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Identifying Drought Tolerant Finger Millet Landraces for the Hills of Nepal

Krishna Hari Ghimire1*, Madhav Prasad Pandey2, Surya Kanta Ghimire3, Hira Kaji Manandhar4, Bal Krishna Joshi5

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Abstract
Finger millet is in the fourth rank among the major cereals in Nepal after rice, maize and wheat. Since it is cultivated in rainy conditions, drought is one of the vital production constraints for this crop. With the objective of enhancing the utilization of native landraces conserved ex situ in genebank, 300 finger millet accessions were evaluated under drought stress and normal conditions at Khumaltar (1,360 masl), Lalitpur, Nepal during 2017 and 2018. In both the years, genotypes were significantly different for the yield and other agronomic characters. Eight different drought tolerant indices namely drought resistance index, geometric mean productivity, harmonic mean, mean productivity, stress susceptibility index, tolerance, yield index and yield stability index for each genotype were calculated using grain yield data recorded from the stress (Yds) and non-stress (Yns) experiment. Majority of the landraces were grouped under moderately susceptible group in both the years followed by moderately tolerant and susceptible group based on all the drought tolerant indices (DTIs). Five landraces, namely NGRC4849, NGRC6487, NGRC04852, NGRC03491 and NGRC6490 with average grain yield of 4670, 3624, 3426, 3191 and 3132 kg/ha, respectively, were identified as stable drought tolerant landraces compared to the released varieties. These landraces could be the potential sources of drought tolerance for finger millet improvement program for the mid-hills of Nepal.

Keywords
Drought tolerance indices; Finger millet; Grain yield; Native landraces; Rainfed farming

1. Introduction

Finger millet [Eleusine coracana (L.) Gaertn., 2n=4x=36] is grown by the East-African and South-Asian farmers for human consumption as well as livestock fodder. It was domesticated in Eastern Africa around 3000 BC and later introduced to the Indian subcontinent around 1000 BC, as reported by Hilu, De Wet and Harlan (1979) and Upadhyaya et al. (2006). Although, it is the fourth important crop of the millet group after sorghum, pearl millet and foxtail millet (Upadhyaya, Gowda and Reddy, 2007), its area and production are not precisely available in many countries since its production statistics is
jointly presented with other crops of the millet group (Upadhyaya et al., 2010). The global finger millet area has been reported as 3.8 million ha, mainly in Uganda, Tanzania, Kenya, Ethiopia, Rwanda and Somalia in Africa, as well as India, Myanmar, Nepal, Sri Lanka, China and Japan in Asia (Bora, 2013; Hittalmani et al., 2017; Kumar et al., 2016; Vetriventhan et al., 2016). It is cultivated in wider altitude ranges from the sea level in India (Upadhyaya et al., 2006) to high mountains (3,130 masl) of Nepal (Bastola et al., 2015; Gaihre, Gauchan and Timsina, 2021; Ghimire et al., 2022). It is a climate resilient crop grown in marginal soils with minimal inputs (Goron et al., 2015). Its grain is considered as nutritionally rich compared to major cereals, with high levels of protein, carbohydrate, dietary fiber, ash, calcium, iron, zinc, polyphenols and soluble fiber (Chandra et al., 2016; Devi et al., 2014; Krishna, Reddy and Kumar, 2021; Nakarani et al., 2020). Since it is a hardy crop grown in marginal soils, it is considered as the future smart crop due to its high nutritional richness with great potentiality to cope with the problem of food and nutrition insecurity in the changing climatic circumstances (Ghimire et al., 2020). Finger millet is called as kodo in Nepali language. Its flour has been commonly used for human food, straw is used as quality fodder for livestock, and whole grains are fermented for making alcoholic beverages (Ghimire et al., 2020). The green as well as dry straw of finger millet is very good animal fodder, which contains about 61% total digestible nutrients (Wafula et al., 2017). The demand of this crop by urban health-conscious consumers is increasing rapidly in recent years. It is nowadays emerging as a crucial element of agricultural tourism in Nepalese homestays serving the traditional recipes such as selroti (a ring bread), dhindo (thick porridge) and raksi (high quality wine) (Ghimire et al., 2017; Gaihre, Gauchan and Timsina, 2021; Joshi, Joshi and Ghimire, 2020).

Finger millet played a vital role in Nepalese economy since it became the fourth important crop of the country after major cereals like rice, maize and wheat (Ghimire et al., 2020). It is cultivated in 265,401 ha area of Nepal producing 326,443 ton grains with average productivity of 1.23 t/ha (MoALD, 2022). More than 90% of the total finger millet produced in the country comes from mid-hill districts where it is totally a rainfed crop (Ghimire et al., 2017; MoALD, 2022). Although, National Genebank is holding 1,055 finger millet accessions in long-term conservation (Genebank, 2022), their utilization in breeding is very less. Breeding the crop varieties is always focused on non-stress environment compared to the stress environment because it is easier to show the research results. However, breeding a crop like finger millet for abiotic stress tolerance is always kept in shadow by national and international research systems (Ghimire et al., 2020). There are only 5 varieties (Okhle-1, Dalle-1, Kabre kodo-1, Kabre kodo-2, Shailung kodo-1) released and one variety (Rato kodo) registered in Nepal during the last five decades (Joshi et al., 2017; Ghimire et al., 2017; SQCC, 2022), but none of these varieties are drought tolerant. Drought is condition of very low soil moisture leading to reduced crop yield (Krishna, Reddy and Kumar, 2021). It is one of the most significant abiotic constraints to plant growth that limits the agricultural productivity worldwide. It is recurrent but unpredictable phenomenon hindering the crop production in rainfed agriculture. Finger millet is considered as a drought resilient crop when compared to other major cereals (Vetriventhan et al., 2016). However, its growth can still be adversely affected by both intermittent and terminal drought stresses in the African and South Asian environments (Kumar et al., 1987;
Mwango, Kimurto and Ojwang, 2022). This is because finger millet is mainly grown by subsistence farmers under rainfed agriculture, which increases the vulnerability of yield loss due to drought stress. Different finger millet genotypes express different degree of tolerance as the crop is grown totally under rainfed agroecology in Nepal. The rainfall pattern in the semi-arid conditions of central to far-western hills is unpredictable and intermittent drought stress occurs frequently during all the crop growth stages. In semi-arid as well as arid environments where millets are predominantly grown, drought is the major abiotic factor for the yield loss (Ghimire et al., 2020; Tadele, 2016). Farmers from Lumbini, Karnali and Far-western provinces of Nepal are experiencing severe drought in recurring years during finger millet growing season. It has been reported that the reproductive and gain filling stages are the most sensitive to drought stress in finger millet, causing the significant reduction of grain yield (Bhavya et al., 2022; Talwar et al., 2020).

Grain yield under drought is a complex trait to evaluate because of its low heritability (Sharma et al., 2022). The yield data under stress and non-stress are useful to identify stable genotypes tolerant to drought stress (Clarke, De Pauw and Townley-Smith, 1992; Mohammadi et al., 2010; Nouri et al., 2011). There are several methods proposed by various researchers to determine different drought tolerance indices (DTIs) to identify drought tolerant genotypes in different crops (Ferede et al., 2020). Among them, drought resistance index (DRI), geometric mean productivity (GMP), harmonic mean (HM), mean productivity (MP), stress susceptibility index (SSI), tolerance (TOL), yield index (YI) and yield stability index (YSI) are some of the commonly used DTIs (Antre et al., 2021; Bhavya et al., 2022; Ferede et al., 2020; Mardeh et al., 2006; Mau et al., 2019; Menezes et al., 2014). This research was aimed to identify finger millet landraces tolerant to reproductive stage drought stress using different DTIs by evaluating native finger millet landraces of Nepal under drought imposed and under normal field conditions over two consecutive years of 2017 and 2018.

2. Methodology

2.1. Plant Materials

This research used 300 native finger millet genotypes including 295 landraces and five released varieties. These diverse genetic resources were collected from 54 districts of six provinces and conserved at National Agriculture Genetic Resources Center (NAGRC) commonly known as Nepal Genebank. District-wise number of landraces has been given in figure 1. Detail passport information (local names, collection districts and geo-coordinates) of these genotypes has been provided in Supplementary Table S1.
2.2. Experiment Site

This experiment was conducted in Khumaltar, Lalitpur, Nepal located at an altitude of 1,360 meter above sea level, north latitude of 27.65° and east longitude of 85.32° representing mid-hill environment of Nepal. The site has fluvial non-calcareous slightly acidic soil with 53.4% sand, 16.5% clay, 2.5% organic matter and pH value of 6.2 (https://soil.narc.gov.np). Data on monthly total rainfall (mm), relative humidity (average, %) and temperature (°C) of the site during finger millet season of both the years has been summarized in table 1.

Table 1: Weather data of experiment site during finger millet growing period (May to November) of 2017 and 2018

<table>
<thead>
<tr>
<th>Month</th>
<th>Relative humidity (%)</th>
<th>Minimum-maximum temperature (°C)</th>
<th>Rainfall (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2017</td>
<td>2018</td>
<td>2017</td>
</tr>
<tr>
<td></td>
<td>ns</td>
<td>ds</td>
<td>ns</td>
</tr>
<tr>
<td>May</td>
<td>76</td>
<td>75</td>
<td>73</td>
</tr>
<tr>
<td>June</td>
<td>81</td>
<td>80</td>
<td>81</td>
</tr>
<tr>
<td>July</td>
<td>82</td>
<td>82</td>
<td>84</td>
</tr>
<tr>
<td>August</td>
<td>81</td>
<td>82</td>
<td>82</td>
</tr>
<tr>
<td>September</td>
<td>79</td>
<td>79</td>
<td>80</td>
</tr>
<tr>
<td>October</td>
<td>79</td>
<td>79</td>
<td>69</td>
</tr>
<tr>
<td>November</td>
<td>75</td>
<td>75</td>
<td>72</td>
</tr>
</tbody>
</table>

Note: ds=drought stress (under white transparent plastic tunnel), ns=non-stress (open field).
2.3. General Methodology

The authors established two parallel set of experiments: one under plastic tunnel creating drought stress (ds) condition, and another in the open field or non-stress (ns) condition. White transparent plastic roof was provided in ds experiment to prevent from the rainfall. For both the experiments, direct seeding was done in raised beds on 17 June 2017 and 8 July 2018. A total of 300 entries were evaluated in alpha lattice design\(^1\) with two replications and 15 blocks. Each plot comprised 10 plants (single row of 1 m length) in ds and 20 plants (single row of 2 m length) in ns with row spacing of 25 cm. For both ds and ns experiments, 20 kg N, 10 kg P\(_2\)O\(_5\) and 10 kg K\(_2\)O per hectare were applied at basal doses, whereas 20 kg/ha N was top-dressed after six weeks of sowing. Manual weeding followed by thinning was done after four weeks of seeding to maintain 10 cm spacing between plants within rows. Sprinkler irrigation was provided at an interval of two weeks till the initiation of flowering in ds but no irrigation was provided in ns field. Soil moisture was recorded from 10 cm depth in a day interval from both ds and ns fields (Ghimire et al., 2020).

