA, 2021). Thus, Bale is the key areas of barley production.

However, barley is widely grown in the Bale Highlands of the Oromia region; its production and productivity are greatly impacted by both biotic and abiotic factors. The main abiotic factors include drought, cold temperatures, and excessive water in the soil, poor soil quality, soil acidity, salinity, hail, and frost. Similarly, the key biotic factors that affect barley production include diseases like scald (*Rhynchosporium secalis*), net spot (*Helminthosporium* spp.), stripe rust (*Puccinia* spp.), powdery mildew (*Erysiphae gaminess*), tuber blight (*Fusarium heterosporium*), covered smut (*Ustilago hordei*), and barley yellow dwarf virus (BYDV); insect pests such as barley shoot fly (*Delia arambourgi* Seguy and *Delia flavibasis* Stein.), Russian aphid (*Diuraphis noxia* Mordvilko), beetle larva (*Melolontha* spp.), and weeds (Dessie, 2018).

Among these insect pests, barley shoot fly is one of the most economically important insect pests of barley in the Bale Highlands, South Eastern Ethiopia with infestation levels often reach up to 100% in susceptible barley genotypes (Mulatu and Grando, 2011; Zeleke *et al*., 2017; Allo *et al*., 2021; Jalata, 2023). This pest causes huge damage to barley by having its larvae migrate to the top of the leaf, move along the leaf whorl, and reach the growth point, through the leaf sheath. Subsequently, the larva cut off the growing point, leading to wilting and drying of the central leaf, known as dead heart, and then feed on rotting plant tissue, resulting in an unpleasant smell when the dead heart is easily removed. Typically, damage occurs within 1 to 4 weeks after seedling emergence, ultimately leading to reduced barley production (Malipatil and Plant Health Australia, 2008; Muluken *et al*., 2009).

To reduce damage caused by this insect pest, some efforts have been made by different researchers, especially in the area of seed dressings, as evidenced by previous studies conducted by Amare (1993) and Tekalign *et al*. (2017). However, due to limited access and high prices, it has not been adopted by farmers (Tafa, 2003). Additionally, insecticides can have harmful effects on human health and the environment (Anjaria and Vaghela, 2024; Jasrotia *et al*., 2024). Furthermore, after the barley seedlings are damaged by this pest, it is

difficult to control it because the larvae feed in the leaf whorls with a downward head. As a result, when chemicals are sprayed on it, they pass down on it without killing (Chamarthi, 2008). Cultural practices such as early planting was also found suitable to control barley shoot fly (Tafa and Bayeh, 2011). But most of the time the rain stops as soon as the barley germinates; because of this, the shoot fly damages the barley crop a lot. This is because the shoot fly has a relationship with the rain, and when there is no rain, barley shoot fly damage the barley extensively in order to obtain moisture from the barley. Therefore, such practices need to be integrated with other pest control methods, like host plant resistance (Teshome *et al*., 2015).

The process of identifying resistant barley genotypes to the barley shoot fly has encountered difficulties, with limited success despite efforts to find resistance from Ethiopian barley landraces such as the Aruso variety in south Eastern Ethiopia, which is known for its resistance to barley shoot fly infestation (Tafa, 2003). In the study area, the development of barley genotypes resistant to the barley shoot fly has been hindered by inadequate information on resistant sources as well as the limited morphological and agronomic traits needed to screen for resistant genotypes. Additionally, there is limited assessment of genetic variability to enhance resistance against the barley shoot fly and a lack of understanding about the mechanisms of resistance in genotypes. Furthermore, there is limited information available on the specific plant traits linked to resistance to this pest infestation. Therefore, screening barley genotypes for important traits and knowledge on the resistance categories of barely genotypes to shoot fly are important aspects of developing resistant or tolerant varieties as one of the best components of integrated pest management.

General Objective

To identify barely genotypes with improved resistance against *Delia flavibasis*

Specific objectives

- To screen barley genotypes with better resistant/tolerance against barley shoot fly,
- To identify morphological and agronomic traits responsible for resistance in barley,
- To assess genetic variability influencing *D. flavibasis* damage, and
- To determine the resistance category of barley genotypes to *D. flavibasis*

2. LITERATURE REVIEW

2.1. Origin and Distribution of Barley

Barley (*Hordeum vulgare* L.) is one of the oldest cereal crop cultivated. The origin of barley is believed to be in the Fertile Crescent region of near- and middle-East, where it was domesticated around 8000- 10,000 BC (Harlan and Zohary, 1966; Zohary and Hopf, 2000). From these areas, barley distributed to other parts of the world, including the Mediterranean basin, highlands of Ethiopia and the Indian subcontinent, the Caucasus and Trans-Caucasus regions, and China (Harlan, 1976). The six-rowed types of barley reached Central and Northern Europe during the fourth and third millenniums BC, while the two-rowed ear types were introduced during the twelfth and thirteenth centuries by the crusaders from the Near-East (Harlan, 1976).

Barley was the main cereal food crop of northern Europe until the 16th century, when it was gradually supplanted by wheat due to culinary preferences. Barley was introduced into North America probably by Columbus in 1492 and later by immigrants and settlers from Europe. The crop is believed to have a multi-centric origin and it could have been domesticated along a broad area from Morocco to Tibet. However, the evidence from archaeology, genetics, and distribution patterns of wild and cultivated barley species available in the Near-East point towards a monocentric origin and domestication (Harlan, 1976).

Barley is widely grown in different regions of the world, including Europe, Asia, Africa, and America. In Ethiopia, barley is an important crop in the highlands, where it is used for food, animal feed, and malt production (CSA, 2019). The crop is also used for traditional brewing and making of injera, flat bread that is a staple food in Ethiopia (Tamiru *et al*., 2019). Barley is adapted to a wide range of environments, from temperate regions to subtropical and tropical highlands, and it can tolerate various soil types and stress conditions (Faria *et al*., 1999; Bonjean and Angus, 2001). However, the distribution of barley is limited by its low tolerance to high temperatures and drought, which restricts its cultivation in some regions (FAO, 2021).

In general, barley is an ancient crop that originated in the Near East and spread to other parts of the world through trade and migration routes. The crop is adapted to a wide range of

environments and is grown in over 100 countries worldwide. In Africa, barley is an important crop in the Mediterranean and Sahel regions, and in Ethiopia and Kenya, it is used for food, feed, and brewing. However, the distribution of barley is limited by abiotic factors like low tolerance to high temperatures, drought, and biotic factors like diseases, insects and weeds (Harlan and Zohary, 1966; Harlan, 1976).

2.2. World and National Barley Production

Barley production is a significant aspect of global agriculture, with implications for food security, trade, and economic development (FAO, 2021). The cultivation of barley plays a significant role in food security and agricultural economies globally, providing staple grains for human consumption, livestock feed, and brewing industries (Gebru *et al*., 2019). Currently, barley is grown commercially in various countries around the world, with major barley-producing nations including European Union, Russia, Australia, Canada, Turkey, United Kingdom, Ukraine, Argentina, United States, Iran, Kazakhstan, Ethiopia, China, India, Morocco, Azerbaijan (USDA, 2023; Shahbandeh, 2024).

In Africa, the top barley producers in 2023/2024 are Ethiopia, Morocco, Algeria, South Africa, and Tunisia. Ethiopia is expected to produce 2.4 million metric tons, making it the largest producer. Morocco and Algeria are forecasted to produce 1.35 million metric tons, and 1.025 million metric tons, respectively. Tunisia and South Africa are also significant producers, with 660,000 and 390,000 metric tons, respectively (Shahbandeh, 2024).

In Ethiopia, barley is an important staple food crop and a source of livelihood for many smallholder farmers, particularly in the highlands where favorable growing conditions exist. The country's agro-ecological diversity and cultural practices contribute to the widespread cultivation of barley in various regions (Assamere *et al*., 2021). It is used for human consumption, animal feed, and traditional brewing of local beer. Barley is an essential crop for food security in country with over 4.5 million farm households producing it, supporting a population of about 22 million in the Ethiopian highlands. Barley is grown as a 'meher' (main season) crop at higher elevations in the Dega regions and also widely cultivated as a 'belg' crop in many areas (Haile, 2018).

The major barley-producing regions in Ethiopia are Oromia, Amhara, Tigray, and the Southern Nations, Nationalities, and Peoples' Region, accounting for about 99.94% of the total national barley production. Barley is also a crucial source of income for farmers, with millions of urban and rural dwellers deriving their livelihoods from processing barley into local drinks such as ‘tella’ and ‘areqae’. Ethiopia Accounts for 25% of the total barley productions in Africa where barley is the principal cereal crop among highlanders. Ethiopia is also recognized as a center of diversity for barley having global significance due to its improved traits, including disease tolerance. In Ethiopia both food and malt barley species is cultivated. Approximately, 85 % of land allocated for barley in Ethiopia is used for food barley production. On the other hand, nearly 150,000 hectares of land (15% of the total barley land) is used for malt barley production, which is the major input for beer production (Meseret, 2016; Tadesse and Derso, 2019).

The crop is grown in diverse rain-fed agro-ecological zones characterized by a wide range of climate and altitude, from 1800 to 3000 meters above sea level, and is well-suited for malting due to its high enzymatic activity, protective hull for the germinating seedling, and use in filtration (Zemede, 2000). However, the barley production and productivity was low compared to recently released other crops like wheat varieties due to lack of improved barley varieties and less contribution of barley on the markets compared to other cash crops. This makes the farmers and other producers to turn their face toward production of cash crops like wheat, maize, and teff. Hence, more attention should be given to barley production and productivity in Ethiopia.

2.3. Major Constraints of Barley Production

Barley (*Hordeum vulgare* L.) is one of the most widely cultivated cereal crops globally, with significant economic and nutritional importance. However, its production is often constrained by various biotic and abiotic factors that can significantly impact yield and quality. The major biotic factors affecting barley production includes: - Insect pests like corn-leaf aphid (*Rhopalosiphum maidis*), Russian wheat aphid (*Diuraphis noxia*), Barley shoot fly (*Delia flavibasis*), are major pests of barley worldwide (Weibull *et al.,* 2003; Malik *et al*., 2013; Nyiraguhirwa *et al.,* 2022). In addition, other important insect pests of barley include the cereal leaf beetle (*Oulema melanopus*), the Hessian fly (*Mayetiola destructor*), and the barley

stem borer (*Chilo partellus*) (Haile and Ali, 1985; Girma *et al*., 1993; Chamarthi, 2008). Aphids can cause significant damage through direct feeding, as well as by transmitting viruses like the barley yellow dwarf virus (Rochow, 1979; Straub and Boothroyd, 1980; Irwin and Goodman, 1981).

Fungal diseases such as scald, net blotch, and spot blotch are significant biotic factors affecting barley production. These diseases can cause significant yield losses and reduce grain quality. Research has focused on developing resistant cultivars and using fungicides to manage these diseases effectively (Fikir, 2022). Viral diseases like barley yellow dwarf virus (BYDV) and barley mosaic virus (BMV) are also important biotic factors and these viruses can cause significant yield losses, and reduce grain quality. Research has focused on developing resistant cultivars and using integrated pest management (IPM) strategies to manage these diseases effectively. Nematodes are microscopic worms that can cause significant damage to barley roots, reducing plant growth and yield. Research has focused on developing resistant cultivars and using nematicides to manage these pests effectively (Vavilov, 1951; Fikir, 2022).

The major abiotic factors affecting barley production includes: - Drought is a significant abiotic factor affecting barley production. Drought can cause significant yield losses and reduce grain quality. Research has focused on developing drought-tolerant cultivars and using irrigation management strategies to manage drought effectively. Additionally, temperature stress is another significant abiotic factor and high temperatures can cause significant yield losses, and reduce grain quality. Research has focused on developing temperature-tolerant cultivars and using heat stress management strategies to manage temperature stress effectively. Also, Salinity is another abiotic factor affecting barley production and high levels of salt can cause significant yield losses and reduce grain quality. Research has focused on developing salt-tolerant cultivars and using irrigation management strategies to manage salinity effectively (Von Bothmer, 1992; Tiwari, 2008). Furthermore, soil fertility is a significant abiotic factor affecting barley production and poor soil fertility can cause significant yield losses, and reduce grain quality. Research has focused on developing fertilizers and using soil management strategies to manage soil fertility effectively (Tiwari, 2008; Yimer, 2021).

Barley production faces several significant constraints that impact the yield and quality of the crop. One of the primary constraints in barley production is the limited research support and inadequate development of improved barley varieties suitable for diverse growing conditions. This lack of focus on varietal development hampers the potential for increased yields and resilience to biotic and abiotic stresses (Tadesse and Derso, 2019). Major constraints of barley production in Ethiopia include poor soil fertility, weed competition, shoot fly incidence, and limited access to modern inputs like fertilizer (Tarekegne *et al*., 1997; Kifle, 2016). Additionally, the lack of disease-resistant and high-yield barley varieties, limited availability of pesticides and fungicides, challenges in accessing affordable fertilizers, and issues related to selling expired products also contribute to the challenges faced by barley farmers in Ethiopia (Kifle, 2016). Furthermore, limited market information, lack of market infrastructure, and fluctuating prices affect farmers' ability to secure competitive prices for their barley produce, highlighting the need for market-oriented agricultural policies (Tarekegne *et al*., 1997).

Barley production is also constrained by inefficient agronomic practices and management approaches. Issues such as poor soil fertility management, inadequate weed control, suboptimal irrigation practices, and limited disease and pest management strategies contribute to reduced productivity and crop health (Kifle, 2016; Shrestha and Lindsey, 2019). Barley cultivation is sensitive to environmental challenges and climate variability, which pose significant constraints to production. Factors such as erratic weather patterns, drought, flooding, and temperature fluctuations can adversely impact barley yields and quality, necessitating strategies for climate risk mitigation and adaptation (Tadesse and Derso, 2019; Gardi *et al.*, 2022; Shuai *et al*., 2023).

Access to markets and price volatility present challenges for barley producers, particularly small-scale farmers. Limited market information, lack of market infrastructure, and fluctuating prices affect farmers' ability to secure competitive prices for their barley produce, highlighting the need for market-oriented agricultural policies (Murray and Brennan, 2009; Samuel Weldeyohanis, 2017; Bezabeh *et al*., 2022). A constraint often faced by barley producers is the lack of access to extension services and training programs that promote best practices in barley cultivation. Insufficient technical guidance, limited knowledge transfer on

modern farming techniques, and a lack of farmer empowerment initiatives hinder the adoption of innovative practices for improved barley production (Boniface *et al*., 2019).

Among these factors, the barley shoot fly damage the barley seedling through the larvae migrate to the top of the leaf, move along the leaf whorl, and reach the growth point, cutting off the growing point and leading to wilting and drying of the central leaf, known as "dead heart" (Malipatil and Plant Health Australia, 2008; Muluken *et al.,* 2009). Integrated pest management (IPM) approaches, combining cultural practices, host plant resistance, and other innovative control methods, have been identified as a promising avenue for more effective and sustainable management of barley insect pests (Teshome *et al*., 2015).

2.4. Description and Biology of Barley Shoot Fly (*Delia flavibasis)*

The biology of barley shoot fly is crucial to understanding its impact on barley production and developing effective pest management strategies. Two species of barley shoot fly have been identified. The first species, *D. arambourgi*, was studied by Davidson in 1969 at Holleta Agricultural Research Center (HARC), while the second species, *D. flavibasis* was studied by Tafa Jobie in 2003 at Sinana Agricultural Research Center (SARC). Both species are known to cause significant yield losses in Ethiopia. They both belong to the order Diptera and the family Anthomyiidae. *Delia flavibasis* is recognized as a major pest of barley in Ethiopia and Kenya (Macharia *et al*., 1986; Tafa, 2003; Mulatu and Grando, 2011). Barley shoot fly (*D.flavibasis)* has complete metamorphosis.

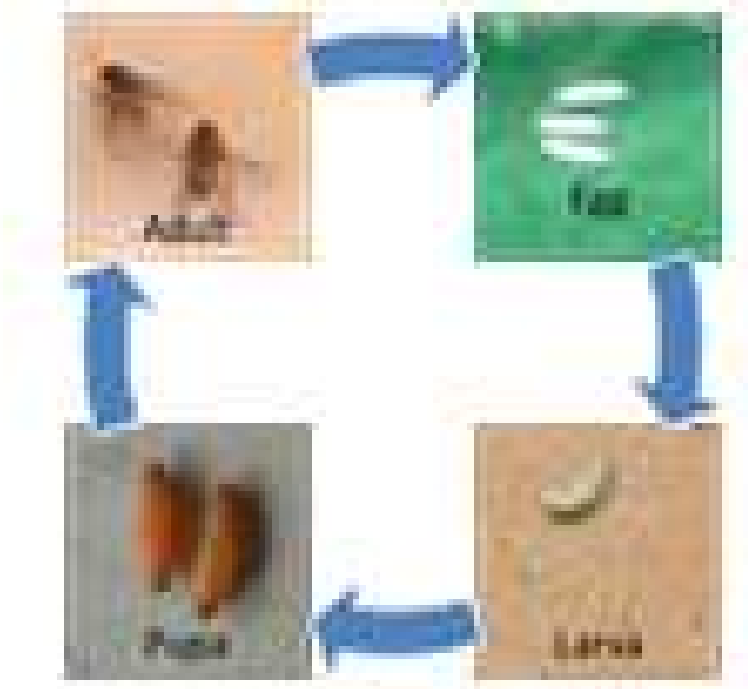

Figure 1.Life cycle of barley shoot fly (Picture taken from the laboratory activity)

Egg is white and elongate-ovoid in shape, resembling rice grains. As observed in both laboratory and field, the eggs may be found singly or in groups (Muluken *et al.,* 2009). Most eggs are typically found in the soil near the base of the plant, at depths ranging from 1 to 3 cm, but they are rarely found on plant parts such as leaves **(**Mallik Malipatil and Plant Health Australia, 2008*).*

Larva is the damaging stage. When fully matured (third instar), it is yellow in color. The young larvae crawl down inside the sheath base of young shoot, where they eat and kill the central shoot. Newly emerged larvae are cylindrical and white. They move up the plant and use their mouth hooks to chew the tender parts of the new shoot, usually just above the first leaf sheath (Tafa, 2003; Muluken *et al.,* 2011).

Pupa is light brown in color and slowly changes to dark brown with age. In the soil, at a depth of 1–3 cm between roots, pupation has occurred. It's similar to *D. Arambourgi*. Under field conditions, it has been observed that pupation is also occurring in the basal stalk of barley seed in rare cases. The adult is looks like the small house fly and it has the ability to fly about 4mm long (SARC, 2004; Mulatu *et al*., 2011).

Egg hatching takes 2.5–3.13 days; the subsequent larval development period is 4.17–5.88 days. The pupal period lasted 7.75–9 days. The overall developmental period (egg to adult) take 14.88–17.67 days. The weights of larvae, pupae, and adults are 3.60–4.02, 3.00–3.63, and 2.13–3.11 mg, respectively (Sharma, 1996; Tafa, 2003; Mulatu and Grando, 2011).

Compared to resistance barley varieties, susceptible barley types had a shorter barley shoot fly life cycle. For instance, the researcher utilizes two resistance varieties—Harbu and Dinsho—and one vulnerable variety, Holker. There was a shorter interval from egg to larval stage on the variety 'Holker' than for 'Dinsho' and 'Harbu'. Larvae were quicker to enter the pre-pupal stage on the susceptible variety compared with the resistant varieties, under both laboratory and field conditions. The number of days required for pre-pupal and pupal stages on 'Holker' was greater (2.26 days) than on 'Harbu' and 'Dinsho' under laboratory conditions (Muluken et *al*., 2009).

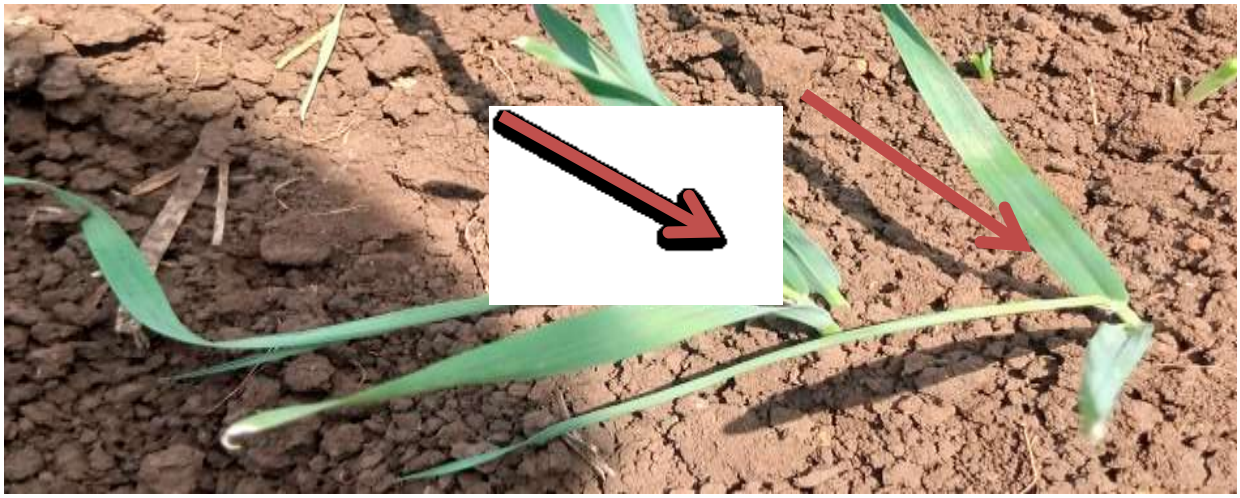

Figure 2. Arrow line shows that barley shoot fly damaging symptoms(Dead heart)(picture taken during the field experiment)

Damage by *D.flavibasis* is at the seedling stage of barley; which make to the typical dead heart symptoms. The young larva migrates to the upper side of the leaf, and moves along the leaf whorl until it reaches the growing point where the larvae cut the growing point. As a result the central leaf dries up forming a dead heart, which can be pulled out easily (Muluken *et al*., 2009).

In general, understanding the biology of the barley shoot fly is crucial for managing its impact on barley production. This pest undergoes complete metamorphosis. The larvae, damaging the central shoot, lead to dead hearts in barley plants. Pupation occurs in the soil, and the adult fly, resembling a small house fly, can fly and is approximately 4mm long. The life cycle from egg to adult spans 14.88-17.67 days, with differences in developmental periods between resistant and susceptible barley varieties. Susceptible barley types have a shorter life cycle, showing significant variations in egg hatching and larval development times. Damage by *D. flavibasis* typically occurs at the seedling stage, manifesting as dead heart symptoms in barley plants.

2.5. Host Range of Barley Shoot Fly

The Barley shoot fly is associated with plants of the grass family, family, like barley (*Hordeum vulgare* L.), maize (*Zea mays*), wheat (*Triticum* spp.), blurish millet (*Pennisetum americanum*) and a few grasses (Hill, 1987). This pest species predominantly infests barley crops during their early growth stages. However, recent studies by SARC (2004) have documented instances of infestation on other grass species related to barley, such as teff (*Eragrostis teff*), wheat (*Triticum* spp.), oat, and maize (*Zea mays*). Among them, barley and teff were the most preferred, these alternative hosts may serve as supplementary breeding grounds for the barley shoot fly under certain environmental conditions. Additionally, observations by Hill (1987) suggest that the season where barley is not cultivated extensively, the barley shoot fly may utilize other grass hosts for oviposition and larval development, with reduced reproductive success compared to its primary host. To effectively manage barley shoot fly infestations, researchers and agricultural practitioners must evaluate the possible expansion of the host range to related grass species and adjust control tactics accordingly.

2.6. Economic Importance of Barley Shoot Fly

Barley shoots fly causes significant yield loss and is becoming an important constraint in barley growing districts of the Bale highlands of Ethiopia (Amare, 1993; Tafa *et al*., 2004). Infestation levels of barley shoot fly in the Bale highlands frequently reach 100% on susceptible varieties such as HB 42, Ardu-10-9-60B, Shege, Beka, Holker, and HB 120; the Bale highlands have become a hot spot for this pest (Amare, 1993; Tafa, 2003). Because of

its devastating effects, especially on improved and exotic genotype of malt barley, the pest is considered to be a major constraint to barley cultivation. At the Sinana on station, heavy infestation usually results in the failure of several trials, particularly those with malt barley and exotic genotypes. In contrast, farmers who grow the local barley cultivar, 'Aruso', often experience low infestation of barley shoot fly in their barley fields, perhaps because the variety has co-existed with the pest for many years (SARC, 2004).

2.7. Morphological Traits Associated to Shoot Fly Resistance

Seedling vigor

Taneja and Leuschner (1985) established a significant negative correlation between seedling vigor and occurrences of dead hearts and oviposition by shoot fly. They found that seedlings with higher vigor tended to experience lower rates of shoot fly infestation. Building upon this foundation, Singh (1998) conducted further investigations, concluding that rapid seedling growth and elongated shoot length can delay larva's access to the base of the shoot, thus reducing susceptibility to shoot fly damage. Additionally, Singh noted that seedlings with elongated and slender leaves during early growth stages exhibited decreased vulnerability to shoot fly attacks. Karanjkar *et al*. (1992) suggested that seedling vigor can be used to select for resistance to shoot fly. However, if the seedling vigor is scored under un-infested conditions, there is no direct effect of seedling vigor on expression of resistance to shoot fly. Contrary to the initial assumption that vigorous growth inherently confers resistance, Dhillon (2004) challenged this notion by demonstrating that vigorously growing plants may paradoxically attract more shoot fly oviposition, potentially leading to greater damage. This underscores the complexity of the interaction between seedling vigor and shoots fly infestation, indicating that while vigor may indirectly influence resistance, its effect depends on various factors including oviposition preference.

Leaf Glossiness

The leaf glossiness(shininess of leaves), characterized by their pale green and reflective surface, likely plays a significant role in influencing the positioning of shoot fly females in sorghum during the seeding stage (Chamarthi, 2008). Nevertheless, the manifestation of leaf shininess appears to be more pronounced during the post-rainy season than during the rainy

season (Gorthy *et al*., 2017). Sorghum genotypes possessing the trait of leaf shininess demonstrate resistance to shoot fly infestation, as evidenced by the prevalence of high leaf glossiness among resistant genotypes (Chamarthi *et al*., 2011).

Seedling color

Mehtre (2006) emphasized the role of seedling color in shoot fly resistance, indicating that traits like leaf glossiness, plumule pigmentation, and trichome density are crucial factors influencing resistance to shoot fly damage. These findings suggest that seedling color, along with other physico-chemical traits like tannin content, moisture levels, and magnesium concentration, play a significant role in determining the susceptibility or resistance of sorghum plants to shoot fly infestation. Recently seedling color was evaluated between landrace and improved barley genotypes (Allo *et al.,* 2020).Therefore, the importance of seedling color as a potential indicator of shoot fly resistance in sorghum genotypes, with specific traits like glossy leaves, pigmented plumules, and high trichome density being associated with resistance, while traits like high soluble sugars and leaf surface wetness are linked to susceptibility. However, in barley genotypes this trait is not deeply studied. Hence, it's important to study the relationship between seedling colors and shoot fly resistance or susceptible barley genotypes for developing strategies to breed resistant barley genotypes and mitigate the impact of this damaging pest on crop yields.

Leaf Width

Allo *et al*., (2020) suggested that the resistance and susceptible barley genotypes showed wider ranges of first leaf width and second leaf width between landrace and improved barley genotypes. However, leaf width was not deeply studied, and it's important to study to it, to select barley shoot fly resistance genotypes.

Seedling Height

Seedling height plays a significant role in reducing shoot fly damage. Patil & Bagde(2017) suggested that taller seedlings are less susceptible to shoot fly. On the other hand, taller plants are more resistant to shoot fly damage compared to shorter ones (Arora *et al*., 2021). This is

because taller plants are less attractive to the shoot fly females for egg laying, and the damage caused by shoot fly is less severe in taller plants. Therefore, seedling height is a crucial morphological trait associated with resistance to shoot fly in sorghum genotypes.

2.8. Agronomic Traits Associated to Shoot Fly Resistance

The Agronomic traits related to barley shoot fly plays a crucial role in enhancing crop productivity and sustainability. Agronomic traits like days to 50% heading, days to 90% maturity, plant height, spike length, seed per kernel, total tillers and productive tillers, biological yield, grain yield, and thousand kernel weight were important traits in selecting shoot fly resistance genotypes. As described by Allo *et al*. (2020), the result of the above agronomic traits showed a wide range of variations among the tested barley genotypes. However, the specific relationship between agronomic traits and shoot fly resistance/susceptibility is not widely studied. Therefore, further research is needed to establish the relationship between these traits and shoot fly resistance, which could lead to the development of more resistant and productive barley genotypes.

2.9. Genetic Diversity of Barley and Its Use in Breeding

The genetic diversity of barley plays a crucial role in ensuring the resilience and sustainability of barley cultivation, especially in the face of changing climatic conditions and environmental degradation (Kumar *et al*, 2020; Saini *et al*., 2020; Ghamkhar *et al*., 2023). Barley genetic resources are conserved in various gene banks and research institutions around the world. Notable collections of barley germplasm are maintained at institutions such as the International Center for Agricultural Research in the Dry Areas (ICARDA) in Lebanon, the Nordic Genetic Resource Center (NordGen) in Scandinavia, the National Small Grains Collection at the United States Department of Agriculture (USDA), and the Ethiopian Biodiversity Institute (EBI) in Ethiopia. These collections are significant for their extensive range of accessions, including wild and cultivated varieties, genetic resources for specific traits of interest, and collections from various geographical regions. The collections are used for research, breeding, and conservation purposes, and they are crucial for maintaining the genetic diversity of barley (Munoz-Amatriaín *et al*., 2014; Getachew *et al*., 2021; Abebe *et*

al., 2023). Efforts to characterize and evaluate the genetic diversity of barley germplasm have been undertaken by various research institutions. For example, the core collection of barley germplasm at ICARDA has been extensively characterized using both morphological and molecular markers, providing valuable insights into the genetic makeup of the collection (Ahmed *et al*., 2015).

In Ethiopia, the genetic diversity of barley germplasm has been the subject of research, with notable efforts to characterize local landraces and improved varieties using morphological and molecular markers (Alemayehu *et al*., 2012; Bekele *et al.,* 2017). However, there remains a need for comprehensive studies that encompass a broader range of barley accessions to fully capture the extent of genetic diversity present within the Ethiopian barley germplasm collections at EBI. Given the importance of genetic diversity in breeding programs, there is a critical need to prioritize the comprehensive characterization of barley germplasm collections, both globally and within Ethiopia, to ensure the effective utilization of genetic resources for the development of improved barley varieties with enhanced resilience, productivity, and adaptability to changing environmental conditions.

2.10. Phenotypic and Genotypic Variability of Barley

The study of phenotypic and genotypic variability in barley is crucial for understanding the genetic diversity of this crop and its implications for agricultural improvement. Variation is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960; Falconer, 1990; Welsh, 1990). Understanding the sources and magnitude of variability among genotypes plays a fundamental role in any crop improvement program to exploit gains from selection (Kassa *et al.,* 2019). Genetic variability is the heart of plant breeding, and genetic variation is the foundation for crop improvement (Welsh, 1990; Sharma, 1998).

The presence of variability among individuals within a population can be estimated by using simple measures of variability, such as range, mean, variance, standard deviation, coefficient of variability, and standard error (Singh *et al*., 2014). Phenotypic variation is observable variation present in traits which include both genotypic and environmental components of

variation, and its magnitude differs under different environmental conditions (Singh and Chaudhary, 1977). The differences between the GCV and PCV indicate the level of environmental variations that contribute a major part in the expression of traits (Majumdar *et al*., 1974).

For successfully selection, information on nature and degrees of variation in populations is necessary (Jalal and Ahmad, 2012; Gebru *et al.,* 2018). Genotypic and phenotypic coefficient of variations can be categorized as low (<10), medium (10-20%), and high (>20%) (Deshmukh *et al*., 1986; Siva Subramanian and Madhavamenon, 1973).

In general, the assessment of phenotypic and genotypic variability in barley is crucial for crop improvement, with genetic variability serving as the foundation for breeding programs. Understanding the sources and magnitude of variability is key to directing selection efforts and developing new barley varieties with enhanced traits.

2.11. Heritability and Genetic Advance in Plant Breeding

The presence of genetic variability is crucial in selecting superior genotypes, but equally important is the heritability of traits, determining their transmission from parents to offspring (Falconer and Mackay, 1996). Heritability serves as a measure of selection value for specific traits and their transmissibility (Poelman and David, 1995). Broad-sense heritability reflects the proportion of total genetic variability to phenotypic variance, while narrow-sense heritability represents the ratio of additive genetic variance to phenotypic variance (Allard, 1960; Falconer and Mackay, 1996).

Heritability values range from zero (environment-driven variation) to one (genetic-driven variation), impacting the efficiency of selection. Traits with heritability above 60% are more efficiently selected due to higher genetic variability and genetic advance (Welsh, 1990). Heritability guides plant breeders in predicting the behavior of future generations and making informed selections.

Genetic advance estimates the expected gain for a specific trait through selection, depending on genetic variability, heritability, and selection intensity (Burton and Devane, 1953; Allard,

1960). It measures the difference in genotypic values between selected and overall populations, with higher variance leading to increased genetic progress. Combining broad-sense heritability with genetic advance enhances the predictive power of selection outcomes, and the heritability values are low (<30%), moderate (30 – 60 %), high (>60%) and genetic advance as percent of mean categorized as low (< 10%), moderate (10–20%) and high (> 20%) as suggested by Robinson *et al*. (1955). Overall, understanding heritability and genetic advance is essential in plant breeding for effective selection of genotypes based on phenotypic performance, guiding breeders in predicting the outcomes of selection and facilitating the advancement of desirable traits in succeeding generations.

