**FIELD SCREENING FOR LEAF CURL DISEASE RESISTANCE IN SUNFLOWER (*Helianthus annuus* L.*)* GENOTYPES**

# **ABSTRACT**

In India, sunflower cultivation is increasingly constrained by leaf curl disease, primarily caused by begomoviruses transmitted by whiteflies. This study aimed to evaluate the resistance of 48 sunflower genotypes to leaf curl disease during the rabi season of 2024–25 at the Regional Agricultural Research Station, Nandyal. Disease severity was assessed at four growth stages using the Percent Disease Incidence (PDI). Significant genotypic variation was observed across all stages. Statistical analysis, including ANOVA and heritability estimates, indicated that environmental influence was minimal, with high heritability and genetic advance suggesting additive gene action in resistance expression. Disease progression parameters such as apparent infection rate and area under the disease progress curve supported these findings. The genotype NDLA-2 × NDI-51 showed consistently low disease incidence. These results highlight potential genotypes for use in breeding programs aimed at improving resistance to leaf curl disease in sunflower, contributing to the development of more resilient hybrids suited for Indian agro-climatic conditions.

# **INTRODUCTION**

Sunflower is a significant contributor to global oilseed production, accounting for approximately 9% of the total and 3.85% of contribution to Indian oil seed production. In India, it is a rapidly growing oilseed crop, particularly in states like Karnataka, Andhra Pradesh, and Telangana, where it plays a crucial role in the agricultural economy. In the 2023–24 period, India produced 1.72 lakh tonnes of sunflower from 1.51 lakh hectares, yielding an average of 1144 kg per hectare.

However, sunflower cultivation in Andhra Pradesh faces substantial challenges due to various diseases, including leaf curl, powdery mildew, necrosis disease and Alternaria leaf spot. These diseases can lead to significant yield losses, ranging from 30% to 74% (Prakash *et al*., 2021). Specifically, in Andhra Pradesh, yield losses due to these diseases were reported to be as high as 43% during manifestation trials conducted from 2012 to 2015 under the All India Coordinated Research Project (AICRP) on Sunflower at the Regional Agricultural Research Station (RARS), Nandyal. (Venkataramanamma *et al*., 2016).

Leaf curl disease in sunflowers is a major problem and is caused by several factors, including viral infections and environmental stressors. Infected plants may exhibit yellowing (chlorosis), mottling, and overall reduced vigor and in severe infections it may lead to significant yield losses. Disease incidence recorded from 24.08 to 56.30%, highest incidence was recorded in Sunbreed-275 hybrid with 56.30% (Vardhini *et al.* 2023). As of now there is no complete resistance against leaf curl is available in cultivated sunflower or any related germplasm even though the differences in susceptibility exist. Early detection and appropriate management strategies are crucial for minimizing the impact of this disease on sunflower production. Breeding for resistance to leaf curl faces the challenge of a gene pool containing only moderate levels of resistance. There is a strong need to identify genotypes/hybrids resistant to leaf curl disease in sunflower.

The objective of the present study was to evaluate a set of sunflower genotypes for resistance to leaf curl disease under field conditions using PDI, AUDPC, apparent infection rate metrics and to identify resistant hybrids for breeding programs.

# **MATERIAL AND METHODS**

The field experiment was conducted during rabi, 2024-25 at regional agricultural research station in Nandyal, Andhra Pradesh, India. The experimental location is situated in a semi-arid tropical region with red sandy loam soils. During the cropping period, average maximum and minimum temperatures ranged between 29°C-34°C and 18°C-22°C, respectively. The field experienced low relative humidity and occasional dry spells typical of the rabi season. These conditions are conducive to the natural incidence and spread of leaf curl disease due to increased whitefly activity.

The experimental material consists of 35 genotypes along with susceptible check KBSH -44 and moderately susceptible check NDSH-1012. Each genotype was evaluated in three replications in single row of length 3m with spacing of 60 x 30 cm. All the recommended agronomical practices were followed throughout the crop growing period. Leaf curl was assessed in each genotype as per the 0– 5 scale proposed by Gururaj Sunkad, *et al.,* (2002) and Venkataramanamma and Prabhakar, (2020) (Table 1). Disease severity was recorded at 15 days interval starting from the appearance of disease symptoms *i.e.*, 30 DAS, 45 DAS (Days After Sowing), 60 DAS and 75 DAS and percent disease incidence (PDI) was evaluated by using below formula suggested by Vander Plank (1963).