2.4. Data Recording and Analysis

Agronomic data on various traits such as days to 50% flowering, days to 80% maturity, grain yield (kg/ha, adjusted to 14% grain moisture) and straw yield (ton/ha after week-sun-drying) were recorded from ds and ns experiments based on whole plot, whereas number of fingers per head was taken from five randomly selected plants. Data were subjected to analysis of variance (ANOVA) and different variability components (mean, standard error of mean, minimum, maximum, probability value, broad sense heritability (\(h^2bs\)) and genetic advance with percentage of mean (GAM) were calculated using 'variability' package (Popat, Patel and Parmar, 2020) of R statistical software (R Core Team, 2020). Various drought tolerance indices (DTIs) were calculated for each genotype using Excel worksheet while referring the relationship of mean grain yield under ds and ns (Table 2). Overall mean (\(\mu\)) and standard deviation (\(\sigma\)) were calculated for each DTIs. Genotypes were grouped in five reaction classes based on DTI values. Higher drought tolerance is considered when the DTI value is higher in case of DRI, GMP, HM, MP, SSI, YI and YSI. Thus, genotype is grouped as tolerant (T) if DTI is above \(\mu+2\sigma\), moderately tolerant (MT) if DTI=\(\mu+\sigma\) to \(\mu+2\sigma\), moderately susceptible (MS) if DTI=\(\mu-\sigma\) to \(\mu+\sigma\), susceptible (S) if DTI=\(\mu-2\sigma\) to \(\mu-\sigma\) and highly susceptible (HS) if DTI is below \(\mu-2\sigma\) (Antre et al., 2021). This is just reverse in case of TOL because the genotype showing greater TOL value means there is higher yield reduction and higher drought sensitivity (Mardeh et al., 2006).

---

\(^1\) Alpha lattice design is a replicated simple experimental design like randomized complete block design (RCBD), but is efficient with large number of treatments where all treatments cannot be adjusted in a homogenous block or in single terraces especially in hills, thus called as an incomplete block design (Akinwale et al., 2021) which is used for the experiments under rainfed conditions, when there were higher CV (%) with RCBD, and gives higher efficiency than the RCBD (Yau et al., 1997).
Table 2: Different drought tolerance indices (DTIs) used in the study

<table>
<thead>
<tr>
<th>DTIs</th>
<th>Formula</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drought resistance index (DRI)</td>
<td>$DRI = Yds \times \left(\frac{Yds}{\bar{Yns}}\right)$</td>
<td>Lan (1998)</td>
</tr>
<tr>
<td>Geometric mean productivity (GMP)</td>
<td>$GMP = (Yns \times Yds)^{0.5}$</td>
<td>Fernandez (1992); Schneider et al. (1997)</td>
</tr>
<tr>
<td>Harmonic mean (HM)</td>
<td>$HM = {2(Yns \times Yds)/(Yns + Yds)}$</td>
<td>Bidinger, Mahalakshmi and Rao (1987); Jafari, Paknejad and Al-Ahamadi (2012)</td>
</tr>
<tr>
<td>Mean productivity (MP)</td>
<td>$MP = (Yds + Yns)/2$</td>
<td>Rosielle and Hamblin (1981)</td>
</tr>
<tr>
<td>Stress susceptibility index (SSI)</td>
<td>$SSI = {1 - (Yds/Yns)}/{1 - (\bar{Yds}/\bar{Yns})}$</td>
<td>Fischer and Maurer (1978)</td>
</tr>
<tr>
<td>Tolerance (TOL)</td>
<td>$TOL = Yns - Yds$</td>
<td>Rosielle and Hamblin (1981); Hessain et al. (1990)</td>
</tr>
<tr>
<td>Yield index (YI)</td>
<td>$YI = Yds/\bar{Yds}$</td>
<td>Gavuzzi et al. (1997)</td>
</tr>
<tr>
<td>Yield stability index (YSI)</td>
<td>$YSI = Yds/Yns$</td>
<td>Bouslama and Schapaugh (1984)</td>
</tr>
</tbody>
</table>

Note: $Yds$=individual genotype yield under drought, $Yns$= individual genotype yield under non-stress, $\bar{Yds}$=average yield of the entries under drought, $\bar{Yns}$=average yield of the entries under non-stress

3. Results

3.1 Soil Moisture Depletion under ds and ns Field

The experiment established under transparent white plastic tunnel preventing from rainfall is called drought stress (ds), whereas experiment in the open field is called as non-stress (ns) experiment. Soil moisture was recorded from 10 random points of both ds and ns experiments at 10 cm depth using soil moisture measuring device. Average soil moisture on every alternate day from mid-August to the first week of November during 2017 and 2018 is plotted in figure 2. Soil moisture depleted from 25% on 16 August to 14% on 10 November of 2017 in ns field conditions, whereas this depletion was from 17% on 16 August to 5% on 10 November of 2017 in ds field conditions. Similarly, during 2018, soil moisture reduction was from 24% on 15 August to 10% on 9 November in ns field, and the same was from 17% on 15 August to 6% on 9 November in ds field conditions. There was a difference of about 11-17% between soil moisture in ns and ds field conditions during the first year (i.e. 2017), but this difference was lower (3-10%) during the second year (i.e. 2018). The crop under ds conditions showed more stress in 2017 than in 2018.
3.2. Variability among Genotypes for Agronomic Traits

Wider variation was recorded among the genotypes under ds and ns conditions for seven different agronomic traits in 2017 and 2018 (Table 3). Grain yield under ds ranged from 39-7,263 kg/ha in 2017 and 81-5,403 kg/ha in 2018; whereas this range was from 137-7,514 kg/ha and 146-6,946 kg/ha, respectively, for 2017 and 2018 under ns conditions. Genotypes differed significantly for days to flowering, number of fingers and grain yield under ds and ns experiments in 2017 as well as in 2018. The genotypes significantly differed for straw yield under ds condition. Genotypes were not significantly different for plant height under ds in both the years, but the difference was significant for the plant height under ns during both the years. The difference among the genotypes was not significant for the root length under ds during both the years. Moderately high to very high heritability ($h^2$) was observed for days to flowering (62.1-93.1%) under ds and ns conditions during both the years, but $h^2$s for grain yield and other traits were found low to medium (11.8-55%) in ds and ns conditions during both the years. High GAM was observed for days to flowering (20.1%-31.2%) under ds (2017 and 2018) and ns (2017 and 2018), for grain yield (60.2-80.7%) under ds (2017), and ns (2017 and 2018), as well as for straw yield (31.2-38.4%) under ds (2017 and 2018). Mean grain yield under drought was 989 and 1,529 kg/ha in 2017 and 2018, respectively. Relative mean grain yield reduction due to drought was 31.65% in
2017 and 1.86% in 2018, suggesting very low impact of drought stress in the second year. This is due to the lower soil moisture difference between ns field and ds field in the second year.

Table 3: Variance components of finger millet genotypes evaluated under drought stress and non-stress conditions for different agronomic traits over two years

<table>
<thead>
<tr>
<th>Trait</th>
<th>Year</th>
<th>Env</th>
<th>Mean ± SE</th>
<th>Range</th>
<th>P-value</th>
<th>H²bs (%)</th>
<th>GAM (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DTF</td>
<td>2017</td>
<td>ds</td>
<td>89 ± 5.86</td>
<td>48-135</td>
<td>0.000</td>
<td>71.2</td>
<td>25.6</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>96 ± 2.88</td>
<td>48-123</td>
<td>0.000</td>
<td>93.1</td>
<td>31.2</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>ds</td>
<td>87 ± 5.93</td>
<td>50-140</td>
<td>0.000</td>
<td>62.1</td>
<td>20.1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>102 ± 2.98</td>
<td>55-130</td>
<td>0.000</td>
<td>91.3</td>
<td>26.4</td>
</tr>
<tr>
<td>EE</td>
<td>2017</td>
<td>ds</td>
<td>8.1 ± 1.93</td>
<td>1.6-19.6</td>
<td>0.263</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>12.1 ± 1.44</td>
<td>2.6-19.8</td>
<td>0.000</td>
<td>38.6</td>
<td>17.2</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>ds</td>
<td>11.8 ± 2.63</td>
<td>2.4-26.4</td>
<td>0.019</td>
<td>11.9</td>
<td>8.24</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>10.2 ± 2.42</td>
<td>2.7-23.4</td>
<td>0.008</td>
<td>14.0</td>
<td>10.4</td>
</tr>
<tr>
<td>FPH</td>
<td>2017</td>
<td>ds</td>
<td>7.5 ± 1.27</td>
<td>2.0-15.0</td>
<td>0.000</td>
<td>18.6</td>
<td>10.1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>6.6 ± 0.75</td>
<td>2.0-11.8</td>
<td>0.000</td>
<td>51.1</td>
<td>24.3</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>ds</td>
<td>9.2 ± 1.16</td>
<td>4.0-14.8</td>
<td>0.000</td>
<td>24.0</td>
<td>10.1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>7.3 ± 0.88</td>
<td>3.4-11.0</td>
<td>0.020</td>
<td>11.8</td>
<td>4.42</td>
</tr>
<tr>
<td>GY</td>
<td>2017</td>
<td>ds</td>
<td>989 ± 564.9</td>
<td>39-7263</td>
<td>0.000</td>
<td>30.2</td>
<td>60.2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>1447 ± 489.7</td>
<td>137-7514</td>
<td>0.000</td>
<td>55.0</td>
<td>80.7</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>ds</td>
<td>1529 ± 498.2</td>
<td>81-5403</td>
<td>0.013</td>
<td>12.9</td>
<td>13.1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>1558 ± 470.8</td>
<td>146-6946</td>
<td>0.000</td>
<td>53.0</td>
<td>72.7</td>
</tr>
<tr>
<td>PH</td>
<td>2017</td>
<td>ds</td>
<td>68 ± 10.66</td>
<td>29-103</td>
<td>0.119</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>81 ± 7.43</td>
<td>32-130</td>
<td>0.000</td>
<td>46.5</td>
<td>17.0</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>ds</td>
<td>122 ± 12.70</td>
<td>53-171</td>
<td>0.795</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>110 ± 8.85</td>
<td>50-151</td>
<td>0.000</td>
<td>34.3</td>
<td>10.0</td>
</tr>
<tr>
<td>RL</td>
<td>2017</td>
<td>ds</td>
<td>15.5 ± 2.26</td>
<td>7.5-27.5</td>
<td>0.115</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>15.2 ± 2.17</td>
<td>7.4-27.8</td>
<td>0.198</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>SY</td>
<td>2017</td>
<td>ds</td>
<td>7.9 ± 1.37</td>
<td>1.9-13.7</td>
<td>0.000</td>
<td>52.2</td>
<td>38.4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ns</td>
<td>9.3 ± 1.62</td>
<td>1.6-16.2</td>
<td>0.000</td>
<td>45.6</td>
<td>31.2</td>
</tr>
</tbody>
</table>

Note: DTF = Days to 50% flowering, EE = Ear exsertion, FPH = Number of fingers per head, GY = Grain yield (kg/ha), PH = Plant height (cm), RL = Root length (cm), SY = Straw yield (t/ha), ds = Stress, ns = Non-stress, SE = Standard error of mean, H²bs = Heritability in broad sense, GAM = Genetic advance with percentage of mean

3.3. Variability among Genotypes for DTIs

Grain yield under ds and ns field conditions was used to calculate different drought tolerant indices of each genotype. High variability was observed among genotypes for all the eight DTIs namely DRI, GMP, HM, MP, SSI, TOL, YI and YSI in both the years (Table 4). Genotype with lower TOL value is preferable since it calculates the yield difference between ns and ds fields, but higher value is desirable for rest of the DTIs.
Table 4: Mean and range of eight various drought tolerant indices over two years