2.12. Management of Barley Shoot Fly

There are many studies have been conducted regarding the management of barley shoot fly, including cultural control, host plant resistance(screening of barley genotypes to shoot fly, category of resistance), chemical control, and integrated management of barley shoot fly (Hussien *et al*., 1993).

2.12.1. Cultural control

Cultural practices (mixed cropping, inter cropping and sowing date) influence insect pests by manipulating the field environment making it unfavorable for the pests. This affects the pest population by increasing the mortality or adversely affecting the natural reduction; or promoting the natural enemies of the pest species (Hill, 1993). Mixed cropping systems influence the abundance, diversity and relative importance of pests and their natural enemies and the yield performance of component crops. The intercrop systems, thus, vary in the structural and spatial relationships between component crops, micro-climatic conditions, their influence on pest incidence and activity of natural enemies (Ogenga *et al*., 1993).

Sowing (planting) dates are important to determine the effect of barley shoot fly and early planting is important to reduce the infestation of barley shoot fly than the late planting. The effect of sowing date on infestation by barley shoot fly was in 2001, 2002 and 2003 in the Bona season at Sinana. Four sowing dates, using two barley genotypes (‘Aruso’ and ‘Holker’), were evaluated for their effect on infestation and yield. Infestation varied significantly among years, with the heaviest level recorded in 2003. Infestation was

significantly higher in the improved variety (‘Holker’) than in the farmer variety (‘Aruso’). Significant differences were observed among the four sowing dates for two infestation scores and grain yield. ‘Aruso’ gave a lower yield in the early sowing dates of 2001 and 2003, but had higher yields than ‘Holker’ in 2002, when there was severe moisture stress. It was also relatively more stable in yield over years and sowing dates. Yield of both the varieties was negatively correlated with infestation. Generally, early sowing significantly minimized infestation and resulted in higher yields than late sowing (Tafa & Muluken , 2007). Limited work has been done on the area of cultural control to control *D.flavibasis* Stein.

2.12.2. Host plant resistance

Host plant resistance is defined as those a plants which enable to avoid, tolerate, or recover from the attacks of insects under conditions that would cause greater injury to other plants of the same species(Chekol *et al*., 2021). Plants respond to herbivore attack through an intricate and dynamic defense system that includes structural barriers, toxic chemicals, and attraction of natural enemies of the target pests (Karban, 2011). Agro-ecology is important to consider the effect of barley shoot fly; due to the barley genotypes stayed in farmer (Landraces) is important to control than exotic, improved variety and malt barley genotypes. Many Ethiopian barley landraces have been reported to possess relative resistance to *D. flavibasis* (Tafa, 2003). Exotic genotypes and malt barley are, in contrast, highly susceptible to the pest. A number of improved barley varieties that were released in the past for the Arsi and Bale areas (Hailu, 1997) were tested for their response to barley shoofly infestation at SARC, and were found to be highly susceptible, with infestations of 85–100% (Amare, 1993; Tesfaye *et al.,* 1997). As a result, the breeding and host plant screening strategy was shifted from working with exotic genotype the utilization of indigenous genotype, particularly local and race collections from Bale Zone. Between 1994 and 2006, almost 6000 Ethiopian barley land races were screened at Sinana for their resistance to *D. flavibasis,* and many relatively resistant genotypes were promoted to yield trials for the release of improved varieties. Therefore, host resistance is one of the principal components in integrated barley shoot fly management practices (Tafa & Muluken, 2007).

2.12.2.1. Screening of barley genotype for resistance to barley shoot fly

The screening of barley genotype for resistance to the barley shoot fly plays a crucial role in enhancing crop productivity and sustainability. Early efforts in this area, as reported by Tafa and Bayeh (2003), 300 landraces obtained from Institute of Biodiversity Conservation and Research(IBCR) were screened and 62 relatively barley shoot fly resistant genotypes were selected, while more recent studies by Allo *et a*l. (2020) compared the landrace, and improved barley genotypes to barley shoot fly.

Additionally, comparison of infestation levels in malt barley and food barley to barley shoot fly were investigated by Tafa and Bayeh (2003) and they suggested that food barley is less susceptible to barley shoot fly than malt barley. The screening process typically involves subjecting diverse barley genotype collections to controlled infestation experiments under laboratory or field conditions. Furthermore, Allo *et al*. (2020) compare and evaluated about 585 barley landraces including 10 improved barley genotypes. Therefore, screening barley genotype for shoot fly resistance is importance for enhancing barley crop productivity and sustainability.

2.12.2.2. Category of resistance

There are three main types of resistance categories in plants: antibiosis, antixenosis, and tolerance. These types of resistance can coexist within a plant, and it may exhibit one or more of these types to impact insect pest populations (Peterson *et al*., 2017). These resistances can be attributed to the morphological and/or biochemical characteristics of the host plant. The mechanisms of resistance includes morphological, physiological, and/or biochemical processes, which can range from simply minimizing the impact of insect attack to adversely affecting the insects' cellular processes, growth, and development (Keneni *et al*., 2011).

2.12.2.2.1. Antixenosis resistance to shoot fly

Non-preference first coined by Painter, later termed as antixenosis by (Kogan and Ortman, 1978).The ovipositional antixenosis in the resistance of barley to the barley shoot fly was studied based on the average number of eggs per plant. The average number of eggs per plant for resistance and susceptible genotypes were 5.6 (for 'Aruso') and 11.3 (for HB-42), respectively. The susceptible genotype had a significantly greater number of eggs per plant

than all the resistant genotypes. The fact that HB-42, compared with the resistant genotypes, had the highest number of eggs per plant is apparently due to higher preference by barley shoot fly for oviposition, which shows that antixenosis is a component of resistance in barley against barley shoot fly(Mulatu and Grando, 2011).

2.12.2.2.2. Antibiosis resistance to shoot fly

Antibiosis mechanisms of resistance against shoot fly was identified based on the larval and pupal periods, larval survival, pupal mortality percent, adult emergence percent, pupal weight(mg), fecundity per female and sex ratio(Male: Female) were collected. The larval period for susceptible genotypes was lower and the pupal period was no significant difference between the susceptible and resistance genotypes. The larval and adult emergence were higher for susceptible than resistance genotypes. The male pupal weight was little variation in each tested genotypes and the female pupal weight for resistance genotypes were lower as compared to the susceptible genotypes, and the female pupal weight is higher than the male pupal weight on all tested genotypes(Dhillon *et al*., 2005).

2.12.2.2.3. Tolerance resistance to shoot fly

The tolerance mechanism refers to the ability of the host plant to with stand an insect population sufficiently (Kogan and Ortman, 1978.).The tolerance mechanism of resistance in barley genotypes against barley shoot fly was determined based on number of dead seedlings due to infestation, crop recovery growth following infestation, and grain yield. The resistant genotypes gave a significantly higher yield relative to the susceptible check, due to the heavy infestation. The number of dead seedlings following infestation for susceptible genotype (HB-42) was 170 per plot, and in contrast for the resistant genotypes were 43–62 per plot. The difference was statistically significant between HB-42 and the resistant genotypes, but was not significant among the resistant genotypes. For visual crop recovery growth following infestation, there was no significant variation among the resistant genotypes, but HB-42 had significantly lower recovery growth compared with the resistant genotypes. The remarkable differences between HB-42 and the resistant genotypes for the number of dead seedlings, crop recovery growth and yield suggest that HB-42 is less tolerant compared with resistant genotypes when exposed to nearly equal levels of barley shoot fly infestation in the field. This

confirms that the resistance of barley genotypes to barley shoot fly is mainly due to tolerance(Mulatu & Grando, 2011).

2.12.3. Chemical control

Many synthetic insecticides have been reported as effective in controlling field and storage insect pests despite their serious environmental consequence (Ogunleye, 2001; Chekol *et al*., 2021).There are different insecticides that used to control barley shoot fly were verified and released at SARC like imidacloprid (Gaucho), tubuconazole (Gaucho Raxil), thiamethoxam (Apron star) and Savera 30FS and others. An insecticide trial conducted at SARC with imidacloprid (Gaucho), tubuconazole (Gaucho Raxil), thiamethoxam (Apronstar) and heterahabditis (Cruiser) showed that heterahabditis (at 50, 75 and 100), thiamethoxam (at 250 and 375) and imidacloprid at 250 g per 100 kg seed were effective as seed dressing against *D. flavibasis*. Imidacloprid reduced infestation and also resulted in excellent control of barley shoot fly (Tafa Jobie & Muluken Goftishu, 2007).

2.12.4. Integrated pest management of barley shoot fly

As the name implies, integrated pest management is the combination of two or more control methods to reduce the pest infestation. It is the best and safe to control pests than other control methods. For example: The application of the recommended chemical and optimum planting can be recommended for the reduction of barley shoot fly in the highland of Guji zone southern Ethiopia and other areas with similar agro-ecological conditions (Yared *et al.,* 2021). The early planting dates and the resistant varieties are recommended as principal components of integrated barley shoot fly management for Bale highlands and other similar agro-ecologies (Tafa Jobie & Muluken Goftishu, 2007).The resistant varieties, recommended fertilizers and insecticides application is beneficial for higher grain yield through reduction of barley shoot fly infestation (SARC, 2019).

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted at Sinana Agricultural Research Center (SARC) on station, which is located in Bale Zone of Oromia National Regional State, South Eastern Ethiopia for two consecutive seasons in 2022/23 and 2023/24. The research center is located at a distance of about 463 km South East of Addis Ababa at 07^0 07' N latitude and 40^0 10' E longitudes and at an altitude of 2400 m.a.s.l. The average annual maximum and minimum temperatures are 21^0C and 9^0C, respectively. The area is characterized by bimodal rainfall pattern with annual precipitation ranging from 750 to 1000 mm. There are two growing seasons locally known in the study area *Ganna* which extends from March to July and *Bona,* from August to December. The soil texture of the area is clay loam having black colour. The soil pH ranges between 6.3 - 6.8 (SARC, 2006). Cereal crops are predominantly grown in the area (Taye and Yifru, 2010; Amanuel *et al*., 2022; Belay, 2023).

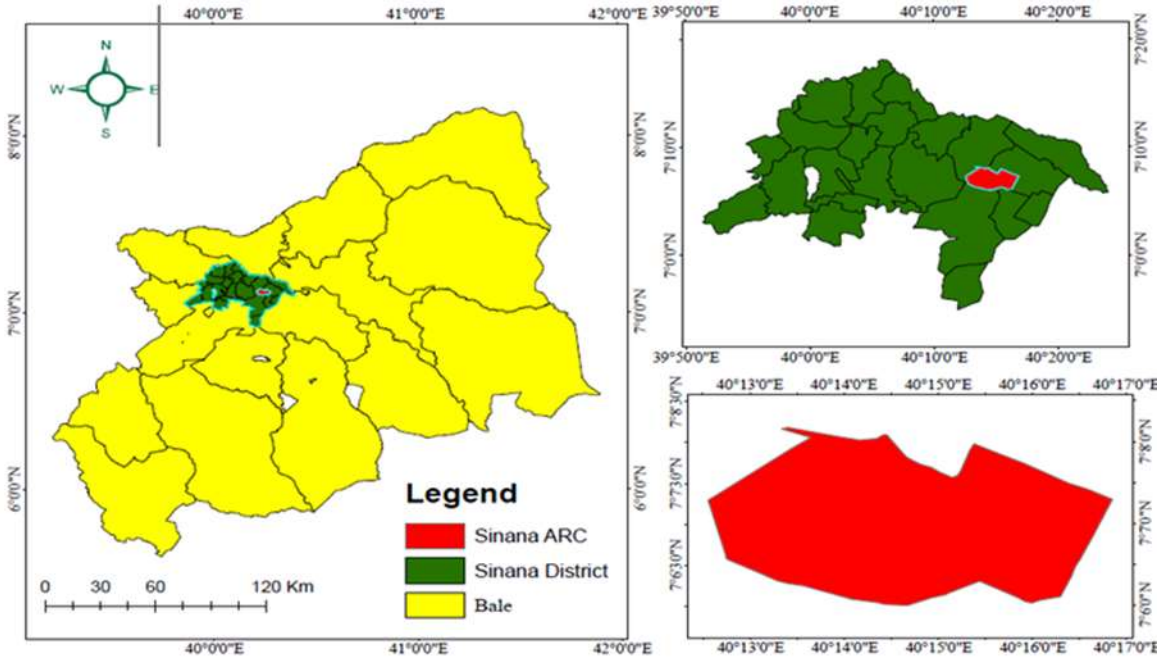

Figure 3. Map of study area

3.2. Experimental Materials

A total of 180 barley genotypes, including 108 landraces, 3 released varieties, and 69 exotic barley genotypes were evaluated in this study (Table 1 &Appendix 1).

Table 1.Description of barley genotypes used in the experiment

Types of Genotype	Source	Accession number or name	No.
Landrace	EBETin	T200,T316,T304,T32,T315,T249,T464,T21,T329,T369,T51,T376,T525,T573,T438,T467,T422,T15,T470,T344,T520,T451,T97, T562,T301,T367,T268,T318,T100,T484,T45,T78,T455,T568,T72,T372,T204,T139,T474,T62,T36,T386,T207,T12,T274,T197,T374,T38,T295,T24,T503,T213,T370,T352,T364,T59,T320,T444,T519,T336,T258,T528,T281,T184,T332,T1,T447,T401,T548,T521,T229,T419,T544,T56,T585,T537,T559,T516,T254,T575,T307,T289,T272,T208,T346,T271,T514,T511,T11,T497,T90,T134,T79,T322,T508,T387,T506,T328,T576,T30,T530,T522,T512,T123,T524,T333,T494,Aruso	108
	SARC	Dinsho and Moata	2
Improved Variety	EBETin	HB-42	1
Exotic Lines	8TH GSBYT-2021	17, 15, 4, 6, 9, 12, 2, 3, 4, 1, 7, 11, 19,139	14
	IBON-2021	114, 96, 66, 88, 15, 90, 51, 50, 61, 59, 113, 100, 29, 102, 55,105	16
	ISBYT-HI-2021	17, 21, 20, 4, 3, 15, 19, 2, 1	9
	IEMBSN-2021	5, 17, 19, 20, 24, 29, 34, 46, 48, 56, 62,67, 69,73, 75, 86, 90, 91, 97, 100, 102, 105, 133, 139, 150, 156, 157, 161, 167, 168	30
		Total number of genotypes screened	180

SARC= Sinana Agricultural Research Center, BETin= Bio and Emerging Technology Institute, ISBYT-HI-21= International Spring Barley Yield Trials for High Input Areas 2021, 8th GSBYT-21=8th Global Spring Barley Yield Trial 2021, IBON-21= International Barley Observation Nursery for HI Input Areas 2021, IEMBSN-21= ICARDA=Ethiopia Malt Barley Special Nursery 2021

3.3. Experimental Procedures

3.3.1. Screening of barely genotypes for resistance to shoot fly

The experiments were laid out in augmented block design consisting of six blocks in which the 176 barely genotypes were planted with non- replications and the three improved varieties (HB-42, Dinsho and Moata) and one local landrace (Aruso) used as checks were replicated six times (ones in each block) to estimate an error variance. The plot area was 0.4 m^2 (0.4 m width * 1m length). The spacing between rows, plots and blocks were 0.2 m, 0.2 m and 1m,

respectively with a total area of 235.4 m^2 (11 m x 21.4m). Seeds were planted manually with a seeding rate of 100 kg ha^{-1}at Sinana Research Centre during 2022/23 cropping season. The agronomic practices such as fertilizer application and hand weeding were applied to the experiments, but plant protection measures (like insecticides, herbicides, fungicides spraying etc.) were avoided. During this time, the collected data were number of eggs per seedling, infestation and dead heart percent, crop recovery, days to 50% heading, days to 90% maturity, plant height, spike length, seed per spike, total tiller, productive tiller, biological yield, grain yield and thousand kernel weights.

3.3.2. Evaluation of morphological and agronomic traits of barley related to barley shoot fly damage in field conditions

Based on the results from screening test, 64 barely genotypes were selected for further agronomic and morphological evaluation. These genotypes were selected based on the results of dead heart obtained from screening genotypes. Out of 64 barley genotypes selected, 21 genotypes had < 20% of dead heart (resistance), 4 genotypes had between 20 to 30% of dead heart (Moderately resistance), 14 genotypes had between 30 to 50 % of dead heart (Susceptible), and the remaining 25 genotypes had > 50 % of dead heart (highly susceptible).The experiment was laid out in 8 x 8 simple lattice designs with two replications. The distance between row to row, rep to rep, block to block, and plot to plot was, 0.2m, 2m, 1.5m, and 0.4m, respectively. All other practices were applied as described in section 3.3.1. Barley shoot fly damage parameters such as eggs per seedling, percentages of infestation and dead heart were collected. Morphological traits like seedling vigor, leaf glossiness, seedling color, first leaf width, second leaf width, and seedling stem length were collected. Likewise, agronomic traits like crop recovery, days to 50% heading, days to 90% maturity, plant height, spike length, seed per spike, total tiller, productive tiller, biological yield, grain yield and thousand kernel weight were also collected.

3.3.3. Category of resistance to shoot fly

3.3.3.1. Insect culture

To multiply barley shoot fly, the susceptible barley genotypes (HB-42) was planted on the field, before plantation of test genotypes. Barley seedlings with dead heart was carefully

collected from the field and put in cages (30cm x 20cm x 20cm) after six days of dead heart formation, the dead heart was covered with moistened soil in the cages up to the depth of 14 cm and kept at room temperature in the laboratory until the emergence of adult fly (Muluken *et al*., 2009).The purpose of adding soil to dead heart in the cages was to provide the pupae with suitable conditions for survival, since in the field pupae normally occurs with or among plant root (Tafa, 2003). The adult of barley shoot fly with an interval of 24h was carefully removed by using siphon trap and were released in cage (50 by 50 by 50 cm). The adult barley shoot fly's diet was made using glucose, brewer's yeast, and distilled water at a ratio of 4:7:10, respectively (Goftishu *et al*., 2009).The diet was changed daily. After three days of conditioning, the shoot flies were used for studies on antixenosis and antibiosis components of resistance to this insect (Chamarthi, 2008).The sex of the shoot fly was identified based on their size, that means; males are smaller than the females (Sharma, 1996; Tafa, 2003) and color (female is gray and male is blackish) (Hill, 1983; Tafa, 2003).

3.3.3.2. Antixenosis or non-preference test

3.3.3.2.1. Multiple choice test

Based on the shoot fly oviposition, infestation, and dead heart parameter results obtained from the first year screening, 12 barley genotypes were selected to study non preference or antixenosis category of resistance to shoot fly under multiple choice test in the field. From the 12 barley genotypes selected, 4 were resistance (T281, T506, T524 and T575), three were moderate resistance (T364, 150, and T123), three were susceptible (55, 168, and T376) and two were standard check (Aruso- as resistance and HB-42- as susceptible). During 2023/2024 main cropping season "Bona", the test material was planted in the field. Each genotype was planted in two rows per plot with 2 m length. The distance between row to row, plot to plot, and block to block was 0.2m, 0.5m and 1.5m, respectively. There were three replications in a randomized complete block design (RCBD). Data collected were eggs per seedling, seedling with egg in percent, and dead heart percent.

3.3.3.2.2. Dual and no-choice test

Antixenosis for oviposition was also studied under dual-choice and no-choice conditions in a rectangular woven cloth-screened cage (Figures 4 and 5). The cage was made from a cloth

mesh to allow air circulation. The above 12 selected genotypes were also used for the study of antixenosis under dual and no-choice conditions. The test genotypes were planted in plastic pots with a potting mixture of black soil, sand, and farmyard manure (2:1:1) (Golla *et al*., 2020). The recommended fertilizer rates were mixed with the soil before planting. Twelve (12) seedlings of each genotype were planted in each plastic pot and thinned to ten (10) seedlings before releasing newly emerged adult flies. For no-choice tests, only one genotype was planted in each pot and put in one cage. For dual-choice tests, there were a pair of pots, one with test genotypes and the other with susceptible control (HB-42) in one cage. A completely randomized design (CRD) with three replications was used in both dual and no-choice tests. A pair of female and male adult barley shoot flies were released into a single pot at 7 days after seedling emergence, during the 1.1-growth stage (first leaf unfolded), as proposed by Muluken *et al.* (2009). The flies were provided with a diet consisting of brewers' yeast, glucose, and water until they were removed from the cages after four days. Numbers of eggs per 10 seedlings, percentages of plants with eggs, and, after five days of infestation, percent of dead heart plants were recorded, following the procedure of Dhillon *et al*. (2005).

3.3.3.3. Antibiosis test

The antibiosis category of resistance was studied under a no-choice test, and 12 selected barley genotypes were planted in the plastic pots covered with net under field conditions to make well-suited conditions (Figure 6). The seedling was inoculated with eggs of *D. flavibasis* at the rate of three per seedling before first leaf folded (Tafa, 2003). Camel hairbrush was used. The eggs were carefully placed at the base of seedlings in each pot using camel hairbrush (Jyoti *et al*., 2001; Tafa, 2003). After 9 days of eggs inoculation, all the dead heart in each genotype was carefully uprooted and put in individual cages (20 cm diameter x 30 cm height) in the laboratory of SARC (Figure 7). The dead heart collected from the field was covered by moistened soil in the plastic cage, up to the depth of 14 cm. The aim of adding the soil to cages was to make suitable conditions for the pupae (Bullock, 1965; Tafa, 2003). The cages were arranged in completely randomized design with four replications**.** Larval and Pupal periods, larval and pupal survival, pupal weight, adult emergence, and fecundity or number of eggs laid per female were collected.

Figure 4. Rectangular woven cloth (30 cm diameter and 40 cm height) tied to two pegs used to recording fecundity *Delia flavibasis* females reared on different paired genotypes (test genotypes vs. HB-42), under dual choice test(From field experiment).

Figure 5. Rectangular woven cloth cages (25 cm diameter and 40cm height) tied to one peg used to recording fecundity *Delia flavibasis* females reared on different genotypes, under no choice test(From field experiment).

Figure 6. Antibiosis category of resistance during eggs inoculated under field conditions and covered with net at SARC on station in 2024(From field experiment)

3.4. Parameters Recorded

3.4.1. Barley shoot fly damage and crop recovery

The barley shoot fly resistance parameters such as number of eggs per plant, number of infested plants and number of dead heart plants were collected under field condition. The number of eggs was recorded at 10 and 13 days after emergence (DAE) by randomly selecting 10 plants per plot, and the number of eggs per plant was calculated by summing the total eggs recorded for ten plants and dividing by ten (Joshi *et al*., 2016).

$$\text{Eggs per plant } = \frac{Number\ of\ eggs\ for\ 10\ \ plants}{10\ plants}$$

The data on number of infested plants was recorded at 13 and 16 DAE by counting the number of infested plants for 2 rows. After that, the infestation/incidence percent was calculated by dividing the number of infected plants by the total plants counted and multiplying by 100. Thus, the rating scales are as follows: when infestation percent is ≤ 20% (resistant); 21 to 40% (moderately resistant); 41 to 60% (susceptible); and 61 to 100% infestation (highly susceptible) (Tafa & Muluken, 2007).

$$\text{Infestation \% } = \frac{Infected\ plants}{Total\ plants\ per\ 2\ rows} x\ 100$$

The dead heart plant was recorded on the 18th DAE by counting the total number of plants per 2 rows and identifying the number of dead heart plants caused by barley shoot fly. The dead heart percentage was calculated by dividing the number of dead heart plants by the total plants counted and multiplying by 100. Then, the rating scale for dead heart is as follows: 0 – 10% is highly resistant, 11 – 20% is resistant, 21 – 30% is moderately resistant, 31 – 50% is susceptible, and above 50% dead heart is highly susceptible (Joshi *et al*., 2016; Allo *et al*., 2020).

$$\text{Dead heart \% } = \frac{Dead\ shoot\ plants}{Total\ plants} x\ 100$$

Crop recovery was recorded based on a 1–5 scale in the fifth week, where 1 = very low recovery growth (0–20%); 2 = low recovery growth (21–40%); 3 = moderate (41–60%); 4 =

moderately high recovery growth (61–80%); and 5 = high recovery growth (81–100%) (Tafa & Muluken, 2007).

3.4.2. Morphological traits of barley genotypes associated with resistance to *D. flavibasis*

The morphological traits collected included seedling vigor, leaf glossiness, seedling color, first leaf width, second leaf width, seedling stem thickness, and seedling stem length.

Seedling vigor: It was recorded based on a combination of height, leaf growth and robustness at 10 DAE on 1–5 rating scale; when 1 = poor seedling vigor , plants showing poor growth, and weak seedlings, 2 = less vigorous, less plant height with poor leaf expansion, and poor adaptation, 3 = moderately vigorous, moderate plant height with moderate number of fully expanded leaves, and fairly good seedling growth, 4 = vigorous , good plant height, good number of fully expanded leaves, and good adaptation and seedling growth, 5= highly vigorous, plants showing maximum height, more number of fully expanded leaves, good adaptation, and robust seedlings (Allo *et al*., 2020).

Leaf glossiness: It was evaluated based on a 1 to 5 rating at 10 DAE in the early morning hours when there was maximum reflection of light from the leaf surfaces (Figure 8). Thus, 1= non-glossy (dark green, dull, broad, and drooping leaves); 2= moderate non-glossy (green, pseudo-shine, broad, and drooping leaves); 3 = moderate glossy (fair green, light shining, medium leaf width, and less drooping leaves); 4 = glossy (light green, less shining, narrow and erect leaves); 5= highly glossy (light green, shining, narrow and erect leaves)(Chamarthi, 2008).

(A) (B) (C)

Figure 7. Leaf glossy (A= highly glossy; B= glossy; C= non-glossy)

Leaf color was recorded 1 to 3 scales as proposed by Mihret *et al*., 2022. Therefore, leaf color 1=Dark green, 2=Medium green, and 3=Light green.

Leaf width: First and second leaf width, was measured by centimeter around their center at 10DAE.

Seedling stem length: It was measured by centimeter starting from bottom (from the soil) to apical meristems or leaf whorl.

Seedling stem thickness was first measured by tied thread to stem and convert it in to centimeter.

3.4.3. Agronomic traits of barley

Plot-based data such as days to 50% heading (DTH), days to 90% maturity (DTM), dry weight of above ground biomass (kg $plot^{-1}$), and grain yield (GY) (g $plot^{-1}$) were recorded on plots basis. Plant-based data such as total number of tiller per plant (TNTPP, in No), productive tiller (PT in No, plant height (PH, in cm), spike length (SL, in cm), and number of seeds per spike (SPS in No.) were measured on ten (10) randomly sampled plants from the rows of each plot (Allo *et al*., 2020).

Table 2. Quantitative agronomic traits recorded (Allo *et al*., 2020)

Trait	Description
DTH	It was recorded in days when about 50% of the plants in a plot produced spikes
DTM	It was recorded in days when about 90% of the plants reached physiological maturity
PH	It was measured in centimeter at physiological maturity from the soil surface to the top of the spike (excluded awns) from 5 randomly selected plants in the central rows
TT	It was determined at maturity by counting all the tillers in numbers from 5 randomly selected plants in the central rows
PT	It was determined at maturity by counting all fertile or productive or seed bearing tillers from the total tiller counted in numbers
SL	It was measured in centimeter (cm) from the bottom of the spike to the tip of the spike excluding the awns from 5 randomly selected spikes from each plot
SPS	It was determined in numbers by counting the number of kernels per spike from randomly selected five spikes per plot
BY	It was recorded as weight of sun-dried of above-ground total plant biomass (grain and straw) in kilograms for each experimental unit
GY	It was recorded in grams $plot^{-1}$ at 12.5 % moisture content
TKW	It was determined in grams based on the weight of 1000 kernels sampled from the grain yields of each plot by weighed with an electronic balance

DTH= Days to 50% heading, DTM= Days to 90% maturity, PH=Plant height, TT=Total Tiller per Plant, PT=Productive Tiller, SL=Spike Length, SPS=Seed Per Spike, BY=Biological Yield, GY=Grain Yield, and TKW=Thousand Kernel Weight.

3.4.4. Antixenosis test

The data collected during the study of antixenosis test were number of eggs 10^{-1} seedlings, percentages of plants with eggs and dead heart percentages of plant.

Number of eggs 10^{-1} seedlings was counted from 10 randomly taken plants per plot and their summation was put in numbers.

Percentages of seedling with eggs were calculated from the percent of seedling that contains eggs from 10 selected plants.

$$\textbf{Dead heart } \% = \frac{Dead\ heart\ seedlings\ per\ 10\ plants}{10\ plants} x\ 100$$

3.4.5. Antibiosis test

Larval and pupal periods in days, pupal weight in milligram, pupation percent in percentages, adult emergence in percent and fecundity per female in numbers were collected during the antibiosis category of resistance.

Larval period (days): It was recorded after egg hatching up to pre-pupation. It is equal to the number of days from the appearance of the dead heart to pupation plus one day (because the dead heart takes one day to realize after the egg hatches). It was recorded separately for each larva, and the mean larval period for each genotype was calculated for the surviving larvae (Dhillon *et al*., 2005).

Larval survival (%): It is the percent of larvae survive out of total dead heart collected for each genotype (Dhillon *et al*., 2005).

Pupa period (days): Measured from days of pre-pupation until reaching adulthood. For each pupa it was measured separately, and for surviving pupae, the average pupal duration of each genotype was calculated.

Pupal weight (mg): It was measured for individual pupa on an electronic balance, within 24 h after pupation. After weighing, the pupae were placed in respective cage on moist soils to avoid the water loss and pupal mortality because of desiccation (Muluken *et al*., 2009).

Adult emergence (%): From the total dead heart collected in each genotype the number of adults that emerged was counted and expressed as a percentage of adult emergences (Dhillon *et al.*, 2005).

Fecundity: Two (2) pair of newly emerged flies, 24 h old, was released into individual cages (30 by 20 by 20 cm) having ten newly emerged seedlings per cage of 1.1-growth stage (first leaf unfolded) for oviposition. The adult flies were provide the diet prepared from glucose, brewer's yeast and distilled water at the ratio of 4:7:10, respectively. The cages were monitored daily to record the number of eggs laid per female in numbers throughout its adult life(Muluken *et al.*, 2009).

3.4.6. Antibiosis indices

The antibiosis indices like growth index, relative growth index, developmental index, adult emergence index, and fecundity index were also calculated following the procedures of Dhillon *et al*. (2005).

$$\text{Growth index} = \frac{\text{Pupation}(\%)}{Larval\ Period(days)}$$

$$\text{Relative growth index} = \frac{\text{growth index on the test genotype}}{\text{growth index on the susceptible check}}$$

$$\text{Developmental index} = \frac{\text{Larval + pupal periods on the test genotype}}{\text{Larval + pupal periods on the susceptible check}}$$

$$\text{Adult emergence index} = \frac{\text{Adult emergence on the test genotype}}{\text{Adult emergence on the susceptible check}}$$

$$\text{Fecundity index} = \frac{\text{Total eggs laid by the insects reared on the test genotype}}{\text{Total eggs laid by the insect reared on susceptible check.}}$$

3.5. Statistical Analysis

All the data (except dual-choice test data) collected for each quantitative trait like agronomic data were subjected to the analysis of variance (ANOVA) after normality was checked using Shapiro-Wilk test. The significance differences between the genotypes were tested by F-tests, while the treatment means w compared by Tukey test and least significant differences (LSD) at P =0.05. For the dual-choice tests, paired t-test (P = 0.05) was used to test the significance of the difference between the test genotype and the susceptible check (HB-42) at P = 0.05 using R.4.1.3 software.

The mathematical model for a simple lattice design is: Pijk = μ + Gi + Rj+ Bk (j) + eijk, Where: - Pijk = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within Replication j; μ = grand mean; Gi = the effect of i^{th} genotype; Rj = the effect of replication j; Bk (j) = the effect of incomplete block k within replication j and eijk = the residual or effect of random error.

To estimation of variance components the phenotypic and genotypic coefficients of variation are calculated according to the procedures suggested by Burton and De Vane (1953).

(a). $\sigma 2g = \frac{MSg - MSe}{r}$ (b). $\sigma 2p = \sigma^2 g + \sigma^2 e$ (c). $PCV = \frac{\sqrt{\sigma 2p}}{\bar{X}} * 100$ (d). $GCV = \frac{\sqrt{\sigma 2g}}{\bar{X}} * 100$

Where: $\sigma 2g$= Genotypic variance, MSe= mean square of error, r=number of replications, $\sigma^2 p$ =Phenotypic variance, σ^2g=Genotypic Variance, σ^2e= Error variance, PCV= Phenotypic coefficient of variation, $\bar{X}$ = Population mean of a character, GCV=Genotypic coefficient of variation.

Heritability in a Broad Sense (H^2) was determined as described by Allard (1999)

$H^2 = \frac{\sigma 2g}{\sigma 2p} * 100$; where H^2= Broad-sense heritability, σ^2g= Genotypic variance, σ^2p= Phenotypic variance**.** The heritability was categorized according to performed by Robinson *et al*. (1949) as low (0–30%), moderate (30–60%), and high (>60%).

Genetic advance (GA), and genetic advance as percentage of mean (GAM) were estimated as devised by Johnson *et al*., (1955). GA = K∗ σp ∗H^2, where: σp = the phenotypic standard deviation of the trait, H^2 = heritability estimate in the broad sense and k = selection differential, where k = 2.063 at 5% selection intensity.

GAM = $\frac{GA}{\bar{X}} * 100$, where $\bar{X}$ is the population mean of a character. GAM was categorized following the procedure of Johnson (1955) as low (0–10%), moderate (10–20%), and high (>20%).