Number of infected plants

Disease incidence % = x 100

Total number of plants

The rate of disease development (r) at different intervals is calculated using the formula outlined by Van der Plank (1963):

r **= (log - log)**

Where:

* **r** = Apparent rate of infection or spread
* **X₁** = Percent disease incidence (PDI) at time t₁
* **X₂** = Percent disease incidence (PDI) at time t₂
* **t₂ - t₁** = Time interval in days between the consecutive observations

Additionally, the Area Under Disease Progress Curve (AUDPC) values were calculated using the PDI at 45, 60, and 75 days after sowing (DAS) for each genotype, employing the formula recommended by Wilcoxson et al. (1975):

AUDPC value = **( Si + Si – 1) × d.**

Where:

* **Sᵢ** = Disease severity at the end of time i
* **k** = Number of successive evaluations
* **Tᵢ - Tᵢ-1** = Constant time interval (15 days)

# **RESULTS AND DISCUSSION**

The PDI values calculated at three intervals were utilized to perform an analysis of variance (ANOVA). The ANOVA revealed significant variations among the genotypes concerning their reaction to leaf curl disease at 30, 45, 60, and 75 DAS (Table 2). Phenotypic coefficient of variance (PCV) is observed slightly greater than Genotypic coefficient of variance (GCV). It implies that the influence of environment over the trait response of genotypes is very low. High heritability and genetic advance as a percentage of mean (GAM) indicate additive gene action, implying great potential for advancement through breeding selection. This indicates a substantial genetic diversity in disease resistance among the evaluated sunflower genotypes.

The PDI values at 30, 45, 60, 75 DAS are furnished in Table 3. After 75 DAS the results of the current investigation displayed that out of 48 genotypes, one genotype NDLA-2 x NDI- 51 showed moderate resistance. 16 genotypes reported moderate susceptibility and 29 genotypes were found susceptible.

At 30 DAS, the disease symptoms were observed in only some of the evaluated genotypes. Among 30 hybrids evaluated the lowest PDI value of 0.0 was observed in 15 hybrids whereas the hybrid CMS 17A x NDI-34 showed the highest PDI of 16.0%. Among checks PHT showed 0.0 PDI value and KBSH-44 exhibited highest PDI of 31.4% indicating susceptibility reaction to disease with score of 4 on 0-5 scale. Among all the genotypes, PDI values ranged from 0.0 to 31.8% with 6.13% mean value. Less PDI of 0.0% was noted in 16 genotypes whereas, highest PDI of 31.8% was noted in KBSH- 44. 16 genotypes demonstrated negative deviation from the mean value. In contrast 14 genotypes showed positive deviation from the mean value.

At 45 DAS, more disease incidence was observed in all entries compared with 30 DAS. Among 30 hybrids evaluated the lowest PDI value of 4.88% was observed in NDLA-2 x NDI-39 whereas the hybrid CMS 17A x NDI-49 showed the highest PDI of 29.67%. Among checks PHT showed 9.8% PDI and KBSH-44 exhibited highest PDI of 51.2% indicating high susceptibility to disease with score of 5 on 0-5 scale. Among all genotypes, PDI values ranged from 4.88% to 51.2%, with 16.89% mean value. 26 genotypes demonstrated greater negative deviation from the mean value. In contrast 7 genotypes showed positive deviation from the mean value.

At 60 DAS, more disease incidence was observed in all entries compared with 45 DAS. Among 30 hybrids evaluated the lowest PDI of 8.71% was observed in NDLA-2 x NDI-51 whereas the hybrid CMS 17A x AKSFI-78 showed the highest PDI of 42.27%. Among checks PHT showed 24.10% PDI and KBSH-44 exhibited highest PDI of 61.00% indicating high susceptibility to disease with score of 5 on 0-5 scale. Among all the genotypes evaluated PDI values ranged from 8.71% to 61.00% with 28.54% mean value. 20 genotypes demonstrated negative deviation from the mean value. In contrast 15 genotypes showed greater positive deviation from the mean value.