<table>
<thead>
<tr>
<th>DIT</th>
<th>Year</th>
<th>Mean</th>
<th>SE</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>DRI</td>
<td>2017</td>
<td>0.87</td>
<td>0.11</td>
<td>0.00</td>
<td>26.82</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1.61</td>
<td>0.10</td>
<td>0.01</td>
<td>13.59</td>
</tr>
<tr>
<td>GMP</td>
<td>2017</td>
<td>1117.1</td>
<td>40.8</td>
<td>100.2</td>
<td>6427.9</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1430.3</td>
<td>31.9</td>
<td>335.8</td>
<td>4227.7</td>
</tr>
<tr>
<td>HM</td>
<td>2017</td>
<td>1037.6</td>
<td>40.7</td>
<td>99.6</td>
<td>6419.9</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1374.7</td>
<td>31.6</td>
<td>275.2</td>
<td>4101.8</td>
</tr>
<tr>
<td>MP</td>
<td>2017</td>
<td>1218.5</td>
<td>41.6</td>
<td>100.8</td>
<td>6436.0</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1493.9</td>
<td>32.7</td>
<td>343.7</td>
<td>4546.5</td>
</tr>
<tr>
<td>SSI</td>
<td>2017</td>
<td>0.09</td>
<td>0.29</td>
<td>-68.53</td>
<td>3.05</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>7.53</td>
<td>1.21</td>
<td>-17.74</td>
<td>141.84</td>
</tr>
<tr>
<td>TOL</td>
<td>2017</td>
<td>460.8</td>
<td>52.2</td>
<td>-2137</td>
<td>4123</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>73.4</td>
<td>51.8</td>
<td>-2185</td>
<td>3931</td>
</tr>
<tr>
<td>YI</td>
<td>2017</td>
<td>1.00</td>
<td>0.05</td>
<td>0.05</td>
<td>6.84</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1.00</td>
<td>0.02</td>
<td>0.10</td>
<td>2.43</td>
</tr>
<tr>
<td>YSI</td>
<td>2017</td>
<td>0.97</td>
<td>0.09</td>
<td>0.03</td>
<td>22.79</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>1.38</td>
<td>0.06</td>
<td>0.11</td>
<td>8.14</td>
</tr>
</tbody>
</table>

Based on the DIT values, all 300 genotypes were divided into five reaction groups namely tolerant, moderately tolerant, moderately susceptible, susceptible and highly susceptible. Number of genotypes in each group for all the DITs during both the years has been presented in table 5. Large numbers of the genotypes were grouped under moderately susceptible group based on DRI (95% and 90%), GMP (84% and 74%), HM (83% and 72%), MP (83% and 78%), SSI (96% and 88%), TOL (70% and 74%), YI (85% and 72%) and GMP (96% and 88%) in 2017 and 2018, respectively. During 2017, 10 genotypes each in GMP and MP, 9 each in HM and YI, 8 in DRI, 7 in TOL and 5 genotypes in GMP were found as tolerant. Similarly, during 2018, maximum of 15 genotypes in SSI, 14 in YSI, 12 in MP, 11 each in DRI and GMP, 9 each in HM and TOL and 7 in YI were grouped as tolerant genotypes. None of the genotypes were found as highly susceptible for 6 out of 8 DITs except SSI and TOL in 2017, whereas 12 genotypes for TOL, 5 for YI and only 1 each for HM and MP were found as highly susceptible in 2018.

Table 5: Number of genotypes under different reaction groups and drought tolerant indices over two years

<table>
<thead>
<tr>
<th>Reaction level</th>
<th>Year</th>
<th>DRI</th>
<th>GMP</th>
<th>HM</th>
<th>MP</th>
<th>SSI</th>
<th>TOL</th>
<th>YI</th>
<th>YSI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tolerant</td>
<td>2017</td>
<td>8</td>
<td>10</td>
<td>9</td>
<td>10</td>
<td>0</td>
<td>7</td>
<td>9</td>
<td>5</td>
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<tr>
<td></td>
<td>2018</td>
<td>11</td>
<td>11</td>
<td>9</td>
<td>12</td>
<td>15</td>
<td>4</td>
<td>7</td>
<td>14</td>
</tr>
<tr>
<td>Moderately tolerant</td>
<td>2017</td>
<td>9</td>
<td>16</td>
<td>22</td>
<td>19</td>
<td>0</td>
<td>37</td>
<td>22</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>22</td>
<td>31</td>
<td>36</td>
<td>25</td>
<td>17</td>
<td>36</td>
<td>32</td>
<td>18</td>
</tr>
<tr>
<td>Moderately susceptible</td>
<td>2017</td>
<td>281</td>
<td>250</td>
<td>247</td>
<td>234</td>
<td>284</td>
<td>207</td>
<td>251</td>
<td>284</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>265</td>
<td>219</td>
<td>214</td>
<td>230</td>
<td>260</td>
<td>219</td>
<td>213</td>
<td>260</td>
</tr>
<tr>
<td>Susceptible</td>
<td>2017</td>
<td>0</td>
<td>22</td>
<td>20</td>
<td>25</td>
<td>9</td>
<td>38</td>
<td>16</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>0</td>
<td>37</td>
<td>38</td>
<td>30</td>
<td>6</td>
<td>27</td>
<td>41</td>
<td>6</td>
</tr>
<tr>
<td>Highly susceptible</td>
<td>2017</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>5</td>
<td>9</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>12</td>
<td>5</td>
<td>0</td>
</tr>
</tbody>
</table>
3.4. Stable Drought Tolerant and Susceptible Genotypes

Genotypes showing tolerant reaction across DTIs and over two years were selected as stable drought tolerant genotypes, whereas genotypes showing susceptible reaction across DTIs and over two years were found as stable susceptible genotypes for drought stress. Five tolerant and five susceptible genotypes with their contrasting reaction levels in each DTI and year have been presented in Table 6. Landraces namely NGRC04849, NGRC06487, NGRC04852, NGRC03491 and NGRC06490 showed tolerant to moderately tolerant reaction in at least 5 out of 8 DTIs during both the years. In contrast, 5 genotypes namely NGRC06485, NGRC04857, NGRC01634, NGRC03503 and NGRC03540 showed moderately susceptible to highly susceptible reactions for at least 7 out of 8 DTIs during both the years.

Table 6: Stable drought tolerant and susceptible finger millet landraces based on drought tolerant indices over two years

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Year</th>
<th>DRI</th>
<th>GMP</th>
<th>HM</th>
<th>MP</th>
<th>SSI</th>
<th>TOL</th>
<th>YI</th>
<th>YSI</th>
</tr>
</thead>
<tbody>
<tr>
<td>NGRC04849</td>
<td>2017</td>
<td>T</td>
<td>T</td>
<td>T</td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>MT</td>
<td>T</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NGRC06487</td>
<td>2017</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td></td>
<td></td>
</tr>
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<td></td>
<td>2018</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NGRC04852</td>
<td>2017</td>
<td>MT</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NGRC03491</td>
<td>2017</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>T</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>MT</td>
<td>T</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NGRC06490</td>
<td>2017</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td>T</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>T</td>
<td>T</td>
<td>T</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>NGRC06485</td>
<td>2017</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>HS</td>
<td>S</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MS</td>
<td>S</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
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</tr>
<tr>
<td>NGRC04857</td>
<td>2017</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>MS</td>
<td>MS</td>
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</tr>
<tr>
<td></td>
<td>2018</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>S</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td>NGRC01634</td>
<td>2017</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>S</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>HS</td>
<td>S</td>
</tr>
<tr>
<td>NGRC03502</td>
<td>2017</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>S</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>HS</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td>NGRC03540</td>
<td>2017</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>MS</td>
<td>S</td>
<td>MS</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>MS</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>HS</td>
<td>S</td>
<td></td>
</tr>
</tbody>
</table>

Mean grain yield performance combined over years of tolerant and susceptible landraces together with 5 released varieties has been presented in figure 3. The highest mean grain yield was produced by NGRC04849 (4,670 kg/ha) followed by NGRC06487 (3,624 kg/ha), NGRC04852 (3,426 kg/ha), NGRC03491 (3,191 kg/ha) and NGRC06490 (3,132 kg/ha). These stable tolerant genotypes produced 149% to 271% higher grain yield over the grand mean (1,259 kg/ha) under drought stress. The susceptible landraces produced grain yield from 172 to 821 kg/ha, which was 35% to 86% lower as compared to grand mean. Four out of five released varieties produced average grain yield higher than grand mean, but much lower than stable tolerant landraces.
4. Discussion

Genebanks conserve genetically diverse genetic resources, which can be utilized to develop high-yielding and stable crop varieties tolerant to various biotic and abiotic stresses, and that contribute to global food security. Finger millet landraces exhibit significant variation in grain yield under different agroecological conditions, but their potential for breeding programs was not efficiently utilized in developing countries, including Nepal, due to limited attention paid to their characterization, evaluation, and pre-breeding activities. Despite the diverse genetic resources conserved in genebanks, less than 10% has been utilized in crop breeding. This is primarily due to insufficient evaluation work especially for the complicated traits like yield under drought (Hodgkin et al., 2003; Nguyen and Norton, 2020). Breeding the finger millet varieties for drought stress tolerance is always at low priority in Nepal, hence not a single variety is released as drought tolerant variety suitable for the dry areas of mid hills (SQCC, 2022).

The weather condition of the natural field is always unpredictable, and rainfall is beyond the control of researchers. To avoid undesirable but unexpected rainfall in the drought screening field, controlled structure with roofing of white transparent plastic sheet was used in this experiment. There was a difference of about 11-17% in soil moisture between under stress and non-stress field conditions during the first year; but this difference was only 3-10% during the second year. The crop under drought showed more stress in 2017 than in 2018. It was reflected in mean grain yield under stress, i.e. 989 kg/ha in 2017 and 1529 kg/ha in 2018. Degree of drought stress was estimated with relative yield reduction under drought compared to the yield under non-stress field conditions. Relative reduction in mean grain yield due to drought stress was 31.65% in 2017 was and 1.86% in 2018, suggesting very low impact of drought stress in the second year. This is due to the lower soil moisture difference between non-stress and stress field conditions in the second year. The yield reduction under drought was not uniform in both the years, suggesting that the...
genotypes do respond differently according to the extent of drought stress (Antre et al., 2021). It is found that this type of controlled structure was effective for screening genotypes under drought stress to avoid unpredictable rainfall. However, high infestation of insects mainly aphids and stem borers was evident due to dryness in such fields. The maximum temperature under ds field was 3-5°C higher compared to ns field. There was very high fluctuation in intra-day relative humidity (25-99%) as per the temperature fluctuation under ds field. The effect of light intensity under the plastic structure was not taken care of.