4. RESULTS AND DISCUSSION

4.1. Screening of Barley Genotype for Resistance to the Barley Shoot Fly

4.1.1. Analysis of variance (ANOVA) of studied characters

The ANOVA for treatment adjustment and block adjustment is presented in Table 3. In the present study, a highly significant ($P < 0.01$) or significant ($P < 0.05$) difference in ANOVA was observed for both treatment-adjusted and block-adjusted values among genotypes (tests), genotypes (tests and checks), checks, and genotypes (tests) vs. checks for all evaluated traits. However, in ANOVA-treatment adjustment, there was no significant difference in productive tiller number in checks, spike length in treatment and genotypes (test and test vs. check), and seed per spike in block (ignoring treatments). Additionally, in ANOVA-block adjustment, there was no significant difference among blocks in all parameters tested, except for days to 50% heading and biological yield (Table 3). The current results are similar to those of Allo *et al*. (2020), who reported significant variations ($P \leq 0.001$) in 13 quantitative characters evaluated among accessions (tests), genotypes (accessions and checks), checks, and accessions (tests) vs. checks. However, the same authors reported no significant difference in grain filling period in genotypes and checks, total tillers per plant, productive tillers per plant, and spike weight in checks, as well as the number of fertile tillers per plant, spike density, and weight in accessions vs. checks. These results indicate a wide range of variations for most agronomic traits from year to year.

4.1.2. Evaluation of different sources of barley genotypes to barley shoot fly

The minimum, maximum, and mean values for quantitative characters and shoot fly resistance components of 107 barley landraces, 69 exotics, and four checks are presented in Table 4. Landrace genotypes exhibited oviposition ranging from 0.70 to 6.95 per plant, with infestation percentages of 7.14 to 89.14 and dead heart percentages of 5.05 to 81.61, while 2.27 to 6.77 oviposition per plant, 20.97 and 98.94 percent infestation, and 17.75 to 92.32 dead heart percent on exotic genotypes. Meanwhile, the check displayed oviposition levels between 1.59 and 6.07 per plant, 14.02 to 84.15 percent infestation, and 9.24 and 75.04 percent dead heart (Table 4). Additionally, other shoot fly qualitative traits for landraces, exotics, and improved

genotypes (checks) showed wider variations (Table 4). The current result is similar to the previous reports of Mehtre (2006), Aruna *et al.* (2011), and Allo *et al.* (2021). In the present study, landrace, improved, and exotic barley genotypes showed the highest, medium, and lowest resistance to shoot fly with oviposition, infestation, and dead heart, with mean values of 3.25, 3.3, and 4.75 numbers per seedling: 36.16%, 44.4%, and 67.67%, respectively. The current result indicates that the barley shoot fly reflects the resistance of different sources of barley genotypes found in field conditions very well. This might be due to the genotypically diverse cultivar resistance, which contrasts with the genetically uniform varieties in terms of shoot fly damage. The results of the current study are consistent with the previous reports of Riyazaddin (2015) and Mendesil *et al.* (2016), who noted that genetically uniform genotypes are more likely to be prone to insect pest damage compared to genotypically diverse genotypes mixtures. However, the mean of landrace genotypes had a lower grain yield compared to other sources of genotype. This might be due to a lower number of tillers per plant, lower plant thickness, and other low agronomic traits of landrace genotypes compared to the improved and exotic genotypes.

4.1.3. Category of resistance barley genotypes based on the mean of barley shoot fly damage parameters

In this experiment, 180 barley genotypes, including four checks, were evaluated for their resistance to barley shoot fly. Based on the oviposition, infestation percent, and dead heart percentage parameters,4 genotypes showed high resistance,37 genotypes exhibited resistance, 31genotypes demonstrated moderate resistance,51 genotypes were susceptible, and 57 genotypes were highly susceptible to barley shoot fly within the ranges of 0-10%, >10 to 20%, >20 to 30%, >30 to 50%, and >50 to 100%, respectively, as per the range defined by Allo *et al*., 2020 (Table 5 and Appendix 2).

Table 3. ANOVA for Treatment and Block Adjustment

ANOVA - treatment adjusted								
Source of variation	DF	OVI	INF	DH	CR	DTH	DTM	TT
Block(ignoring Treatments)	5	7.94**	557.8**	534.2**	1.45**	179.5**	385.8**	2.77*
Treatment(eliminating Blocks)	179	2.50**	647.7**	583.4**	1.03**	163.4**	242.3**	6.47**
Treatment: Check	3	23.7**	6516.4**	5369**	15.4**	1444.5**	1823.3**	17.9**
Treatment: Test and Test vs. Check	176	2.14**	547.7**	501.8**	0.78**	141.5**	215.4**	6.27**
Residuals	15	0.06	10.06	5.13	0.11	11.90	25.70	0.77
Source of variation	DF	PT	PH	SL	SPS	BY	GY	TKW
Block(ignoring Treatments)	5	2.21*	647.6**	4.51*	69.07^{ns}	0.39**	4298.7**	65.20**
Treatment(eliminating Blocks)	179	3.13**	376.0**	1.53^{ns}	65.24*	0.29**	2196.4**	42.35**
Treatment: Check	3	1.33^{ns}	1120.1**	9.83**	99.30*	1.95**	7318.9**	91.75**
Treatment: Test and Test vs. Check	176	3.16**	363.3**	1.39^{ns}	64.66*	0.26**	2109.1**	41.51**
Residuals	15	0.51	26.18	1.02	26.66	0.02	86.89	5.69
ANOVA - block adjusted								
Source of variation	DF	OVI	INF	DH	CR	DTH	DTM	TT
Treatment(ignoring Blocks)	179	2.7**	663.2**	598.1**	1.07**	167.3**	251.3**	6.51**
Treatment: Check	3	23.7**	6516.4**	5369**	15.4**	1444.5**	1823.3**	17.9**
Treatment: Test	175	2.4**	564.9**	517.1**	0.81**	145.7**	223.4**	6.35**
Treatment: Test vs. Check	1	3.2**	295.5**	456.5**	2.06**	123.9**	406.4**	0.62^{ns}
Block(eliminating Treatments)	5	0.12^{ns}	3.60^{ns}	8.60^{ns}	0.08^{ns}	38.4*	65.28^{ns}	1.13^{ns}
Residuals	15	0.06	10.06	5.13	0.11	11.90	25.70	0.77
Source of variation	DF	PT	PH	SL	SPS	BY	GY	TKW
Treatment(ignoring Blocks)	179	3.17**	392.7**	1.58^{ns}	66.80*	0.30**	2311.9**	44.09**
Treatment: Check	3	1.33^{ns}	1120.1**	9.83**	99.30*	1.95**	7318.9**	91.75**
Treatment: Test	175	3.22**	381.8**	1.44^{ns}	61.85*	0.27**	2097.2**	43.28**
Treatment: Test vs. Check	1	0.13^{ns}	131.4*	0.63^{ns}	835**	0.35**	24868**	43.39*
Block(eliminating Treatments)	5	0.49^{ns}	47.5^{ns}	2.86^{ns}	13.30^{ns}	0.08*	161.14^{ns}	3.01^{ns}
Residuals	15	0.51	26.18	1.02	26.66	0.02	86.89	5.69

^{ns} P > 0.05; * P <= 0.05; ** P <= 0.01; DF=Degree Freedom, OVI=Oviposition, INF=Infestation, DH=Dead heart, CR=Crop Recovery, DTH=Days to 50% Heading, DTM=Days to Maturity, TT=Total Tiller, PT=Productive Tiller, PH=Plant Height, SL=Spike Length, SPS=Seed Per Spike, BY=Biological Yield, GY=Grain yield and TKW=Thousand kernel weight.

Table 4.Minimum, maximum, mean, coefficient of variation and standard error of means (SE) for quantitative characters and shoot fly resistance components of different source of barley genotypes

Traits	Landrace genotypes					Exotic genotypes					Standard check				
	Min	Max	Mean	CV	SE	Min	Max	Mean	CV	SE	Min	Max	Mean	CV	SE
Eggs seedling^{-1}	0.7	6.95	3.25	18.19	0.16	2.27	6.77	4.75	17.47	0.14	1.59	6.07	3.3	5.26	0.31
IINF (%)	7.14	89.84	36.16	19.67	1.86	20.97	98.94	67.67	9.18	2.96	14.02	84.15	44.4	7.4	5.42
DH (%)	5.05	81.61	30.15	21.69	1.76	17.75	92.32	59.58	11.76	2.89	9.24	75.04	36.5	5.42	4.99
CR(1-5)	0.56	4.48	2.72	22.02	0.1	1.38	4.82	3.23	10.59	0.13	0.85	4.76	3.23	7.79	0.27
DTH(days)	50.87	88.87	67.8	11.24	1.18	53.13	94.88	80.7	11.41	1.38	51.33	90.08	68.5	4.63	2.64
DTM(days)	94.3	143.04	116.35	7.42	1.55	98.29	144.54	131.72	9.21	1.39	90.08	139.83	115.3	4.51	3.19
TT(no)	1.12	10.58	5.22	34.48	0.19	4.45	13.22	8.59	31.58	0.32	3.64	9.46	6.19	8.36	0.35
FT(no)	1.08	8.1	4.28	33.68	0.16	3.31	10.08	6.29	27.43	0.25	2.84	6.24	4.85	6.75	0.18
PH(cm)	37.21	124.99	79.7	14.54	2.54	43.07	124.52	82.61	12.46	2.54	62.8	108.7	84.7	2.92	2.7
SL(cm)	4.77	10.58	8.18	15.17	0.11	4.57	12.03	8.2	17.52	0.24	5.21	11.5	8.39	13.3	0.32
SPS(no)	21.64	65.99	40.03	14.92	0.94	24.9	64.54	43.04	17.28	1.33	36.09	60.79	48.08	9.44	1.15
BY(Kg/plot)	0.32	2.58	1.2	27.98	0.06	0.56	2.24	1.41	42.64	0.06	0.43	2.00	1.38	8.89	0.1
GY(gram plot^{-1})	0	192.94	88.98	34.67	5.18	52.97	230.17	126.43	12.29	5.69	86.21	191.86	140.24	5.27	5.96
TKW(grams)	20.98	55.18	35.49	15.37	0.61	29.22	54.94	42.17	13.2	0.89	33.85	51.69	39.48	3.5	0.84

Min=Minimum, Max=Maximum, CV=Coefficient of Variation, SE=Standard Error, OVI seedling-1= Number of Eggs Laid Per Seedling, IINF (%) =Infestation in Percentages, DH(%)=Dead Heart in Percentages, CR(1-5)=Crop Recovery 1 to 5 Scoring Scale, DTH(Days)=Days to 50% Heading in Days, DTM(Days)=Days to 90% Maturity in Days, TT(no)=Total Tiller in Number. PT(no)=Productive Tiller in Number, PH(cm)=Plant Height in Centimeters SL(cm)=Spike Length in Centimeter, SPS(no)=Seed Per Spike in Numbers, BY(Kg/Plot)=Biological Yield in Kilogram Per Plot, GY(gram plot-1)=Grain Yield in gram per plot, TKW(grams)=Thousand Kernel Weight in Grams.

Table 5. Resistance category of barley genotypes based on the mean of dead heart of shoot fly

S.No	Genotypes	No.	RC
1	T249,T62,T506,T524	4	HR
2	T200,T32,T464,T329,T369,T438,T467,T562,T301,T367,T318,T482,T45,T78,T455,T568,T72,T372,T204,T374,T24,50,T281,T401,149,T544,T575,T208,T11,T90,T328,T576,139,T512,T333,Dinsho,Aruso	37	R
3	20,T315,2,T21,T51,T525,T573,6,T15,9,T520,T97,T36,T38,T370,T352,T364,T521,T56,T537,T289,T497,T134,T322,T508,T387,T522,150,T123,157,T494	31	MR
4	T316,T304,3,15,T422,T470,T344,2,3,T100,19,96,T139,T474,T386,88,T207,T12,T274,T197,90,T503,T213,113,T519,29,T528,T332,T1,T447,T548,T29,T419,20,T559,T516,T254,T307,T272,T346,T271,T514,T79,T30,T530,156,167,Moata	51	S
5	17,21,4,19,17,4.T376,12,T451,4,T268,1,7,11,114,66,15,T295,51,61,59,T59,T320,100,T444,T336,T258,T184,102,55,105,5,17,19,24,29,34,46,48,56,62,67,69,73,75,86,T511,90,91,97,100,102,105,133,161,168,HB-42	57	HS

S.No=Sequence number, No. =Amount in number, RC=Resistance Category, HR=highly resistance, R=Resistance, MR=Moderately resistance, S=Susceptible, HS=Highly susceptible

4.2. Evaluation of Shoot Fly Damage, Morphological, and Agronomic Traits of Resistance to *D. flavibasis*

4.2.1. Analysis of variance

The results of mean squares and coefficient of ANOVA are presented in Table 6. The analysis of variances showed that there were highly significant ($P<0.001$) differences for all traits among the 64 barley genotypes evaluated. This finding is in line with the previous report of Allo *et al*. (2020). This suggested that there is variation of genotype under field conditions in order to identify better performing genotypes for barley shoot fly resistance.

Table 6. Mean squares and coefficient of variability for 21 traits of 64 barley genotypes evaluated at SARC during the 2023/2024 Bona season

Characters	Rep (DF=1)	Block(Rep) (DF=14)	Genotypes (DF=63)	Error (DF=49)	CV (%)
Oviposition	0.37	0.27	6.894e-12 ***	1.40	19.1
Infestation	0.27	0.26	6.455e-12 ***	2.42	24.2
Dead heart	0.10	0.36	1.219e-09 ***	2.19	29.7
Crop recovery	0.57	0.45	4.249e-05 ***	0.10	25.1
Seedling vigor	0.01 **	0.52	7.14e-10 ***	0.12	24.9
Leaf glossiness	0.26	0.41	2.163e-12 ***	0.11	19.9
Seedling color	0.79	0.59	<2e-16 ***	0.08	19.4
First leaf width	0.01**	0.27	< 2.2e-16 ***	0.01	8.3
Second leaf width	0.21	0.08	< 2e-16 ***	0.01	5.7
Seedling stem length	0.47	0.27	<2e-16 ***	0.11	8.8
Seedling stem thickness	0.02*	0.46	1.167e-09 ***	0.01	11.6
Days to heading	0.21	0.20	3.11e-12 ***	0.36	2.8
Days to maturity	0.48	0.82	3.133e-08 ***	0.47	2.7
Total tiller	0.50	0.64	<2e-16 ***	0.14	8.8
Productive tiller	0.74	0.15	1.154e-13 ***	0.12	10.7
Plant height	0.55	0.03 *	2.425e-10 ***	1.23	7.5
Spike length	0.17	0.86	2.528e-08 ***	0.13	10.9
Seed per spike	0.02 *	0.07	4.295e-09 ***	0.96	13.7
Biomass	0.31	0.41	<2e-16 ***	0.05	12.7
Grain yield	0.44	0.013 *	1.603e-14 ***	1.80	6.1
Thousand kernel weight	0.38	0.36	5.36e-09 ***	0.33	5.5

** = Highly Significant (P <0.01); * = Significant (P<0.05), and NS=Non-Significant (P>0.05); Rep=Replication; DF=Degree Freedom; CV=Coefficient of Variation.

4.2.2. Mean comparison of barley shoot fly damage parameters

The mean performances of 64 barley genotypes for shoot fly damage parameters evaluated are presented in Appendix Table 3 and Table 7. The barley shoot fly damage parameters were highly significantly different (p = 0.001) among the 64 barley genotypes evaluated (Appendix 3). The genotype mean values for shoot fly oviposition, infestation, dead heart, and crop recovery ranged from 14.06 (T11) to 62.46 (T376), 15.90 (T467) to 91.31 (HB-42), 11.86 (T369) to 81.09 (T376), and 0.63 (90) to 4.78 (T281), respectively. Among the evaluated barley genotypes, the five lowest mean shoot fly oviposition, percentage of infestation, dead heart percentage, and highest crop recovery scale were recorded on T11, T464, T506, T62, and T123 genotypes with the values 14.06, 19.72, 16.32, and 4.12; 16.35, 15.90, 14.97, and 4.01; 16.51, 18.71, 15.78, and 4.00; 17.44, 18.76, 16.99, and 4.78; 18.42, 25.18, 19.12, and

4.00, respectively. Likewise, the five highest shoot fly with oviposition, infestation, dead heart, and lowest crop recovery recorded were T376, 21, 11, 2, and 66 barley genotypes with the values of 62.46, 87.63, 81.09, and 0.75; 61.63, 89.19, 80.07, and 2.50; 61.26, 80.01, 65.20, and 3.10; 60.76, 90.61, 79.74, and 1.74; 60.01, 83.50, 76.84, and 2.00, respectively. These results show that there is variation in barley genotypes for barley shoot fly with oviposition, infestation percentage, dead heart percentage, and crop recovery scoring scale. This finding is in line with the previous report of Allo et al. (2020). The genotypes with the lowest number of oviposited, percentage of infestation, dead heart percentage, and highest crop recovery are important traits of barley shoot fly resistance genotypes (Tafa and Bayeh, 2011; Yogeswari *et al*., 2019; Allo *et al*., 2020).

4.2.3. Morphological traits of barley genotypes associated to *Delia flavibasis*

The mean performances of 64 barley genotypes for morphological traits evaluated at SARC in 2023/24 are presented in Appendix 4 and Table 8. Seedling vigor, leaf glossiness, seedling color, first leaf width, second leaf width, seedling stem length, and seedling stem thickness were highly significant differences ($p<0.001$) among the genotypes evaluated (Appendix 4, Table 8).

Seedling vigor and leaf glossiness

The genotypes T11, T123, T524, T249, and T90 exhibited the highest seedling vigor, while genotypes 168, 11, 17, HB-42, and 90 showed the lowest seedling vigor in the current study. This might be due to resistance genotypes have longer internodes, longer stems, and faster initial plant growth. As a result, the first instar larvae are delayed in reaching the growing tip due to the quick growth of barley seedlings and decreasing the probability of dead heart formation. The present investigation are similar with previous results of Satish *et al*. (2009); Gorthy *et al*. (2017); Abinaya *et al*. (2019); Allo *et al*., 2020.

Similarly, T249, 6, Aruso, T24, and T575 displayed the highest leaf glossiness, whereas 2, HB-42, T258, 168, and 12 exhibited the lowest leaf glossiness. This is also might be due to the glossy leaves have high light reflected from leaves and influences the orientation of shoot flies toward their host plants, reducing the oviposition, reduce infestation percent, and reduce dead heart percentages. This result is aligning with the earlier findings of Sharma, 1993; Kiranmayee *et al*. (2016). Significantly, higher leaf

In general, the result of the current study indicates that, there is a negative association between barley shoot damage parameters and seedling vigor and leaf glossiness. This might be due to the fact that high leaf glossiness and seedling vigor was decrease oviposition, infestation, and dead heart. This result is in agreement with the findings of Abinaya *et al*. (2019), who reported that genotypes that have a low oviposition, infestation, and dead heart percentage exhibit high seedling vigor and leaf glossiness. This suggests that genotypes with lower barley shoot fly resistance component parameters and high leaf glossiness and seedling vigor are resistant barley genotypes.

Seedling Color

Among the evaluated barley genotypes, most of the seedling colors for resistant, moderate, and susceptible genotypes were light green, medium green, and dark green, respectively. This might be due to influencing the behavior and preferences of insects, and through releasing chemical defenses. That means, the high green brightness have been low ovipositional preferences by barley shoot fly than other colors. While the dark green colors have been high moisture content and preferred by shoot fly than others. In addition, many of the green plants release tannin chemicals; which is used to detect insect herbivores. In this study the tannin concentration might be different based on their capacity of green. This result is similar to the previous finding in the main bona season report (Tafa, 2003). Therefore, this result shows that seedling color can indeed play a key role in attracting or deterring shoot fly in barley genotypes.

The leaf width

T364, T11, T506, T62, and T45 were the top five resistant barley genotypes, based on the results of the first leaf width and second leaf width, with values of 0.51 cm, 0.52 cm, 0.50 cm, 0.52 cm, and 0.54 cm, and 0.34 cm, 0.38 cm, 0.35 cm, 0.36 cm, and 0.37 cm, respectively. Similarly, the top five susceptible barley genotypes screened were 66, 19, 17, 90, and 21 for both first and second leaf width, with values of 1.02 cm, 1.01 cm, 1.02 cm, 0.99 cm, and 0.99 cm, and 0.94 cm, 0.93 cm, 0.93 cm, 0.94 cm, and 0.93 cm, respectively (Table 8). The results observed for leaf width were similar to the results in previous studies (Kiranmayee *et al*., 2016; Allo *et al*., 2020). This result confirms that wider leaves are more susceptible than narrower leaves to barley shoot fly. This could be due to the lack of moisture content on the

narrower leaves and upright leaves of barley genotypes being associated with reduced shoot fly infestation, making it more difficult for the shoot fly to lay eggs and for the larvae to feed on the plant tissues.

Seedling stems length

The tallest and shortest seedling stem lengths were recorded for the T281 and 24 genotypes, with mean values of 7.01 cm and 3.39 cm, respectively (Table 8). In the current study, a taller seedling stem length was found to reduce barley shoot fly infestation. This result is consistent with the previous findings of Patil and Bagde (2017), who reported that entries with greater seedling height were observed to be less susceptible to shoot fly infestation than those with lower seedling height. Similar results were also reported by Nadeem *et al*. (2005); Balikai (2011). This is because the insect lays its eggs mainly under the seedling; when it turns into a larva, it leaves the ground and climbs the plant, entering the plant through the apical meristem, by the head. During this time, various events, such as rain, wind, and other factors, prevent it from entering the apical meristem because the longer the stem length, the longer it takes to enter the plant. Therefore, seedling stem length can also play a key role in controlling barley shoot infestation.

4.2.4. Agronomic traits of barley genotypes

The mean performances of 64 barley genotypes for various agronomic traits, such as days to 50% heading, days to 90% maturity, plant height, total tiller, productive tiller, spike length, seed per spike, biomass yield, grain yield, and thousand kernel weights, exhibited highly significant differences ($p<0.001$) among the evaluated genotypes. These results are detailed in Appendix Table 5 and Table 9.

Days to 50 % heading

The study revealed highly significant differences ($P<0.001$) in days to 50% heading among the genotypes, as documented in Appendix 5. The range for days to 50% heading was from 61.00 to 78.00 days, with a mean value of 70.11 days (Table 9). The values observed for days to 50% heading in the current study were found to be similar to those reported in previous studies (Chamarthi, 2008; Allo *et al*., 2020). The lowest and highest mean days to 50 %

heading were observed for Dinsho and T45, in the resistant and susceptible barley genotypes, with values of 61.56 days and 76.12 days, respectively (Table 9). This indicates that resistant genotypes flowered early; while susceptible barley genotypes took more days. This is because, barley genotypes affected by barley shoot fly, replace themselves by tillering itself, may increase the days to 50% flowering.

Days to 90% maturity

Days to 90% maturity ranged from 105.00 days to 131.00 days with a mean value of 114.60 days (Table 9). The results showed that the barley shoot fly susceptible genotypes like HB-42, 4, T451, T519, and T45 were significantly higher number of days than all other varieties to reach physiological maturity. On the other hand, genotypes T90, T123, 6, Aruso and T575 were significantly lower number of days than all other varieties to reach physiological maturity (Table 9). The present result showed a wide range of variations for days to maturity. The results in the current study are in line with the previous findings (Mohammed *et al., 2018;* Allo *et al*., 2020). This might be associated with the shorter days to 90 % maturity among evaluated genotypes, resulting lowest infestation percentage and highest grain yield. Therefore, breeders have managed to reduce the time of maturity by selecting early cultivars in order to develop shoot fly resistance genotypes.

Plant height

Most of the resistant genotypes produced significantly taller plants than susceptible genotypes. This result is in line with the findings of Chamarthi (2008); Satish *et al*. (2009), who reported that shoot fly resistance lines have rapid initial plant growth. Hence, plant height can play a key role in reducing the impact of barley shoot fly infestation. Therefore, by maintaining taller genotypes through appropriate cultivation practices or using barley varieties that naturally have long heights, researchers and farmers can help reduce the risk of barley shoot fly infestation.

Spike Length

In the present study, most of the susceptible genotypes produced shorter spikes than the resistance genotypes. The current result is consistent with the findings of Mengesha *et al*. (1990) who reported that the susceptible millet genotype to ergot was shorter spikes than the

resistance genotypes. The differences in the spike length by the barley genotypes could be attributed to shoot fly infestation. This shows that evaluated barley genotypes responded differently to the infestation level in terms of spike length.

Seed per kernel

Seeds per spike ranged from 21.53 to 69.80 numbers with a mean value of 43.41 numbers (Table 9). The genotypes showed a wide range of variation for seed per kernel. Number of kernels spike^{-1} increased with decreasing infestation percentage of barley shoot fly.

Total tillers and productive tillers

Analysis of variance showed significant results ($P < 0.001$) indicating differences in the numbers of total tillers and productive tillers (Appendix Table 5). In the current study, it was observed that most susceptible genotypes produced a higher number of total tillers and fertile tillers compared to the resistant genotypes. This may be attributed to the presence or absence of rainfall. If the affected plants by barley shoot fly, receive sufficient rainfall or moisture, the susceptible barley genotypes show a significant increase in the number of tillers. That means if there enough rainfall, there is high tiller; but if not, it can damaged 100%. Therefore, the tiller capacity of susceptible barley genotypes is positively associated with rainfall (Tafa 2003). This finding is also consistent with Abinaya *et al*. (2019), who reported that the number of tillers is higher in plants with high shoot fly infestation. However, in comparison to resistant genotypes, susceptible genotypes produced lower values for other agronomic parameters related to yield. Therefore, it's important to develop barley genotypes resistance to barley shoot fly with low moisture percentages.

Biological yield

Biomass yield ranged from 0.50 to 2.50 kg per plot with a mean value of 1.33 kg per plot (Table 6). A decreasing infestation percentage resulted in higher biomass production for most barley genotypes. The major genotypes with higher biomass yield were T506, T524, T464, T467, T11, T369, T575, T281, and T249. On the other hand, genotypes 161, 90, 66, 96, 150, 51, T301, T45, and T268 had lower mean values of biomass yield (Table 9). These results indicate that the shoot fly damage parameters were negatively associated with biomass

production. This result is in agreement with the findings of Reddy et *al*., 2012; Arora *et al*., 2021.

Grain yield

The analysis of variance indicated a highly significant difference ($P < 0.001$) among genotypes evaluated in grain yield (Appendix Table 5 and Table 9). The grain yield ranged from 91.75(161) to 192.50(T281) grams per plot, with a mean value of 138.86 grams per plot (Table 9). Among the evaluated barley genotypes, T281, 157, T576, T90, and T524 were the top five in grain yields, with values of 189.57, 178.05, 176.61, 175.13, and 171.70 grams per plot, respectively. On the other hand, 161, HB-42, 66, 167, and 105, with average values of 91.75, 93.40, 104.99, 113.64, and 115.68 grams per plot, were the five genotypes with the lowest grain yields (Table 9).

In the present study, resistant genotypes showed the highest grain yield, while susceptible ones showed the lowest grain yield. This result is in agreement with the findings of Tafa (2003); Mulatu *et al*. (2011), who reported that the resistant genotypes produced a significantly higher, yield. This confirms that the highest grain yield of the barley genotype is mainly due to the lowest shoot fly damage parameters.

Thousand Kernel weight (TKW)

The analysis of variance showed that the genotypes differed significantly ($P < 0.001$) in thousand kernel weight (Appendix Table 5). The average number of thousand kernel weight ranged from 29.10(HB-42) grams to 50.80(T281) grams, with a mean value of 37.78 grams (Table 6). The results of the study showed that there is genetic variation among the tested genotypes concerning the thousand kernel weight. This result is in agreement with the findings of Rachon (2002).

Table 7. Mean performance of 64 barley genotypes for shoot fly resistance component parameters and crop recovery evaluated at SARC in 2023/24

Entry	Eggs 10 Seedling^{-1}	Infestation (%)	Dead Heart (%)	Crop Recovery(1-5)
T11	14.06 ^{u}	19.72 $^{p-u}$	16.32 $^{p-q}$	4.12 $^{a-c}$
T123	18.42 $^{r-u}$	25.18 $^{n-u}$	19.12 $^{o-q}$	4.00 $^{a-d}$
1	53.20 $^{a-h}$	73.62 $^{a-i}$	62.25 $^{a-j}$	3.01 $^{b-g}$
T208	20.85 $^{o-u}$	24.83 $^{n-u}$	18.00 $^{p-q}$	3.89 $^{a-d}$
2	60.76 $^{a-c}$	90.61 ^{a}	79.74 $^{a-c}$	1.74 $^{g-j}$
T213	34.46^{j-p}	47.25 $^{i-o}$	31.83 $^{l-q}$	3.99 $^{a-d}$
3	49.85 $^{a-j}$	58.54 $^{e-l}$	47.42 $^{g-n}$	3.76 $^{a-e}$
T24	40.36 $^{h-n}$	53.76 $^{h-m}$	14.41 $^{p-q}$	2.25 $^{e-i}$
4	52.91 $^{a-h}$	83.05 $^{a-f}$	62.20 $^{a-j}$	2.99 $^{b-g}$
T249	19.09 $^{p-u}$	16.86 $^{t-u}$	48.55 $^{e-m}$	3.99 $^{a-d}$
T258	44.91 $^{d-l}$	63.08 $^{b-k}$	49.81 $^{d-m}$	3.24 $^{a-g}$
5	52.25 $^{a-h}$	81.18 $^{a-g}$	68.96 $^{a-g}$	2.00 $^{f-j}$
6	25.61 $^{n-u}$	18.54 $^{q-u}$	15.72 $^{p-q}$	4.00 $^{a-d}$
T268	53.81 $^{a-h}$	76.74 $^{a-h}$	62.47 $^{a-j}$	1.75 $^{g-j}$
Aruso	23.00 $^{o-u}$	16.24 ^{u}	14.74 $^{p-q}$	4.00 $^{a-d}$
T281	17.99 $^{r-u}$	20.59 $^{o-u}$	16.90 $^{p-q}$	4.78 ^{a}
12	52.46 $^{a-h}$	73.75 $^{a-i}$	59.54 $^{a-k}$	3.25 $^{a-g}$
T295	49.81 $^{a-j}$	78.91 $^{a-h}$	67.32 $^{a-h}$	2.75 $^{c-g}$
15	42.66 $^{f-l}$	57.46 $^{f-l}$	47.90 $^{f-n}$	2.88 $^{b-g}$
T30	32.49 $^{k-r}$	34.333 $^{l-u}$	27.56 $^{m-q}$	3.26 $^{a-g}$
T301	34.18 $^{j-q}$	45.55 $^{j-q}$	34.28 $^{k-q}$	3.10 $^{b-g}$
17	56.51 $^{a-g}$	85.19 $^{a-e}$	74.70 $^{a-f}$	2.75 $^{c-g}$
T364	35.93 $^{i-o}$	44.44 $^{k-r}$	31.20 $^{l-q}$	3.51 $^{a-f}$
19	54.54 $^{a-h}$	72.05 $^{a-j}$	63.08 $^{a-j}$	2.75 $^{c-g}$
T369	20.56 $^{o-u}$	16.97 $^{s-u}$	11.86 ^{q}	4.38 $^{a-b}$
20	32.19 $^{k-s}$	43.96 $^{k-s}$	38.57 $^{i-q}$	3.25 $^{a-g}$
T372	20.64 $^{o-u}$	25.54 $^{n-u}$	18.42 $^{p-q}$	3.99 $^{a-d}$
21	61.63 $^{a-b}$	89.19 $^{a-b}$	80.07^{a-b}	2.50 $^{d-h}$
T376	62.46 ^{a}	87.63 $^{a-c}$	81.09 ^{a}	0.75 $^{i-j}$
HB-42	52.09 $^{a-h}$	91.31 ^{a}	80.14 $^{a-b}$	2.74 $^{c-g}$
T401	26.72 $^{m-u}$	28.31 $^{m-u}$	20.68 $^{n-q}$	3.50 $^{a-f}$
T45	40.17 $^{h-n}$	55.28 $^{g-m}$	47.29 $^{g-n}$	2.76 $^{c-g}$
29	30.88 $^{l-t}$	43.81 $^{k-t}$	32.69 $^{k-q}$	3.74 $^{a-e}$
T451	52.96 $^{a-h}$	66.09 $^{a-k}$	50.82 $^{d-m}$	3.38 $^{a-f}$
51	58.47 $^{a-e}$	85.81 $^{a-d}$	74.94 $^{a-f}$	0.87 $^{i-j}$
T464	18.76 $^{q-u}$	18.28 $^{r-u}$	16.80 $^{p-q}$	3.90 $^{a-d}$
55	53.04 $^{a-h}$	79.95 $^{a-h}$	70.21 $^{a-g}$	2.16 $^{f-i}$
T467	16.35 $^{t-u}$	15.90 ^{u}	14.97 $^{p-q}$	4.01^{a-d}
59	57.40 $^{a-f}$	84.24 $^{a-f}$	76.38 $^{a-d}$	1.74^{g-j}
T506	16.51 $^{s-u}$	18.71 $^{q-u}$	15.78 $^{p-q}$	4.00 $^{a-d}$
66	60.01 $^{a-d}$	83.50 $^{a-f}$	76.84 $^{a-d}$	2.00 $^{f-j}$
90	50.28 $^{a-i}$	79.54 $^{a-h}$	67.59 $^{a-h}$	0.63 ^{j}
96	42.98 $^{e-l}$	68.19 $^{a-k}$	46.14 $^{g-o}$	2.50 $^{d-h}$