At 75 DAS, disease was observed in almost all genotypes. Among 30 hybrids evaluated the lowest PDI of 8.71% was observed in NDLA-2 x NDI-51 whereas the hybrid CMS 17A x AKSFI-78 showed the highest PDI of 46.43%. Among checks PHT showed 24.1% PDI and KBSH-44 exhibited highest PDI of 73.1% indicating high susceptibility to disease with score of 5 on 0-5 scale. Among all the genotypes evaluated PDI values ranged from 8.71% to 73.10% with 30.21% average. 22 genotypes showed negative deviation from the mean. In contrast 13 genotypes showed a positive deviation from the mean.

By analyzing the PDI scores obtained, we can conclude that there is an increase in disease susceptibility of almost all genotypes from 30 DAS to 75 DAS. The similar results were obtained in the experiment conducted by Deepa *et al.* (2017) where there is an increased susceptibility of genotypes to leaf curl disease from 30 DAS to 90 DAS. Saddam (2016) conducted a study to examine seasonal incidence of leaf curl disease in sunflower and reported that PDI values were reaching up to 80% during the rabi season.

The apparent rate of infection ‘r’ value for leaf curl is summarized in Table 4 for three intervals i.e., between 30-45 DAS, 45-60 DAS and 60-75 DAS along with average rate of infection and AUDPC (Area Under Disease Progress Curve). Between 30-45 days interval among 30 hybrids evaluated, 15 hybrids showed no infection where as nine hybrids showed zero ‘r’ value and hybrid NDLA-2 x NDI-34 showed high ‘r’ value of 0.029. And among checks PHT showed no infection where as TNTSH-1 showed high ‘r’ value of 0.03. Between 45-60 days interval among 30 hybrids evaluated 7 hybrids showed no infection zero ‘r’ value and hybrid NDLA-2 x NDI-39 showed high ‘r’ value of 0.01. And among checks KBSH-44 showed zero ‘r’ value where as PHT showed high ‘r’ value of 0.004. Between 60-75 days interval among 30 hybrids evaluated, 28 hybrids showed zero ‘r’ value and hybrids CMS 17A x NDI-24, NDLA-2 x NDI-24 showed high ‘r’ value of 0.001. And all checks showed zero ‘r’ value.

The average ‘r’ values ranged from 0.00 (IMS 265A x NDI-50, CMS 17A x NDI- 32, CMS 17A x NDI-50, NDLA-2 x NDI-51, NDLA-2 x RHA-1055 and NDLA-2 X NDI-50) to 0.011 (NDLA-2 x NDI-34 and TNTSH-1). The genotypes NDI-50, NDLA-2 x NDI-39 and NDLA-2 x AKSFI-78 exhibited ‘r’ value of 0.005 and NDSI-3 exhibited ‘r’ value of 0.004. Even though these genotypes exhibited higher rate of disease spread, the disease severity was low in contrast to other genotypes lines with lower ‘r’ value and high initial disease infection. In KBSH-44, high early- stage disease development in combination with low ‘r’ value shows late spread of disease. High early-stage disease infection coupled with higher ‘r’ value is identified in all highly susceptible genotypes Fig.1. These findings demonstrated that a low apparent infection rate does not always reflect a genotype’s resistance to disease. While the 'r' value alone may not be a reliable indicator of resistance, it can still serve as a useful tool for analyzing disease progression across different genotypes and it was detailed by Wilcoxson *et al.* (1975) he emphasized that while 'r' measures the speed of disease spread, it must not be used alone to declare a genotype resistant. Nargund (1989) reported that apparent infection rate (r) should be integrated with AUDPC for accurate disease progression analysis and Reddy *et al*. (2023) also stated that low 'r' value alone cannot indicate the genotypes resistance to disease in their experiment, field screening of sunflower genotypes for powdery mildew disease resistance.

The AUDPC was derived for each genotype using the PDI values obtained and represented in Table 4 and Fig.2. AUDPC values were used to compare the rates of disease progression amongst genotypes. Among hybrids the AUDPC values ranged from 108.88 (NDLA-2 x NDI-51) to 504 (CMS 17A x NDI-49). Among checks the AUDPC values ranged from 229.74 (PHT) to 855.9 (KBSH-44). Among all genotypes NDLA-2 x NDI-51 showed least AUDPC value of 108.88 and KBSH- 44 exhibited highest AUDPC value of 822.90. The mean value of AUDPC is 315.45. Genotypes with low AUDPC values develop disease at a slower rate than genotypes with high AUDPC values. So, with the results obtained we can conclude that NDLA-2 x NDI-51 developed disease at slower rate whereas KBSH-44 developed disease at faster rate compared to all other genotypes.