Singh (2001) explained greater than 80% the heritability values as very high, 60-79% the heritability values as moderately high, 40-59% the heritability values as medium, and less than 40% the heritability values as low. According to this delineation, moderately high to very high level of $h^2$bs for required days to flowering are observed. Medium $h^2$bs for grain yield under ns conditions and low $h^2$bs under ds conditions during both the years indicated the inheritance of grain yield mostly controlled by environmental variation. Previous reports by Anuradha et al. (2020); Bezaweletaw et al. (2006); Lule et al. (2012); Wolie, Dessalegn and Belete (2023) showed comparatively higher heritability in finger millet as compared to our estimates. Lower estimates of $h^2$bs in the study may be due to smaller plot size and single location (Teklu, Kebede and Gebremichael, 2014). This suggests the need of evaluation in multiple locations with larger plot size for effective selection of genotypes. Genetic advance as percentage of mean (GAM) values less than 10% are considered as low, 10-20% as moderate and more than 20% as high (Johnson, Robinson and Comstock, 1955). Based on this demarcation, the high genetic advance was estimated for days to flowering under ds and ns conditions in both the years. Similarly, grain yield under ds (2017), ns (2017 and 2018) and straw yield under ds (2017) showed high GAM. Sharma et al. (2022) reported higher $h^2$bs and GAM in finger millet as compared to the estimates of this study. Significant difference among the genotypes was observed for days to flowering, ear exerions, number of fingers per head, grain yield and straw yield, but the difference was not significant for plant height and root length under ds conditions. Similar results have reported that finger millet genotypes were not significantly different for root length under drought (Aparna and Bhargavi, 2017) and grain yield under drought stress was not correlated with root length (Simbagije, 2016). In contrast, morphological traits such as shoot length and root length are important traits under drought stress conditions (Mukami et al., 2019; Murtaza et al., 2016; Mwango, Kimurto and Ojwang, 2022).

Genotypes showing significant variability in grain yield under ds conditions suggest genotypic tolerance to drought stress. It is difficult to make conclusion just by looking at the yield performance under stress condition; thus, the comparative yield performance of genotypes under drought stress and non-stress conditions are useful to identify stable drought tolerant genotypes (Clarke, De Pauw and Townley-Smith, 1992; Mohammadi et al., 2010; Moosavi et al., 2008; Naghavi, Aboughadareh and Khalili, 2013; Nouri et al., 2011). Genotypes displaying high yield variation under drought stress and non-stress conditions cannot be measured as a stable drought tolerant genotype even if it yielded high under drought (Ali and El-Sadek, 2016). There are several methods proposed by various researchers to determine different DTIs in different crops to identify stable genotypes tolerant to drought. Among them, DRI, GMP, HM, MP, SSI, TOL, YI and YSI are some of the commonly used DTIs (Antre et al., 2021; Bhavya et al., 2022; Darkwa et al., 2016; Ferede et al., 2020; Mardeh et al.,
2006; Mau et al., 2019; Menezes et al., 2014; Naghavi, Aboughadareh and Khalili, 2013). High values of DRI, SSI, YI and YSI confirmed drought tolerance in different crops whereas high value of GMP, HM and MP confirmed the stable genotypes giving high yield at various levels of drought stress as well as non-stress condition (Ferede et al., 2020; Ghasemi and Farshandfar, 2015; Mohammadi et al., 2010; Naghavi, Aboughadareh and Khalili, 2013; Yousefi, 2015). In contrary to other DTIs, lower TOL value is desirable to be concluded as genotypes less sensitive to drought stress (Clarke, De Pauw and Townley-Smith, 1992; Mardeh et al., 2006; Rosielle and Hamblin, 1981). However, the selection only based on low TOL value was not effective to detect high yielding genotypes (Rizza et al., 2004). Stability in grain yield performance under both the ds and ns conditions is important to detect genotypes with stable drought tolerance (Mardeh et al., 2006). Based on the reaction levels exhibited by the genotypes across DTIs, five landraces namely NGRC04849, NGRC06487, NGRC04852, NGRC03491 and NGRC06490 were identified as stable tolerant landraces under drought conditions in this study because they showed tolerant to moderately tolerant reaction for at least 5 out of 8 DTIs during both the years. These stable landraces should be utilized in different ways: as donors in breeding program, further evaluation in larger plots at multiple locations, bringing into formal seed system after registration as a variety.

5. Conclusion

Wide variation was observed within Nepalese finger millet genotypes for agronomic traits under drought. Based on grain yield under stress and non-stress experiments, eight drought tolerant indices were used to identify stable drought tolerant landraces. Based on these indices, five promising landraces are identified, namely NGRC4849 from Rukum, NGRC6487 from Sindhuli, NGRC04852 from Sindhupalchok, NGRC03491 from Dolakha and NGRC6490 from Sindhuli district. These landraces have average grain yield ranging from 3,100 to 4,600 kg/ha showing stability compared to the released varieties under both drought and non-stress condition of mid-hill environments. This finding could provide strong avenues to enhance the use of native finger millet landraces and to accelerate the breeding process of this future smart nutrient-dense cereal. Since none of the finger millet varieties released so far is recommended for drought-prone areas, these selected landraces are being tested in larger plots under national coordinated varietal trials by Hill Crops Research Program (HCRP) throughout the country. Besides, these landraces could be listed into the national gazette as a variety, deployed to the analogous hilly environments to enrich the varietal options enhancing food security of the country.

6. Acknowledgments

This research was funded by UNEP/GEF in coordination with Bioversity International. We acknowledge the logistic support received from Agriculture and Forestry University (AFU), Nepal Agricultural Research Council (NARC) and National Agriculture Genetic Resources Center (NAGRC) for the field experiments. We extend our sincere gratitude to all farmers who provided seeds of these landraces.
7. Supplementary Table S1

Passport details of 300 finger millet genotypes received from National Agriculture Genetic Resources Center (Genebank), Nepal used in this research. Supplementary Table S1 is appended as zip file.

8. References


Authors’ Declarations and Essential Ethical Compliances

Authors’ Contributions (in accordance with ICMJE criteria for authorship)

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Funding
Research fund was available from UNEP/GEF through Alliance of Bioversity International-CIAT but no fund was available for writing and publication of this paper.

Research involving human bodies or organs or tissues (Helsinki Declaration)
The author(s) solemnly declare(s) that this research has not involved any human subject (body or organs) for experimentation. It was not a clinical research. The contexts of human population/participation were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) or ethical obligation of Helsinki Declaration does not apply in cases of this study or written work.

Research involving animals (ARRIVE Checklist)
The author(s) solemnly declare(s) that this research has not involved any animal subject (body or organs) for experimentation. The research was not based on laboratory experiment involving any kind animal. The contexts of animals were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) or ethical obligation of ARRIVE does not apply in cases of this study or written work.

Research on Indigenous Peoples and/or Traditional Knowledge
The author(s) solemnly declare(s) that this research has not involved any Indigenous Peoples as participants or respondents. The contexts of Indigenous Peoples or Indigenous Knowledge were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) and Self-Declaration in this regard are appended.

Research involving Plants
The author(s) solemnly declare(s) that this research has involved the plants for experiment or field studies. Some contexts of plants are also indirectly covered through literature review. Thus, during this research the author(s) obeyed the principles of the Convention on Biological Diversity and the Convention on the Trade in Endangered Species of Wild Fauna and Flora.
Research Involving Local Community Participants (Non-Indigenous) or Children
The author(s) solemnly declare(s) that this research has directly involved local community participants or respondents belonging to non-Indigenous peoples. But, this study did not involve any child in any form directly. The contexts of different humans, people, populations, men/women/children and ethnic people are only indirectly covered through literature review. A sample copy of the Consent Form implying prior informed consent (PIC) of the respondents is appended.

(Optional) PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses)
The author(s) has/have NOT complied with PRISMA standards. It is not relevant in case of this study or written work.

Competing Interests/Conflict of Interest
Author(s) has/have no competing financial, professional, or personal interests from other parties or in publishing this manuscript. There is no conflict of interest with the publisher or the editorial team or the reviewers.

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To see original copy of these declarations signed by Corresponding/First Author (on behalf of other co-authors too), please download associated zip folder [Declarations] from the published Abstract page accessible through and linked with the DOI: https://doi.org/10.33002/aa030101
ETHICAL CLEARANCE CERTIFICATE

Research Involving Indigenous Peoples and Traditional Knowledge

Declaration by the Principal Investigator

I certify that the study titled: "Identifying Drought Tolerant Finger Millet Landraces for the Hills of Nepal", (ref: na202022), does not involve collection of data or information on (an) Indigenous land, including reserve, settlement, and land governed under a self-government rule/agreement; the study does not involve any of the criteria for participation, including membership in an indigenous community, group of communities, or organization, including urban indigenous populations; the study does not seek inputs from participants (members of the indigenous community) regarding a community’s cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices; and the study does not involve Aboriginal identity or membership in an indigenous community used or be used as a variable for the purpose of analysis. The present study is conducted on government research stations and does not involve any Indigenous Peoples or Communities. I hereby declare the same and confirm that all personnel associated with the present study have read this application and have agreed to comply with procedures described and any conditions imposed by the World Intellectual Property Organization (WIPO), Geneva, with regards to research on Indigenous Peoples and/or Traditional Knowledge.

Principal Investigator: [Signature]

Date: 07-06-2023

Declaration by Head of the Organization/Research Committee

I have read this application and am satisfied that the study does not involve capturing and collection of data or information of the Indigenous Community's cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices. The study fully complies with the legislation and the general principles of the World Intellectual Property Organization (WIPO), Geneva.

Head of the Organization/Research Committee

Date: 7/6/23
SELF-DECLARATION FORM
Research on Indigenous Peoples and/or Traditional Knowledge

The nature and extent of community engagement should be determined jointly by the researcher and the relevant community or collective, taking into account the characteristics and protocols of the community and the nature of the research.

If your research involved/involves the Indigenous Peoples as participants or respondents, you should fill in and upload this Self-Declaration and/or Prior Informed Consent (PIC) from the Indigenous Peoples. [Please read carefully https://grassrootsjournals.org/credibility-compliance.php#Research-Ethics]

1. Conditions of the Research

1.1 Was or will the research (be) conducted on (an) Indigenous land, including reserve, settlement, and land governed under a self-government rule/agreement or?

   No

1.2 Did/does any of the criteria for participation include membership in an Indigenous community, group of communities, or organization, including urban Indigenous populations?

   No

1.3 Did/does the research seek inputs from participants (members of the Indigenous community) regarding a community’s cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices?

   No

1.4 Did/will Aboriginal identity or membership in an Indigenous community used or be used as a variable for the purposes of analysis?

   No

2. Community Engagement

2.1 If you answered “Yes” to questions 1.1, 1.2, 1.3 or 1.4, have you initiated or do you intend to initiate an engagement process with the Indigenous collective, community or communities for this study?

   Not Applicable

2.2 If you answered “Yes” to question 2.1, describe the process that you have followed or will follow with respect to community engagement. Include any documentation of
consultations (i.e., formal research agreement, letter of approval, PIC, email communications, etc.) and the role or position of those consulted, including their names if appropriate:

Not Applicable

3. No Community Consultation or Engagement

If you answered “No” to question 2.1, briefly describe why community engagement will not be sought and how you can conduct a study that respects Aboriginal/Indigenous communities and participants in the absence of community engagement.

Not Applicable

Name of Principal Researcher: Krishna Hari Ghimire
Affiliation of Principal Researcher:
   1. Senior Scientist (S-4), National Agriculture Genetic Resources Center, Nepal Agricultural Research Council, Nepal
   2. PhD Student, Department of Genetics and Plant Breeding, Agriculture and Forestry University, Chitwan, Nepal

Signature: 

Date: 7/6/2023

Declaration: Submitting this note by email to any journal published by The Grassroots Institute is your confirmation that the information declared above is correct and devoid of any manipulation.
INFORMATION AND CONSENT FORM FROM RESPONDENTS
(Non-Indigenous or Indigenous Respondents)
*This form was translated into local language for the respondents*

Title of the Research: Identifying Drought Tolerant Finger Millet Landraces for the Hills of Nepal

Principal Researcher: Krishna Hari Ghimire
National Agriculture Genetic Resources Center (Genebank)
Nepal Agricultural Research Council (NARC)

Research Supervisor: Self

A) INFORMATION TO PARTICIPANTS

1. Objectives of the research
To evaluate native finger millet landraces under drought stress condition, identify promising landraces and enhanced their utilization in developing high yielding varieties for the hills of Nepal.