T519	41.34 g-m	60.17 d-l	46.88 g-n	2.90 b-g
Dinsho	24.19 o-u	18.37 r-u	16.98 p-q	3.75 a-e
105	53.93 a-h	78.93 a-h	64.60 a-j	2.49 d-h
T524	19.82 p-u	19.65 p-u	18.01 p-q	4.00 a-d
T562	32.50 k-r	46.28 j-p	33.72 k-q	3.37 a-f
113	45.39 c-l	57.68 f-l	50.79 d-m	3.26 a-g
114	46.38 b-l	64.66 a-k	52.98 b-m	1.06 h-j
139	47.57 a-k	62.74 b-k	52.78 c-m	2.75 c-g
150	40.96 g-n	49.66 i-n	38.140 i-q	3.10 b-g
T575	19.11 p-u	19.06 q-u	16.96 p-q	4.01 a-d
157	40.72 h-n	48.21 i-n	37.96 j-q	3.38 a-f
161	52.88 a-h	78.05 a-h	68.42 a-h	1.18 h-j
Moata	47.38 a-k	62.20 c-k	41.28 h-p	3.01 b-g
168	50.26 a-i	83.66 a-f	75.53 a-e	2.25 e-i
T576	24.24 o-u	26.58 n-u	16.58 p-q	3.24 a-g
11	61.26 a-b	80.01 a-h	65.20 a-i	3.10 b-g
100	57.60 a-f	84.35 a-f	74.50 a-f	2.75 c-g
T62	17.44 r-u	18.76 q-u	16.99 p-q	3.99 a-d
24	53.25 a-h	73.80 a-i	62.70 a-j	3.12 b-g
167	42.83 e-l	69.32 a-k	55.54 a-l	2.25 e-i
T90	21.65 o-u	19.55 p-u	16.36 p-q	3.99 a-d
Mean	39.92	54.15	44.97	3.02
CV (%)	19.1	24.2	29.7	25.1

a, b, c,….u means with different letters in a row are significantly different; CV(%)=Coefficient of Variation

Table 8. Mean performance of 64 barley genotypes for morphological traits

Entry	SV	LG	SC	FLW	SLW	SSL	SST
T11	5.02 ^{a}	4.49 $^{a-b}$	3.03 ^{a}	0.52 $^{o-q}$	0.38 $^{q-u}$	6.46 $^{a-e}$	0.60 $^{i-m}$
T123	5.01^{a}	3.99 $^{a-d}$	3.01 ^{a}	0.62 $^{k-q}$	0.43 $^{o-r}$	6.30 $^{a-e}$	0.56 $^{k-m}$
1	1.98 $^{e-g}$	2.01 $^{h-j}$	0.99 ^{d}	0.95 ^{a}	0.63 $^{a-f}$	3.91 $^{o-u}$	0.89 $^{a-b}$
T208	3.01^{c-e}	2.98 $^{d-h}$	2.01 $^{b-c}$	0.54 $^{o-q}$	0.43 $^{o-r}$	6.11 $^{a-g}$	0.63 $^{h-m}$
2	1.51 $^{f-g}$	0.98 ^{j}	1.00 ^{d}	0.79 $^{b-i}$	0.58 $^{f-j}$	4.65 $^{k-p}$	0.79 $^{a-h}$
T213	2.50 $^{d-f}$	2.00 $^{h-j}$	1.00 ^{d}	0.82 $^{a-i}$	0.51 $^{k-n}$	4.49 $^{k-s}$	0.81 $^{a-e}$
3	2.00 $^{e-g}$	3.73 $^{b-e}$	1.49 $^{c-d}$	0.92 $^{a-b}$	0.63 $^{a-f}$	3.51 $^{t-u}$	0.87 $^{a-c}$
T24	2.50 $^{d-f}$	2.24 $^{g-i}$	1.51 $^{c-d}$	0.61 $^{k-q}$	0.40 $^{p-t}$	6.20 $^{a-f}$	0.59 $^{j-m}$
4	2.01 $^{e-g}$	2.99 $^{d-h}$	1.51 $^{c-d}$	0.89 $^{a-d}$	0.61 $^{a-g}$	3.99 $^{o-u}$	0.78 $^{a-h}$
T249	5.01 ^{a}	5.01 ^{a}	3.02 ^{a}	0.52 $^{o-q}$	0.39 $^{q-u}$	6.68 $^{a-d}$	0.50 ^{m}
T258	1.53 $^{f-g}$	1.48 $^{i-j}$	1.02 ^{d}	0.84 $^{a-h}$	0.53 $^{j-m}$	4.06 $^{n-u}$	0.87 $^{a-c}$
5	1.99 $^{e-g}$	1.97 $^{h-j}$	0.97 ^{d}	0.77 $^{d-i}$	0.54 $^{h-k}$	3.66 $^{q-u}$	0.68 $^{e-l}$
6	4.5 $^{a-b}$	5.02 ^{a}	2.97 ^{a}	0.58 $^{o-q}$	0.42 $^{o-r}$	6.24 $^{a-f}$	0.56 $^{k-m}$
T268	2.51 $^{d-f}$	1.49 $^{i-j}$	1.49 $^{c-d}$	0.91 $^{a-c}$	0.65 $^{a-b}$	3.94 $^{o-u}$	0.92 ^{a}
Aruso	4.99 ^{a}	5.02 ^{a}	3.00 ^{a}	0.59 $^{m-q}$	0.42 $^{o-r}$	6.40 $^{a-e}$	0.57 $^{j-m}$
T281	4.5 $^{a-b}$	4.52 $^{a-b}$	2.49 $^{a-b}$	0.51 $^{p-q}$	0.40 $^{p-t}$	7.01 ^{a}	0.53 $^{l-m}$
12	2.01 $^{e-g}$	1.49 $^{i-j}$	1.02 ^{d}	0.93 ^{a}	0.66 ^{a}	4.01 $^{o-u}$	0.88 $^{a-b}$
T295	2.5 $^{d-f}$	3.27 $^{c-g}$	0.99 ^{d}	0.90 $^{a-d}$	0.60 $^{b-i}$	4.02 $^{o-u}$	0.78 $^{a-h}$
15	2 $^{e-g}$	2.49 $^{f-i}$	1.03 ^{d}	0.90 $^{a-e}$	0.65 $^{a-c}$	3.77 $^{p-u}$	0.86 $^{a-c}$
T30	3.98 $^{a-c}$	3.00 $^{d-h}$	2.01 $^{b-c}$	0.63 $^{k-p}$	0.40 $^{p-t}$	5.91 $^{c-h}$	0.58 $^{j-m}$
T301	2.51 $^{d-f}$	2.50 $^{f-i}$	0.99 ^{d}	0.52 $^{o-q}$	0.47 $^{m-o}$	5.80 $^{d-i}$	0.51 ^{m}
17	1.50 $^{f-g}$	1.99 $^{h-j}$	1.02 ^{d}	0.93 ^{a}	0.62 $^{a-f}$	3.95 $^{o-u}$	0.88 $^{a-c}$
T364	2.48 $^{d-f}$	4.25 $^{a-c}$	3.01 ^{a}	0.51 $^{p-q}$	0.34 ^{u}	6.26 $^{a-f}$	0.51 ^{m}
19	1.98 $^{e-g}$	2.01 $^{h-j}$	1.01^{d}	0.93 ^{a}	0.63 $^{a-f}$	3.82 $^{p-u}$	0.87 $^{a-c}$
T369	4.98 ^{a}	4.50 $^{a-b}$	3.00 ^{a}	0.60 $^{l-q}$	0.40 $^{p-t}$	6.12 $^{a-g}$	0.61 $^{i-m}$
20	3.00 $^{c-e}$	2.51 $^{f-i}$	0.99 ^{d}	0.64 $^{j-o}$	0.44 $^{o-q}$	5.37 $^{f-k}$	0.54 $^{l-m}$
T372	3.00 $^{c-e}$	3.02 $^{d-h}$	1.47 $^{c-d}$	0.58 $^{n-q}$	0.46 $^{n-p}$	6.41 $^{a-e}$	0.53 $^{l-m}$
21	1.51 $^{f-g}$	1.49 $^{i-j}$	0.99 ^{d}	0.93 ^{a}	0.62 $^{a-f}$	4.50 $^{k-r}$	0.84 $^{a-e}$
T376	1.51 $^{f-g}$	1.49 $^{i-j}$	1.02 ^{d}	0.90 $^{a-d}$	0.62 $^{a-f}$	4.01 $^{o-u}$	0.82 $^{a-e}$
HB-42	1.50 $^{f-g}$	1.00 ^{j}	0.98 ^{d}	0.89 $^{a-e}$	0.43 $^{o-r}$	3.67 $^{q-u}$	0.80 $^{a-g}$
T401	3.51 $^{b-d}$	4.00 $^{a-d}$	2.50 $^{a-b}$	0.55 $^{o-q}$	0.42 $^{o-r}$	6.86 $^{a-b}$	0.50 ^{m}
T45	2.99 $^{c-e}$	3.50 $^{b-f}$	1.52 $^{c-d}$	0.54 $^{o-q}$	0.37 $^{r-u}$	6.93 ^{a}	0.57 $^{j-m}$
29	3.51 $^{b-d}$	2.50 $^{f-i}$	1.50 ^{cd}	0.72 $^{g-l}$	0.55 $^{g-k}$	5.22 $^{g-l}$	0.69 $^{d-l}$
T451	1.99 $^{e-g}$	3.52 $^{b-f}$	0.99 ^{d}	0.79 $^{c-i}$	0.55 $^{h-k}$	5.04 $^{h-m}$	0.79 $^{a-g}$
51	1.51 $^{f-g}$	2.01 $^{h-j}$	1.01 ^{d}	0.85 $^{a-g}$	0.66 ^{a}	4.32 $^{l-t}$	0.80 $^{a-g}$

T464	4.99 ^{a}	4.99 ^{a}	2.98 ^{a}	0.63 $^{k-p}$	0.41 $^{p-s}$	6.90 ^{a}	0.59 $^{j-m}$
55	0.98 ^{g}	2.51 $^{f-i}$	1.00 ^{d}	0.94 ^{a}	0.58 $^{d-j}$	4.15 $^{m-u}$	0.84 $^{a-e}$
T467	4.98 ^{a}	4.51 $^{a-b}$	2.99 ^{a}	0.61 $^{k-q}$	0.41 $^{p-s}$	6.78 $^{a-c}$	0.58 $^{j-m}$
59	2.51 $^{d-f}$	1.99 $^{h-j}$	0.99 ^{d}	0.90 $^{a-c}$	0.59 $^{b-i}$	3.75 $^{p-u}$	0.76 $^{a-i}$
T506	3.98 $^{a-c}$	4.99 ^{a}	3.00 ^{a}	0.50 ^{q}	0.35 $^{s-u}$	6.28 $^{a-f}$	0.56 $^{k-m}$
66	2.02 $^{e-g}$	1.99 $^{h-j}$	1.02 ^{d}	0.94 ^{a}	0.63 $^{a-f}$	3.57 $^{s-u}$	0.73 $^{b-j}$
90	1.50 $^{f-g}$	1.50 $^{i-j}$	0.99 ^{d}	0.94 ^{a}	0.62 $^{a-f}$	3.69 $^{q-u}$	0.89 $^{a-b}$
96	2.00 $^{e-g}$	2.75 $^{e-h}$	1.018 ^{d}	0.89 $^{a-e}$	0.63 $^{a-f}$	4.07 $^{n-u}$	0.80 $^{a-f}$
T519	2.51 $^{d-f}$	2.48 $^{f-i}$	1.50 $^{c-d}$	0.76 $^{e-j}$	0.54 $^{i-m}$	5.18 $^{h-l}$	0.77 $^{a-i}$
Dinsho	4.99 ^{a}	4.97 ^{a}	2.98 ^{a}	0.51 $^{p-q}$	0.63 $^{a-f}$	6.77 $^{a-c}$	0.58 $^{j-m}$
105	2.50 $^{d-f}$	2.25 $^{g-i}$	1.00 ^{d}	0.90 $^{a-c}$	0.64 $^{a-e}$	4.01 $^{o-u}$	0.88 $^{a-c}$
T524	5.01 ^{a}	4.99 ^{a}	3.00 ^{a}	0.56 $^{o-q}$	0.34 $^{t-u}$	6.32 $^{a-e}$	0.54 $^{l-m}$
T562	2.53 $^{d-f}$	3.49 $^{b-f}$	2.53 $^{a-b}$	0.60 $^{l-q}$	0.41 $^{p-s}$	6.92 ^{a}	0.53 $^{l-m}$
113	1.98 $^{e-g}$	1.51 $^{i-j}$	1.00 ^{d}	0.86 $^{a-f}$	0.54 $^{i-k}$	3.98 $^{o-u}$	0.84 $^{a-e}$
114	2.48 $^{d-f}$	2.01 $^{h-j}$	0.99 ^{d}	0.93 ^{a}	0.55 $^{h-k}$	4.48 $^{k-s}$	0.92 ^{a}
139	2.01 $^{e-g}$	2.99 $^{d-h}$	2.02 $^{b-c}$	0.71 $^{i-n}$	0.48 $^{m-o}$	5.95 $^{b-h}$	0.71 $^{c-k}$
150	2.50 $^{d-f}$	3.02 $^{d-h}$	0.97 ^{d}	0.83 $^{a-i}$	0.48 $^{l-o}$	4.52 $^{k-r}$	0.77 $^{a-i}$
T575	4.98 ^{a}	4.99 ^{a}	3.02 ^{a}	0.55 $^{o-q}$	0.41 $^{p-s}$	6.13 $^{a-g}$	0.58 $^{j-m}$
157	3.49 $^{b-d}$	2.99 $^{d-h}$	1.97 $^{b-c}$	0.71 $^{h-m}$	0.42 $^{o-r}$	4.79 $^{j-o}$	0.64 $^{g-m}$
161	1.98 $^{e-g}$	2.51 $^{f-i}$	0.99 ^{d}	0.89 $^{a-c}$	0.54 $^{i-l}$	3.93 $^{o-u}$	0.85 $^{a-d}$
Moata	2.48 $^{d-f}$	2.51 $^{f-i}$	0.99 ^{d}	0.90 $^{a-c}$	0.59 $^{d-j}$	4.93 $^{i-n}$	0.86 $^{a-c}$
168	1.50 $^{f-g}$	1.49 $^{i-j}$	0.98^{d}	0.85 $^{a-f}$	0.59 $^{c-j}$	4.00 $^{o-u}$	0.76 $^{a-i}$
T576	2.52 $^{d-f}$	3.01 $^{d-h}$	2.00 $^{b-c}$	0.73 $^{f-k}$	0.44 $^{o-q}$	5.63 $^{e-j}$	0.64 $^{f-m}$
11	1.50 $^{f-g}$	1.99 $^{h-j}$	0.98 ^{d}	0.92 $^{a-b}$	0.65 $^{a-d}$	3.60 $^{r-u}$	0.83 $^{a-e}$
100	2.99 $^{c-e}$	2.76 $^{e-h}$	1.01 ^{d}	0.87 $^{a-e}$	0.51 $^{k-n}$	4.57 $^{k-q}$	0.82 $^{a-e}$
T62	3.49 $^{b-d}$	3.50 $^{b-f}$	2.50 $^{a-b}$	0.52 $^{o-q}$	0.36 $^{s-u}$	6.82 $^{a-c}$	0.50 ^{m}
24	2.01 $^{e-g}$	2.51 $^{f-i}$	1.49 $^{c-d}$	0.95 ^{a}	0.61 $^{a-h}$	3.39 ^{u}	0.88 $^{a-b}$
167	1.99 $^{e-g}$	2.49 $^{f-i}$	1.00 ^{d}	0.89 $^{a-e}$	0.58 $^{e-j}$	4.01 $^{o-u}$	0.86 $^{a-c}$
T90	5.00 a	4.52 $^{a-b}$	2.98 ^{a}	0.58 $^{o-q}$	0.42 $^{o-r}$	6.45 $^{a-e}$	0.51 ^{m}
Mean	2.84	2.95	1.68	0.75	0.51	5.08	0.71
CV (%)	24.9	19.9	19.4	8.3	5.7	8.8	11.6

a, b, c,….u means with different letters in a row are significantly different; CV(%)=Coefficient of Variation; SV=Seedling Vigor; LG=Leaf Glossiness; SC=Seedling Color; FLW=First Leaf Width; SLW=Second Leaf Width; SSL=Seedling Stem Length; SST=Seedling Stem Thickness

Table 9. Mean performance of 64 barley genotypes for agronomic traits

Entry	DTH	DTM	PH	TT	PT	SL	SPS	BM	GY	TKW
T11	65.95 p-s	110.51 n-v	113.03 a-f	6.17 k-t	4.97 m-v	9.38 a-e	56.05 a-f	2.20 ab	150.00 f-m	43.30 b
T123	63.27 rst	106.21 v	110.62 a-g	6.56 g-q	5.46 i-s	9.56 a-d	56.04 a-f	1.93 b-e	134.12 j-v	39.88 b-j
1	69.64 g-p	114.76 g-q	99.46 d-q	6.84 e-n	5.97 e-n	5.58 u-x	44.60 e-s	0.80 p-s	135.20 j-u	38.04 d-o
T208	74.24 a-e	116.74 e-m	102.87 b-n	3.29 z	3.08 A	9.22 a-g	42.75 h-u	1.44 g-l	151.81 f-j	38.12 c-o
2	72.39 a-m	114.37 g-r	77.71 xyzAB	7.35 c-i	7.05def	5.88 s-x	42.96 h-t	0.80 p-s	139.43 h-r	37.80 d-p
T213	72.55 a-l	116.07 f-o	91.11 l-z	7.68 c-g	6.11 e-m	7.91 e-p	36.44 m-w	1.50 f-k	137.20 i-t	38.72 c-n
3	69.44 h-p	110.23 o-v	94.09 i-v	9.25 ab	6.04 e-n	7.63 h-r	37.88 l-w	1.50 f-k	151.04 f-k	39.53b-k
T24	70.73 c-n	119.52 d-g	108.67 a-i	4.92 vwx	4.46 q-z	7.76 f-r	54.77 a-h	1.01 n-q	133.75 j-w	36.44f-s
4	72.62 a-l	130.10 a	93.05 j-w	9.50 a	6.75 d-h	7.43 i-s	30.23 uvw	1.20 k-o	130.93 n-x	36.25h-s
T249	61.81 t	108.39 s-v	95.04 h-t	7.31 c-k	3.84 v-zA	9.91 ab	31.63 t-w	2.00 bcd	150.54 f-k	40.52 b-g
T258	69.22 j-p	116.42 f-n	86.86 o-z	7.17 d-l	6.38 e-j	5.60 t-x	42.99 g-t	1.00 n-q	132.39 l-w	36.34 g-s
5	74.49 a-d	115.81 g-o	92.26 k-x	6.72 f-p	6.32 e-k	7.85 e-p	35.76 n-w	0.90 o-r	121.42 r-y	34.13o-t
6	62.98 r-t	107.54 u-v	114.30 a-d	5.63 o-w	4.58 q-y	9.73 ab	57.12 a-d	2.00 bcd	143.48 g-q	39.86 b-j
T268	72.32 a-m	113.94 g-s	77.44 yzAB	6.93 e-n	5.66 g-q	6.12 r-w	32.22 r-w	0.80 p-s	122.97 r-y	33.78 p-t
Aruso	62.85 r-t	107.83 u-v	101.68 b-o	5.60 p-w	5.22 i-t	9.81 ab	61.33 ab	1.80 c-f	159.17 c-g	39.94 b-i
T281	71.92 b-m	110.30 o-v	110.62 a-g	4.98 uvw	4.23 s-zA	8.74 a-k	56.91 a-e	2.10 bc	189.57 a	50.59 a
12	69.07 k-q	119.11 d-g	89.66 m-z	9.20 ab	8.66 ab	8.35 b-n	42.77 h-u	1.40 h-m	149.08 f-n	39.17 b-n
T295	73.09 a-j	115.46 g-p	83.95 r-A	7.64 c-h	5.82 f-p	6.80 n-v	31.75 t-w	0.90 o-r	116.63 v-y	36.51 f-s
15	70.07 f-o	117.25 e-l	83.65 s-zA	8.2-2 bcd	5.40 i-s	7.19 k-t	32.69 q-w	1.30 i-n	130.31 o-x	37.52 d-p
T30	68.92 l-q	116.87 e-m	97.98 f-t	9.21 ab	5.88 f-o	8.15 c-o	41.66 i-u	1.40 h-m	154.22 e-i	39.81 b-j
T301	70.73 c-n	121.83 c-f	94.44 i-u	6.18 j-t	5.29 i-s	6.34 p-w	38.53 l-w	0.70 qrs	124.59 r-x	33.79 p-t
17	73.46 a-g	116.38 f-n	79.01 v-zAB	9.41 ab	7.62 bcd	8.41 a-m	50.89 b-k	1.50 f-k	164.52 b-f	37.18 d-r
T364	73.87 a-f	111.68 l-v	99.03 e-r	6.41 i-s	5.57 h-r	8.76 a-j	54.31 a-h	1.50 f-k	144.20 g-q	38.40 c-n
19	69.32 j-p	113.19 h-u	93.52 j-w	7.72 c-f	6.24 e-l	7.41 i-s	34.30 q-w	0.81 p-s	129.74 p-x	36.61e-s
T369	66.67 o-r	109.18 q-v	114.23 a-e	5.14 t-w	4.55 q-z	9.82 ab	57.54 abc	2.20 ab	137.99 i-s	40.58 b-f
20	70.52 d-o	116.60 e-m	76.90 yzAB	5.38 r-w	4.64 p-y	7.56 i-r	38.66 k-w	0.90 o-r	148.12 f-o	37.95 d-p
T372	69.12 j-q	112.92 i-u	103.84 a-m	5.32 s-w	4.66 o-y	8.50 a-l	44.97 d-q	1.49 f-k	155.82 e-h	37.64 d-p
21	74.50 a-d	114.38 g-r	70.07 AB	9.51 a	6.45 d-i	6.68 o-v	47.38 c-o	1.00 n-q	139.43 h-r	38.23c-o
T376	74.07 a-f	113.74 g-t	65.02 B	7.03 e-m	5.13 k-u	5.42 vwx	35.83 n-w	1.10 m-p	137.03 i-t	33.00 r-u
HB-42	69.19 j-q	122.29 c-e	104.94 a-l	5.56 q-w	4.02 t-zA	6.27 q-w	29.11 vw	0.90 o-r	93.40 z	29.10 u
T401	72.34 a-m	111.37 m-v	116.75 ab	3.63 yz	3.32 zA	8.72 a-k	47.26 c-p	1.69 d-h	150.12 f-l	37.66 d-p
T45	76.12 a	128.29 a-b	101.90 b-o	5.33 s-w	4.99 m-v	6.21 r-w	38.93 j-w	0.80 p-s	134.72 j-v	36.80 d-r
29	72.03 b-m	112.21 j-u	104.72 a-l	6.78 f-o	5.35 i-s	8.90 a-i	44.21 f-t	1.25 j-n	147.68 f-p	38.14 c-o

T451	73.28 a-i	125.88 a-c	96.08 g-t	7.96 cde	6.42 d-i	6.77 o-v	44.79 e-r	1.31 i-n	143.93 g-q	40.26 b-h
51	72.49 a-l	117.85 d-j	78.84 w-zAB	10.29 a	8.96 a	7.194 k-s	33.42 q-w	0.70 qrs	121.83 r-y	35.67 j-s
T464	69.43 i-p	112.49 j-u	107.98 a-j	5.67 o-w	5.03 l-v	9.70 abc	62.57 ab	2.25 ab	148.10 f-p	39.43 b-l
55	72.53 a-l	117.56 d-k	97.85 f-t	7.11 e-m	5.82 f-p	7.50 i-r	43.05 g-t	1.10 l-p	133.63 j-w	36.03 i-s
T467	61.83 t	111.37 m-v	114.09 a-e	7.32 c-j	6.38 e-j	9.95 a	55.68 a-f	2.20 ab	147.39 f-p	42.33 bc
59	70.67 d-n	113.18 h-u	89.26 m-z	5.64 o-w	4.89 n-w	6.90 m-v	36.12 m-w	1.19 k-o	132.17 m-w	37.34 d-q
T506	62.24 st	110.30 o-v	107.00 a-k	5.46 q-w	5.15 j-t	9.66 abc	55.31 a-g	2.45 a	155.75 e-h	40.82 b-e
66	74.62 a-c	115.01 g-q	85.27q-zA	8.33 bc	6.69 d-h	6.93 m-v	35.26 o-w	0.59 rs	104.99 yz	33.14 q-u
90	74.19 a-e	114.18 g-s	77.07 yzAB	7.17 d-l	6.70 d-h	7.01 l-u	34.82 p-w	0.51 s	119.42 t-y	34.05 o-t
96	68.86 l-q	118.82 d-h	86.06 p-z	9.34 ab	8.39 abc	6.68 o-v	34.68 p-w	0.60 rs	127.69 q-x	35.35 k-s
T519	67.39 n-q	123.24 b-d	95.01 h-t	5.54 q-w	3.65xyzA	7.8 e-q	29.26 vw	1.10 m-p	124.69 r-x	34.97 n-s
Dinsho	61.56 t	108.84 r-v	115.03 abc	6.01 m-v	4.68 o-y	9.50 a-d	57.91 abc	1.75 d-g	139.38 h-r	39.58 b-k
105	68.42 m-q	117.99 d-j	76.90 yzAB	8.32 bcd	6.25 e-l	7.73 g-r	35.63 o-w	0.80 p-s	115.68 wxy	37.85 d-p
T524	65.26 q-t	111.92 k-v	106.83 a-k	7.64 c-h	7.16cde	9.31 a-f	64.15 a	2.25 ab	171.70 a-e	40.86 bcd
T562	74.07 a-f	114.30 g-s	101.18 c-o	4.96vwx	3.50yzA	8.75 a-k	50.45 b-l	1.54 f-j	158.08 d-g	37.93 d-p
113	73.40 a-h	119.38 d-g	98.03 f-s	5.79 n-w	4.86 n-x	7.70 g-r	29.33 vw	1.60 e-i	133.91 j-v	37.52 d-p
114	72.34 a-m	115.23 g-p	83.39 s-zA	5.46 q-w	4.36 r-z	4.34 x	40.14 i-v	1.20 k-o	162.46 b-f	36.83 d-r
139	75.50ab	110.29 o-v	92.12 k-y	9.54 a	6.90 def	9.16 a-h	48.11 c-n	1.55 f-j	133.28 k-w	39.36b-m
150	74.29 a-e	115.52 g-p	85.50 q-z	4.97 u-x	4.57 q-y	8.02 d-o	37.74 m-w	0.70 qrs	117.23 v-y	35.19 m-s
T575	61.57 t	107.85t-v	115.46abc	6.03 l-v	3.94 u-zA	9.86ab	54.94 a-h	2.10bc	159.81 b-g	40.34 b-h
157	68.86 l-q	112.73 i-u	96.88 g-t	5.36 r-w	4.98 m-v	8.91 a-i	48.64 c-m	1.61 e-i	178.05 ab	40.18 b-i
161	70.47 e-o	112.75 i-u	79.47 u-zAB	7.35 c-i	7.02 def	7.24 j-s	27.50 w	0.50 s	91.75 z	30.17 tu
Moata	70.84 c-n	118.43 d-i	90.89 l-z	6.12 l-u	4.83 n-x	7.76 f-r	44.16 f-t	1.10 m-p	120.68 s-y	36.63 d-s
168	68.93 l-q	114.19 g-s	82.82 t-zA	6.50 h-r	5.26 i-s	4.79 wx	44.26 f-t	1.20 k-o	132.06 m-w	38.83 c-n
T576	72.02 b-m	111.70 l-v	103.26 b-m	3.81 xyz	3.72w-zA	8.78 a-j	51.08 b-j	1.40 h-m	176.61 abc	48.04 a
11	72.43a-l	116.94 e-m	94.15 i-v	7.67 c-h	5.91 f-n	7.45 i-s	39.93 i-w	1.20 k-o	121.93 r-y	36.33 g-s
100	72.36 a-m	113.75 g-s	106.63 a-k	6.35 i-s	5.12 k-u	6.99 l-u	32.12 s-w	1.30 i-n	118.20 u-y	35.14 n-s
T62	72.98 a-k	109.83 p-v	100.89 c-p	4.81wx	3.89 v-zA	8.96 a-i	51.66 a-i	1.75 d-g	147.56 f-p	38.83 c-n
24	71.07 c-n	113.99 g-s	88.18 n-z	7.18 c-l	6.05 e-n	7.47 i-r	33.22 q-w	1.09 m-p	119.45 t-y	35.27 l-s
167	70.53 d-o	109.28 q-v	88.07 o-z	7.34 c-j	6.82 d-g	6.85m-v	36.01 n-w	0.80 p-s	113.64 xy	32.55stu
T90	63.06 r-t	105.90 v	118.23 a	4.76 wxy	4.58 q-y	9.63 a-d	55.79 a-f	2.00 bcd	175.13 a-d	39.52 b-k
Mean	70.11	114.57	95.41	6.71	5.50	7.86	43.41	1.33	138.86	37.78
CV (%)	2.8	2.7	7.5	8.8	10.7	10.9	13.7	12.7	6.1	5.5

a, b, c,….z means with different superscripts in a row are significantly different; CV(%)=Coefficient of Variation; DTH=Days to Heading in Days; DTM= Days to Maturity in Days; PH=Plant Height in Centimeter; TT=Total Tiller Plant^{-1} in Numbers; PT=Productive Tiller Plant^{-1} in Number; Spike Length in Centimeter; Seed Spike^{-1} in Numbers; BY=Biological Yield in Kilogram Plot^{-1}; GY=Grain Yield in Gram Plot^{-1}; TKW=Thousand Kernel Weight in Gram.

4.3. Genetic Variability Analysis of Barley Genotypes to Shoot Fly

The 64 barley genotypes were evaluated at SARC in 2023/24 for variance components, heritability percentages, and genetic parameters for 21 quantitative traits related to shoot fly resistance, morphological traits, yield, and yield components. The results of this evaluation are presented in Table 10.

4.3.1. The estimation of phenotypic and genotypic coefficients of variation

In the current study, the phenotypic variance (σ^2p) ranged from 0.0107 for the second leaf width to 753.25 for infestation, while the genotypic variance (σ^2g) varied from 0.0097 for the second leaf width to 570.86 for infestation (Table 10). GCV and PCV were categorized as low (<10%), moderate (10 to 20%), and high (>20%) (Sivasubramaniam and Menon, 1973; Deshmukh *et al*., 1986.

The GCV and PCV values were notably high for several traits, including the first leaf width (20.62 and 22.32), the number of total tillers per plant (22.7 and 24.3), seedling stem length (22.72 and 24.44), productive tiller (21.86 and 24.6), seed per spike (20.06 and 24.94), crop recovery (25.44 and 35.81), biological yield (37.04 and 39.2), oviposition 10 $Seedling^{-1}$ (34.73 and 39.88), leaf glossiness (37.51 and 42.5), seedling vigor (39.46 and 46.6), infestation (44.13 and 50.7), seedling color (47.1 and 50.84), and dead heart (46.1 and 55.09), respectively. For the second leaf width (19.23 and 20.2) and seedling stem length (18.02 and 21.43), the GCV was moderate while the PCV was high. Additionally, the GCV and PCV values were moderate for spike length (15.5 and 18.7), grain yield (13 and 14.75), and plant height (11.97 and 14.6); respectively (Table 10). This suggests that the genotype may be manifested in the phenotype and that the success of selection based on the phenotypic performance of these traits. Conversely, it suggests the presence of significant variability, providing abundant opportunity for improvement through selection. The current result is similar to the outcomes reported by Fikre et *al*. (2015); Garome *et al.*, 2022.

The traits with the lowest GCV and PCV values were days to heading (5.12 and 5.86), days to 90% maturity (3.84 and 4.7), and thousand kernel weight (8.12 and 9), respectively. This shows that environmental factors had a greater influence on these traits compared to genetic factors, suggesting that the potential to improve these traits through direct selection of better

performing genotypes is limited. The results in the current study are in line with the previous findings of Garome et *al*. (2022) who reported the lowest GCV and PCV were estimated for days to 50% heading, and day to 90% maturity.

4.3.2. Broad sense heritability (H^2)

In the current study, the estimated broad-sense heritability values ranged from 50.43 % for crop recovery to 90.65 % for second leaf width (Table 10). According to Allo *et al*. (2020) the heritability values were categorized as low (<40 percent), moderate (40–60 percent), and moderately high (>60 - 79 percent), and very high heritability (> 80%).

Based on this range, the findings indicate high heritability for traits such as seedling color (86.3%), first leaf width (85.71%), second leaf width (90.62%), seedling stem length (86.36%), total tiller (87.22), and biological yield (88.89) as shown in Table 10. This suggests that the observed variation is mainly controlled by genetic factors and is less influenced by the environment, thus allowing for potential improvement through selection. However, it's important to note that high heritability alone does not always guarantee significant genetic gain for effective selection and improvement. Instead, higher heritability combined with a greater estimate of GCV and GAM is essential for this purpose. This finding aligns with previous research by Ali *et al.* (2002); Garome *et al*. (2022), suggesting that high heritability alone may not be sufficient for effective selection. Additionally, Udeh and Ogbu (2011) reported that greater heritability combined with increased GCV and GAM estimates is important for significant genetic gain through effective selection and improvement.

4.3.3. Genetic advance as a percent of the mean (GAM)

The current study showed that, genetic advance as a percent of the mean (GAM) ranged from 6.54 % for days to 90% maturity to 89.9 % for seedling color, indicating that selecting the top 5% of the base population could lead to advancements of 6.54 % to 89.9 % over the base population mean(Table 10).

Genetic advance (GA) as a percentage of the mean was higher for all traits, except days to 90% maturity (6.54%), and thousand kernel weight (13.78)(Table 10). This indicates that environmental factors have little impact on these traits, and significant enhancement for these

traits could be accomplished through direct selection. These traits are believed to be controlled by additive genes.The current result is consistent to the previous findings of Allo *et al*. (2020) who reported high genetic advance for plant height, spike length, seed per spike, total tiller per plant, fertile tiller per plant, spike weight, grain yield, 1000 seed weight, dead heart, oviposition, seedling vigour, seedling color, and crop recovery.