The categorization of genotypes based on DIS value is summarized in (Table 5), which revealed that there was no clear correlation between Disease Incidence Scale (DIS) values and the apparent infection rate ('r'), suggesting that relying solely on the 'r' value may not provide an accurate assessment of disease resistance. From the table, we observe that no genotypes fall into the “Highly resistant” (Scale-0) or “Resistant” (Scale-1) categories thus, no ‘r’ values are associated with these categories. A single genotype is categorized as “Moderately resistant” (Scale-2) with an ‘r’ value of 0.00 this also aligns well, as here ‘r’ value is very low. The “Moderately susceptible” (Scale-3) and “Susceptible” (Scale-4) categories show overlapping and indistinguishable ‘r’ value ranges 0.0 – 0.011 and 0.0–0.0107, respectively. This overlap suggests that even as the DIS moves from 3 to 4 (indicating more disease severity), the ‘r’ values do not clearly increase. In the “Highly susceptible” category (Scale-5), the ‘r’ values (0.00033 and 0.00067) are low. These values are lower than many observed in the “Moderately susceptible” and “Susceptible” categories, contradicting the expectation that higher DIS values should correspond to higher ‘r’ values. The similar results were obtained for Reddy *et al*. (2023), in a field experiment conducted to screen powdery mildew disease in sunflower and results obtained showed the variability of AUDPC values and the complex relationship between DIS and 'r' values.

# **CONCLUSION**

The evaluation of sunflower genotypes for resistance to leaf curl disease revealed significant genetic variability in disease reaction. PDI values consistently increased from 30 to 75 DAS, indicating progressive disease development. Among the evaluated genotypes, NDLA-2 x NDI-51 emerged as a moderately resistant hybrid, with the lowest AUDPC and favorable disease progression characteristics. The apparent infection rate (r) was found to be an inconsistent indicator of resistance, reinforcing the need to interpret it alongside PDI and AUDPC values. The moderate heritability and genetic advance estimates suggest that resistance to leaf curl disease is governed by additive gene action, making it amenable to improvement through selection. Genotypes like NDLA-2 x NDI- 51 can serve as valuable donors in breeding programs targeting the development of high-yielding, disease-tolerant sunflower hybrids. The integration of resistant genotypes into cultivation practices is essential for enhancing sunflower productivity and sustainability in diverse agro-climatic regions. The identified moderately resistant genotype NDLA-2 × NDI-51, can be utilized in hybrid development through marker-assisted backcrossing or incorporation into line × tester schemes to introgress resistance while retaining desirable agronomic traits.

# **AKNOWLEDGEMENT**

The author is thankful to Acharya N. G. Ranga Agricultural University and ICAR- Indian Institute of Oilseed Research, Hyderabad for providing assistance in conducting the research work.

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**Table 1. Based on disease incidence, the entries were categorized by following 0-5 scale (Gururaj Sunkad, et al., 2002 and Venkataramanamma and Prabhakar, 2020)**

|  |  |  |
| --- | --- | --- |
| **Score** | **Disease reaction** | **Disease incidence (% average)** |
| 0 | I/HR (Immune/Highly resistant) | No infection or 0% to 1% |
| 1 | R (Resistant) | 1.1 to 5% |
| 2 | MR (Moderately susceptible) | 5.1 to 10% |
| 3 | MS (Moderately susceptible) | 10.1 to 25% |
| 4 | S (Susceptible) | 25.1 to 50% |
| 5 | HS (Highly susceptible) | Above 50% |

**Table 2. Analysis of variance for PDI at different stages**

**PDI at**

**different growth Mean Sum SE CD Heritability**

**stages of Squares Mean CV (m) (5%) (bs) PCV GCV GAM**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Treatment** | **Error** |  | | | | | | | |
| **PDI@30 DAS** | 111.13\*\* | 0.71 | 6.13 | 13.73 | 0.59 | 1.69 | 0.99 | 121.5 | 121.2 | 248.80 |
| **PDI@45 DAS** | 226.78\*\* | 3.41 | 16.89 | 10.93 | 1.29 | 3.71 | 0.99 | 63.10 | 62.59 | 127.96 |
| **PDI@60 DAS** | 247.86\*\* | 8.28 | 28.54 | 10.08 | 2.01 | 5.79 | 0.97 | 39.01 | 38.35 | 77.68 |
| **PDI@75 DAS** | 332.02\*\* | 9.12 | 30.21 | 10.00 | 2.1 | 6.08 | 0.97 | 42.65 | 42.06 | 85.45 |

\* and \*\* significant at 5% and 1% LOS, respectively. bs= broad sense.