2. Participation in research
The researcher will ask you several pertinent questions. This interview will be recorded in written form and should last about 50-60 minutes. The location and timing of the interview will be determined by you, depending on your availability and convenience.

3. Risks and disadvantages
There is no particular risk involved in this project. You may, however, refuse to answer any question at any time or even terminate the interview.

4. Advantages and benefits
You will receive intangible benefits even if you refuse to answer some questions or decide to terminate the interview.

5. Confidentiality
Personal information you give us will be kept confidential. No information identifying you in any way will be published. In addition, each participant in the research will be assigned a code and only the researcher will know your identity.

6. Right of withdrawal
Your participation in this project is entirely voluntary and you can at any time withdraw from the research on simple verbal notice and without having to justify your decision, without consequence to you. If you decide to opt out of the research, please contact the researcher at the telephone number or email listed below. At your request, all information concerning you can also be destroyed. However, after the outbreak of the publishing process, it is impossible to destroy the analyses and results on the data collected.
B) CONSENT

Declaration of the participant
⇒ I understand that I can take some time to think before agreeing or not to participate in the research.
⇒ I can ask the research team questions and ask for satisfactory answers.
⇒ I understand that by participating in this research project, I do not relinquish any of my rights, including my right to terminate the interview at any time.
⇒ I have read this information and consent form and agree to participate in the research project.
⇒ I agree that the interviews be recorded in written form by the researcher: Yes (   ) No (   )

Signature of the participant : __________________ Date : __________________

Surname : ______________________________ First name : __________________________

Researcher engagement

I explained to the participant the conditions for participation in the research project. I answered to the best of my knowledge the questions asked and I made sure of the participant's understanding. I, along with the research team, agree to abide by what was agreed to in this information and consent form.

Signature of the researcher: __________________ Date : 07-06-2023

Surname: Ghimire First name: Krishna Middle name: Hari

⇒ Should you have any questions regarding this study, or to withdraw from the research, please contact to Krishna Hari Ghimire by e-mail ghimirekh@gmail.com

⇒ If you have any concerns about your rights or about the responsibilities of researchers concerning your participation in this project, you can contact to National Agriculture Genetic Resources Center, Nepal Agricultural Research Council by email joshibalak@yahoo.com
The Drivers of Changes in the State of Agrobiodiversity

Bal Krishna Joshi*,1, Devendra Gauchan2, Pushpatti Chaudhary3, Kamal Aryal4, Ram Krishna Shrestha5

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Abstract

The diversity of agricultural genetic resources is decreasing over the years and sites across the world. With the objectives of determining the drivers and their impact on agrobiodiversity particularly in Nepal, different methods e.g., focus group discussion, transact walk, key informant survey, and literature survey were used. Among the 16 broad categories of drivers, the most important drivers in terms of negative impact on agrobiodiversity were the: 1) advancements and innovations in science and technology, 2) changes in land and water use and management, 3) alternative business and information flow, 4) population growth and urbanization, and 5) markets and trade. The most important specific driver is exotic varieties and breeds among 90 specific drivers. The earthquake of 2015 was a major disaster having damaged much local agricultural diversity in more than 14 districts of Nepal. Expansion of area for agricultural production, the establishment of a new settlement and various types of developmental activities have caused a loss of many wild relatives of agricultural species and wild edible species. Threat to crop diversity is high in rice, banana, cucumber, and tomato due to replacement of old cultivars by modern varieties. Threat to rice bean, horse bean, and foxtail millet is due to low priority given by growers and consumers. Invasive alien species like Parthenium, Eupatorium spp. and Lantana camara have had a significant effect on diversity and ecosystem services. The least affected agrobiodiversity components are microbial genetic resources. The important drivers e.g., exotic genotypes, external inputs, monogenotype-based monoculture policy and climate changes, should be given due attention to control and manage for better management of agrobiodiversity.

Keywords

Agrobiodiversity; Genetic diversity; Drivers of changes; Genetic resources

1. Introduction

Estimate of the total species in the world is 8.7 million (BBC, 2011). Among them, about 30% species are agriculture-related. However, only 12 plant and 5 animal species provide 75% of the world’s food (FAO, 1999). Out of 50,000 edible plants from the 320,000 plant species, only 150 to 200 are used by humans. Only 3 plants - rice, maize, and wheat - contribute nearly 60% of
calories and proteins obtained by humans from plants. Animals provide some 30% of human requirements for food and agriculture, and 12% of the world's population lives entirely on products from ruminants (FAO, 1999). Thus, agrobiodiversity is the most important sector of biodiversity fulfilling needs of human welfare and environmental security. In general, agrobiodiversity is divided into 6 components namely crop, forage, livestock, agro-insect, agro-microbial, and aquatic agri-genetic resources (Joshi et al., 2019, 2020). Each component is further divided into 4 sub-components and they are domesticated/cultivated, semi-domesticated, wild relatives, and wild edible species. There are about 6,618 species related to agriculture in Nepal (Joshi et al., 2008, 2017a, 2017b, 2020; Joshi, Ghimire and Singh, 2018; MoFSC, 2014). Diversity is being maintained at ecosystem, species, varietal/breed/strain, genotypic and allelic levels. Three agroecozones i.e., mountain, temperate and tropical agricultural zones along with 18 agroecosystems, are the major factors for creating and maintaining diversity in Nepal. This diversity has been conserved and promoted through different conservation initiatives (Joshi et al., 2008; 2017a). However, this life-sustaining native agrobiodiversity pool is under threat of loss owing to different factors and reasons.

FAO (2019) has estimated the loss of 75% of plant genetic diversity is attributed to the farmers worldwide who have replaced their local varieties and landraces by genetically-uniform and high-yielding varieties. Similarly, 30% of livestock breeds are at risk of extinction, meaning that 6 breeds are lost each month. In Nepal, the estimated loss in different components of agricultural biodiversity is 50% in crop genetic resources, 40% in forage genetic resources, 40% in livestock genetic resources, 30% in aquatic genetic resources, 20% in insect genetic resources, and 20% in microbial genetic resources (Joshi et al., 2020). Such loss is higher at the genotypic level.

Agrobiodiversity is under threat due to the use of high-yielding varieties, destruction of natural habitat, overgrazing, land fragmentation, commercialization of agriculture, indiscriminate use of pesticides, population growth and urbanization, and changes in farmers’ priorities (Joshi et al., 2017b; MoFSC, 2000). The most important drivers affecting the extent and distribution of agricultural biodiversity have been the commercialization of agriculture, weak policy and regulatory framework and climate change, population growth, and technological advancements (Ghale, 1999; Shrestha and Shrestha, 1999; Upreti and Upreti, 2002). There have been rapid changes and losses in genetic diversity because of the cumulative effects of various factors, which are also termed as “drivers of change” (Chaudhary et al., 2006; Sthapit et al., 2012). To manage agrobiodiversity properly over a long period, the drivers of changes in agrobiodiversity are very important to know. Therefore, this study was carried out to assess the drivers of changes that could help adopt effective measures, good practices, and strategies towards the management of agrobiodiversity.

2. Methodology

The impact of drivers of change depends on the types and components of agrobiodiversity. In this study, agrobiodiversity was divided into 5 components: food plant genetic resources (FPGR), forage genetic resources (FGR), animal genetic resources (AnGR), aquatic genetic resources (AqGR), and insect-microbial genetic resources (IMGR) (Joshi et al., 2020).
Food plant genetic resources (FPGR) encompass domesticated and wild plant species and varieties that hold direct value for humans. Forage genetic resources (FGR) include all plant species used for livestock feeding, while aquatic genetic resources (AgGR) comprise edible plant and animal species existing in aquatic environments. Animal genetic resources (AnGR) consist of edible animal species, and insect-microbial genetic resources (IMGR) encompass beneficial and economically significant species of insects and microbes.

General drivers of change in these components (Table 1) were compiled based on existing literature (Chaudhary et al., 2020; Chaudhary, Uphtey and Rimal, 2016; FAO, 2019). Specific drivers were identified through authors' experiences, literature review, and interactions with key individuals. The list of potential specific drivers (Table 1) was shared and discussed with the respondents. The effects of these drivers on the six components of agrobiodiversity were assessed through focus group discussions and key informant surveys conducted in 2018 and 2019. Focus group discussions took place in three locations (Palpa, Kathmandu, and Parwanipur), involving over 200 participants. Additionally, 25 key individuals were interviewed. A survey format developed by using Google Forms was also distributed through online channels. Noteworthy cases were documented during the focus group discussions. For each driver, the trend on agrobiodiversity was assessed during the survey as strongly increasing (2), increasing (1), stable (0), decreasing (-1), or strongly decreasing (-2). In cases where information was unavailable or unknown, it was recorded as "NK" (not known) or "NA" (not applicable). The impacts of specific drivers were also evaluated during the survey and supplemented with insights from the existing literature.

3. Findings and Discussion

All participants reported the loss of landraces in all the studied sites. Key informants also shared their experiences regarding the impact of different drivers at various sites and time periods. The participants demonstrated a good understanding of specific drivers and their role and contribution to agrobiodiversity. Any factor that directly or indirectly affects agrobiodiversity in a particular area over time and space is referred to as a driver. Drivers can be categorized as direct or indirect. Direct drivers, such as the promotion of modern varieties, play a significant role in replacing native crop diversity. Conversely, efforts are required to minimize the impact of indirect drivers on diversity. For instance, climate change is an indirect driver influenced by human activities, making it challenging to mitigate its impact on agrobiodiversity. Drivers can be further grouped into broad categories and specific drivers (refer to Table 1). Analyzing specific drivers within the context of broad category drivers is crucial and effective in controlling the negative impact on agrobiodiversity. Drivers can also be classified as natural or anthropogenic (refer to Figure 1). Specific drivers are listed across three levels of diversity: ecosystem, species, and genetic.