Conversely, traits like days to 90% maturity, and 1000 seed weight shows low genetic advances as a percentage of the mean. This shows that, non-additive gene expression for shoot fly resistance, which may require heterosis breeding for improvement. This result is similar to the previous findings of Jilo et *al*. (2018) who reported low genetic advance for days to 50% heading and days to 90% maturity. This indicating that, no additive gene expression of these traits. Therefore, selection based on these traits may not be effective, but heterosis breeding might be necessary for improving these traits.

On the other hand, traits such as days to 90% maturity and 1000 seed weight demonstrate minimal genetic advance as a proportion of the average. This suggests that non-additive gene expression is involved in resistance to shoot fly, which may necessitate heterosis breeding for enhancement. This outcome is consistent with the earlier findings of Jilo *et al*. (2018), who observed limited genetic advance for days to 50% heading and 90% maturity, indicating non-additive gene expression for these traits. Consequently, selecting based on these traits may not be effective, but heterosis breeding may be essential for improving them.

4.3.4. Broad sense heritability (H^2) and genetic advance as a percent of the mean (GAM)

In this study, traits such as seedling color (86.30% and 89.90%), first leaf width (85.71% and 39.25), second leaf width (90.65% and 37.72%), seedling stem length (86.36% and 43.50%), total tiller (87.22% and 43.70%), and biological yield (88.89% and 72.12%) show high heritability, and genetic advance as a percentage of the mean, respectively(Table 10). This suggests that there is minimal influence from environmental factors and potential for improvement through direct selection. These traits are likely controlled by additive genes. This result was corroborating to the previous findings of Garome *et al. (*2022) who reported that a high level of heritability and a significant genetic advance as a percentage of the mean for both thousand seed weight and yield per plant.

Conversely, traits such as days to 50% heading (76.09% and 9.20%) and days to 90% maturity (68.07% and 6.54%) displayed high heritability but limited genetic progress as a percentage of the mean. This implies non-additive gene expression for shoot fly resistance, suggesting a potential requirement for heterosis breeding to facilitate improvement. This outcome aligns with the findings of Alemu *et al.* (2016), who similarly observed high heritability with minimal genetic advancement as a percentage of the mean for days to 50% heading and days to 90% maturity.

Table 10. Components of variance, heritability, and genetic parameters for 21 quantitative traits

Traits	Ranges	Mean ± SE	σ^2p	σ^2g	PCV (%)	GCV (%)	H^2 (%)	GA	GAM (%)
OVI	12.00 – 64.00	39.9 ± 5.53	253.44	192.18	39.88	34.73	75.83	24.87	62.30
INF	12.85 - 93.50	54.15 ± 9.5	753.25	570.86	50.70	44.13	75.79	42.85	79.13
DH	8.60 - 87.10	44.97 ± 9.6	613.73	429.90	55.09	46.10	70.05	35.75	79.50
CR	0.25 – 4.80	3.02 ± 0.54	1.17	0.59	35.81	25.44	50.43	1.13	37.24
SV	1.00 – 5.00	2.84 ± 0.50	1.75	1.26	46.60	39.46	72.00	1.96	68.86
LG	1.00 – 5.00	2.95 ± 0.42	1.57	1.22	42.50	37.50	77.71	2.01	68.20
SC	1.00 – 3.00	1.68 ± 0.23	0.73	0.63	50.84	47.10	86.30	1.51	89.90
DTH	61.00 - 78.00	70.11 ±1.42	16.90	12.86	5.86	5.12	76.09	6.45	9.20
PH	52.40– 126.7	95.41± 5.60	193.61	130.5	14.60	11.97	67.40	19.32	20.25
SL	3.80 – 10.50	7.86 ± 0.58	2.16	1.50	18.70	15.50	69.44	2.10	26.50
L1	0.46 – 0.98	0.75 ± 0.05	0.028	0.024	22.32	20.62	85.71	0.29	39.25
L2	0.33 – 0.68	0.51 ± 0.02	0.0107	0.0097	20.20	19.23	90.65	0.19	37.72
SSL	3.23 – 70.00	5.08 ± 0.32	1.54	1.33	24.44	22.72	86.36	2.21	43.50
SST	0.43 -0.94	0.71 ± 0.06	0.0232	0.0164	21.43	18.02	70.69	0.22	31.21
TT	3.00 – 10.33	6.71 ± 0.41	2.66	2.32	24.30	22.70	87.22	2.93	43.70
PT	2.87 – 9.00	5.50 ± 0.44	1.83	1.45	24.60	21.86	79.23	2.20	40.00
SPS	21.53 – 69.80	43.41 ± 4.6	117.30	75.82	24.94	20.06	64.64	14.42	33.23
DTM	105 – 131	114.6 ± 2.1	28.50	19.40	4.70	3.84	68.07	7.50	6.54
BY	0.50 – 2.50	1.33 ± 0.12	0.27	0.24	39.20	37.04	88.89	0.96	72.12
GY	84.50 -195.50	138.9 ± 6.9	419.40	325.50	14.75	13.00	77.61	32.74	23.58
TKW	27.60 – 50.80	37.8 ± 1.50	13.86	9.41	9.85	8.12	67.89	5.21	13.78

OVI=Oviposition; INF=Infestation, DH=Dead Heart; CR=Crop Recovery; SV=Seedling Vigor; LG=Leaf Glossiness; SC=Seedling Color; DTH=Days To 50% Heading; PH=Plant Height; SL=Spike Length; L1=First Leaf Width; L2=Second Leaf Width; SSL=Seedling Stem Length; SST=Seedling Stem Thickness; TT=Total Tiller; PT=Productive/Fertile Tiller; SPS=Seed Per Spike; Days to Maturity; BY=Biological Yield; GY=Grain Yield: TKW=Thousand Kernel Weight; SE=Standard Error; σ^2p=Phenotypic Variance, σ2g=Genotypic Variance; PCV=Phenotypic Coefficient of Variation; GCV=Genotypic Coefficient of Variation; H^2=Heritability, GA=Genetic Advance; GAM= Genetic Advance as Percentage of Mean.

4.4. Correlation among Barley Shoot Fly Damage Parameters, Morphological and Agronomic Traits of Barley Genotypes under Field Conditions

Correlation between major barley shoot fly damage parameters, morphological and agronomic traits of barley genotypes are given in Table 11. Among morphological traits evaluated, seedling vigor, leaf glossiness, seedling color, and seedling stem length were negatively and highly significant correlated ($P<0.001$) with shoot fly oviposition, infestation and dead hearts. This shows that the barley genotypes with high amount of eggs, infestation and dead hearts have low amount of seedling vigor, leaf glossiness, seedling color, and seedling stem length. However, (Sekar *et al*., 2018) reported highly significant and but positive correlation of seedling vigor, leaf glossiness with shoot fly oviposition and dead hearts. However, first leaf width, second leaf width and seedling stem thickness were positively and highly significant correlated ($P< 0.001$) with shoot fly oviposition, infestation and dead hearts. This revealed that, the highest leaf width, and seedling stem thickness of barley genotype have high amount of shoot fly oviposition, infestation and dead hearts. In line with this, Allo *et al*. (2020) reported that significant and negative, non-significant and negative, significant and positive, significant and negative, non-significant and positive, and significant and positive correlation of first leaf width with dead heart, second leaf width with dead heart, first leaf width with shoot fly oviposition, second leaf width with shoot fly oviposition, first leaf width with infestation, and second leaf width with infestation, respectively. As well as, among various agronomic trait like crop recovery, plant height, spike length, seed per spike, biomass, grain yield and thousand kernel weight were negatively and highly significant associated ($p<0.001$) with shoot fly oviposition, infestation and dead hearts. In line with previous studies, (Allo *et al*., 2020) reported that negative and significant correlation of majority of these agronomic traits. This shows that resistance barley genotypes have high crop recovery, plant height, spike length, seed per spike, biomass, grain yield and thousand kernel weight, compared to susceptible barley genotypes. On the other hand, days to heading, days to maturity, total tiller, and productive (fertile) tiller were significantly and positively associated ($p<0.001$) with shoot fly oviposition, infestation and dead heart. The days to 50% flowering was positively and significantly correlated with the expression of barley shoot fly (Mohammed *et al*., 2015). This indicates that, the barley genotypes with long days to heading and maturity have high shoot fly oviposition, infestation and dead heart.

Table 11. Phenotypic (below the diagonal) and genotypic (above the diagonal) Pearson correlation coefficients of 21 traits in barley genotypes tested in SARC during the 2023/2024 growing season

	OVI	INF	DH	CR	SV	LG	SC	DTH	PH	SL	L1
OVI	**1** **	0.99 **	1.00 **	-0.85 **	-0.92 **	-0.90 **	-0.94 **	0.63 **	-0.81 **	-0.90 **	0.93 **
INF	0.96 **	**1** **	0.99**	-0.88 **	-0.93 **	-0.95 **	-0.98 **	0.64 **	-0.83 **	-0.94 **	0.93 **
DH	0.93 **	0.98 **	**1** **	-0.92 **	-0.90 **	-0.95 **	-0.98 **	0.61 **	-0.82 **	-0.94 **	0.92 **
CR	-0.73 **	-0.77 **	-0.76 **	**1** **	0.78 **	0.98 **	0.90 **	-0.57 **	0.86 **	0.98 **	-0.78 **
SV	-0.81 **	-0.84 **	-0.80 **	0.66 **	**1** **	0.97**	0.99 **	-0.78 **	0.86 **	0.93 **	-0.85 **
LG	-0.72 **	-0.75 **	-0.73 **	0.55 **	0.78 **	**1** **	0.97 **	-0.66 **	0.91 **	0.92 **	-0.85 **
SC	-0.76 **	-0.77 **	-0.71 **	0.56 **	0.78 **	0.83 **	**1** **	-0.69 **	0.88 **	0.93 **	-0.88 **
DTH	0.55 **	0.56 **	0.52 **	-0.45 **	-0.67 **	-0.56 **	-0.58 **	**1** **	-0.58 **	-0.65 **	0.47 **
PH	-0.69 **	-0.69 **	-0.67 **	0.68 **	0.65 **	0.57 **	0.63 **	-0.46 **	**1** **	0.79 **	-0.78 **
SL	-0.66 **	-0.69 **	-0.66 **	0.59 **	0.63 **	0.66 **	0.73 **	-0.43 **	0.59 **	**1** **	-0.77 **
L1	0.83 **	0.83 **	0.79 **	-0.59 **	-0.71 **	-0.69 **	-0.76 **	0.41 **	-0.65 **	-0.61 **	**1** **
L2	0.81 **	0.82 **	0.78 **	-0.57 **	-0.71 **	-0.71 **	-0.75 **	0.36 **	-0.65 **	-0.62 **	0.90 **
SSL	-0.81 **	-0.80 **	-0.77 **	0.56 **	0.72 **	0.723 **	0.79 **	-0.37 **	0.63 **	0.63 **	-0.90 **
SST	0.74 **	0.75 **	0.71 **	-0.53 **	-0.66 **	-0.65 **	-0.69 **	0.36 **	-0.59 **	-0.57 **	0.90 **
TT	0.47 **	0.46 **	0.43 **	-0.26 **	-0.34 **	-0.26 **	-0.36 **	0.10 ^{NS}	-0.45 **	-0.25 **	0.50 **
PT	0.43 **	0.43 **	0.40 **	-0.30 **	-0.33 **	-0.29 **	-0.38 **	0.12 ^{NS}	-0.41 **	-0.27 **	0.46 **
SPS	-0.61 **	-0.65 **	-0.62 **	0.54 **	0.63 **	0.63 **	0.76 **	-0.43 **	0.52 **	0.59 **	-0.61 **
DTM	0.45 **	0.46 **	0.41 **	-0.25 **	-0.44 **	-0.43 **	-0.53 **	0.47 **	-0.26 **	-0.47 **	0.33 **
BM	-0.70 **	-0.72 **	-0.67 **	0.66 **	0.72 **	0.72 **	0.81**	-0.53 **	0.65 **	0.67 **	-0.63 **
GY	-0.54 **	-0.57 **	-0.55 **	0.47 **	0.45 **	0.48 **	0.56 **	-0.21 *	0.42 **	0.49 **	-0.52 **
TKW	-0.55 **	-0.58 **	-0.56 **	0.53 **	0.49 **	0.50 **	0.54 **	-0.28 **	0.44 **	0.45 **	-0.47 **

Table 11 (Continued)

	L2	SSL	SST	TT	PT	SPS	DTM	BM	GY	TKW
OVI	0.91 **	-0.92 **	0.92 **	0.61 **	0.63 **	-0.89 **	0.57 **	-0.84 **	-0.65 **	-0.69 **
INF	0.91 **	-0.93 **	0.90 **	0.59 **	0.63 **	-0.91 **	0.62 **	-0.88 **	-0.72 **	-0.75 **
DH	0.90 **	-0.93 **	0.87 **	0.59 **	0.64 **	-0.87 **	0.58 **	-0.86 **	-0.71 **	-0.75 **
CR	-0.77 **	0.79 **	-0.77 **	-0.44 **	-0.56 **	0.87 **	-0.39 **	0.94 **	0.79 **	0.87 **
SV	-0.83 **	0.86 **	-0.84 **	-0.47 **	-0.53 **	0.93 **	-0.71 **	0.88 **	0.62 **	0.70 **
LG	-0.82 **	0.84 **	-0.84 **	-0.36 **	-0.43 **	0.94 **	-0.61 **	0.86 **	0.61 **	0.69 **
SC	-0.87 **	0.87 **	-0.88 **	-0.40 **	-0.43 **	0.95 **	-0.69 **	0.90 **	0.64 **	0.67 **
DTH	0.40 **	-0.42 **	0.43 **	0.15 ^{NS}	0.21 ^{NS}	-0.68 **	0.57 **	-0.65 **	-0.31 *	-0.41 **
PH	-0.76 **	0.81 **	-0.81 **	-0.62 **	-0.57 **	0.72 **	-0.29 *	0.81 **	0.51 **	0.57 **
SL	-0.76 **	0.76 **	-0.80 **	-0.35 **	-0.36 **	0.84 **	-0.61 **	0.88 **	0.62 **	0.68 **
L1	0.96 **	-0.98 **	1.01 **	0.58 **	0.57 **	-0.78 **	0.42 **	-0.70 **	-0.64 **	-0.59 **
L2	**1** **	-0.94 **	0.97 **	0.63 **	0.59 **	-0.81 **	0.41 **	-0.73 **	-0.66 **	-0.60 **
SSL	-0.87 **	**1** **	-0.99 **	-0.56 **	-0.58 **	0.84 **	-0.42 **	0.73 **	0.69 **	0.64 **
SST	0.84 **	-0.82 **	**1** **	0.60 **	0.61 **	-0.80 **	0.44 **	-0.69 **	-0.65 **	-0.54 **
TT	0.54 **	-0.48 **	0.47 **	**1** **	0.86 **	-0.32 *	0.18 ^{NS}	-0.31 *	-0.24 ^{NS}	-0.24 ^{NS}
PT	0.48 **	-0.45 **	0.42 **	0.85 **	**1** **	-0.28 *	0.13 ^{NS}	-0.41 **	-0.25 *	-0.31 *
SPS	-0.60 **	0.67 **	-0.57 **	-0.24 **	-0.19 *	**1** **	-0.78 **	0.90 **	0.79 **	0.75 **
DTM	0.33 **	-0.32 **	0.33 **	0.16 ^{NS}	0.13 ^{NS}	-0.51 **	**1** **	-0.56 **	-0.42 **	-0.46 **
BM	-0.65 **	0.66 **	-0.55 **	-0.29 **	-0.34 **	0.75 **	-0.44 **	**1** **	0.74 **	0.78 **
GY	-0.53 **	0.56 **	-0.48 **	-0.20*	-0.21 *	0.70 **	-0.348 **	0.67 **	**1** **	0.88 **
TKW	-0.49 **	0.53 **	-0.44 **	-0.18 *	-0.20 *	0.68 **	-0.35 **	0.64 **	0.78 **	**1** **

*=($p<0.05$); **=($p<0.01$); NS=Non significant; OVI=Oviposition; INF=Infestation, DH=Dead Heart; CR=Crop Recovery; SV=Seedling Vigor; LG=Leaf Glossiness; SC=Seedling Color; DTH=Days To Heading; PH=Plant Height; SL=Spike Length; L1=First Leaf Width; L2=Second Leaf Width; SSL=Seedling Stem Length; SST=Seedling Stem Thickness; TT=Total Tiller; PT=Productive/Fertile Tiller; SPS=Seed Per Spike; Days to Maturity; BY=Biological Yield; GY=Grain Yield:TKW=Thousand Kernel-Weight.

4.5. Antixenosis for Oviposition

4.5.1. Multiple choice test

The average oviposition preference and damage caused by female barley shoot fly on 12 barley genotypes during a multi-choice test in the field at SARC in 2023/2024 are shown in Table 12. Highly significant differences ($p<0.001$) were observed for all parameters tested among the evaluated genotypes, indicating that the barley shoot fly showed a preference for oviposition under multi-choice test conditions (Appendix 6).

The average number of eggs laid per seedling ranged from 2.03 to 4.43 eggs at 10 days after seedling emergence (DAE), and 1.83 to 4.30 eggs at 13 days after seedling emergence (DAE). The lowest number of eggs per seedling was recorded on the resistance genotypes T281, T506, T524, T575, and Aruso compared to susceptible check, HB-42. Hence, the resistance genotypes were less preferred for oviposition by barley shoot fly. On the other hand, intermediate amount of eggs per seedling were recorded on the, T364, 150, and T123 genotypes. While, the highest number of eggs per seedling was recorded on the susceptible genotype 55, 168, T376, and HB-42 as compared to resistance check Aruso (Table 12). The results demonstrate that during oviposition, female barley shoot fly distinguish between the barley genotypes that was studied. Under multi-choice tests, the shoot flies laid less egg on the resistance genotypes than the susceptible genotypes. This confirms that, resistant genotype is unattractive for oviposition.This result was corroborating the results of Dhillon *et al. (*2005) who reported non-preference genotype by insects is often projected as a property of the plant to render it unattractive for oviposition, feeding, or shelter. This might be due to the morphological traits of barley genotypes at seedling stage has a strong influence on the oviposition of shoot fly females. This result is also, consistent with that of Vikal *et al.* (2020) who reported that plant morphology has a strong impact on shoot fly damage, especially seedling characteristics that physically reduce feeding, oviposition, and shelter. Therefore, the present results also indicated that oviposition non-preference is the primary component of resistance to shoot fly under multi-choice test field conditions. The current result is consistent to the previous findings of Dhillon *et al*. (2005).

Likewise, seedlings with eggs were significantly varied ($p<0.001$) among genotypes. Seedlings with eggs ranged from 55.90 to 94.93%, and 47.10 to 96.20 % at 10 and 13 DAE, respectively (Table 12). Genotypes T281, T506, T524, and T575 had significantly lower proportion of seedlings with eggs as compared to the susceptible check, HB-42, though on par with the resistance check, Aruso. Even though, the genotypes 55, 168, and T376 had higher proportion of seedlings with eggs as compared to the resistance check, Aruso, but concurrent with the susceptible check, HB-42, but there were a few exceptions. This revealed that, there is clear significance difference among the genotypes evaluated for shelter under multi choice test. In this study, resistance genotypes were less preferred or unattractive for shelter under multi choice test than susceptible genotypes. This result is in line with the previous report of Dhillon *et al. (*2005); Vikal *et al.* (2020).

As well as, the dead hear percentage was highly significant difference ($p< 0.001$) under multi choice test among genotypes tested (Appendix 6). The dead heart percentages were ranged from 17.07(T575) to 56.83% (T376) at 18 DAE (Table 12). The dead heart percentages were significantly lower in T281, T506, T524, and T575 genotypes as compared with susceptible check, HB-42; while the dead hearts percentages were higher in 55, 168, and T376 genotypes as compared to resistance check, Aruso (Table 12).This indicates that, resistance genotypes were less damaged than susceptible genotypes. Similarly, genotypes preferred for oviposition also show heavy dead heart formation (Rana *et al*., 1975; Unnithan & Reddy, 1985; Dhillon *et al*., 2005).

Table 12. Average oviposition preference and damage by the barley shoot fly females on 12 barley genotypes under multi-choice test in the field at SARC 2023/2024

	Eggs seedling^{-1}		Seedlings with eggs (%)		Dead hearts (%)
Genotypes	10DAE	13 DAE	10DAE	13DAE	18DAE
T281	2.47^{d}	2.33^{c}	57.83^{c}	59.47^{c}	17.82^{e}
T506	2.67^{d}	2.43^{c}	56.20^{c}	53.03^{cd}	16.14^{e}
T524	2.03^{e}	1.83^{d}	55.90^{c}	47.10^{d}	15.80^{e}
T575	2.03^{e}	2.23^{c}	62.13^{c}	58.77^{c}	15.07^{e}
T364	3.47^{c}	3.40^{b}	71.37^{b}	70.17^{b}	29.23^{d}
150	3.53^{c}	3.37^{b}	73.30^{b}	71.33^{b}	29.47^{d}
T123	3.57^{c}	3.50^{b}	71.47^{b}	69.93^{b}	29.00^{d}
55	4.00^{b}	4.20^{a}	93.90^{a}	89.67^{a}	51.30^{b}
168	4.07^{b}	4.00^{a}	89.49^{a}	88.38^{a}	43.57^{c}
T376	4.43^{a}	4.30^{a}	94.93^{a}	96.20^{a}	56.83^{a}
HB-42(S)	4.27^{ab}	4.10^{a}	92.13^{a}	93.30^{a}	54.80^{a}
Aruso(R)	2.67^{d}	2.53^{c}	56.30^{c}	55.30^{cd}	18.03^{e}
Mean	3.45	3.65	78.06	71.05	31.42
SE ±	0.12	0.11	2.77	2.84	1.19
CV (%)	26	27.09	21.8	24.03	50.11
LSD(p= 0.05)	0.31401	0.3226847	8.09184	8.278988	3.465931

Means in a row followed by different letter are significantly different; DAE=Days after Emergence; SE=Standard Error; CV=coefficient of variation, LSD=Least Significant Differences =Susceptible; R=Resistance

4.5.2. No-choice test

The average oviposition preference and damage by the barley shoot fly females on 12 barley genotypes under no-choice test in the field at SARC 2023/2024 are presented in Table 13. The analysis results indicated that the number of eggs per seedling and percentages of dead heart were significantly differences ($p<0.001$). However, the percentage of eggs with seedling was not statistically significant, under no choice condition test; in the cage with pot culture (Appendix 7). This shows that non-preference for oviposition is strong resistance components under no- choice tests. This result is in contrary to the previous findings of Dhillon *et al*. (2005) who reported that there were no significant differences in number of eggs among the

genotypes tested and non-preference for oviposition was no strong resistance components under no-choice conditions.

The mean of oviposition preference was highly significant differences ($p<0.001$) under no choice test conditions. The average number of eggs per seedling on different barley genotypes under no choice test in the pot ranged from 2.73 to 4.83 numbers and 2.67 to 4.80 numbers at 10 and 13 DAE, respectively (Table 13). The lowest mean number of eggs per seedling under no choice tested was observed on T281, T506, T524, and T575 genotypes compared to susceptible check HB-42; though on par with resistance check, Aruso. On the other hand, the highest mean number of eggs per seedling was recorded on 55, 168, and T376 compared to resistance check Aruso; though on par with susceptible check, HB-42. Other shows medium level of mean number of eggs per seedling. This result indicates that, oviposition behavior of the barley shoot fly shows very clear resistance in different barley genotypes in field conditions under no choice test. Corroborating the results of this study, Esayas *et al*. (2016) reported that oviposition behavior in the pea weevil reflects very well the resistance of different genotypes of field pea found in a field situation. Even though, seedlings with eggs were not exhibit significant ($p=0.05$) among genotypes (Table 13).This finding is in line with the previous reports of Dhillon *et al.* (2005). This shows that there is not clear significance difference among the genotypes evaluated for shelter under no-choice test situation.

However, the dead heart percentage was highly significant varied ($p< 0.001$) under no- choice test (Appendix 7). This result is also in contrary with the result obtained by Dhillo *et al*. (2005). The lowest and highest dead heart percentages were recorded on resistance (T506) and susceptible (168) genotypes with the values of 53.23% and 84.03%, respectively. The dead heart percentages were significantly lower in T506, T524, T281, and T575 genotypes as compared with susceptible check, HB-42; while the dead hearts percentages were higher in 55, 168, and T376 genotypes as compared to resistance check, Aruso (Table 13).This confirms that, resistance genotypes were less damaged than susceptible genotypes. Consequently, genotypes preferred for oviposition also show heavy dead heart formation (Rana *et al*., 1975; Unnithan & Reddy, 1985; Dhillon *et al*., 2005). Additionally, this result is contrasted by Kumar *et al*. (2008), who reported that, there is no clear evidence of antixenosis for oviposition under no choice conditions.

Table 13. Average oviposition preference and damage by the *D. flavibasis* females on 12 barley genotypes under no-choice test in the field at SARC 2023/2024

Genotypes	Eggs seedling^{-1}		Seedlings with eggs (%)		Dead hearts (%)
	10DAE	13 DAE	10DAE	13DAE	18DAE
T281	3.20^{c}	3.17^{e}	98.23^{a}	99.00^{a}	56.63^{ef}
T506	3.17^{c}	3.10^{e}	98.43^{a}	99.60^{a}	53.23^{f}
T524	2.73^{d}	2.67^{e}	99.50^{a}	99.10^{a}	56.67^{ef}
T575	2.73^{d}	2.70^{e}	99.00^{a}	99.60^{a}	55.80^{ef}
T364	3.87^{b}	4.07^{bcd}	98.57^{a}	98.40^{a}	68.73^{d}
150	4.00^{b}	3.77^{d}	99.30^{a}	99.53^{a}	68.63^{d}
T123	4.07^{b}	3.93^{cd}	100.00^{a}	98.93^{a}	69.38^{cd}
55	4.63^{a}	4.80^{a}	98.40^{a}	98.83^{a}	74.53^{bc}
168	4.80^{a}	4.40^{abc}	100.00^{a}	100.00^{a}	84.03^{a}
T376	4.83^{a}	4.53^{ab}	98.90^{a}	98.73^{a}	72.30^{cd}
HB-42(S)	4.57^{a}	4.60^{ab}	100.00^{a}	99.23^{a}	79.27^{ab}
Aruso(R)	2.87^{cd}	2.83^{e}	99.20^{a}	99.10^{a}	58.73^{e}
Mean	3.79	4.60	99.13	99.17	66.50
SE ±	0.14	0.21	0.66	0.64	1.79
CV (%)	21.60	22.00	11.50	10.20	15.30
LSD(P = 0.05)	0.3981892	0.5659193	1.931213	1.85347	5.212016

Means in a row followed by different letters are significantly different; DAE=Days After Emergence; SE=Standard Error; CV=coefficient of variation, LSD=Least Significant Differences; S=Susceptible; R=Resistance

4.5.3. Dual-choice test

The study examines the average number of eggs per plant, seedlings with eggs, and dead hearts under dual choice conditions, in relation to susceptible check (HB-42) are presented on Table 14. Dual choice test experiment was conducted in cage with pot culture by pairing each of eleventh test genotypes with the susceptible check, HB-42, in order to see the genotype influence on ovipositional antixenosis of barley shoot fly.

The number of eggs per seedling, seedlings with eggs, and dead hearts were ranged from 1.20 - 2.66eggs, 42.55 – 96.87 % and 20.32 – 54.92 % in test genotypes; and 2.22 to 3.75 eggs, 94 to 99.57 %, and 53.82 – 85.43% in susceptible check (HB-42), respectively. The average number of eggs per seedling was less preferred for the genotypes T281, T506, T524, T575, and Aruso, compared with the susceptible genotypes, HB-42. However, the average number of eggs per seedling for susceptible genotypes (55, 168, and T376) was on par with

susceptible genotypes (HB-42) (Table 14). Under dual choice test, the shoot fly laid more eggs on susceptible genotypes than the resistance genotypes. This indicates that the susceptible genotype is highly preferred for oviposition under dual choice test. This result is similar to the previous report of Dhillon *et al*. (2005); Mendesil *et al*. (2016). Likewise, the percentage of plants with eggs was less preferred on the genotypes T506, T524, T575, T281 and Aruso compared to the susceptible check (HB-42). This indicates that there is less preference for resistance genotypes compared to susceptible genotypes. However, the genotypes like 55,168, and T376 were on par or no statistical significance with susceptible check (HB-42). Similarly, the percentage of dead hearts is less preferred for the resistance genotypes than susceptible check, HB-42. Even though, the percentage of dead hearts genotypes for 55, 168, and T376 were on par with the susceptible check (HB-42). In general, the preference for certain traits in the shoot fly may be used to develop pest management techniques like intercropping and trap cropping, under dual choice test. The combination of resistance and susceptible barley genotypes reduced ovipositional and damage parameters, could be used as intercropping and trap cropping. This might be due to reduced result shoot fly damage parameters, during combination of resistance (T575, T524, T506 and T281) and susceptible check (HB-42). This result is in line with the previous report of Esayas *et.al*. (2016).

Table 14. Average oviposition preference and damage by the barley shoot fly females on 12 barley genotypes under dual choice conditions, in relation to susceptible check (HB-42) in the cages in the field at SARC 2023/2024

Genotypes	Eggs plant^{-1}				Percentages of plants with eggs				Dead heart percentages			
	Test entry	HB-42	t-value	P-value	Test entry	HB-42	t-value	P-value	Test entry	HB-42	t-value	P-value
T281	1.25	3.55	62.99**	1.909e-08	52.05	98.75	17.99**	9.754e-06	24.40	82.38	30.76**	6.813e-07
T506	1.20	3.75	28.81**	9.438e-07	46.48	99.57	28.78**	9.482e-07	20.42	83.42	22.12**	3.511e-06
T524	1.25	3.65	65.73**	1.544e-08	42.55	99.23	26.24**	1.503e-06	20.32	83.12	40.97**	1.633e-07
T575	1.47	3.53	18.33**	8.893e-06	53.33	98.75	36.92**	2.747e-07	20.70	78.62	44.38**	1.096e-07
T364	1.86	3.07	4.89**	0.004527	63.0	99.05	13.53**	3.957e-05	39.90	66.68	11.72**	7.962e-05
150	1.76	3.05	7.25**	0.0007809	60.98	94.00	6.35**	0.001435	38.38	65.12	31.44**	6.114e-07
T123	1.66	2.70	18.09**	9.495e-06	60.33	95.4	5.21**	0.003436	41.07	64.78	12.84**	5.101e-05
55	2.43	2.32	1.23^{ns}	0.2722	96.00	94.47	0.51^{ns}	0.6312	54.37	56.77	1.14^{ns}	0.3042
168	2.66	2.22	2.35^{ns}	0.06596	96.87	95.15	0.45^{ns}	0.6689	53.75	53.82	0.038^{ns}	0.9712
T376	2.23	2.25	0.24^{ns}	0.822	91.20	95.87	1.49^{ns}	0.1974	54.92	59.10	2.56^{ns}	0.05084
Aruso	1.22	3.52	25.72**	1.661e-06	54.80	99.4	17.39**	1.154e-05	20.92	85.43	34.26^{ns}	3.985e-07

4.6. Antibiosis Test for Developmental Period

The average developmental parameters measured for *D. flavibasis* life cycle on 12 barley genotypes are presented in Table 15. Highly significant genotype difference ($p<0.001$) were noted for all developmental parameters recorded (Appendix 8).

The larval period was ranged between 6.04 days for T376 to 7.26 days for T524. Larval period was longer than one day on T506 (7.25), T524(7.26), and approximately longer one day on T575,T281 and Aruso (6.93 to 7.00 days) as comparable to the susceptible check HB-42(6.19 days). In comparable to the resistance check, Aruso (7.00 days), the larval period was also approximately shorter one day in susceptible genotypes of 55, 168, T376, and HB-42. The pupal period was ranged from 9.27 days in T376 to 10.23 days in T524. The resistance genotypes T281, T524, T506, T575, and Aruso had longer pupal period than other susceptible genotypes. This suggests that susceptible genotypes had shorter larval and pupal periods in contrast to resistance genotypes. The pupal weights ranged from 3.26 grams to 3.80 grams. The highest pupal weights were found in susceptible barley genotypes 55, 168, T376, and HB-42, with values of 3.80, 3.78, 3.70, and 3.76 grams, respectively. In contrast, the lowest pupal weights were observed in resistant barley genotypes T281, T506, T524, T575, and Aruso with values of 3.39, 3.26, 3.28, 3.40 and 3.37 grams, respectively.

Pupation and adult emergence percentages were ranged from 69.91% to 83.33% and 59.11% to 77.78%, respectively. The resistance genotypes T281, T506, T524, T575, and Aruso showed lower pupation and adult emergence percentages compared to the susceptible check HB-42. Conversely, susceptible genotypes 55, 168, T376, and HB-42 exhibited higher pupation and adult emergence percentages compared to the resistance check Aruso. The number of fecundity per female was ranged from 16.00(T506) to 18.36(168). More number of eggs was laid under the susceptible genotypes than the resistance genotypes. Therefore, based on the evidence presented, there is clear indication of antibiosis mechanisms of resistance in barley against shoot fly. These findings align with the results of Singh and Verma (1988); and Dhillon *et al*. (2005). However, these results contradict the earlier findings of Tafa (2003), who reported no significant differences between resistant and susceptible barley genotypes, except for the weight of adult flies ($p<0.01$).