**Table 3. Percent disease incidence of Leaf curl disease at different growth stages**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sl.**  **No.** | **Genotypes** | | **30 days** | | | | **45 days** | | | **60 days** | | | **75 days** | | |
| **PDI** | | **Score on 0-5**  **scale** | **Host Reaction** | **PDI** | **Score on 0-5**  **scale** | **Host Reaction** | **PDI** | **Score on 0-5**  **scale** | **Host Reaction** | **PDI** | **Score on 0-5**  **scale** | **Host Reaction** |
|  | **Crosses** | |  | |  |  |  |  |  |  |  |  |  |  |  |
| 1 | IMS 265A X NDI-24 | | 0.00 | | 0 | HR | 15.48 | 3 | MS | 28.18 | 4 | S | 28.18 | 4 | S |
| 2 | IMS 265A X NDSI-3 | | 6.93 | | 2 | MR | 6.93 | 1 | R | 25.54 | 4 | S | 25.54 | 4 | S |
| 3 | IMS 265A X NDI-39 | | 6.46 | | 2 | MR | 6.46 | 1 | R | 33.48 | 4 | S | 33.48 | 4 | S |
| 4 | IMS 265A X NDI-51 | | 0.00 | | 0 | HR | 8.33 | 2 | MR | 16.67 | 3 | MS | 16.67 | 3 | MS |
| 5 | IMS 265A X NDI-49 | | 10.80 | | 3 | MS | 10.80 | 3 | MS | 36.93 | 4 | S | 36.93 | 4 | S |
| 6 | IMS 265A X RHA-1055 | | 8.83 | | 2 | MR | 8.83 | 1 | R | 33.65 | 4 | S | 33.65 | 4 | S |
| 7 | IMS 265A X NDI-32 | | 0.00 | | 0 | HR | 17.42 | 3 | MS | 20.63 | 3 | MS | 20.63 | 3 | MS |
| 8 | IMS 265A X NDI-50 | | 0.00 | | 0 | HR | 13.39 | 3 | MS | 13.39 | 3 | MS | 13.39 | 3 | MS |
| 9 | IMS 265A X AKSFI-78 | | 9.43 | | 2 | MR | 9.43 | 2 | MR | 25.66 | 4 | S | 25.66 | 4 | S |
| 10 | IMS 265A X NDI-34 | | 6.35 | | 2 | MR | 6.35 | 2 | MR | 28.18 | 4 | S | 29.18 | 4 | S |
| 11 | CMS 17A X NDI-24 | | 6.27 | | 2 | MR | 20.86 | 3 | MS | 30.99 | 4 | S | 40.59 | 4 | S |
| 12 | CMS 17A X NDSI-3 | | 0.00 | | 0 | HR | 9.09 | 2 | MR | 33.57 | 4 | S | 33.57 | 4 | S |
| 13 | CMS 17A X NDI-39 | | 10.05 | | 2 | MR | 10.05 | 2 | MR | 41.43 | 4 | S | 41.43 | 4 | S |
| 14 | CMS 17A X NDI-51 | | 0.00 | | 0 | HR | 14.58 | 3 | MS | 21.83 | 3 | MS | 21.83 | 3 | MS |
| 15 | CMS 17A X NDI-49 | | 15.48 | | 3 | MS | 29.67 | 4 | S | 42.26 | 4 | S | 42.26 | 4 | S |