Table 1: General and specific drivers along with their impact on agrobiodiversity based on the focus group discussion and literature review

<table>
<thead>
<tr>
<th>SN</th>
<th><strong>General drivers</strong></th>
<th><strong>Specific drivers</strong></th>
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<td>1.</td>
<td>Advancements and innovations</td>
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<tr>
<td>SN</td>
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| 1  | in science and technology | artificial selection, improved technology, extension strategy, mechanization, formal seed system, widely adopted variety/breed promotion, recommendation of single variety for larger areas, introduction, commercial agriculture, protected farming | • 80% of Tarai goats got adulterated by Jamunapari goat  
• Murrah buffalo, a single breed occupied about 40% of buffalo-rearing households |
| 2  | Changes in land and water use and management | The settlement, dam construction, road construction, hydropower, abandonment of land, monogentotyping, water use in non-agriculture, encroachment | • Converting land to the city, the road in Biratnagar, Lothar, and Kailali resulted in the complete loss of wild rice  
• About 60% of agricultural land in the majority of city areas was converted to other business |
| 3  | Pollution and external inputs | Toxic effects, chemicals, exotic seeds and breeds, dust, industrial and sewage, solid waste, plastic, air pollution | • 100% aquatic diversity lost in some areas due to chemical pollution  
• 100% native diversity of crops, bees, fish, and animals lost due to exotic genotypes in some areas |
| 4  | Climate change | Temperature rise, drought, erratic rainfall, change in snowfall | • Many tropical crop species are now possible to grow in mountain areas  
• 100% native diversity of some crop species lost in some areas due to drought  
• Complete crop failure was observed in some species in some areas due to high temperature |
| 5  | Natural disasters | Earthquakes, flooding, landslides, pandemic diseases, hailstone, cyclones, hurricanes, thunderstorms, and lightning | • About 10% of crop diversity was lost due to earthquake in 10 districts  
• 100% farming land along with native genetic resources were lost in some localities |
| 6  | Alternative livelihood options and information flow | Non-farm business (hotel, tourism, job, industry, trade), media, traditional knowledge, education, non-native language | • 80 to 100% of households shifted their business from agriculture to non-agriculture in some localities  
• Only 5% of educated people engaged in agriculture  
• All households near Yarssagummba growing areas prefer to collect this species rather than cultivating native crops and breed diversity |
| 7  | Pests, diseases, alien invasive species | Armyworm, blast, late blight, foot and mouth disease, bird flu, swine flu, citrus decline, banana wilt, parthenium, lantana camera, Gandi bug | • The population of different bee species was reduced by 15%  
• 80% of soil biodiversity lost in some areas  
• 90% of native diversity lost due to alien invasive species in some areas |
| 8  | Natural selection | Different domains for seed production and cultivation, pollinators, mutation, habitat degradation | • About 60% of seeds/saplings are from other than cultivating areas  
• Natural selection did not get a chance to favor almost all domesticated species |
<table>
<thead>
<tr>
<th>SN</th>
<th>General drivers</th>
<th>Specific drivers</th>
<th>Some cases/impact</th>
</tr>
</thead>
<tbody>
<tr>
<td>9.</td>
<td>Over-exploitation and overharvesting</td>
<td>Overexploitation, overharvesting, poaching, grazing</td>
<td>• The amount of edible ferns was reduced by 25%</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• Availability of wild edible fruits and vegetables was reduced by 40%</td>
</tr>
<tr>
<td>10.</td>
<td>Human-wildlife conflict</td>
<td>Crop and livestock-fish depredation</td>
<td>• Monkeys, wild boars, wild elephants, tigers, porcupines, squirrels, and bear affected about 10-50% of total agrobiodiversity</td>
</tr>
<tr>
<td>11.</td>
<td>Population Growth and Urbanization</td>
<td>Development activities, human-made disturbance, hydropower plants, roads, buildings, industry, dam, human-made sound, lighting in the night, vehicle</td>
<td>• About 60% of native crop diversity lost due to Budhi Gandaki hydropower</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• 50% of farmers depend on an agro-vet for their seeds requirement</td>
</tr>
<tr>
<td>12.</td>
<td>Markets and trade</td>
<td>Market demand, value chain, access to markets, illegal trade, cost of production</td>
<td>• Only about 10% of native products get to market</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• The majority of the native products are not well-processed, labeled, and packed</td>
</tr>
<tr>
<td>13.</td>
<td>Changing economic, socio-political, and cultural factors</td>
<td>Changes in food choice, preferences, labor shortage, migration, land fragmentation, political instability, increased remittance</td>
<td>• 95% of items in farmer’s fields, kitchens, research stations, and supermarkets are from outside the country</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• More than 50% of city dwellers ignore native food cultures and prefer exotic products</td>
</tr>
<tr>
<td>14.</td>
<td>Migration</td>
<td>Outmigration, temporary migration to the city, shifting to city/plain areas, girl migration after marriage</td>
<td>• About 50% of native genetic resources were lost due to migration in some areas</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• In some location, 50% of agricultural land remain barren</td>
</tr>
<tr>
<td>15.</td>
<td>Incentives</td>
<td>Subsidy, training and visit, free distribution, cash reward, materials rewards</td>
<td>• The incentive is only for improved variety and breed</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• Native agrobiodiversity never includes in training and education program</td>
</tr>
<tr>
<td>16.</td>
<td>Policies</td>
<td>Commercialization, agriculture fair, promotional activities, single variety promotion</td>
<td>• Only uniform variety has been entered into the formal seed system</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>• The awarding system is only for improved variety and breed</td>
</tr>
</tbody>
</table>

Multiple factors and actions are driving agrobiodiversity loss in Nepal, leading to various impacts. Several cases highlight the impact of drivers on agrobiodiversity. For instance, following the introduction of the Masuli rice variety in the Tarai region of Nepal in 1973, approximately 60% of rice landraces were lost within a decade. Similarly, the introduction of the Jamunapari goat in the Tarai region resulted in 80% of Tarai goats being crossbred with this exotic breed. Ajaya Chaudhary, a farmer from Rupandehi, observed a complete loss of aquatic animals (goge, sutuahi, native fishes, earthworms, etc.) and native weeds due to the use of herbicides and pesticides. Heavy machinery for soil preparation, along with chemical fertilizers and pesticides, has led to the loss of soil biodiversity, rendering the soil lifeless. Construction of an irrigation channel from Chepe River to Rainas in Lamjung
district resulted in the loss of two dozen upland rice landraces (Ghaiya) from Rainas. Similarly, Palungtar, Gorkha witnessed a 90% loss of native rice landraces due to the factors like outmigration, urbanization, and the adoption of improved varieties (KH Ghimire, personal communication). Additionally, the use of pesticides has led to the scarcity of local mushrooms (Govrechayu, jharichayu, kalodungechayu, padkechayu) in many areas of Nepal.

Figure 1: Different types of drivers over ecosystem, species, and genotype levels.

As mentioned in table 2, the top five drivers with the most negative impact on agrobiodiversity, in order, are: advancements and innovations in science and technology, changes in land and water use and management, alternative business and information flow, population growth and urbanization, and markets and trade. Almost all drivers have a detrimental effect on all five components of agrobiodiversity. A study conducted by the Ministry of Agriculture and Livestock Development (Joshi et al., 2017b) identified pollution and external inputs as an important driver affecting the extent and distribution of associated biodiversity in Nepal over the past 10 years. Unplanned and unregulated rural roads emerged as a significant threat to agrobiodiversity across all seven provinces of Nepal (refer to Table 3). However, the threat of overexploitation of plant species was relatively low in Lumbini province compared to other provinces. The impacts of different drivers are described below.
### Table 2: Effect of drivers on components of agrobiodiversity in Nepal

<table>
<thead>
<tr>
<th>SN</th>
<th>Driver</th>
<th>FPGR</th>
<th>FGR</th>
<th>AnGR</th>
<th>AqGR</th>
<th>IMGR</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Advancements and innovations in science and technology</td>
<td>-2</td>
<td>0</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
</tr>
<tr>
<td>2</td>
<td>Changes in land and water use and management</td>
<td>-2</td>
<td>-1</td>
<td>-1</td>
<td>-2</td>
<td>-1</td>
</tr>
<tr>
<td>3</td>
<td>Pollution and external inputs</td>
<td>-2</td>
<td>0</td>
<td>-1</td>
<td>-1</td>
<td>-2</td>
</tr>
<tr>
<td>4</td>
<td>Climate change</td>
<td>-2</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>5</td>
<td>Natural disasters</td>
<td>-2</td>
<td>-1</td>
<td>-2</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>6</td>
<td>Alternative business and information flow</td>
<td>-1</td>
<td>0</td>
<td>-1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>Pests, diseases, alien invasive species</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>0</td>
</tr>
<tr>
<td>8</td>
<td>Natural selection</td>
<td>-1</td>
<td>0</td>
<td>-1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>Over-exploitation and overharvesting</td>
<td>-1</td>
<td>-2</td>
<td>-2</td>
<td>-1</td>
<td>0</td>
</tr>
<tr>
<td>10</td>
<td>Human-wildlife conflict</td>
<td>-1</td>
<td>0</td>
<td>-1</td>
<td>-1</td>
<td>0</td>
</tr>
<tr>
<td>11</td>
<td>Population growth and urbanization</td>
<td>-2</td>
<td>-2</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>12</td>
<td>Markets and trade</td>
<td>-2</td>
<td>-1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>13</td>
<td>Changing economic, socio-political, and cultural factors</td>
<td>-1</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>14</td>
<td>Migration</td>
<td>-2</td>
<td>1</td>
<td>-1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>15</td>
<td>Incentives</td>
<td>-1</td>
<td>0</td>
<td>-1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>16</td>
<td>Policies</td>
<td>-1</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

**Code description:** Trends are strongly increasing (2), increasing (1), stable (0), decreasing (-1), or strongly decreasing (-2), no information available, not known (NK), and not applicable, (NA). FPGR, food plant genetic resources; FGR, forage genetic resources; AnGR, animal genetic resources; AqGR, aquatic genetic resources; and IMGR, insect-microbial genetic resources.

### Table 3: Threat assessment of agrobiodiversity in different states of Nepal

<table>
<thead>
<tr>
<th>Threat</th>
<th>Province</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Koshi</td>
</tr>
<tr>
<td>Loss of agrobiodiversity</td>
<td>High</td>
</tr>
<tr>
<td>Improper use of pesticides</td>
<td>High</td>
</tr>
<tr>
<td>Urbanization</td>
<td>High</td>
</tr>
<tr>
<td>Lack of incentives to conserve local landraces</td>
<td>Moderate</td>
</tr>
<tr>
<td>Overharvesting of plant species</td>
<td>Moderate</td>
</tr>
<tr>
<td>Climate change</td>
<td>High</td>
</tr>
<tr>
<td>Unplanned and unregulated rural roads</td>
<td>Very High</td>
</tr>
<tr>
<td>Overexploitation of plant species</td>
<td>High</td>
</tr>
<tr>
<td>Alien Invasive Plant species</td>
<td>Moderate</td>
</tr>
<tr>
<td>Loss of local landraces</td>
<td>Moderate</td>
</tr>
<tr>
<td>Loss of wild relatives</td>
<td>Moderate</td>
</tr>
<tr>
<td>Increased vulnerability to pests and diseases</td>
<td>Moderate</td>
</tr>
</tbody>
</table>

**NA = is not available.** **Source:** MoFE (2018)
3.1 Advancements and Innovations in Science and Technology

The participants expressed that modern uniform varieties have replaced their traditional landraces. Dependency on external stakeholders for inputs has further accelerated the loss of genetic diversity and traditional knowledge. The commercialization of agriculture promotes monoculture and the use of modern and hybrid varieties, which are major contributors to genetic erosion, as they replace local and diverse landraces (Shrestha and Shrestha, 1999; Joshi et al., 2020; Chaudhary et al., 2006). This trend has resulted in a narrow genetic base and increased vulnerability among resource-poor farmers, as well as the loss of native agrobiodiversity. For example, out of 1,800 indigenous and wild species of rice, only one variety is commonly cultivated in the Tarai region (Shrestha and Upadhyay, 1999). Several indigenous vegetable varieties are on the brink of extinction due to the widespread use of hybrid seeds (Shrestha and Shrestha, 1999).