Table 15. The average developmental parameters of *D. flavibasis* on 12 barley genotypes under laboratory condition (SARC, 2023)

Genotypes	Larval Period (days)	Pupal period (days)	Pupal weight (mg)	Pupation (%)	Adult Emergence (%)	Fecundity Female^{-1}
T281	6.93^{b}	10.16^{ab}	3.39^{cd}	70.37^{e}	60.92^{e}	16.19^{e}
T506	7.25^{a}	10.19^{ab}	3.26^{e}	69.91^{e}	59.11^{e}	16.00^{e}
T524	7.26^{a}	10.23^{a}	3.28^{de}	70.20^{e}	60.29^{e}	16.07^{e}
T575	6.98^{b}	10.18^{ab}	3.40^{c}	70.37^{e}	60.54^{e}	16.33^{e}
T364	6.54^{c}	9.59^{c}	3.53^{b}	74.07^{cde}	66.40^{d}	16.96^{d}
150	6.58^{c}	9.54^{c}	3.53^{b}	79.32^{abc}	72.38^{c}	17.13^{cd}
T123	6.53^{c}	9.59^{c}	3.54^{b}	83.33^{a}	77.78^{a}	17.40^{c}
55	6.08^{de}	9.40^{d}	3.80^{a}	80.29^{ab}	76.63^{ab}	18.19^{ab}
168	6.06^{de}	9.37^{de}	3.78^{a}	83.33^{a}	77.39^{a}	18.36^{a}
T376	6.04^{e}	9.27^{e}	3.70^{a}	77.73^{bc}	73.67^{bc}	18.07^{ab}
HB-42(S)	6.19^{d}	9.37^{de}	3.76^{a}	76.68^{bcd}	76.45^{ab}	17.91^{b}
Aruso(R)	7.00^{b}	10.09^{b}	3.37^{cde}	72.22^{de}	61.11^{e}	16.23^{e}
Mean	6.62	9.75	3.53	75.65	68.56	17.07
SE±	0.05	0.04	0.04	1.81	1.24	0.15
LSD(P=0.05)	0.14	0.10	0.11	5.28	3.62	0.43
CV (%)	6.81	4.00	5.58	7.44	11.37	5.28

Means in a row followed by different letters are significantly different; SE=Standard Error; CV=coefficient of variation, LSD=Least Significant Differences; S =Susceptible Check; R=Resistance Check

4.7. Antibiosis indices

The average antibiosis indices of barley shoot fly on 12 barley genotypes were presented in Table 16. Highly significant genotype differences ($p<0.001$) were observed for all recorded parameters (Appendix 9). The growth, relative growth, developmental, adult emergence and fecundity indices were ranged between 9.65(T506) to 13.74(161), 0.78(T506 and T524) to 1.11(168), 0.98(T376) to 1.12(T506 and T524), 0.77(T506) to 1.02(T123), and 0.89(T506) to 1.03(168), respectively. The growth, relative growth, adult emergence and fecundity indices were lower in susceptible genotypes than the resistance genotypes. However, the developmental index was higher in resistance genotypes than the susceptible genotypes. This shows that, the barley shoot fly complete her life cycle within a short period of days in susceptible genotypes than the resistance genotypes. The results in the current study are in line with the previous findings of Chamarthi, 2008; except fecundity index.

Table 16. Average antibiosis indices of barley shoot fly on 12 barley genotypes (SARC, South Eastern Ethiopia, 2023/2024)

Genotypes	GI	RGI	DI	AEI	FI
T281	10.15^{e}	0.82^{e}	1.10^{b}	0.80^{e}	0.90^{e}
T506	9.65^{e}	0.78^{e}	1.12^{a}	0.77^{e}	0.89^{e}
T524	9.66^{e}	0.78^{e}	1.12^{a}	0.79^{e}	0.90^{e}
T575	10.09^{e}	0.81^{e}	1.10^{b}	0.79^{e}	0.91^{e}
T364	11.32^{d}	0.91^{d}	1.04^{c}	0.87^{d}	0.95^{d}
150	12.06^{cd}	0.97^{cd}	1.04^{c}	0.95^{c}	0.96^{cd}
T123	12.76^{bc}	1.03^{bc}	1.04^{c}	1.02^{a}	0.972^{c}
55	13.21^{ab}	1.07^{ab}	0.99^{de}	1.00^{ab}	1.02^{ab}
168	13.74^{a}	1.11^{a}	0.99^{de}	1.01^{a}	1.03^{a}
T376	12.87^{bc}	1.04^{bc}	0.98^{e}	0.96^{bc}	1.01^{ab}
HB-42(S)	12.40^{bc}	1.00^{bc}	1.00^{d}	1.00^{ab}	1.00^{b}
Aruso(R)	10.31^{e}	0.83^{e}	1.10^{b}	0.80^{e}	0.91^{e}
Mean	11.52	0.93	1.05	0.90	0.95
SE ±	0.30	0.024	0.004	0.02	0.01
LSD(P<0.05)	0.86	0.07	0.013	0.05	0.024
CV (%)	13.13	13.13	5.01	11.37	5.28

Means with superscripts in a row are significantly different; SE=Standard error; CV=coefficient of variation, LSD=Least significant differences; S =Susceptible check; R=Resistance check.GI=Growth index, RGI=Relative growth index, DI=Developmental index, AEI=Adult emergence index, and FI=Fecundity index.

5. SUMMARY, CONCLUSION AND RECOMMENDATIONS

Barley is the most important cereal crop in the world, primarily grown for food, feed, and malting purposes. However, its production is affected by many biotic and abiotic factors and among the biotic factors insect pests have been identified as a major limiting factor. Among biotic factors, barley shoot fly (*D. flavibasi*s) is the most common and affect barley at the seedling stage, and leading to reduction in the production and productivity of barley. The present study was conducted to screen barley genotypes, identify morphological and agronomic traits for selection and assess genetic variability to this pest, and determine the resistance category of barley genotypes to barley shoot fly.

During the main cropping seasons of 2022 and 2023, a total of 180 barley genotypes were screened for resistant to barely shoot fly. Different levels of resistance were recorded with 4 highly resistant 37 showing resistant, 31 moderately resistant, 51 susceptible and 57 highly susceptible genotypes. Landrace genotypes showed the highest resistance to barley shoot fly based shoot flies damage parameters including oviposition, infestation percent, and dead heart percent. Subsequently, 64 barley genotypes were selected to study for further identification of morphological and agronomic traits to select resistant barley genotypes to shoot fly. Traits like seedling vigor, leaf glossiness, seedling color, leaf width, seedling stem length, time to flowering and maturity, plant height, spike length, seed per spike, total tillers, fertile tillers, biomass yield, grain yield, and thousand kernel weight were used for screening and selecting resistance genotypes. Genetic variability was also considered important traits for improving barley genotypes to shoot fly. Traits with high heritability and genetic advance indicate minimal environmental influence, while low genetic advances suggest non additive gene expression may need heterosis breeding for improvement. Another study focused on the resistance category of barley genotypes against to *D. flavibasis* examined antixenosis and antibiosis. Twelve (12) barley genotypes were selected based on the results of the dead heart percentages from the last year screening. In multiple choice tests, there is a significant difference in eggs per seedling, seedling with eggs and dead heart percentages. Landrace genotypes, T281, T506, T524, T575, and Aruso (resistance check) were less preferred by barley shoot fly compared to the susceptible check (HB-42). In no choice test, significant differences were found in number of eggs per seedling and dead heart percentages among

genotypes, but the percentage of seedling with eggs was not statistically significant. In dual choice tests resistance barley genotypes (T281, T506, T524, T575, and Aruso) were less preferred for oviposition, shelter, and feeding compared to susceptible genotypes (55, 168 and T376). Similarly, the antibiosis test revealed highly significant variations among genotypes for all developmental parameters of *D. flavibasis*. These findings suggests that understanding the biology, behavior and population dynamics of the barley shoot fly is crucial for effective resistance breeding program for barely in order to manage the barley shoot fly.

In conclusion, the present study has shown that the barley shoot fly is becoming an important threat to barley production in the South Eastern of Ethiopia. This study also confirms the presence of variation in barley genotypes against shoot fly infestation. On the other hand, significant variation in infestation was observe among genotypes with different morphological and agronomic traits. These variations suggest that selecting resistant genotypes based on shoot fly infestation, morphological, and agronomic traits is important for resistant barely genotypes. Additionally, determining genotypic and phenotypic coefficients of variation, heritability, and genetic advance is important for understanding genetic diversity and potential for improvement through selection. Furthermore, antixenosis and antibiosis resistance were found the most prominently functioning of resistance forms to the barley shoot fly.

Overall, the study identified varying levels of resistance among different sources of barley genotypes to the barley shoot fly. Therefore, it is recommended to continue screening a larger collection of genotypes to identify and select those with high levels of resistance for further breeding programs. In this study the morphological and agronomic traits identified were recommended for screening barley genotypes to the barley shoot fly. However, further research should focus on understanding other morphological traits like trichome density, biochemical traits such as soluble sugar, moisture, protein, tannins, polyphenols, and lignin, and nutritional traits like nitrogen, potassium, calcium, magnesium, and other microelements and their relation to the barley shoot fly.

Moreover, genetic variability in barely genotypes was found to be important in improving barley genotypes for resistance to the barley shoot fly. Future studies should confirm the genes involved for resistant barley genotypes to the barley shoot fly using molecular markers. In general, barley genotypes T281, T506, T524, and T575 could be important in breeding

programs aimed at developing resistance to barley shoot fly. Landrace barley genotypes have shown superior potential in terms of resistance against barley shoot fly, suggesting the need for further systematic screening of barley landraces to exploit their potential for resistance to barley shoot fly breeding programs.

6. REFERENCES

Abebe, T.D., Abate, A. and Leon, J., 2023. Genetic diversity within landraces of barley (*Hordeum vulgare* L.) and its implications on germplasm collection and utilization. Genetical Resources and Crop Evolution, 70, 1985-1998.

Abinaya, Kumaravadivel, Varanavasiappan, & Kavithamani., 2019. Screening the genotypes of sorghum (*Sorghum bicolor* (L.) Moench) BC1 F3 generation of the cross CO (S) 28 x IS18551 for shoot fly (*Atherigona ssoccata* (Rond.) resistance.

Ahmed, M., Smith, J., & Jones, R., 2015. Genetic Diversity Assessment of Barley Germplasm at ICARDA. Journal of Agricultural Genetics, 20(3), 112-125.

Alemayehu Keba Beyene., 2024. An overview of Ethiopia's Barley Productivity, Import QuantityandConsumption.ScienceFrontiers,5(1),pp.1-3.

Alemayehu, T., Gebremedhin, W., & Tadesse, A., 2012. Genetic Diversity and Characterization of Ethiopian Barley Germplasm. Ethiopian Journal of Agricultural Sciences, 20(1), 45-58.

Alemu, F. Mekbib, and T. Desalegn., 2016. Estimation of genetic and phenotypic correlation coefficients and path analysis of yield and yield contributing traits of bread wheat (*Triticum aestium* L.) genotypes, International Journal of Natural Resource Ecology and Management, vol. 1, no. 4, pp. 145–154.

Allard, R.W., 1960. Principles of plant breeding. John Willey and Sons. Inc. New York, 485.

Allo A. Dido, B. J. K. Singh, Dawit T. Degefu, K. T. & M. S. R. K., 2021. Diversity and resistance components analysis of barley landraces to barley shoot fly (*Delia flavibasis*). Journal of Plant Diseases and Protection, pp. 139–152. https://doi.org/10.1007/s41348-020-00364-4.

Amanuel Tekalign, Tadele Tadesse, and Belay Asmare., 2022. Registration of Hora, Small-red Seed Food Type Common Bean (*Phaseolus vulgaris*) Varieties for Midland Areas of Bale and East Bale, Southeast Ethiopia. Plant, 10(1), pp. 36-39.

Amare Andargie., 1993. Infestation and damage level of barley shoot fly (*Delia arambourgi*) at Sinana. In: Proceedings of the Joint Conference of the Ethiopian Phytopathological Committee and the Committee of Ethiopian Entomologists. Addis Ababa, Ethiopia, 5-6 March 1992. Crop Protection Society of Ethiopia (CPSE), Addis Ababa, pp. 28.

Anjaria, P. and Vaghela, S., 2024. Toxicity of agrochemicals: Impact on environment and human health. Journal of Toxicological Studies, 2(1).

Arora, N., Mishra, S.P., Nitnavare, R.B., Jaba, J., Kumar, A.A., Bhattacharya, J., Sohu, R.S., & Sharma, H.C., 2021. Morpho-physiological traits and leaf surface chemicals as

markers conferring resistance to sorghum shoot fly (*Atherigona soccata* Rondani). Field Crops Research, 261, p.108029.

Aruna, C., Bhagwat, V.R., Sharma, V., Hussain, T., Ghorade, R.B., Khandalkar, H.G., Audilakshmi, S., & Seetharama, N., 2011. Genotype× environment interactions for shoot fly resistance in sorghum (*Sorghum bicolor* (L.) Moench): response of recombinant inbred lines. Crop Protection, 30(6), pp.623-630.

Assamere, A., Mamuye, A., Amare, K., & Fiseha, M., 2021. Diversity, distribution, agronomic and post-harvest management of local barley (*Hordeum vulgare* L.) variety in South Wollo, Ethiopia. PLOS ONE, 16(5), p.e0250899.

Ayoub, L., Yaqoob, M., Zahoor, S., Wani, F.F., Irshad, S.S., Gull, A., & Sheikh, M.A., 2024. Role of Induced Resistance in Insect-Pest Management. In: Plant Resistance to Insects in Major Field Crops, pp. 249-277. Singapore: Springer Nature Singapore.

Bedada, W., Karltun, E., Lemenih, M., & Tolera, M., 2014. Long-term addition of compost and NP fertilizer increases crop yield and improves soil quality in experiments on smallholder farms. Agriculture, Ecosystems & Environment, 195, pp. 193-201.

Bekele, A., Tesfaye, K., & Wondimu, B., 2017. Comprehensive Study on the Genetic Diversity of Barley Germplasm in Ethiopia. Journal of Plant Genetics and Breeding, 25(3), 112-125.

Belay., 2023. Genetic Variability and Relationship Among Yield, Yield Related Traits and Quality Attributes in Small Seeded Common Bean (*Phaseolus Vulgaris* L.) Genotypes at Goro and Ginnir, Southeast Ethiopia. MSc thesis. Alemaya University, Ethiopia.

Bezabeh, A., Beyene, F., Haji, J., & Lemma, T., 2022. Evaluating the commercialization of smallholder malt barley farmers via vertical coordination in Arsi highlands, Oromia region, Ethiopia. Cogent Economics & Finance, 10(1), p.2125660.

Boniface, P.J., Jose, A.M., & Husain, A.S., 2019. Training needs of farmers and agricultural extensionists on selected information technology enabled systems for agriculture. Journal of Extension Education, 31(1).

Bonjean, A.P. and Angus, W.J., 2001. Barley: origin, botany, culture, winter hardiness, genetics utilization, pests. USDA Agriculture Handbook 338.

Bullock, J.A., 1965. The control of Hylemya *Arambourg*i Seguy (Diptera: Anthomyiidae) on barley. Bulletin of Entomological Research, 55, pp. 645–661.

Burton, G.W. and Devane, D.E., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy Journal, 45(10), pp. 478-481.

Chamarthi, S. K., 2008a. Bio-ecology and Management of Aphid, *Rhopalosiphum maidis* (Fitch) on Barley, *Hordeum vulgare* Linn. (M.Sc. Thesis). Chaudhary Charan Singh Haryana Agricultural University, Hisar, India.

Chamarthi, S.K., 2008b. Biochemical mechanisms of resistance to shoot fly, *Atherigona soccata* (Rondani) in sorghum, Sorghum bicolor (L.) Moench (Doctoral dissertation, Jawaharlal Nehru Technological University).

Chamarthi, S.K., Sharma, H.C., Sahrawat, K.L., Narasu, L.M. and Dhillon, M.K., 2011. Physico-chemical mechanisms of resistance to shoot fly, *Atherigona soccata* in sorghum, Sorghum bicolor. Journal of Applied Entomology, 135(6), pp. 446-455.

Chekol, G. M., Wakgari, M., & Damte, T., 2021. Resistance Mechanism in Lentil (*Lens Culinaris* Medikus) Genotype To Pea Aphid (*Acyrthosiphon pisum* HARRIS) Haramaya Re. March. https://doi.org/10.13140/RG.2.2.32063.64165.

CSA., 2019. Agricultural Sample Survey: Area and Production of Crops (Private Peasant Farms), Report on Area and Production of Crops (Private Peasant Farms), Vol. II. Statistical Bulletin 582. Central Statistical Agency, Addis Ababa, Ethiopia.

CSA., 2021.The Federal Democratic Republic of Ethiopia Report on Area and Production of Major. I.

Daniel Tadesse and Beyene Derso., 2019. The status and constraints of food barley production in the North Gondar highlands, North Western Ethiopia.

Davidson A., 1969. Effect of some systemic insecticides on an infestation of the barley shoot fly, *Delia arambourgi* in Ethiopia. East African Agricultural and Forestry Journal, 34, pp. 422–425.

Deshmukh, S.N., Basu, M.S., & Reddy, P.S., 1986. Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences, vol. 56, pp. 515–518.

Dessie, A., 2018. Cereal crops research achievements and challenges in Ethiopia. International Journal of Research Studies in Agricultural Sciences, 4(6), pp. 23-29.

Dhillon M. K., 2004. Effects of cytoplasmic male-sterility on resistance to sorghum shoot fly, *Atherigona soccata* (Rondani). Ph.D. Thesis, 382 pp. Department of Entomology, Chaudhary Charan Singh Haryana Agricultural University, Hisar 125004, Haryana, India.

Dhillon, M. K., Sharma, H. C., Singh, R., & Naresh, J. S., 2005. Mechanisms of resistance to shoot fly, *Atherigona soccata* in sorghum. Euphytica, 144(3), pp. 301–312. https://doi.org/10.1007/s10681-005-7400-4.

Dwivedi, S. A., & Pandit, T. R., 2024. Host Plant Resistance and Sustainable Management of Insect Pests. In: Antimicrobial Resistance in Agriculture and its Consequences, pp. 95-110. CRC Press.

Ephrem Adamu., 2024. Response of Barley (*Hordeum Vulgare* L.) Genotypes to Soil Acidity, At Hula District, Sidama Region, Ethiopia. Middle East Research Journal of Agriculture and Food Sciences, 4(1), pp. 1-14.

Esayas Mendesil., 2015. Evaluation of plant resistance in field pea by host plant choice behavior of pea weevil (*Bruchus pisorum* L.). Acta Universitatis Agriculturae Sueciae, (2015: 101).

Esayas Mendesil., 2016. Oviposition preference of pea weevil, *Bruchus pisorum* L. among host and non-host plants and its implication for pest management.

Falconer, D. S., 1990. Introduction to Quantitative Genetics, 3rd Edition. John Wiley and Sons, Inc., New York.

Falconer, D.S. and Mackay, F.C.T., 1996. Introduction to Quantitative Genetics, 4th Edition. Longman Group Limited. Harlow, Essex, England: 108-183.

FAO., 2021. World Food and Agriculture. Rome: Food and Agriculture Organization of the United Nations.

Faria, L., Costa, J., Rava, C., Peloso, M., Melo, L., Carneiro, G., Soares, D., Díaz, J., Abreu, A. and Faria, J., 1999. Barley: origin, botany, culture, winter hardiness, genetics, utilization, pests. Dados de catalogação na fonte:(Marlene Cravo Castillo–CRB-10/744), 27(1), p.31.

Fikir Desalew. (2022). Review On Genetic Variability of Ethiopian Barley (*Hordeum Vulgare* L.) Genotypes for Acid Soil Stress Tolerance. International Journal of Research Studies in Agricultural Sciences (IJRSAS), 8(6), 1-5.

Fikre, S. Alamerew, and Z. Tadesse., 2015. Genetic variability studies in bread wheat (*Triticum aestivum* L.) genotypes at Kulumsa agricultural research center, south east Ethiopia. Journal of Biology, Agriculture and Healthcare, vol. 5, no. 5, pp. 2224–3208.

Gahukar, R. T., 1987. Population dynamics of sorghum shoot fly, *Atherigona soccata* (Diptera: Muscidae), in Senegal. Environmental Entomology, 16(4), pp. 910-916.

Gardi, M.W., Memic, E., Zewdu, E. and Graeff-Hönninger, S., 2022. Simulating the effect of climate change on barley yield in Ethiopia with the DSSAT-CERES-Barley model. Agronomy Journal, 114(2), pp.1128-1145.

Garome Shifaraw Geneti, Sentayehu Alamerew Kebede, and Techale Birhan Mekonnen., 2022. Genetic Variability and Association of Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes in Gechi District, South West Ethiopia. Hindawi Advances in Agriculture, Article ID 7132424, 17 pages. https://doi.org/10.1155/2022/7132424.

Gebru, A., Mekbib, F., & Lakew, B., 2018. Estimation of Genetic Variability of Malt Barley (*Hordeum vulgare* l.) Varieties for Yield, Yield Related Trait, North Eastern Ethiopia. International Journal of Plant Biology & Research, 6(6): 1105.

Gebru, K.M., Rammelt, C., Leung, M., Zoomers, A. and van Westen, G., 2019. Inclusive malt barley business and household food security in Lay Gayint district of northern Ethiopia. Food Security, 11, pp.953-966.

Getachew, T., Mekonnen, T., Assefa, A., & Gebremedhin, T., 2021. Agro-morphological traits-based genetic diversity assessment in Ethiopian barley (*Hordeum vulgare* L.) landrace collections from Bale highlands, Southeast Ethiopia. Agriculture & Food Security, 10(1), 58. DOI: 10.1186/s40066-021-00335-4.

Ghamkhar, K., Williams, W.M. and Brown, A.H.D. (eds.)., 2023. Plant genetic resources for the 21st century: the OMICS era. CRC Press.

Girma, H., Haile, A., & Abate, T. (1993). Insect pests of barley in Ethiopia. Barley and Wheat Improvement Program, Institute of Agricultural Research, Addis Ababa, Ethiopia.

Golla, S. K., Sharma, H. C., Rajasekhar, P., Mishra, S. P., & Jaba, J., 2020. Biochemical components of wild relatives of chickpea confer resistance to pod borer, *Helicoverpa armigera*. Arthropod-Plant Interactions, 14(5), pp. 623–639. https://doi.org/10.1007/s11829.

Gorthy, S., Narasu, L., Gaddameedi, A., Sharma, H. C., Kotla, A., Deshpande, S. P., & Are, A. K., 2017. Introgression of shoot fly (*Atherigona soccata* L. Moench) resistance QTLs into elite post-rainy season sorghum varieties using marker assisted backcrossing (MABC). Frontiers in Plant Science, 8, pp. 1494.

Haile, A., & Ali, M., 1985. Insect pests of barley in Ethiopia. In Barley and Wheat Improvement Program, Institute of Agricultural Research, Addis Ababa, Ethiopia.

Haile, M.Y., 2018. Review on barley breeding and its status in Ethiopia. International Journal of Research Studies in Agriculture and Science, 4(9), pp. 13-21.

Hailu Gebere., 1997. Improved barley varieties for Bale and Arsi zones. In: Abera Deressa and Beyene Seboka (eds.), Research Achievements and Technology Transfer Attempts in South eastern Ethiopia. Proceedings of the Second Technology Generation Transfer and Gap Analysis Workshop, 9–11 July 1996, Nazret, Ethiopia.

Harlan, J.R. and Zohary, D., 1966. Distribution of Wild Wheat and Barley. Science, 153: 1074–1080.

Harlan, J.R., 1976. Barley, *Hordeum vulgare* (*Gramineae-triticineae*). In: N.W. Simmonds, ed., Evolution of Crop Plants. Longman Group, London, pp. 93-98.

Hill, D.S., 1983. Agricultural Insect Pests of the Tropics and Their Control (2nd ed.), Cambridge University Press, Cambridge, 746pp.

Hill, D.S., 1987. Agricultural Insect Pests of Temperate Regions and Their Control. Cambridge University Press, Cambridge, UK.

Hill, D.S., 1993. Agricultural insect pests of the tropics and their control, 2nd edition. Cambridge University press, Cambridge, 746.

Hussien, M.L.A., Melde, C. and Wetzel, T., 1993. Investigations on the effects of seed treatment of winter wheat with Decis (*deltamethrin*), Filitox (*metamidophos*) and Baythroid (*cyfluthrin*) against larvae of the wheat bulb fly (*Delia coarctata* Fall). Journal of Phytopathology and Plant Protection, 28, pp. 147–154.

Irwin, M. E., & Goodman, R. M., 1981. Ecology and control of barley yellow dwarf. In D. Pimentel (Ed.), CRC Handbook of Pest Management in Agriculture (Vol. 1, pp. 269-293).

Jalal Al-Tabbal, J. and Al-Fraihat, A.H., 2012. Genetic Variation, Heritability, Phenotypic and Genotypic Correlation Studies for Yield and Yield Components in Promising Barley Genotypes. Journal of Agricultural Science, 4, pp. 193-210.

Jalata, Z., 2023. Barley Production Trend, Breeding Efforts, Achievements and Constraints: The case of Ethiopia. Journal of Agriculture, Food and Natural Resources, 1(2), pp. 70-82.

Jan, S., Iram, S., Bashir, O., Shah, S.N., Kamal, M.A., Rahman, S., Kim, J., & Jan, A.T., 2024. Unleashed Treasures of Solanaceae: Mechanistic Insights into Phytochemicals with Therapeutic Potential for Combatting Human Diseases. Plants, 13(5), pp. 724.

Jasrotia, R., Langer, S., & Dhar, M., 2024. Pesticide impacts on humans. In: Pesticides in a Changing Environment, pp. 203-222. Elsevier.

Jilo, T., Tulu, L., Birhan, T. and Beksisa, L., 2018. Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia. Journal of Plant Breeding and Crop Science, 10(10), pp.281-289.

Joshi, S., Hussain, T., Kirar, V. S., & Nagar, R., 2016. *Atherigona soccata*, 9(July 2011), pp. 23–26.

Jyoti, J.L., Shelton, A.M. and Earle, E.D., 2001. Identifying sources and mechanisms of resistance in crucifers for control of cabbage maggot (Diptera: Anthomyiidae). Journal of Economic Entomology, 94(4), pp.942-949.

Karanjkar, R.R., Chundurwar, R.D., & Borikar, S.T., 1992. Correlations and path analysis of shoot fly resistance in sorghum. Journal of Maharashtra Agricultural Universities, 17, pp. 389-391.

Karban, R., 2011. The ecology and evolution of induced resistance against herbivores. Functional Ecology, 25, pp. 339-47.

Kassa Mammo, Dagne Wegary, Dagnachew Lule and Firew Mekbib., 2019. Genetic variability of common bean (*Phaseolus vulgaris* L.) genotypes under sole and maize-bean cropping.

Keneni, G., Bekele, E., Getu, E., Imtiaz, M., Damte, T., Mulatu, B. and Dagne, K., 2011. Breeding food legumes for resistance to storage insect pests: potential and limitations. Sustainability, 3(9), pp.1399-1415.

Kifle, S.M., 2016. Review on barley production and marketing in Ethiopia. Journal of Economics and Sustainable Development, 7(9), pp.91-100.

Kiranmayee, K.U., Kishor, P.K., Hash, C.T. and Deshpande, S.P. 2016. Evaluation of QTLs for shoot fly (*Atherigona soccata*) resistance component traits of seedling leaf blade glossiness and trichome density on sorghum (*Sorghum bicolor*) chromosome SBI-10L. Tropical Plant Biology, 9, pp.12-28.

Kogan, M., & Ortman, E. E., 1978. Antixenosis - a new term proposed to replace Painter's "non-preference" modality of resistance. Entomology Society of America, 24, pp. 175-176.

Kumar, C.S., Sharma, H.C., Narasu, M.L. and Pampapathy, G., 2008. Mechanisms and diversity of resistance to shoot fly, *Atherigona soccata* in Sorghum bicolor. Indian Journal of Plant Protection, 36(2), pp.249-256.

Kumar, P., Banjarey, P., Malik, R., Tikle, A.N. and Verma, R.P.S., 2020. Population structure and diversity assessment of barley (*Hordeum vulgare* L.) introduction from ICARDA. Journal of Genetics, 99(1), p.70.

Lev-Yadun, S., 2021. Avoiding rather than resisting herbivore attacks is often the first line of plant defence. Biological Journal of the Linnean Society, 134(4), pp. 775-802.

Macharia, M., & Mueke, J. M., 1986. Resistance of barley varieties to barley fly, *Delia flavibasis* Stein (Diptera: Anthomyiidae). Insect Science and its Application, 7, pp. 75–77.

Majumdar, M.K., Chatterjee, S.D., Bose, S.D.P. and Bhattacharya, G., 1974. Variability inter relationships and coefficient analysis for some quantitative characters in okra (*Abelmoschus esculentus* (L) Moench). Indian Agriculture Journal, 18: 13-20.

Malik, M. F., Nawaz, M., Haider, Z., Hanif, M. S., & Iqbal, A., 2013. Screening of barley germplasm against corn leaf aphid, Rhopalosiphum maidis (Fitch) (Homoptera: Aphididae). Pakistan Journal of Zoology, 45(1), 1-6.

Mallik Malipatil and Plant Health Australia., 2008. Industry Biosecurity Plan for the Grains Industry.

Manetas, Y., 2006. Flora-Morphology, Distribution, Functional Ecology of Plants, 201, pp. 163-177.

Mehtre, S.P., 2006. Genetic diversity analysis, QTL mapping and marker-assisted selection for shoot fly resistance in sorghum (*Sorghum bicolor* (L,) Moench) (Doctoral dissertation, Marathwada Agricultural University, Parbhani).

Mengesha, M.H., Rao, S.A. and Reddy, C.R., 1990. Characteristics and potential uses of some genetic stocks of pearl millet in the world collection. Indian Journal of Plant Genetic Resources, 3(01), pp.1-7.

Mesay Yami., 2020. Malt Barley Value Chain in Arsi and West Arsi highlands of Ethiopia. Research on Humanities and Social Sciences, 10(18).

Meseret Shiferaw., 2016. Determinants of Smallholder Farmers' Production and Marketing of Malt Barley in Ethiopia.

Mihret Yirgu, Mulugeta Kebede, Tileye Feyissa, Berhane Lakew, Aemiro Bezabih Woldeyohannes., 2022. Morphological variations of qualitative traits of barley (*Hordeum vulgare* L.) Accessions in Ethiopia.

Mohammed, R., Are, A.K., Munghate, R.S., Gaddameedi, A., Polavarapu Bilhan, K.K. and Sharma, H.C., 2018. Pattern of genetic inheritance of morphological and agronomic traits of sorghum associated with resistance to sorghum shoot fly, *Atherigona soccata*. Euphytica, 214, pp.1-20.

Mohammed, R., Munghate, R.S., Are, A.K., Polavarapu, K.K.B., Reddy, B.V. and Sharma, H.C., 2016. Components of resistance to sorghum shoot fly, *Atherigona soccata*. Euphytica, 207, pp.419-438.

Mulatu, B., & Grando, S. (Eds)., 2011. Barley Research and Development in Ethiopia. Proceedings of the 2nd National Barley Research and Development Review Workshop. 28-30 No.

Muluken G., Emana G. and Tadele T., 2011. Biology and population dynamics of *Delia flavibasis* Stein (Diptera: Anthomyiidae) in Bale, Ethiopia. Barley Research and Development in Ethiopia, p. 173.

Muluken Goftishu, Tadele Tefera, and Emana Getu., 2009. Biology of barley shoot fly *Delia flavibasis* Stein (Diptera: Anthomyiidae) on resistant and susceptible barley cultivars. November 2006, HARC, Holetta, Ethiopia. ICARDA, PO Box 5466, Aleppo, Syria, pp. 157-172.

Muñoz-Amatriaín, M., Cuesta-Marcos, A., Hayes, P.M. and Muehlbauer, G.J., 2014. Barley genetic variation: implications for crop improvement. Briefings in Functional Genomics, 13(4), pp. 341-350.

Murray, G.M. and Brennan, J.P., 2009. The current and potential costs from diseases of barley in Australia (p. 59). Barton, ACT, Australia: Grains Research and Development Corporation.

Nadeem, M. H., Sadaqat, A. H., & Khan, I. H., 2005. Genetic potential of high forage yielding sorghum x sudangrass hybrids for resistance to stem borer (*Chilo partellus*) and shoot fly (*Atherigona soccata*). Pak. Entomol. Vol. 27, pp. 57-62.

Nyiraguhirwa, D., Niyonzima, F. N., & Uwimana, B., 2022. Genetic diversity and population structure analyses in barley (*Hordeum vulgare*) against corn-leaf aphid, *Rhopalosiphum maidis* (Fitch). Frontiers in Plant Science, 14, 1188627.

Ogenga-Latigo, M. W., Balidawa, C. W., & Ampofo, J. K. O., 1993. Factors influencing the incidence of black bean aphid on common beans intercropped with maize. African Crop Science Journal, 1, pp. 49-58.

Ogunleye, R. F., 2001. Comparative effectiveness of Gamalin 20, Audrex 40 and Vetox 85 in controlling *Eurema hacabe* (L.) a defoliator of Parkia biglobossa. Journal of Science in Education and Technology, 5, pp. 77-80.

Painter, R. H., 1928. Notes on the injury to plant cells by chinch bug feeding. Annals of the Entomological Society of America, 21(2), pp. 232-242.

Patil, S.P. and Bagde, A.S., 2017. Physio–chemical resistance mechanism of sorghum genotypes against shoot fly (*Atherigona soccata*) (Rondani). Int J Curr Microbiol App Sci, 6(9), pp. 2742-2746.

Pawlak, I. G., Dallacort, S., Paloschi, C. L., Brun, E. J., Colombo, F. C., Maciel, R. M. A., Abati, R., Cechim, F. E., Lozano, E. R., Mazaro, S. M., & Potrich, M., 2024. Preference of *Thaumastocoris peregrinus* (Hemiptera: Thaumastocoridae) and biochemical analysis of different genetic materials of Eucalyptus. Arthropod-Plant Interactions, 1-10.