| 16 | CMS 17A X RHA-1055 | | 14.36 | | 3 | MS | 14.36 | 2 | MR | 34.85 | 4 | S | 34.85 | 4 | S |
| 17 | CMS 17A X NDI-32 | | 0.00 | | 0 | HR | 21.11 | 3 | MS | 21.11 | 3 | MS | 21.11 | 3 | MS |
| 18 | CMS 17A X NDI-50 | | 0.00 | | 0 | HR | 28.57 | 4 | S | 28.57 | 4 | S | 28.57 | 4 | S |
| 19 | CMS 17A X AKSFI-78 | | 15.50 | | 3 | MS | 25.83 | 4 | S | 42.27 | 4 | S | 46.43 | 4 | S |
| 20 | CMS 17A X NDI-34 | | 16.02 | | 3 | MS | 16.02 | 3 | MS | 40.07 | 4 | S | 40.07 | 4 | S |
| 21 | NDLA-2 X NDI-24 | | 0.00 | | 0 | HR | 11.58 | 3 | MS | 16.24 | 3 | MS | 23.27 | 3 | MS |
| 22 | NDLA-2 X NDSI-3 | | 0.00 | | 0 | HR | 7.12 | 2 | MR | 12.08 | 3 | MS | 12.08 | 3 | MS |
| 23 | NDLA-2 X NDI-39 | | 0.00 | | 0 | HR | 4.88 | 1 | R | 13.40 | 3 | MS | 13.40 | 3 | MS |
| 24 | NDLA-2 X NDI-51 | | 0.00 | | 0 | HR | 8.71 | 2 | MR | 8.71 | 2 | MR | 8.71 | 2 | MR |
| 25 | NDLA-2 X NDI-49 | | 7.18 | | 2 | MR | 9.31 | 2 | MR | 26.80 | 3 | MS | 26.80 | 4 | S |
| 26 | NDLA-2 X RHA-1055 | 0.00 | | 0 | | HR | 14.17 | 3 | MS | 14.17 | 3 | MS | 14.17 | 3 | MS |
| 27 | NDLA-2 X NDI-32 | | 6.79 | | 2 | MR | 17.15 | 3 | MS | 17.15 | 3 | MS | 17.15 | 3 | MS |
| 28 | NDLA-2 X NDI-50 | | 0.00 | | 0 | HR | 16.73 | 3 | MS | 18.86 | 3 | MS | 18.86 | 3 | MS |
| 29 | NDLA-2 X AKSFI-78 | | 0.00 | | 0 | HR | 5.21 | 2 | MR | 14.17 | 3 | MS | 14.17 | 3 | MS |
| 30 | NDLA-2 X NDI-34 | | 2.38 | | 1 | R | 9.17 | 2 | MR | 24.41 | 3 | MS | 24.41 | 3 | MS |
|  | **Checks** | |  | |  |  |  |  |  |  |  |  |  |  |  |
| 1 | NDSH-1012 | | 20.89 | | 3 | MS | 28.60 | 4 | S | 41.90 | 4 | S | 48.80 | 4 | S |
| 2 | KBSH-44 | | 31.79 | | 4 | S | 51.20 | 5 | HS | 61.00 | 5 | HS | 73.10 | 5 | HS |
| 3 | KBSH-78 | | 8.25 | | 2 | MR | 12.90 | 3 | MS | 35.80 | 4 | S | 35.80 | 4 | S |
| 4 | TNTSH-1 | | 2.50 | | 1 | R | 15.80 | 3 | MS | 25.00 | 3 | MS | 27.50 | 4 | S |
| 5 | PHT | | 0.00 | | 0 | HR | 9.80 | 2 | MR | 24.10 | 3 | MS | 24.10 | 3 | MS |