The use of hybrid varieties in Nepal since 1995 has shown a significant rise: 620% in tomato, 123% in cauliflower, 260% in carrot, 447% in brinjal, 146% in okra, and 100% in cabbage. A study conducted in six districts representing three agroecological domains (Mountain, Hill, and Tarai) indicated the introduction of 29 varieties of cereals, 10 varieties of legumes, 14 varieties of fruits, and 56 varieties of vegetables within a span of 20 years. Varietal diversities of indigenous vegetables (particularly bitter gourd, snake gourd, broadleaf mustard, pumpkin, sponge gourd, and radish) and cereals (rice and finger millet) are at high risk of extinction. Many landraces have been reported as endangered in crops such as rice, maize, buckwheat, finger millet, legumes, fruits, vegetables, and medicinal plants (Sthapit et al., 2012; Upadreti and Ghale, 2000). Similarly, the introduction of exotic forage varieties has led to genetic erosion in forage species. Native oat and vetch species were previously cultivated by farmers, but with the introduction of high-yielding oat and vetch cultivars, the native species have been replaced and lost. A similar situation exists with tree fodders.

In recent years, the adoption of bee foraging practices by commercial bee farms, which involve exotic bee species, has positively affected the pollination of crops such as rapeseed, mustard, and others in Chitwan, Dang, Surkhet, as well as apple in Jumla districts. However, the promotion of exotic bees has led to a reduction in the population of native bee species. Similar cases can be observed in livestock and fish commercialization. The populations of pure Yak and Nak have drastically declined, making Yak a rare animal in the northern Himalayan ranges.

While certain technologies, such as biotechnology, have a positive effect on creating and maintaining diversity in animal and plant genetic resources (AnGR and PGR), the indiscriminate introduction of exotic breeding animals and varieties has resulted in cross-breeding with local animals and landraces, leading to under-utilization of native resources and ultimately their loss. The recent expansion of artificial insemination has also shifted attention away from animal biodiversity.

3.2 Changes in Land and Water Use and Management

Many participants have shared their own experiences regarding changes in land use. They have expressed an interest in converting agricultural land to other businesses if it proves to be more suitable and profitable. In peri-urban areas, farmers are more profit-oriented, which has led to the gradual replacement of
traditional farming systems with commercial vegetable cultivation. As a result, the area under traditional crops, as well as their varieties and landraces, has decreased. Land fragmentation has also contributed to farmers opting for food crops instead of forage, leading to a decline in forage diversity. Furthermore, both land and human resources have shifted from agricultural activities to non-agricultural businesses.

The scarcity of water sources significantly drives the utilization of agrobiodiversity. The aquatic environment in the mid-hills is primarily affected by river damming for hydropower, while in the southern plains, the encroachment of wetlands, lakes, and swamps for irrigation purposes is a major factor. Continuous deforestation poses a significant threat to forest biodiversity. Nepal experienced a 1.4% loss in forest area between 1990 and 2000 (FAO, 2010). The factors driving the loss of forest habitats and agricultural land include encroachment for settlements, expansion of cultivation using exotic breeds/varieties, and the development of infrastructure such as schools, hospitals, temples, and water storage tanks (DOR, 2010).

3.3 Pollution and External Inputs

Participants reached a consensus that pollution of soil, water, and air, primarily caused by chemicals, poses a significant risk to numerous genetic resources, placing them at the brink of extinction. The use of external inputs, including exotic genetic resources, has emerged as a major driver contributing to the loss of native genetic diversity. This driver has a particularly pronounced impact on crop and insect-microbial genetic resources. In Panauti of Kavrepanchok, for instance, local farmers have reported a scarcity of native bees, which they attribute to the heavy use of pesticides. Furthermore, they estimate that approximately 70% of soil biodiversity has been lost as a result of these practices.

3.4 Climate Change

Climate change is a widely discussed issue, and many participants have shared their experiences on this topic. The increasing annual temperatures have adversely affected crop growth cycles, resulting in reduced yield and productivity. Precipitation plays a crucial role in determining the success of crop production (Thomas et al., 2007; Viglizzo et al., 1997). The existing plant varieties in various regions may not be well adapted to the new production conditions. Alarming signs of a sharp and sustained decline in food security have already emerged in Nepal, such as a significant decrease in winter food crop harvests across all regions in 2009. The crop sector has also faced major challenges due to outbreaks and spread of minor diseases, pests, and unwanted weeds (Chaudhary et al., 2011; Tiwari et al., 2010). Farmers have reported the extinction of plant species, with the Seti River Valley of the Kaski district witnessing a reduction from 77 rice landraces to only 11 (Rijal et al., 1998).

Changes in soil, temperature, humidity, sunshine, and water availability are altering the ability of certain species, varieties, and breeds to survive in their respective environments. Tree lines and species are migrating to higher elevations, while species already residing at the highest elevations face the challenge of having nowhere else to go.
Farmers in the Mustang and Manang districts have experienced improved apple sizes and have been able to grow cauliflower, cabbage, chilli, tomato, and cucumber due to climate shifts (Dahal, 2005). There have been reports of better sizes and tastes of local fruits (Dahal, 2005). Rice cultivation is now possible at altitudes up to 2,400 meters in Murza VDC of Myagdi district in Western Nepal (Dahal, 2006). The delayed monsoon has disrupted cropping patterns, maturity periods, and planting and harvesting times, resulting in thousands of hectares of fallow farmland (Regmi and Adhikari, 2007). In 2006, drought in the Eastern region of Nepal caused a 30% decrease in rice production, while heavy flooding in 2006 and 2008 destroyed crops in several places in Western Nepal (Paudel et al., 2006). Farmers have also observed the effects of climate change on beekeeping, insect and pest intensity, and other impacts on rain-fed agriculture, such as changes in the timing of fruit tree and coffee flowering, decline in local grass species, and reduced size of some fodder trees (Regmi et al., 2009). Changes in snowfall patterns, including duration and reduced amounts during winter, have also affected vegetation, including crops and animal genetic resources. Animals kept under the transhumant migratory system, such as sheep and yak, are particularly vulnerable to climate change, resulting in declining numbers and increased mortality.

The emergence of tropical insect pests and diseases at higher altitudes has become a common occurrence. For instance, *Citrus psylla*, whitefly, and armyworm are becoming problematic in these areas. Additionally, common cockroaches and mosquitoes are now being observed in high hill and mountainous regions where they were not previously seen. Outbreaks of snails and slugs have also been frequently reported. Abundant populations of *Lissachatina fulica* were found in Biratnagar, Jaleshwor, and Birgunj, and in recent years, it has spread to the western limits of the Western Development Region of the Terai and extended north across the Siwalik Hills to Makwanpur, Chitwan, and Tanahun (Budha and Fred, 2008).

Long-duration droughts have led to the drying up of ponds and wetlands, while heavy rainfall has caused flooding, resulting in the loss of fish and sweeping away of pond and wetland waters. Rainfall-induced landslides, degradation, and filling of wetlands and lakes have devastating effects on various types of biodiversity, including associated biodiversity. According to the Millennium Ecosystem Assessment (2005), changing climatic conditions are likely to become the leading direct driver of biodiversity loss by the end of this century. The Intergovernmental Panel on Climate Change has estimated that a temperature increases greater than 1.5 degrees Celsius could put 20-30% of species at a higher risk of extinction, with the risk increasing with further temperature rise (IPCC, 2007).

3.5 Natural Disasters

Participants recounted the devastating earthquake of 2015 and its profound impact on human survival, as well as the scarcity of genetic resources. Natural disasters, such as earthquakes, flooding, and landslides, have had a significant impact on agrobiodiversity (Joshi and Gauchan, 2017). The mid-hills, which are known for their rich agrobiodiversity, have been among the most affected areas by such disasters. The earthquake of 2015 resulted in the loss of a large number of livestock and the depletion of native crop diversities, leading to
the erosion of soil biodiversity and the disruption of the seed system. According to Joshi and Gauchan (2017), approximately 10% of the total local crop diversity, based on landraces, was lost in 10 districts of Nepal as a result of the devastating earthquake in 2015.

3.6 Alternative Livelihood Options and Information Flow

Many farmers have opted to pursue alternative businesses such as hotels, jobs, or other entrepreneurial ventures instead of engaging in agricultural activities. As a consequence, numerous genetic resources possessed by these farmers have lost, and agricultural land has been left barren. The influence of advertisements and promotional information also plays a crucial role in determining the choice of genotypes for cultivation and other purposes.

3.7 Insect Pests, Diseases, and Alien Invasive Species

In all studied sites, there have been reports of new pests, diseases, and invasive species. This phenomenon is commonly observed in Nepal (Tiwari et al., 2010; Chaudhary et al., 2011). These newly introduced or unintentionally introduced insect pests and diseases have had a significant impact on native genetic resources. Farmers often face challenges from common problematic pests such as aphids, caterpillars, cutworms, blight, *Alternaria* spp. of fungus, blast, and others, which prompt them to seek alternative solutions. Furthermore, emerging and re-emerging animal diseases like foot and mouth disease, hemorrhagic septicemia, black quarter in cattle and buffaloes, Peste des petits in Ruminants (PPR) in goats and sheep, and bird flu in poultry cause substantial damage to livestock diversity. Many native breeds are not typically vaccinated or provided with medicines against parasites, leading to reduced productivity. In addition, several alien invasive species such as *Lantana camara*, *Mikania micrantha*, *Chromolaena odorata*, and *Eichhornia crassipes* pose a threat to native genetic resources in both forested and cultivated areas (Tiwari et al., 2010; Chaudhary et al., 2011).

3.8 Natural Selection

Farmers typically do not practice seed selection for future plantations but instead rely on purchasing seeds each year from commercial farms and shops. This practice suggests that natural selection does not play a significant role in the selection of seeds for the next planting season. In the field of agriculture, particularly in breeding programs, nature’s influence in selecting genetic resources is almost non-existent. The selection made by farmers and breeders may not always result in successful outcomes in the subsequent season’s planting. It is common for seeds to be produced in locations other than the actual production sites, which can lead to genotypes experiencing complete failure in their performance due to environmental shocks or mismatches.

3.9 Overexploitation, Overgrazing, and Overharvesting

The overexploitation of high-value species has emerged as a significant threat to their survival in their natural habitats. The excessive commercial
harvesting of medicinal plants, both legally and illegally, poses a direct danger to high-value species such as yarchagumba (*Ophiocordyceps sinensis*), jatamansi (*Valeriana jatamansi*), sarpagandha (*Rauwolfia serpentina*), and many others. Uncontrolled forest fires present a serious hazard, particularly in the Siwalik region and high-altitude areas. Many of these fires are intentionally set by local communities to clear land for agriculture or to promote the early growth of grass for livestock grazing. Recurrent forest fires cause significant damage, hindering the regeneration and growth of seedlings, destroying non-timber forest products, harming ground flora and fauna, and inhibiting the development of understory vegetation. This ultimately leads to the transformation of forests into open areas with relatively low biodiversity. Overgrazing in forests has had detrimental effects on seedling regeneration and growth, resulting in forest degradation in various locations. Additionally, the over-harvesting of many wild foods such as bamboo shoots (*Tusa*), ferns (*Niuro/Daunde*), certain medicinal plants, and wild animals has put them at risk of extinction.

3.10 Human-Wildlife Conflict

Due to the persistent issue of wildlife disturbances, such as monkeys, boars, and wild elephants, many farmers have been compelled to make changes either in the choice of agricultural species or in their agri-businesses altogether. The presence of wildlife poses a significant threat as they often destroy crop fields and consume or damage planted seeds. In order to mitigate these challenges and minimize losses, farmers have resorted to altering their agricultural practices or exploring alternative income-generating activities. The need to protect crops from wildlife encroachment has driven farmers to adapt and seek solutions that are more compatible with the local wildlife dynamics.