Perez-Harguindeguy, N., Diaz, S., Garnier, E., Lavorel, S., Poorter, H., Jaureguiberry, P., Bret-Harte, M.S., Cornwell, W.K., Craine, J.M., Gurvich, D.E., & Urcelay, C., 2016. Corrigendum to: New handbook for standardised measurement of plant functional traits worldwide. Australian Journal of Botany, 64(8), pp. 715-716.

Peter, A. J., Shanower, T. G., & Romeis, J., 1995. The role of plant trichomes in insect resistance: a selective review. Phytophaga, 7, pp. 41-63.

Peterson, R. K. D., Higley, L. G., & Pedigo, L. P., 2017. "Integrated Pest Management and Plant Resistance: A Comprehensive Review." Journal of Agricultural Entomology, 25(3), 112-125.

Peterson, R. K., Varella, A. C., & Higley, L. G., 2017. Tolerance: the forgotten child of plant resistance. PeerJ, 5, e3934.

Poehlman, J.M. and David, A.S., 1995. Breeding Field Crops, 4th Edition. Ames: Iowa State University Press, USA, 494.

Rana, B. S., Tripathi, D. P., Balakotaiah, K., Damodar, R., & Rao, N. G. P., 1975. Genetic analysis of some exotic × Indian crosses in sorghum selection for shoot fly resistance. Indian J Genet, 35, pp. 350–355.

Reddy, B.V., Reddy, P.S., Sadananda, A.R., Dinakaran, E., Ashok Kumar, A., Deshpande, S.P., Srinivasa Rao, P., Sharma, H.C., Sharma, R., Krishnamurthy, L. and Patil., 2012.

Postrainy season sorghum: Constraints and breeding approaches. Journal of SAT Agricultural Research, 10(1), pp.1-12.

Riyazaddin, M., 2015. Genetic variability for shoot fly resistance, grain characteristics, and yield in the postrainy season sorghums (Doctoral dissertation, Osmania University, Hyderabad).

Riyazaddin, M., Kavi Kishor. P.B., Ashok Kumar, A., Reddy, B.V., Munghate, R.S. and Sharma, H.C; 2015. Mechanisms and diversity of resistance to sorghum shoot fly, *Atherigona soccata*. Plant Breeding, 134(4), pp.423-436.

Robinson, H. F., Comstock, R.E. and Harvey, P.H., 1955. Estimates of heritability and the degree of dominance in maize. Agronomy of Journal, 41: 353-359.

Rochow, W. F., 1979. Transmission of barley yellow dwarf virus by aphids. In K. F. Harris & K. Maramorosch (Eds.), Aphids as Virus Vectors (pp. 359-377).

Saini, P., Saini, P., Kaur, J.J., Francies, R.M., Gani, M., Rajendra, A.A., Negi, N., Jagtap, A., Kadam, A., Singh, C. and Chauhan, S.S., 2020. Molecular approaches for harvesting natural diversity for crop improvement. In: Rediscovery of genetic and genomic resources for future food security, pp. 67-169.

Samuel Weldeyohanis ., 2017. Value Chain Analysis of Malt Barley (*Hordeum vulgare* L.): The Case of Lemu Bilbilo Woreda, East Arsi Zone, Oromia National Regional State of Ethiopia. Jimma University MSc Thesis.

Santamaria ME, Arnaiz A, Rosa-Diaz I, González-Melendi P, Romero-Hernandez G, Ojeda-Martinez DA, Garcia A, Contreras E, Martinez M, Diaz I., 2020. Plant Defenses Against Tetranychus urticae: Mind the Gaps. Plants, 9(4), 464.

SARC. 2004., 2019. Entomology Progress Report for 2004/05, and 2018/209. SARC, Sinana, Ethiopia.

Satish, K., Srinivas, G., Madhusudhana, R., Padmaja, P. G., Nagaraja Reddy, R., Murali Mohan, S., & Seetharama, N., 2009. Identification of quantitative trait loci for resistance to shoot fly in sorghum [*Sorghum bicolor* (L.) Moench]. Theoretical and Applied Genetics, 119, pp. 1425-1439.

Shahbandeh., 2024. Major barley producers worldwide in 2023/2024, by country (in million metric tons).

Sharma J.R., 1998, .Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited, Publishers, New Delhi, 432.

Sharma, H.C., 1996. Crop Protection Compendium: Sorghum shoot fly, *Atherigona soccata.* Electronic Compendium for Crop Protection. Wallingford, U.K, CAB International.

Sharma, H.C., Bhagwat, V.R. and Padmaja, P.G., 2008. Techniques to screen sorghums for resistance to insect pests.

Shiferaw, T. and Tadele, M., 2022. Genetic Diversity of Ethiopian Barley (Hordeum vulgare L.) Genotypes Based on Multivariate Statistical Analysis for Acid Soil Tolerance.

Shrestha, R.K. and Lindsey, L.E., 2019. Agronomic management of malting barley and research needs to meet demand by the craft brew industry. Agronomy Journal, 111(4), pp. 1570-1580.

Shuai, H.A.O., Yan-ling, S.O.N.G., Shuang, S.U.N. and Chun-yi, W.A.N.G., 2023. Review on the impacts of climate change on highland barley production in Tibet Plateau. Chinese Journal of Agrometeorology, 44(05), p. 398.

SINGH and VERMA .1988. Antibiosis Mechanism of Resistance to Stem Borer.

Singh, J., Prasad, L. C., Madakemohekar, A. H., & Bornare, S. S., 2014. Genetic variability and character association in diverse genotypes of barley (*Hordeum vulgare* L.). The International Quarterly of Journal of Life Sciences, 9(2), 759-761.

Singh, R.K. and Chaudhary., 1977. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi-Ludhiana India.

Singh, S. P., 1998. Field efficacy of some bio-pesticides against shoot fly and stem borer in forage sorghum. Forage Research, 24, pp. 177-178.

Sivasubramaniam and Menon., 1973a. “Inheritance of short stature in rice,” Madras Agricultural Journal, vol. 60, pp. 1129–1133.

Sivasubramanian, S., and P. Madhavamenon., 1973b. "Genotypic and phenotypic variability in rice." Madras Agricultural Journals, 60(9-13): 1093-1096.

Stephens, J.F., 1834. Illustrations of British Entomology, Or a Synopsis of Indigenous Insects: Containing Their Generic and Specific Distinctions, with an Account of Their Metamorphoses, Times of Appearance, Localities, Food, and Economy, as Far as Practicable. Embellished with Coloured Figures of the Rarer and More Interesting Species. Haustellata 4 Vols. Mandibulata 7 Vols. Supplement 1 (Vol. 4).

Straub, R. W., & Boothroyd, C. W., 1980. Barley yellow dwarf virus. In M. K. Corbett & H. D. Sisler (Eds.), Plant Diseases and Vectors: Ecology and Epidemiology (pp. 301-328).

Tadesse, D. and Derso, B., 2019. The status and constraints of food barley production in the North Gondar highlands, North Western Ethiopia. Agriculture & Food Security, 8, pp. 1-7.

Tafa Jobie and Bayeh Mulatu., 2006. Research achievements in barley shoot fly in Ethiopia.

Tafa Jobie and Bayeh Mulatu., 2011. Research achievements in barley shoot fly in Ethiopia. Barley Research and Development in Ethiopia, p. 157.

Tafa Jobie, Tadesse Gebremedhin & Sakhuja, P.K., 2004. Ovipositional antixenosis in some barley accessions to barley shoot fly. Pest Management Journal of Ethiopia, 8, pp. 51–57.

Tafa Jobie., 2003. Mechanisms of resistance in barley accessions to shoot fly, *Delia flavibasis* Stein. MSc thesis. Alemaya.

Tafa, J. and Muluken., 2007. Effect of sowing date on infestation of barley shoot fly on barley in southeastern Ethiopia. African Crop Science Conference Proceedings 8, pp. 1-6.

Tafa, J., 2007. *Delia flavibasis Stein* (Diptera: Anthomyiidae) as a major pest of wheat in the major cereal belt, southeast Ethiopia. In 8th African Crop Science Society Conference, El-Minia, Egypt, 27-31 October 2007 (pp. 965-969). African Crop Science Society.

Tamiru, A.M., Gebrehiwot, M., and Tefera, T., 2019. Traditional and modern uses of barley (Hordeum vulgare L.) in Ethiopia: a review. Journal of Cereals and Crop Science, 83: 129-135.

Taneja, S.L. and Leuschner, K., 1985. Resistance screening and mechanisms of resistance in sorghum to shoot fly. In: Proceedings, International Sorghum Entomology Workshop, 15-21 July, 1984, Texas A&M University, College Station, Texas, USA (Kumble, V. ed.): International.

Tarekegne, A., Gebre, H. and Francis, C.A., 1997. Yield limiting factors to food barley production in Ethiopia. Journal of Sustainable Agriculture, 10(2-3), pp. 97-113.

Taye Belachew and Yifru Abera ., 2010. Response of maize (*Zea mays* L.) to tied ridges and…

Teetes, G.L., Seshu Reddy, K.V., Leuschner, K., and House, L.R., 1983. Sorghum insect identification handbook. Information Bulletin No.12. Patancheru, A.P., India; International Crops Research Institute for the Semi-Arid Tropics.

Tekalign, Z., Bekele, H. and Tamirat, N., 2017. Evaluation of Seed Dressing Pesticides on Barely Shoot Fly, *Delia flavibasis* and Barely Stripe, *Pyrenophora graminea* Disease in South-Eastern Ethiopia. Journal of Plant Sciences, 5, pp. 29-33.

Teklemariam, S. S., Bayissa, K. N., Matros, A., Pillen, K., Ordon, F., & Wehner, G., 2022. The genetic diversity of Ethiopian barley genotypes in relation to their geographical origin. PLoS ONE, 17(5). https://doi.org/10.1371/journal.pone.0260422

Tesfaye Getachew, Mulugeta Amsalu & Kassahun Tesfaye., 1997. Varietal improvement on major crops in Bale zone of Oromiya Region, pp. 45–50, in: Abera Deressa and Beyene Seboka (eds.). Research Achievements and Technology Transfer Attempts in South eastern Ethiopia. Proceedings of the Second Technology Generation, Transfer and Gap Analysis Workshop, 9–11 July 1996, Nazret, Ethiopia.

Teshome, A., Mendesil, E., Geleta, M., Andargie, D., Anderson, P., Rämert, B., Seyoum, E., Hillbur, Y., Dagne, K., and Bryngelsson, T., 2015. Screening the primary gene pool of field pea (*Pisum sativum* L. subsp. sativum) in Ethiopia for resistance against pea weevil (*Bruchus pisorum* L.). Genetic Resources and Crop Evolution, 62, pp.525-538.

Tiwari, V., 2008. Growth and Production of Barley. Encyclopedia of Life Support Systems (EOLSS).

Transmission of barley yellow dwarf virus by aphids. In K. F. Harris & K. Maramorosch (Eds.), Aphids as Virus Vectors (pp. 359-377).

Udeh and Ogbu., 2011. "Principal component analysis of body measurements in three strains of broiler chicken," Science World Journal, vol. 6, no. 2, pp. 11–14.

Unnithan, G.C. & Reddy, K.V.S., 1985. Oviposition and infestation of the sorghum shoot fly, *Atherigona soccata* Rondani, on certain sorghum cultivars in relation to their relative resistance and susceptibility. Insect Sci Applic, 6, pp. 409–412.

USDA., 2023. World agricultural production. Ekonomika APK, 7, 5965.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants. Chron Bot, 13(1), 1-366.

Vikal, Y., Kaur, A., Jindal, J., Kaur, K., Pathak, D., Garg, T., Singh, A., Singh, P., & Yadav, I., 2020. Identification of genomic regions associated with shoot fly resistance in maize and their syntenic relationships in the sorghum genome. Plos one, 15(6), e0234335.

Von Bothmer, R., 1992. The wild species of Hordeum: Relationships and potential use for improvement of cultivated barley.In: PR Shewry, ed. Barley: Genetics, Biochemistry, Molecular Biology and Biotechnology. C.A.B International, Wallingford, Oxford, pp. 3-18.

Weibull, J., Ronquist, F., & Brishammar, S., 2003. Free amino acid composition of leaf exudates and phloem sap: a comparative study in oats and barley. Plant Physiology, 92(1), 222-226..

Welsh, J.R., 1990. Fundamentals of Plant Genetic and Breeding. John Wiley and Sons. New York.

Yared, T., Seyoum, A., Girma, T., Kabna, A., & Obsa, C., 2021. Integrated Management of Barley Shoot fly at highland of Guji zone southern Ethiopia. Acad. Res. J. Agri. Sci. Res., 9(1), pp. 23-30.

Yawson, D.O., Adu, M.O., & Armah, F.A., 2020. Impacts of climate change and mitigation policies on malt barley supplies and associated virtual water flows in the UK. Scientific Reports, 10(1), 376.

Yimer, A. H., 2021. Influence of Organic Fertilizers on Productivity of Barley: A Review. Agricultural Science Digest, 41(2), 1-5.

Yirgu, M., Kebede, M., Feyissa, T., Lakew, B., & Woldeyohannes, A.B., 2022. Morphological variations of qualitative traits of barley (*Hordeum vulgare* L.) accessions in Ethiopia. Heliyon, 8(10).

Yogeswari, P., Rani, C.S., Rao, G.R., & Manoj, V., 2019. Influence of bio-physical factors on shoot fly infestation in different sorghum genotypes cultivated under zero tillage in rice fallows. J. Entomol Zool. Stud, 7(1), pp. 808-814.

Yousuf, P., Razzak, S., Parvaiz, S., Rather, Y.A., & Lone, R., 2024. Role of Plant Phenolics in the Resistance Mechanism of Plants against Insects. In: Plant Phenolics in Biotic Stress Management, pp. 191-215. Singapore: Springer Nature Singapore.

Zeleke, T., Hundie, B., & Negash, T., 2017. Evaluation of Seed Dressing Pesticides on Barely Shoot Fly, *Delia flavibasis* and Barely Stripe, *Pyrenophora graminea* Disease in South-Eastern Ethiopia. Journal of Plant Sciences, 5(1), pp. 29-33.

Zemede, A., 2000. Barley production in Ethiopia. Proceedings of the first barley research review workshop, 16-19 October, Addis Ababa, IAR/ICARDA.

Zohary, D., & Hopf, M., 2000. Domestication of plants in the Old World: The origin and spread of cultivated plants in West Asia, Europe, and the Nile Valley. Oxford University Press.

7. APPENDICES

List of Appendix Table

Appendix 1. Entry number, source, description and types of screening barley genotypes

S.No	Entry No.	Source	Description	Barley types
1	17	ISBYT-HI-20/21	Exotic Line	Food Barley
2	21	ISBYT-HI-20/21	Exotic Line	Food Barley
3	T200	BETin	Landrace	Malt Barley
4	20	ISBYT-HI-20/21	Exotic Line	Food Barley
5	4	ISBYT-HI-20/21	Exotic Line	Malt Barley
6	T316	BETin	Landrace	Food Barley
7	T304	BETin	Landrace	Food Barley
8	3	ISBYT-HI-20/21	Exotic Line	Malt Barley
9	T32	BETin	Landrace	Food Barley
10	15	ISBYT-HI-20/21	Exotic Line	Food Barley
11	19	ISBYT-HI-20/21	Exotic Line	Food Barley
12	T315	BETin	Landrace	Malt Barley
13	T249	BETin	Landrace	Food Barley
14	2	ISBYT-HI-20/21	Exotic Line	Malt Barley
15	T464	BETin	Landrace	Food Barley
16	T21	BETin	Landrace	Malt Barley
17	1	ISBYT-HI-20/21	Exotic Line	Malt Barley
18	T329	BETin	Landrace	Malt Barley
19	T369	BETin	Landrace	Irregular
20	17	8TH GSBYT-20/21	Exotic Line	Malt Barley
21	15	8TH GSBYT-20/21	Exotic Line	Malt Barley
22	T51	BETin	Landrace	Food Barley
23	4	8TH GSBYT-20/21	Exotic Line	Food Barley
24	T376	BETin	Landrace	Food Barley
25	T525	BETin	Landrace	Malt Barley
26	T573	BETin	Landrace	Malt Barley
27	T438	BETin	Landrace	Malt Barley
28	T467	BETin	Landrace	Malt Barley
29	T422	BETin	Landrace	Malt Barley
30	6	8TH GSBYT-20/21	Exotic Line	Food Barley
31	T15	BETin	Landrace	Irregular
32	9	8TH GSBYT-20/21	Exotic Line	Malt Barley
33	T470	BETin	Landrace	Malt Barley
34	T344	BETin	Landrace	Irregular
35	12	8TH GSBYT-20/21	Exotic Line	Malt Barley
36	2	8TH GSBYT-20/21	Exotic Line	Food Barley
37	T520	BETin	Landrace	Food Barley

Appendix 1(Continued)

S.No	Entry No.	Source	Description	Barley types
38	3	8TH GSBYT-20/21	Exotic Line	Food Barley
39	T451	BETin	Landrace	Malt Barley
40	T97	BETin	Landrace	Irregular
41	4	8TH GSBYT-20/21	Exotic Line	Food Barley
42	T562	BETin	Landrace	Malt Barley
43	T301	BETin	Landrace	Food Barley
44	T367	BETin	Landrace	Malt Barley
45	T268	BETin	Landrace	Malt Barley
46	1	8TH GSBYT-20/21	Exotic Line	Food Barley
47	T318	BETin	Landrace	Food Barley
48	T100	8TH GSBYT-20/21	Exotic Line	Malt Barley
49	7	8TH GSBYT-20/21	Exotic Line	Food Barley
50	T482	BETin	Landrace	Irregular
51	T45	BETin	Landrace	Food Barley
52	11	8TH GSBYT-20/21	Exotic Line	Malt Barley
53	T78	BETin	Landrace	Irregular
54	T455	BETin	Landrace	Food Barley
55	19	8TH GSBYT-20/21	Exotic Line	Food Barley
56	T568	BETin	Landrace	Malt Barley
57	T72	BETin	Landrace	Malt Barley
58	T372	BETin	Landrace	Food Barley
59	T204	BETin	Landrace	Food Barley
60	114	IBON-20/21	Exotic Line	Food Barley
61	96	IBON-20/21	Exotic Line	Food Barley
62	T139	BETin	Landrace	Food Barley
63	T474	BETin	Landrace	Malt Barley
64	T62	BETin	Landrace	Food Barley
65	66	IBON-20/21	Exotic Line	Food Barley
66	T36	BETin	Landrace	Malt Barley
67	T386	BETin	Landrace	Malt Barley
68	88	IBON-20/21	Exotic Line	Food Barley
69	T207	BETin	Landrace	Malt Barley
70	T12	BETin	Landrace	Food Barley
71	T274	BETin	Landrace	Food Barley
72	T197	BETin	Landrace	Malt Barley
73	15	IBON-20/21	Exotic Line	Malt Barley
74	T374	BETin	Landrace	Food Barley
75	T38	BETin	Landrace	Food Barley

Appendix 1(Continued)

S.No	Entry No.	Source	Description	Barley types
76	T295	IBON-20/21	Exotic Line	Malt Barley
77	90	IBON-20/21	Exotic Line	Food Barley
78	T24	BETin	Landrace	Food Barley
79	51	IBON-20/21	Exotic Line	Malt Barley
80	T503	BETin	Landrace	Food Barley
81	T213	BETin	Landrace	Malt Barley
82	50	IBON-20/21	Exotic Line	Malt Barley
83	61	IBON-20/21	Exotic Line	Food Barley
84	T370	BETin	Landrace	Food Barley
85	59	IBON-20/21	Exotic Line	Food Barley
86	T352	BETin	Landrace	Food Barley
87	113	IBON-20/21	Exotic Line	Malt Barley
88	T364	BETin	Landrace	Irregular
89	T59	BETin	Landrace	Food Barley
90	T320	BETin	Landrace	Food Barley
91	100	IBON-20/21	Exotic Line	Food Barley
92	T444	BETin	Landrace	Food Barley
93	T519	BETin	Landrace	Malt Barley
94	T336	BETin	Landrace	Irregular
95	29	IBON-20/21	Exotic Line	Malt Barley
96	T258	BETin	Landrace	Irregular
97	T528	BETin	Landrace	Irregular
98	T281	BETin	Landrace	Food Barley
99	T184	BETin	Landrace	Food Barley
100	102	IBON-20/21	Exotic Line	Food Barley
101	T332	BETin	Landrace	Irregular
102	T1	BETin	Landrace	Food Barley
103	55	IBON-20/21	Exotic Line	Malt Barley
104	T447	BETin	Landrace	Irregular
105	105	IBON-20/21	Exotic Line	Food Barley
106	T401	BETin	Landrace	Irregular
107	T548	BETin	Landrace	Malt Barley
108	T521	BETin	Landrace	Malt Barley
109	5	IEMBSN-20/21	Exotic Line	Malt Barley
110	T229	BETin	Landrace	Malt Barley
111	17	IEMBSN-20/21	Exotic Line	Malt Barley
112	19	IEMBSN-20/21	Exotic Line	Malt Barley
113	T419	BETin	Landrace	Irregular

Appendix 1(Continued)

S.No	Entry No.	Source	Description	Barley types
114	20	IEMBSN-20/21	Exotic Line	Malt Barley
115	149	BETin	Landrace	Malt Barley
116	24	IEMBSN-20/21	Exotic Line	Malt Barley
117	T544	BETin	Landrace	Food Barley
118	29	IEMBSN-20/21	Exotic Line	Malt Barley
119	T56	BETin	Landrace	Food Barley
120	34	IEMBSN-20/21	Exotic Line	Malt Barley
121	T585	BETin	Landrace	Malt Barley
122	46	IEMBSN-20/21	Exotic Line	Malt Barley
123	T537	BETin	Landrace	Food Barley
124	48	IEMBSN-20/21	Exotic Line	Malt Barley
125	T559	BETin	Landrace	Malt Barley
126	T516	BETin	Landrace	Malt Barley
127	T254	BETin	Landrace	Food Barley
128	56	IEMBSN-20/21	Exotic Line	Malt Barley
129	T575	BETin	Landrace	Food Barley
130	62	IEMBSN-20/21	Exotic Line	Malt Barley
131	T307	BETin	Landrace	Food Barley
132	T289	BETin	Landrace	Food Barley
133	67	IEMBSN-20/21	Exotic Line	Malt Barley
134	T272	BETin	Landrace	Malt Barley
135	T208	BETin	Landrace	Malt Barley
136	69	IEMBSN-20/21	Exotic Line	Malt Barley
137	T346	BETin	Landrace	Irregular
138	73	IEMBSN-20/21	Exotic Line	Malt Barley
139	T271	BETin	Landrace	Malt Barley
140	75	IEMBSN-20/21	Exotic Line	Malt Barley
141	T514	BETin	Landrace	Food Barley
142	86	IEMBSN-20/21	Exotic Line	Malt Barley
143	T511	BETin	Landrace	Malt Barley
144	T11	BETin	Landrace	Malt Barley
145	T497	BETin	Landrace	Food Barley
146	90	IEMBSN-20/21	Exotic Line	Malt Barley
147	T90	BETin	Landrace	Irregular
148	T134	BETin	Landrace	Malt Barley
149	91	IEMBSN-20/21	Exotic Line	Malt Barley
150	T79	BETin	Landrace	Malt Barley
151	T322	BETin	Landrace	Food Barley

Appendix 1(Continued)

S.No	Entry No.	Source	Description	Barley types
152	97	IEMBSN-20/21	Exotic Line	Malt Barley
153	T508	BETin	Landrace	Malt Barley
154	100	IEMBSN-20/21	Exotic Line	Malt Barley
155	T387	BETin	Landrace	Malt Barley
156	102	IEMBSN-20/21	Exotic Line	Malt Barley
157	T506	BETin	Landrace	Malt Barley
158	T328	BETin	Landrace	Irregular
159	105	IEMBSN-20/21	Exotic Line	Malt Barley
160	T576	BETin	Landrace	Food Barley
161	T30	BETin	Landrace	Irregular
162	133	IEMBSN-20/21	Exotic Line	Malt Barley
163	T530	BETin	Landrace	Food Barley
164	T522	BETin	Landrace	Malt Barley
165	139	IEMBSN-20/21	Exotic Line	Malt Barley
166	T512	BETin	Landrace	Malt Barley
167	150	IEMBSN-20/21	Exotic Line	Malt Barley
168	156	IEMBSN-20/21	Exotic Line	Malt Barley
169	T123	BETin	Landrace	Malt Barley
170	157	IEMBSN-20/21	Exotic Line	Malt Barley
171	161	IEMBSN-20/21	Exotic Line	Malt Barley
172	T524	BETin	Landrace	Food Barley
173	T333	BETin	Landrace	Food Barley
174	T494	BETin	Landrace	Food Barley
175	167	IEMBSN-20/21	Exotic Line	Malt Barley
176	168	IEMBSN-20/21	Exotic Line	Malt Barley
177	Dinsho(R. Check)	SARC	Improved Variety	Food Barley
178	Aruso (R. Check)	HARC	Local Genotypes	Food Barley
179	Moata (S. Check)	BETin	Improved Variety	Malt Barley
180	HB-42 (S. Check)	HARC	Local Genotypes	Food Barley

ISBYT-HI-2021=International Spring Barley Yield Trial for High Input Areas 2021, BETin=Biotechnology Emerging Technology Institute, 8TH GSBYT-21= 8^{TH} Global Spring Barley Yield Trial 2021, IEMBSN-21=ICARDA Ethiopia Malt Barley Special Nursery 2021, IBON-2021=International Barley Observation Nursery for Hi-input Areas 2021, SARC= Sinana Agricultural Research Center, HARC= Holleta Agricultural Research Center, R-Check=Resistance-Check, and S-Check=Susceptible-Check.

Appendix 2. Entry number, adjusted means of each trait, and categorization of screening barley genotypes for susceptibility or resistance to barley shoot fly, *Delia flavibasis* Stein based on dead heart recorded during the 2022/2023

Entry No.	OVI	INF	DH	CR	DTH	TT	PT	DTM	PH	SL	SPS	BY	GY	TKW	RC
17	4.29	70.47	63.85	3.97	83.08	11.2	8.49	131.12	90.26	9.05	54.17	1.45	143.38	42.37	HS
21	5.19	88.58	71.35	3.97	73.08	8.31	6.19	120.12	95.26	7.55	45.77	1.35	126.38	40.37	HS
T200	1.29	19.57	15.65	2.85	50.08	3.51	3.39	91.12	106.46	6.65	35.57	0.75	101.38	40.37	R
20	2.39	48.47	29.15	4.47	83.08	5.71	4.39	131.13	88.36	9.68	69.17	1.75	184.28	42.37	MR
4	4.39	68.48	58.15	3.77	54.08	14.4	10.19	90.12	72.46	7.35	42.17	1.55	138.58	46.37	HS
T316	3.59	36.27	32.25	2.67	51.08	5.91	3.72	88.12	58.36	6.35	35.67	0.7	70.18	30.57	S
T304	3.59	44.68	40.15	1.77	83.08	7.81	5.63	131.13	55.36	6.26	42.32	0.25	31.28	27.77	S
3	4.29	52.97	44.95	3.97	71.08	7.31	4.99	117.12	82.56	9.55	35.82	1.75	153.08	45.37	S
T32	1.29	21.47	14.25	3.47	51.08	3.51	3.42	91.12	101.86	5.59	39.65	1.25	119.48	35.37	R
15	3.79	51.48	44.15	3.57	79.08	6.16	4.24	127.12	80.36	5.85	46.07	1.25	137.08	39.37	S
19	4.09	80.98	73.75	3.87	80.08	10.5	7.69	127.13	76.66	6.35	52.9	1.29	145.38	35.37	HS
T315	2.29	32.97	29.45	2.47	69.08	5.51	4.29	118.12	72.66	7.05	33.82	0.45	66.38	38.57	MR
T249	0.99	16.18	7.05	3.6	51.08	2.71	2.49	91.13	96.86	7.35	58.07	2	147.21	38.37	HR
2	2.29	31.77	23.35	3.97	52.08	6.11	4.69	93.12	98.46	11.5	44.57	1.15	169.68	46.37	MR
T464	1.29	18.78	16.25	3.97	53.08	4.39	4.39	95.12	96.86	6.05	54.17	1.75	137.98	39.37	R
T21	1.79	31.87	26.15	2.97	83.08	5.71	4.69	131.12	85.16	5.85	43.4	0.65	69.94	35.47	MR
1	3.19	39.27	37.45	2.97	64.08	7.51	5.19	107.12	92.46	5.93	46.82	1.71	159.05	44.57	S
T329	1.39	26.07	18.45	3.59	53.08	5.71	5.19	92.12	118.56	7.85	41.9	1.25	103.71	40.37	R
T369	1.54	21.27	17.55	3.47	53.08	3.41	3.19	93.12	99.86	7.68	44.32	1.62	120.28	40.37	R
17	4.89	88.48	82.45	2.97	83.08	6.91	5.02	131.12	70.26	7.05	33.77	1.25	95.48	38.87	HS
15	4.09	54.47	47.65	3.22	80.08	6.51	5.19	130.12	79.66	7.05	39.27	1.49	121.38	40.37	S
T51	3.09	28.77	22.75	3.37	50.08	6.71	5.69	93.12	85.36	5.88	37.82	1.15	93.38	36.77	MR
4	4.39	68.47	59.85	2.57	67.08	7.01	4.69	120.12	82.46	5.32	47.99	0.75	94.68	41.37	HS
T376	4.54	85.57	76.55	0.77	75.08	3.21	2.19	126.12	50.36	7.45	30.9	0.25	15.6	29.97	HS
T525	2.29	25.07	21.35	1.97	49.08	4.98	4.19	93.12	58.16	7.45	23.9	0.65	59.31	37.97	MR
T573	1.79	22.27	20.45	2.1	52.08	3.91	3.19	95.12	80.46	6.75	41.57	0.88	79.57	35.47	MR
T438	0.59	17.47	12.45	3.37	49.08	6.31	6.19	89.12	112.46	7.85	43.77	1.61	117.95	39.07	R

Appendix 2(Continued)

T467	0.59	18.28	11.15	3.22	57.08	5.89	5.89	108.12	117.36	8.45	49.07	2.15	139.53	42.77	R
T422	3.04	39.98	32.65	1.47	82.08	4.61	3.39	129.12	54.36	7.55	22.07	0.25	32.48	28.87	S
6	2.09	26.97	20.05	4.17	77.08	6.41	4.32	123.12	110.36	5.57	48.57	1.25	171.18	47	MR
T15	2.59	35.68	27.18	2.79	78.33	7.01	5.95	125.38	76.5	6.02	33.38	1.1	72.02	31.53	MR
9	2.49	28.37	20.38	3.79	56.33	9.41	6.95	100.38	118.5	9.12	41.38	1.7	183.99	52.03	MR
T470	3.69	48.68	39.78	2.29	76.33	10.7	7.95	130.38	73.4	5.12	19.88	1.1	76	33.93	S
T344	4.19	44.68	35.18	1.54	80.33	5.51	3.95	132.38	50.2	8.15	34.78	0.6	39.89	27.93	S
12	5.29	62.38	55.98	2.79	74.33	11.2	8.75	131.38	101.3	7.47	41.58	1.85	142.69	51.73	HS
2	4.19	58.38	40.88	4.04	90.33	8.01	5.95	142.38	102.5	8.72	59.68	1.5	164.09	46.63	S
T520	2.69	33.78	24.68	2.29	58.33	7.41	5.75	100.38	65.4	8.82	29.38	0.98	67.53	28.73	MR
3	4.49	44.88	39.08	3.79	89.33	8.81	6.55	141.38	102.5	5.72	47.48	1.9	156.49	47.27	S
T451	6.19	64.88	55.08	1.79	87.33	9.41	6.95	140.38	60.3	8.92	35.98	1.25	63.09	33.73	HS
T97	2.89	33.18	22.88	2.79	58.33	4.21	3.67	106.38	82.6	10.3	45.21	0.85	100.82	30.83	MR
4	4.59	59.38	50.08	2.79	82.33	9.41	6.25	134.38	97.9	7.32	49.88	1	111.19	45.64	HS
T562	2.19	19.88	17.28	3.19	56.33	3.88	3.45	99.38	106.6	8.17	45.08	1.4	138.49	42.93	R
T301	1.59	20.38	13.98	4.19	59.33	5.21	4.75	104.38	106.7	8.32	51.38	2.3	262.39	54.03	R
T367	1.69	21.88	17.08	2.92	61.33	4.41	3.85	106.38	101.25	9.12	36.58	1.3	112.19	35.03	R
T268	4.39	66.97	54.98	3.29	88.33	10.8	7.95	142.38	88.7	7.74	43.71	2.1	165.12	37.53	HS
1	5.19	85.78	72.78	3.79	86.33	6.81	4.95	140.38	93.5	7.02	47.71	1.1	149.87	46.83	HS
T318	1.69	27.17	17.48	3.19	58.33	3.26	3.25	102.38	106.3	8.82	41.13	1.9	111.89	34.53	R
T100	4.44	51.88	43.68	2.39	88.33	7.61	6.19	141.38	67.6	8.92	37.88	0.85	94.54	30.83	S
7	4.19	80.38	71.28	2.59	90.33	10.1	6.25	142.38	63.6	5.92	50.18	0.6	87.94	30.73	HS
T482	2.44	28.88	19.58	2.19	62.33	8.01	6.95	114.38	107.7	8.92	47.08	1.8	118.2	39.23	R
T45	2.26	20.07	18.93	4.03	53.33	4.82	4.26	102.12	104.54	9.29	59.78	2.08	165.32	40.89	R
11	6.59	84.38	77.68	2.79	88.33	6.51	3.95	141.38	83.5	6.12	41.38	1.1	128.14	39.03	HS
T78	1.86	24.48	17.63	3.83	51.33	7.92	6.86	98.13	95.24	7.99	46.83	1.53	134.49	35.49	R
T455	1.69	24.27	18.48	3.42	54.33	5.01	4.35	106.38	103.7	8.52	39.98	1.6	129.82	36.45	R
19	4.49	60.68	47.98	3.94	87.33	7.31	4.75	142.38	99.6	7.82	52.68	1.1	156.44	39.23	S
T568	2.19	26.18	17.88	2.79	56.33	4.01	3.95	102.38	103.7	7.92	33.63	1.35	118.44	34.24	R
T72	2.59	21.37	18.28	3.04	60.33	5.01	4.35	106.38	91.4	10	36.08	1.35	120.49	38.23	R