HR= highly resistant, R= resistant, MR= moderately resistant, S= susceptible, HS=highly susceptible

**Table 4. Apparent rate of infection “r” values and AUDPC values for leaf curl resistance in sunflower genotypes**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sl.**  **No.** | **Genotypes** | **30 to 45 days** | **45 to 60 days ‘r’** | **60 to 75 days ‘r’** | **Average ‘r’** | **AUDPC** |
|  | **Crosses** |  |  |  |  |  |
| 1 | IMS 265A X NDI-24 | - | 0.002 | 0.000 | 0.001000 | 288.71 |
| 2 | IMS 265A X NDSI-3 | 0.000 | 0.008 | 0.000 | 0.002667 | 243.49 |
| 3 | IMS 265A X NDI-39 | 0.000 | 0.009 | 0.000 | 0.003000 | 299.55 |
| 4 | IMS 265A X NDI-51 | - | 0.004 | 0.000 | 0.002000 | 166.68 |
| 5 | IMS 265A X NDI-49 | 0.000 | 0.005 | 0.000 | 0.001667 | 357.94 |
| 6 | IMS 265A X RHA-1055 | 0.000 | 0.006 | 0.000 | 0.002000 | 318.56 |
| 7 | IMS 265A X NDI-32 | - | 0.001 | 0.000 | 0.000500 | 241.83 |
| 8 | IMS 265A X NDI-50 | - | 0.000 | 0.000 | 0.000000 | 167.38 |
| 9 | IMS 265A X AKSFI-78 | 0.000 | 0.005 | 0.000 | 0.001667 | 263.14 |
| 10 | IMS 265A X NDI-34 | 0.000 | 0.009 | 0.000 | 0.003000 | 261.44 |
| 11 | CMS 17A X NDI-24 | 0.008 | 0.001 | 0.001 | 0.003333 | 376.35 |
| 12 | CMS 17A X NDSI-3 | - | 0.006 | 0.000 | 0.003000 | 297.19 |
| 13 | CMS 17A X NDI-39 | 0.000 | 0.005 | 0.000 | 0.001667 | 386.03 |
| 14 | CMS 17A X NDI-51 | - | 0.002 | 0.000 | 0.001000 | 236.59 |
| 15 | CMS 17A X NDI-49 | 0.002 | 0.001 | 0.000 | 0.001000 | 504 |
| 16 | CMS 17A X RHA-1055 | 0.000 | 0.003 | 0.000 | 0.001000 | 369 |
| 17 | CMS 17A X NDI-32 | - | 0.000 | 0.000 | 0.000000 | 263.88 |
| 18 | CMS 17A X NDI-50 | - | 0.000 | 0.000 | 0.000000 | 357.13 |
| 19 | CMS 17A X AKSFI-78 | 0.002 | 0.001 | 0.000 | 0.001000 | 495.29 |
| 20 | CMS 17A X NDI-34 | 0.000 | 0.003 | 0.000 | 0.001000 | 420.64 |
| 21 | NDLA-2 X NDI-24 | - | 0.002 | 0.001 | 0.001500 | 197.23 |
| 22 | NDLA-2 X NDSI-3 | - | 0.004 | 0.000 | 0.002000 | 126.16 |
| 23 | NDLA-2 X NDI-39 | - | 0.010 | 0.000 | 0.005000 | 124.86 |
| 24 | NDLA-2 X NDI-51 | - | 0.000 | 0.000 | 0.000000 | 108.88 |
| 25 | NDLA-2 X NDI-49 | 0.002 | 0.005 | 0.000 | 0.002333 | 265.43 |
| 26 | NDLA-2 X RHA-1055 | - | 0.000 | 0.000 | 0.000000 | 177.06 |
| 27 | NDLA-2 X NDI-32 | 0.007 | 0.000 | 0.000 | 0.002333 | 231.34 |
| 28 | NDLA-2 X NDI-50 | - | 0.000 | 0.000 | 0.000000 | 225.08 |
| 29 | NDLA-2 X AKSFI-78 | - | 0.009 | 0.000 | 0.004500 | 132.29 |
| 30 | NDLA-2 X NDI-34 | 0.029 | 0.005 | 0.000 | 0.011333 | 234.81 |
|  | **Checks** |  |  |  |  |  |
| 1 | NDSH-1012 | 0.001 | 0.001 | 0.000 | 0.000667 | 526.88 |
| 2 | KBSH-44 | 0.001 | 0.000 | 0.000 | 0.000333 | 822.90 |
| 3 | KBSH-78 | 0.003 | 0.003 | 0.000 | 0.002000 | 353.89 |
| 4 | TNTSH-1 | 0.030 | 0.002 | 0.000 | 0.010667 | 279.15 |
| 5 | PHT | - | 0.004 | 0.000 | 0.002000 | 229.74 |

**Table 5. Categorization of the sunflower genotypes for leaf curl resistance based on disease incidence scale.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Disease Reaction** | **Disease Incidence Scale** | **No. of genotypes** | **Range of ‘r’ values** |
| Highly resistant | 0 | Nil | - |
| Resistant | 1 | Nil | - |
| Moderately resistant | 2 | 1 | 0.00 |
| Moderately susceptible | 3 | 14 | 0.0-0.0113 |
| Susceptible | 4 | 19 | 0.0-0.010667 |
| Highly susceptible | 5 | 1 | 0.000333 & 0.000667 |

**Fig.1.** **Average r value of leaf curldisease for moderately resistant and highly susceptible genotypes**

**Fig.2.** **Average AUDPC value of leaf curldisease for moderately resistant and highly susceptible genotypes**