Appendix 2(Continued)

T372	2.39	25.98	18.28	3.79	58.33	5.01	4.58	102.38	108.5	7.32	35.98	1.53	130.37	38.93	R
T204	2.19	26.87	15.88	3.29	56.33	6.31	5.45	98.38	103.3	8.72	44.18	1.7	113.04	33.63	R
114	5.79	78.68	65.28	2.79	89.33	8.01	5.65	143.38	77.6	5.82	42.63	1.9	113.19	40.23	HS
96	4.56	45.6	37.55	3.92	80.83	8.16	6.87	127.88	85.74	7.93	44.92	1.93	162.93	37.13	S
T139	6.26	60.7	48.25	0.67	85.83	3.66	2.69	135.88	53.84	9.13	39.42	0.58	27.55	25.03	S
T474	3.96	40.6	30.35	2.67	78.83	8.16	6.14	124.88	71.64	9.63	37.62	0.98	96.48	37.33	S
T62	1.36	18.1	8.25	3.92	56.83	2.96	3.34	100.88	103.14	8.13	44.87	1.93	143.45	33.83	HR
66	6.56	94.1	85.25	1.42	86.83	6.96	4.44	133.88	66.44	6.63	51.12	0.88	106.04	35.33	HS
T36	2.76	30.6	21.75	3.17	88.83	4.76	4.34	136.88	85.74	8.33	33.82	1.98	94.69	35.43	MR
T386	4.16	39.6	36.55	2.17	85.83	4.16	3.54	137.88	54.14	9.07	36.37	0.73	62.4	33.33	S
88	4.76	43.6	37.55	3.92	75.83	6.86	3.84	121.88	106.64	7.33	59.72	1.08	156.64	36.33	S
T207	4.16	44.4	33.95	1.55	74.83	5.16	4.04	120.88	50.54	10.1	38.45	0.73	40.95	27.53	S
T12	3.96	39.8	36.55	2.92	84.83	7.16	5.54	136.88	71.74	7.83	32.62	1.08	78.9	29.33	S
T274	3.96	41.4	33.35	1.17	84.83	5.16	3.67	137.88	48.94	8.63	42.12	0.83	29.48	28.73	S
T197	5.46	52.6	41.75	1.79	73.83	3.89	3.14	124.88	60.74	8.93	37.95	0.88	42.1	30.13	S
15	4.96	73.62	56.45	3.67	80.83	8.66	5.54	131.88	88.14	9.03	42.12	0.88	134.01	49.83	HS
T374	1.86	17.9	15.25	3.52	56.83	5.56	5.39	100.88	104.14	9.13	44.42	1.83	133.7	38.03	R
T38	2.96	35.2	25.75	2.67	70.83	2.66	2.48	121.88	80.64	8.38	33.2	1.01	71.2	26.93	MR
T295	4.96	71.8	64.65	1.42	86.83	3.86	2.84	137.88	45.84	10.9	38.32	0.78	37.54	38.83	HS
90	4.26	57.6	38.95	3.92	70.83	6.86	5.14	124.88	96.94	8.38	63.95	1.94	163.63	37.83	S
T24	1.56	17.4	10.55	3.92	65.83	5.16	5.17	114.88	113.74	10.2	49.12	2.08	152.53	38.43	R
51	5.46	81.6	71.05	3.67	86.83	9.76	7.54	137.88	71.84	9.63	40.62	1.68	140.13	39.33	HS
T503	3.96	44.4	35.95	1.8	86.83	4.16	3.54	137.88	58.74	8.33	50.12	0.88	58.85	32.13	S
T213	5.46	49.1	40.55	1.42	83.83	5.26	4.14	135.88	51.54	8.88	39.42	0.83	33.1	30.13	S
50	1.96	27.6	17.05	3.92	64.83	7.56	7.54	112.88	115.74	9.53	46.92	2.08	194.71	37.93	R
61	5.16	85.6	76.65	2.52	86.83	6.96	4.94	136.88	72.84	6.63	48.92	1.08	92.1	34.53	HS
T370	2.76	31.9	24.85	1.92	70.83	2.76	2.54	125.88	86.79	8.13	54.12	1.08	90.5	33.43	MR
59	4.96	69.6	58.25	3.92	84.83	6.56	5.29	136.88	115.84	8.03	58.92	1.08	152.84	40.16	HS
T352	2.66	32.1	23.95	2.32	60.83	0.76	0.94	105.88	89.59	7.93	37.92	1.08	92.3	27.73	MR
113	5.46	64.6	49.55	3.42	83.83	3.96	2.54	134.88	111.74	9.93	51.92	1.08	136.41	41.43	S

Appendix 2(Continued)

T364	2.16	36.7	24.9	3.52	60.83	5.16	4.67	109.88	84.79	7.63	35.82	0.98	86	32.73	MR
T59	6.76	91.4	82.35	1.55	76.83	7.76	4.29	127.88	45.74	8.13	51.42	0.78	38.71	33.83	HS
T320	6.71	63.67	59.98	2.42	75.83	11.5	8.28	127.13	47.04	9.31	36.88	0.83	47.54	29.89	HS
100	5.41	79.38	76.38	3.87	88.83	7.26	4.78	138.13	79.94	7.81	46.48	0.58	130.11	46.59	HS
T444	5.71	84.18	78.98	1.62	86.83	3.66	1.98	131.13	39.04	9.61	31.91	0.58	19.61	37.59	HS
T519	5.91	53.88	48.38	1.85	75.83	6.76	5.08	129.13	47.84	7.86	35.58	0.83	26.68	35.29	S
T336	6.71	71.08	66.18	1.65	87.83	5.06	3.48	141.13	61.04	8.91	34.33	0.58	37.81	31.29	HS
29	5.01	48.38	36.48	4.22	74.83	6.66	5.73	127.13	81.84	9.44	42.08	2.08	152.92	41.59	S
T258	5.21	74.97	67.98	1.55	87.83	6.66	4.58	136.13	52.74	8.61	38.28	0.78	34.73	32.59	HS
T528	4.21	38.87	33.78	2.22	72.83	5.66	4.28	128.12	56.74	8.01	45.68	0.88	46.59	38.59	S
T281	2.01	16.12	13.78	4.22	61.83	10.7	9.48	101.12	89.94	9.86	43.58	2.38	191.77	38.19	R
T184	5.61	68.98	63.28	1.97	87.83	5.46	3.78	136.13	49.94	5.91	42.28	0.58	44.99	34.59	HS
102	5.21	89.77	85.08	2.22	90.83	6.36	4.48	141.12	69.04	8.21	46.68	0.98	87.89	37.39	HS
T332	3.71	39.58	37.48	3.1	72.83	4.66	3.48	131.13	70.24	8.61	42.08	1.31	87.32	34.09	S
T1	6.11	41.38	37.08	2.72	67.83	4.26	3.13	113.13	62.84	8.61	49.88	0.83	77.39	38.99	S
55	5.81	79.38	77.58	4.22	89.83	9.16	5.61	141.13	80.04	8.85	41.58	0.83	151.3	52.39	HS
T447	4.71	46.87	42.48	2.97	75.83	5.46	4.08	127.13	53.74	8.81	41.88	1.03	58.99	35.39	S
105	4.71	82.37	76.38	3.42	77.83	12.1	8.48	131.12	79.44	7.61	59.38	1.28	124.93	34.66	HS
T401	1.81	17.88	16.48	3.85	61.83	6.66	6.48	105.13	91.54	8.41	54.08	2.08	145.2	36.79	R
T548	5.21	46.38	42.28	2.35	78.83	6.66	4.88	131.12	51.04	10.6	34.58	0.88	52.03	46.99	S
T521	2.01	23.27	20.03	4.22	68.83	5.66	4.98	121.13	107.94	10	50.08	2.48	148.25	50.59	MR
5	4.71	82.58	79.08	3.97	85.83	9.46	7.18	141.13	78.64	9.41	40.08	1.58	134.81	54.79	HS
T229	5.51	47.37	44.78	1.72	69.83	5.66	3.98	119.13	37.94	9.21	42.28	0.98	34.69	44.69	S
17	5.21	54.87	51.18	4.22	88.83	11	7.98	140.12	79.04	10.3	42.08	1.83	154.59	41.59	HS
19	4.41	75.98	70.58	4.22	86.83	8.16	7.08	139.13	83.84	7.31	39.08	2.48	133.69	46.89	HS
T419	4.21	34.48	33.78	2.02	76.83	3.66	2.78	126.13	59.64	9.21	39.18	0.58	43.84	31.29	S
20	4.51	52.38	47.28	3.62	84.83	9.06	7.23	136.13	78.94	9.34	40.08	1.08	124.69	40.59	S
149	2.31	17.68	18.08	3.72	59.83	7.66	6.74	105.13	87.04	8.41	32.08	1.88	107.36	38.99	R
24	5.51	60.38	55.38	3.92	82.83	5.66	5.48	135.13	72.74	7.91	39.91	2.58	139.75	45.19	HS
T544	2.21	21.68	16.18	3.72	62.83	3.86	3.33	114.13	93.74	8.61	41.48	1.45	119.86	36.61	R
29	5.21	58.37	53.38	3.22	87.83	7.36	5.48	141.12	73.84	10.2	40.58	1.38	119.49	39.59	HS

Appendix 2(Continued)

T56	2.36	28.38	23.13	2.78	54.33	3.28	2.76	103.12	101.24	7.19	34.53	1.33	96.39	37.39	MR
34	4.86	67.67	59.83	2.79	77.33	6.42	4.56	130.13	71.64	9.44	36.95	1.08	107.99	38.89	HS
T585	4.16	36.98	34.13	2.78	64.33	6.42	4.39	114.13	77.64	10.6	32.53	0.98	92.06	47.09	S
46	4.66	83.87	75.13	1.59	83.33	11.8	8.51	134.12	75.54	10.2	36.03	1.51	87.65	38.09	HS
T537	2.36	23.68	20.03	3.66	55.33	6.42	5.66	96.13	103.24	7.59	52.23	1.58	119.75	33.9	MR
48	5.06	84.88	77.93	2.48	83.33	8.32	5.76	133.13	77.54	9.19	37.86	1.84	114.57	35.19	HS
T559	4.36	40.38	39.33	1.78	68.33	6.42	4.66	123.13	51.24	8.59	33.73	0.83	51.09	29.69	S
T516	4.36	44.38	35.28	2.66	70.33	6.42	5.06	126.13	68.34	9.09	31.95	1.08	87.04	37.1	S
T254	4.06	36.08	33.78	3.03	61.33	5.42	4.26	112.12	83.34	9.59	34.23	0.83	93.93	34.29	S
56	5.86	84.87	76.13	1.87	82.33	9.82	5.38	135.12	68.54	9.89	32.03	1.08	81.09	46.19	HS
T575	0.86	18.18	16.43	3.43	51.33	7.42	7.06	93.12	110.64	8.59	53.33	2.08	182.19	41.69	R
62	5.56	83.38	78.33	2.33	81.33	12.9	9.51	132.12	72.54	8.71	31.13	1.08	96.2	35.59	HS
T307	2.86	33.18	31.28	3.33	71.33	2.92	2.39	125.13	85.44	7.79	44.83	1.68	98.13	31.99	S
T289	3.06	36.88	28.73	2.66	62.33	3.12	2.38	114.13	75.24	7.69	44.03	1.31	76.05	26.09	MR
67	5.86	86.88	79.28	2.43	71.33	11.9	9.26	127.13	56.64	9.59	37.73	1.58	97.29	46.89	HS
T272	4.36	48.67	43.13	1.43	81.33	6.42	4.52	135.13	60.34	8.81	30.73	0.68	41.5	29.59	S
T208	2.36	24.88	19.13	4.03	59.33	2.98	2.76	110.13	107.54	7.89	41.53	2.08	145.76	39.29	R
69	6.36	65.38	58.13	3.03	85.33	8.42	6.76	138.13	74.34	9.29	34.23	2.08	121.69	52.99	HS
T346	4.36	40.38	35.08	2.16	67.33	5.82	4.46	120.13	58.24	10.2	35.13	0.83	61.66	32.39	S
73	4.66	90.88	86.88	2.03	85.33	11.9	6.26	136.13	63.64	10.2	45.33	0.83	110.69	43.89	HS
T271	3.86	36.68	33.83	2.53	67.33	6.42	4.76	120.13	98.54	8.39	35.83	0.58	88.24	40.29	S
75	5.06	84.37	78.38	2.83	82.33	8.02	6.76	132.12	89.24	7.59	32.93	2.08	119.09	51.19	HS
T514	4.36	43.87	37.93	2.53	67.33	6.02	4.26	122.12	68.44	9.09	46.33	0.98	63.99	26.99	S
86	6.26	85.87	82.23	1.53	81.33	10	6.76	135.13	56.64	8.82	30.13	2.33	54.92	28.99	HS
T511	6.66	83.18	78.68	0.66	84.33	7.29	4.76	135.13	43.44	6.59	20.36	0.58	22.67	19.99	HS
T11	1.66	19.17	12.88	4.03	54.33	5.42	5.26	98.13	119.54	10.7	37.53	2.08	154.7	54.19	R
T497	2.76	34.17	28.43	3.33	67.33	5.02	4.11	124.13	87.34	9.74	41.73	1.36	101.57	33.29	MR
90	5.26	90.78	86.33	2.03	85.33	11.4	8.96	134.13	68.54	9.39	30.53	1.83	91.19	35.09	HS
T90	1.86	23.88	18.33	3.53	51.33	3.92	3.66	97.13	103.24	8.69	35.53	2.08	171.83	44.09	R
T134	2.99	25.6	20.6	3.27	57.58	2.64	2.33	99.38	95.43	7.4	34.83	0.91	83.56	32.09	MR
91	4.59	84.3	75.6	1.94	89.58	12	8.08	141.38	47.83	9.03	41.83	0.81	55.37	29.39	HS

Appendix 2(Continued)

T79	3.99	40.4	32.6	1.57	73.58	3.54	2.48	123.38	80.63	8.1	37.83	0.64	50.63	31.59	S
T322	4.49	33.8	29.6	2.07	71.58	2.64	1.96	125.38	48.53	5.63	35.03	0.51	40.79	28.79	MR
97	4.79	73.8	65.2	2.82	89.58	5.84	4.08	141.38	75.53	7.2	36.33	0.76	89.16	33.09	HS
T508	2.69	27.9	20.4	2.57	57.58	3.64	3.08	101.38	56.43	7.9	39.83	0.86	63.93	33.79	MR
100	5.89	86.8	80.5	2.57	85.58	6.84	4.98	141.38	64.73	7.5	35.83	0.91	86.96	33.19	HS
T387	3.49	31.6	24.2	2.57	65.58	4.04	3.58	112.38	73.73	8.8	34.63	1.04	82.56	35.69	MR
102	5.29	82.8	71.2	2.07	71.58	7.04	4.71	126.38	74.03	7.23	32.73	0.81	75.72	38.69	HS
T506	1.09	3.4	1.5	4.07	58.58	5.04	5.08	106.38	100.63	9	35.83	1.91	137.36	42.29	HR
T328	0.89	20.8	16.3	3.57	68.58	5.04	4.58	116.38	98.43	8.1	36.03	1.41	104.06	36.79	R
105	5.39	83.6	76.9	1.57	77.58	9.94	7.28	126.38	60.73	6.3	35.66	1.36	39.7	29.19	HS
T576	1.99	18.6	11	4.07	66.58	4.04	3.88	119.38	114.03	6.13	54.33	2.11	182.91	45.69	R
T30	4.69	44.9	36.8	2.47	85.58	6.04	4.58	135.38	58.63	6.5	46.13	0.61	42.61	32.69	S
133	4.99	83.6	74	1.54	83.58	8.64	6.38	135.38	65.83	6.4	29.83	1.41	48.36	47.59	HS
T530	4.49	41.9	35.2	2.47	73.58	5.04	3.58	127.38	62.53	6.4	36.33	0.71	58.26	34.29	S
T522	3.19	34.8	24.2	2.37	56.58	4.04	3.48	111.38	61.73	7.1	35.03	0.96	54.92	42.19	MR
139	2.39	23.8	18.6	4.57	59.58	14	11.08	106.38	98.43	8	46.33	1.41	190.27	43.19	R
T512	1.49	26.8	17.1	3.27	67.58	4.04	3.88	119.38	105.83	7.4	40.33	1.66	113.82	36.79	R
150	2.99	27.2	23.8	3.37	62.58	5.64	4.83	118.38	80.43	9.12	46.33	1.21	123.13	43.69	MR
156	3.99	54.3	47.3	3.22	79.58	12	9.1	126.38	81.63	7.43	35.33	0.91	110.08	42.39	S
T123	2.99	27.9	22.8	2.82	71.58	3.44	3.08	127.38	82.53	6.03	31.33	1.41	90.63	37.19	MR
157	2.19	27.8	22.8	4.67	64.58	8.74	6.88	116.38	104.7	10.6	45.33	0.91	203.07	51.99	MR
161	5.19	81.3	75.9	3.87	85.58	7.54	5.58	139.38	77.83	7.01	38.03	1.61	133.16	47.09	HS
T524	1.49	7.5	3.9	4.07	57.58	7.14	6.98	99.38	97.43	6.3	52.83	1.91	173.39	43.69	HR
T333	1.49	24.8	17.9	3.37	55.58	2.54	2.21	96.38	101.3	7.3	39.75	0.91	106.86	34.59	R
T494	2.69	27.6	24.1	3.07	71.58	3.24	2.88	123.38	72.63	6.3	41.66	0.86	84.78	28.29	MR
167	4.39	52.3	44	3.87	88.58	7.74	5.96	139.38	85.83	9.2	44.53	1.31	137.99	43.19	S
168	5.59	84.3	75.7	3.07	87.58	7.84	4.98	139.38	90.73	6.3	35.53	0.91	102.48	40.09	HS
Dinsho	1.8	18.9	12.95	3.93	57.5	4.51	4.34	103.17	95.94	9.3	48.67	1.65	149.2	39.49	R
Aruso	1.68	15.2	10.98	4.53	56.33	5.27	5.2	101.83	93.48	8.86	52.01	1.91	174.12	43.63	R
Moata	4.32	59.37	49.18	3.6	79.5	7.6	5.43	128.67	75.85	8.68	47.32	1.45	140.93	40.08	S
HB-42	5.75	83.53	72.8	0.91	87	8.04	4.9	135.83	67.78	6.44	42.22	0.59	90.85	34.16	HS

OVI=Eggs seedling-1, INF=Infestation Percentages, DH=Dead Heart Percentages, CR=Crop Recovery measured by 1-5 scale, DTH=Days to 50% Heading in Days, TT=Total Tiller in Numbers, PT=Productive or Fertile Tillers in Numbers, DTM=Days to 90% Maturity in Days, PH=Plant Height in Centimeters, SL=Spike Length in Centimeters, SPS=Seed Per Spikes in Numbers, BY=Biological Yield in KgPlot-1,GY=Grain Yield in Grams Plot-1,TKW=Thousand Kernel Weight in Grams, RC=Resistance Category, HR=Highly Resistance, R=Resistance, MR=Moderately Resistance, S=Susceptible and HS=Highly Susceptible

Appendix 3. Analyses of variance for barley shoot fly damage parameters

Characters	Source	DF	Sum Sq.	Mean of Sq.	F value	Pr (>F)
OVI(No.)	Replications	1	47.8	47.78	0.8228	0.3688
	Genotypes(unadj)	63	28073.8	445.62	7.6746	6.894e-12 ***
	Block in rep(adj)	14	1014.5	72.47	1.2480	0.2735
	Intrablock error	49	2845.1	58.06		
INF (%)	Replications	1	211	211.02	1.2272	0.2734
	Genotypes(unadj)	63	83419	1324.11	7.7004	6.455e-12 ***
	Block in rep(adj)	14	3065	218.91	1.2731	0.2578
	Intrablock error	49	8426	171.95		
DH (%)	Replications	1	512	512.20	2.8652	0.09686
	Genotypes(unadj)	63	65749	1043.63	5.8380	1.219e-09 ***
	Block in rep(adj)	14	2822	201.57	1.1276	0.35928
	Intrablock error	49	8759	178.76		
CR(1-5)	Replications	1	0.185	0.18529	0.3207	0.5738
	Genotypes(unadj)	63	111.137	1.76408	3.0532	4.249e-05 ***
	Block in rep(adj)	14	8.255	0.58964	1.0205	0.4495
	Intrablock error	49	28.312	0.57779		

***= (P<0.001); OVI (No.) = Oviposition in Numbers; INF (%) = Infestation Percentage; DH (%) =Dead Heart percentages; CR (1-5) =Crop Recovery with Scoring Rates of 1 to 5

Appendix 4. Analysis of variance for morphological traits of barley genotypes

Characters	Source	DF	Sum Sq	Mean of Sq	F value	Pr(>F)
SV(1-5)	Replications	1	3.781	3.7813	7.5417	0.008408 **
	Genotypes(unadj)	63	189.875	3.0139	6.0112	7.14e-10 ***
	Block in rep(adj)	14	6.651	0.4751	0.9475	0.517597
	Intrablock error	49	24.568	0.5014		
LG(1-5)	Replications	1	0.439	0.43945	1.2801	0.2634
	Genotypes(unadj)	63	176.045	2.79436	8.1396	2.163e-12 ***
	Block in rep(adj)	14	5.114	0.36526	1.0640	0.4114
	Intrablock error	49	16.822	0.34330		
SC(1-3)	Replications	1	0.008	0.00781	0.0737	0.7872
	Genotypes(unadj)	63	85.367	1.35503	12.7822	<2e-16 ***
	Block in rep(adj)	14	1.298	0.09269	0.8744	0.5896
	Intrablock error	49	5.194	0.10601		
FLW(cm)	Replications	1	0.0291	0.029101	7.5017	0.008571 **
	Genotypes(unadj)	63	3.2705	0.051913	13.3824	< 2.2e-16 ***
	Block in rep(adj)	14	0.0680	0.004855	1.2515	0.271281
	Intrablock error	49	0.1901	0.003879		
SLW(cm)	Replications	1	0.00138	0.0013781	1.6224	0.20876
	Genotypes(unadj)	63	1.28109	0.0203347	23.9393	< 2e-16 ***
	Block in rep(adj)	14	0.02050	0.0014643	1.7238	0.08096
	Intrablock error	49	0.04162	0.0008494		
SSL(cm)	Replications	1	0.104	0.10351	0.5198	0.4744
	Genotypes(unadj)	63	181.050	2.87381	14.4301	<2e-16 ***
	Block in rep(adj)	14	3.493	0.24953	1.2529	0.2704
	Intrablock error	49	9.759	0.19915		
SST(cm)	Replications	1	0.03850	0.038503	5.6886	0.02099 *
	Genotypes(unadj)	63	2.49542	0.039610	5.8521	1.167e-09 ***
	Block in rep(adj)	14	0.09574	0.006838	1.0103	0.45874
	Intrablock error	49	0.33166	0.006769		

SV =Seedling Vigor, LG=Leaf Glossiness, SC=Seedling color, FLW=First Leaf Width, SLW (cm) =Second Leaf Width, SSL =Seedling Stem Length, SST =Seedling Stem Thickness.

Appendix 5. Analysis of variance for agronomic traits of barley genotypes

Characters	Source	DF	Sum Sq	Mean of Sq	F value	Pr(>F)
DTH(Days)	Replications	1	6.13	6.1250	1.6451	0.2057
	Genotypes(unadj)	63	1874.47	29.7535	7.9916	3.11e-12 ***
	Block in rep(adj)	14	71.44	5.1031	1.3707	0.2035
	Intrablock error	49	182.43	3.7231		
DTM(Days)	Replications	1	4.96	4.961	0.5036	0.4813
	Genotypes(unadj)	63	3016.09	47.874	4.8592	3.133e-08 ***
	Block in rep(adj)	14	88.65	6.332	0.6427	0.8158
	Intrablock error	49	482.76	9.852		
PH(cm)	Replications	1	18.1	18.10	0.3559	0.55356
	Genotypes(unadj)	63	20418.1	324.10	6.3719	2.425e-10 ***
	Block in rep(adj)	14	1484.4	106.03	2.0846	0.02975 *
	Intrablock error	49	2492.3	50.86		
PT(No.)	Replications	1	0.039	0.0390	0.1119	0.7395
	Genotypes(unadj)	63	206.630	3.2798	9.4158	1.154e-13 ***
	Block in rep(adj)	14	7.256	0.5183	1.4880	0.1513
	Intrablock error	49	17.068	0.3483		
TT(No.)	Replications	1	0.163	0.1629	0.4662	0.498
	Genotypes(unadj)	63	313.462	4.9756	14.2372	<2e-16 ***
	Block in rep(adj)	14	4.043	0.2888	0.8264	0.638
	Intrablock error	49	17.124	0.3495		
SL(cm)	Replications	1	1.438	1.4379	1.9436	0.1696
	Genotypes(unadj)	63	229.332	3.6402	4.9203	2.528e-08 ***
	Block in rep(adj)	14	6.079	0.4342	0.5869	0.8622
	Intrablock error	49	36.252	0.7398		

Appendix 5(Continued)

Characters	Source	DF	Sum Sq	Mean of Sq	F value	Pr(>F)
SPS(No.)	Replications	1	215.4	215.428	6.0742	0.01727 *
	Genotypes(unadj)	63	12163.9	193.077	5.4440	4.295e-09 ***
	Block in rep(adj)	14	872.2	62.302	1.7566	0.07405
	Intrablock error	49	1737.8	35.466		
BY(kg/plot)	Replications	1	0.030	0.03001	1.0472	0.3112
	Genotypes(unadj)	63	32.524	0.51625	18.0122	<2e-16 ***
	Block in rep(adj)	14	0.428	0.03060	1.0676	0.4083
	Intrablock error	49	1.404	0.02866		
GY(gm/plot)	Replications	1	44	43.68	0.6078	0.43938
	Genotypes(unadj)	63	46925	744.83	10.3633	1.603e-14 ***
	Block in rep(adj)	14	2394	170.97	2.3787	0.01293 *
	Intrablock error	49	3522	71.87		
TKW(gm)	Replications	1	3.44	3.4420	0.7954	0.3768
	Genotypes(unadj)	63	1465.73	23.2656	5.3766	5.36e-09 ***
	Block in rep(adj)	14	68.18	4.8698	1.1254	0.3610
	Intrablock error	49	212.03	4.3272		

*** = (P<0.001); * = (P<0.05); DTH=Days to Heading in Days, DTM=Days to Maturity in Days, PH=Plant Height in Centimeter, PT=Productive or Fertile Tillers Plant^{-1} in Numbers, TT=Total Tillers Plant^{-1} in Numbers, SL=Spike Length in Centimeter, SPS=Seed Per Spikes in Numbers, BY=Biomass Yield in Kilogram Plot^{-1}, GY=Grain Yield in Grams Plot^{-1}, TKW=Thousand Kernel Weight in Grams.

Appendix 6. Analysis of variance oviposition preference and damage by the barley shoot fly, *Delia flavibasis* females on 12 barley genotypes under multi-choice test in the field

Traits	Sources of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Eggs plant-1 at 10 DAE	Genotypes	11	24.4267	2.22061	73.28	1.035e-14 ***
	Replication	2	0.1667	0.08333	2.75	0.0859
	Residuals	22	0.6667	0.0303		
	Total	35	25.2601			
Eggs plant-1 at 13 DAE	Genotypes	11	25.2031	2.29119	70.7178	1.509e-14 ***
	Replication	2	0.1672	0.08361	2.5807	0.09844
	Residuals	22	0.7128	0.0324		
	Total	35	52.23			
Seedling with eggs at 10 DAE	Genotypes	11	8287.7	753.42	30.4928	9.192e-11 ***
	Replication	2	9.8	4.9	0.1982	0.8217
	Residuals	22	543.6	24.71		
	Total	35	8841.1			
Seedling with eggs at 13 DAE	Genotypes	11	9623.8	874.89	40.7098	4.842e-12 ***
	Replication	2	106.5	53.24	2.4771	0.1071
	Residuals	22	472.8	21.49		
	Total	35	10203.1			
Dead heart at 18 DAE	Genotypes	11	8576.5	779.68	169.0767	<2e-16 ***
	Replication	2	0.1	0.04	0.0079	0.9921
	Residuals	22	101.5	4.61		
	Total	35	8678.1			

***=(P<0.001); DAE=Days After Emergence

Appendix 7. Analysis of variance oviposition preference and damage by the barley shoot fly, *Delia flavibasis* females on 12 barley genotypes under no-choice test in the field

Traits	Source of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Eggs plant^{-1} at 10 DAE	Genotypes	11	22.116	2.01051	36.009	3.236e-12 ***
	Residuals	24	1.34	0.05583		
	Total	35	23.456			
Eggs plant^{-1} at 13 DAE	Genotypes	11	7.7831	0.70755	5.1667	0.0003819 ***
	Residuals	24	3.2867	0.13694		
	Total	35	11.0698			
Seedling with eggs at 10 DAE	Genotypes	11	13.952	1.2684	0.9658	0.5009^{ns}
	Residuals	24	31.520	1.3133		
	Total	35	45.472			
Seedling with eggs at 13 DAE	Genotypes	11	6.5589	0.59626	0.4929	0.8892^{ns}
	Residuals	24	29.0333	1.20972		
	Total	35	35.5922			
Dead heart at 18 DAE	Genotypes	11	3393.9	308.535	32.254	1.09e-11 ***
	Residuals	24	229.6	9.566		
	Total	35	3623.5			

***= (P<0.001); ns=Non-Significant; DAE=Days after Emergence

Appendix 8. Analysis of variance for the average developmental parameters of *D. flavibasis* on 12 barley genotypes under laboratory condition (SARC, 2023)

Traits	Source of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Larval period (days)	Genotypes	11	6.9495	0.63177	96.7	< 2.2e-16 ***
	Residuals	24	0.1568	0.00653		
	Total	35	7.1063			
Pupal period (days)	Genotypes	11	4.9241	0.44764	116.95	< 2.2e-16 ***
	Residuals	24	0.0919	0.00383		
	Total	35	5.016			
Pupal weight(grams)	Genotypes	11	1.2535	0.113954	26.639	8.738e-11***
	Residuals	24	0.10267	0.004278		
	Total	35	1.35617			
Pupation (%)	Genotypes	11	873.49	79.408	8.0866	1.086e-05 ***
	Residuals	24	235.67	9.82		
	Total	35	1109.16			
Adult Emergence (%)	Genotypes	11	2014.71	183.156	39.608	1.122e-12 ***
	Residuals	24	110.98	4.624		
	Total	35	2125.69			
Fecundity per female	Genotypes	11	26.8514	2.44104	37.561	2.026e-12 ***
	Residuals	24	1.5597	0.06499		
	Total	35	28.4111			

*****=(P<0.001)**

Appendix 9. Analysis of variance for the average Antibiosis indices of *D. flavibasis* on12 barley genotypes under laboratory condition (SARC, 2023)

Traits	Source of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Growth index	Genotypes	11	73.697	6.6997	25.448	1.429e-10 ***
	Residuals	24	6.319	0.2633		
	Total	35	80.016			
Relative Growth Index	Genotypes	11	0.47958	0.043598	25.448	1.429e-10 ***
	Residuals	24	0.04112	0.001713		
	Total	35	0.5207			
Developmental index	Genotypes	11	0.095781	0.0087073	149.95	< 2.2e-16 ***
	Residuals	24	0.001394	0.0000581		
	Total	35	0.097175			
Adult emergence index	Genotypes	11	0.3447	0.0313361	39.608	1.122e-12 ***
	Residuals	24	0.01899	0.0007911		
	Total	35	0.36369			
Fecundity Index	Genotypes	11	0.08371	0.00761	37.561	2.026e-12 ***
	Residuals	24	0.004862	0.0002026		
	Total	35	0.088572			

*****=(P<0.001)**

Appendix 10. Temperature and rainfall data of Sinana Agricultural Research Center

Average monthly temperature and rainfall for the 2022				Average monthly temperature and rainfall for the 2023		
Month	Temperature (^{0}C)		Total Rainfall(mm)	Temperature (^{0}C)		Total Rainfall(mm)
	Maximum	Minimum		Maximum	Minimum	
January	22.7	8.4	4	22.4	7.8	10
February	24.1	9.7	3	23.9	9.3	1
March	24.1	10.5	19	21.2	10.7	167
April	21.7	11	134	20.4	10.1	162
May	22.4	10.7	27	20.3	11	101
June	21.8	11	27	21.3	11.5	19
July	19.3	11	172	21.2	11.9	91
August	19.3	10.8	179	20.3	11	82
September	19.7	10.7	92	20.9	11.6	147
October	18.7	9.6	181	19.4	10.5	147
November	19.6	7.6	21	18.8	8.9	116
December	21.4	7.7	2	21.3	7.9	2
Mean	21.23	9.89	72	20.95	10.2	87
Total			**861**			**1,045**

Appendix 11. Average daily temperature of the laboratory during 2024 antibiosis test at Sinana Agricultural Research Center

Date	Month	Date	Month
	October		October
1	21.02	17	20.02
2	20.68	18	26.35
3	21.02	19	22.02
4	21.35	20	24.35
5	21.02	21	19.02
6	21.68	22	20.02
7	20.35	23	20.35
8	19.35	24	21.35
9	22.68	25	23.35
10	23.02	26	20.02
11	21.68	27	21.35
12	22.68	28	22.02
13	23.02	29	21.35
14	20.35	30	18.35
15	20.02	31	22.02
16	20.35		
Mean			**21.36**