3.11 Population Growth and Urbanization

The farmers who participated in the study appeared to be less informed about one particular driver of biodiversity loss. However, based on the available literature and insights from key informants, it is evident that increased population pressure, widespread poverty, and environmental degradation are the major severe threats to flora and fauna diversity in Nepal (Upreti, 2000; Yonzon, 2000). The population growth rate is estimated at 0.61% per year, with a corresponding growth rate of 2.3% per year for principal agriculture production. The combination of small landholdings and mounting population pressure has resulted in challenges in maintaining existing agrobiodiversity.

Unplanned rapid urbanization, the absence of appropriate land use policies, and weak institutional arrangements have placed enormous pressure on land resources, leading to the loss of agrobiodiversity. The rapid migration from rural to urban areas is posing significant socio-economic and conservation-related threats (NPC, 1998). In the Tarai region, such as Chitwan, Banke, and Kanchanpur, the loss of agrobiodiversity is attributable to swift urbanization, the expansion of feeder roads, construction of buildings and industrial facilities (Upreti and Upreti, 2002). Additionally, wetland sites, which are important habitats for indigenous crop species, are degrading and being lost due to encroachment, conversion into rice fields, fish ponds, extended settlements, and sedimentation (Siwakoti and Tiwari, 2007).
The changes in demand for livestock products, driven by population growth, urbanization, and higher income, have also had an impact on the diversity of livestock, poultry, and fish species. Urbanization and industrialization have further contributed to the reduction of grazing lands, negatively affecting animal genetic resources (AnGR) and forage diversity.

3.12 Markets and Trade

Market access and options play a crucial role in ensuring the sustainability of native genetic resources in agricultural production. The promotion of supermarkets and the availability of frozen food items have become an emerging trend, with a significant portion of the market consisting of imported goods, often overlooking local products. This can undermine the demand for and market opportunities of indigenous agricultural products.

However, on a smaller scale, certain native agricultural products hold high market value, leading to the continued cultivation of specific landraces, breeds, or strains. These products enjoy a niche market and are often sought after due to their unique characteristics or cultural significance. Examples of such native products that are exported include yak cheese, chyangra meat, large cardamom, Jumli bean, Jumli marshi (a type of rice), wool, and pashmina. The export value of these products incentivizes their continued production and contributes to their conservation.

In this way, the market plays a dual role, both posing challenges to local products through the dominance of imported goods but also providing opportunities for the conservation and preservation of native genetic resources when there is a high market demand and value for specific indigenous products.

3.13 Economic, Socio-Political, and Cultural Factors

The participants in the study acknowledged that as household economies improve, there is a tendency for individuals to move away from agriculture. Engaging in other non-agricultural businesses or occupations is often associated with higher social status. These values and reputations attached to non-agribusiness pursuits have significantly contributed to the loss of agrobiodiversity. Socio-cultural diversity, including food cultures and dietary habits, is closely intertwined with agrobiodiversity.

In many cases, women play a crucial role in determining the continued growth and preservation of genetic resources. Women are primarily responsible for growing local crops, managing wild relative plants, and maintaining their cultivation (Howard, 2003). However, changing socio-cultural dynamics and shifting dietary patterns in rural communities have led to the erosion of traditional food habits. The easy availability and appeal of fast foods with different tastes have influenced dietary choices. As a result, there has been a decline in women's knowledge of processing, preparation, and storage techniques associated with traditional foods. This erosion of knowledge, along with changing dietary habits, has had adverse effects on genetic diversity, family food security, and overall health.

It is important to recognize the role of women in agricultural practices and the preservation of agrobiodiversity. Empowering women and promoting their active participation and leadership in decision-making processes related to
agriculture and food systems can contribute to the conservation and promotion of genetic resources, food security, and sustainable agricultural practices.

3.14 Migration

Land abandonment in the studied sites is a growing concern, primarily driven by migration and labor shortage. This trend has had a direct impact on the gradual decline of local genetic resources. For instance, in the Panchase region (Kaski, Parbat, and Syangja districts), approximately 20-25% of cultivable land has been left uncultivated due to the migration of entire households to urban areas. In Samibhanjyang, Lamjung, around 50% of farming households have migrated to urban and plain areas, resulting in 50% of the land being left barren. This pattern of migration has led to the loss of almost 80% of traditional agricultural genetic resources in the area.

Agriculture in Nepal is undergoing a process of feminization due to male outmigration. This shift in gender dynamics in agriculture, along with the increased flow of remittances, has had implications for agrobiodiversity. The rising rate of outmigration is a significant driver of change in women’s roles in agriculture and the management of agrobiodiversity (Desai and Banerji, 2008; Maharjan, Bauer and Knerr, 2012). The shortage of labor, combined with the availability of remittance money and cheap substitutes in the market, has led to the abandonment of local crops such as Ghaiya rice and Kauno (Bhattari, Belin and Ford, 2015). The labor-intensive nature of processing Kauno, in particular, has added to the drudgery experienced by women, further contributing to its abandonment.

Addressing the challenges of land abandonment, labor shortage, and gender dynamics in agriculture is crucial for the conservation and preservation of agrobiodiversity. Creating supportive policies, providing access to resources and technologies, and empowering women in agricultural decision-making can help mitigate these threats and ensure the sustainable management of genetic resources.

3.15 Incentives

Farmers were initially unaware of the incentives associated with their own genetic resources. Consequently, they were persuaded to adopt modern varieties through the provision of incentives. Both monetary and non-monetary rewards are exclusively applicable to released, registered, and improved uniform varieties and breeds. However, this system promotes uniformity and a single genotype across large areas, leading to the displacement of localized genetic diversity.

3.16 Policies

Farmers were initially unaware of the policies regarding the management of agrobiodiversity, leading to a lack of attention towards its conservation in current policies. Native traditional crop landraces and livestock breeds have been significantly affected due to inadequate policy measures, strategies, and institutional support for farmers, as well as poor seed maintenance and exchange practices. In Nepal, the Seed Act 2045 (1988) fails to prioritize the informal "farmers-to-farmers" and non-formal seed management system, which has long
been in existence (Timsina, 2000) and accounts for over 90% of the seed flow (Joshi et al., 2020). The country's agricultural policy leans more towards monoculture and promotes improved varieties and breeds/strains to enhance production and productivity, contradicting conservation policies and neglecting the preservation and utilization of on-farm genetic diversity. Numerous indigenous crop and livestock diversities are disappearing, yet the existing regulatory framework is ineffective in protecting the loss of valuable agrobiodiversity (Joshi et al., 2020; Upreti and Upreti, 2002).

The expansion of tourism areas, particularly in regions abundant in agrobiodiversity, has accelerated the loss of biodiversity (Shrestha and Shrestha, 1999; Yonzon, 2000). National policies, strategies, and action plans do not fully incorporate the provisions of the Convention on Biological Diversity (CBD) and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGFRA). Nepal's membership in the World Trade Organization (WTO) limits the effective implementation of CBD (Chaudhary, 1999) as the provisions of the Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS) conflict with the biodiversity conservation goals outlined in the CBD (Adhikari, Belbase, and Ghale, 2000).

4. Conclusion

More than 90 specific drivers have been identified as having a negative impact on agrobiodiversity. The effects of these drivers vary over time and across different locations. Among the components of agrobiodiversity, crop biodiversity is particularly affected due to the introduction of exotic varieties. Understanding these drivers is crucial for effectively planning and mitigating their adverse effects on agrobiodiversity. Various good practices have been implemented to ensure the availability of agrobiodiversity. These practices include the development of site-specific polymorphic varieties, evolutionary populations, cultivar mixtures, agro gene sanctuaries, provision of incentives, market guarantees for native genetic resources, geographical indication tags, community gene banks, school field gene banks, agro-insect field gene banks, dedicated structures, and land areas for conservation, among others. It is essential to urgently develop strategies and action plans in the country to minimize the negative impact of these drivers on agrobiodiversity. The aforementioned good practices should be widely and extensively implemented throughout the country to safeguard existing genetic diversity for long-term availability.

5. Acknowledgments

The study was supported by the Ministry of Agriculture and Livestock Development and the Nepal Agricultural Research Council. We extend our gratitude to Ajay Chaudhary and Krishna Hari Ghimire for their valuable information and insights. We also express our deep appreciation to the farmers and stakeholders who actively participated in this study from various regions of the country. Their contributions were invaluable to the success of this research.
6. References


Authors’ Declarations and Essential Ethical Compliances

Authors’ Contributions (in accordance with ICMJE criteria for authorship)

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Research involving human bodies or organs or tissues (Helsinki Declaration)
The author(s) solemnly declare(s) that this research has not involved any human subject (body or organs) for experimentation. It was not a clinical research. The contexts of human population/participation were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) or ethical obligation of Helsinki Declaration does not apply in cases of this study or written work.

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The author(s) solemnly declare(s) that this research has not involved any animal subject (body or organs) for experimentation. The research was not based on laboratory experiment involving any kind animal. The contexts of animals were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) or ethical obligation of ARRIVE does not apply in cases of this study or written work.

Research on Indigenous Peoples and/or Traditional Knowledge
The author(s) solemnly declare(s) that this research has not involved any Indigenous Peoples as participants or respondents. The contexts of Indigenous Peoples or Indigenous Knowledge were only indirectly covered through literature review. Therefore, an Ethical Clearance (from a Committee or Authority) and Self-Declaration in this regard are appended.

Research involving Plants
The author(s) solemnly declare(s) that this research has involved the plants for experiment or field studies. Some contexts of plants are also indirectly covered through literature review. Thus, during this research the author(s) obeyed the

Research Involving Local Community Participants (Non-Indigenous) or Children
The author(s) solemnly declare(s) that this research has directly involved local community participants or respondents belonging to non-Indigenous peoples. But, this study did not involve any child in any form directly. The contexts of different humans, people, populations, men/women/children and ethnic people are only indirectly covered through literature review. A sample copy of the Consent Form implying prior informed consent (PIC) of the respondents is appended.

(Optional) PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses)
The author(s) has/have NOT complied with PRISMA standards. It is not relevant in case of this study or written work.

Competing Interests/Conflict of Interest
Author(s) has/have no competing financial, professional, or personal interests from other parties or in publishing this manuscript. There is no conflict of interest with the publisher or the editorial team or the reviewers.

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To see original copy of these declarations signed by Corresponding/First Author (on behalf of other co-authors too), please download associated zip folder [Declarations] from the published Abstract page accessible through and linked with the DOI: https://doi.org/10.33002/aa030102
ETHICAL CLEARANCE CERTIFICATE

Research Involving Indigenous Peoples and Traditional Knowledge

Declaration by the Principal Investigator

I certify that the study titled: "The drivers of changes in the state of agrobiodiversity", (ref: aa03-01-01), does not involve collection of data or information on (an) Indigenous land, including reserve, settlement, and land governed under a self-government rule/agreement; the study involves the criteria for participation, including membership in an indigenous community, group of communities, or organization, including urban indigenous populations; the study seeks inputs from participants (members of the indigenous community) regarding a community's cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices; and the study does not involve Aboriginal identity or membership in an indigenous community used or be used as a variable for the purpose of analysis. The present study is conducted on farming communities. I hereby declare the same and confirm that all personnel associated with the present study have read this application and have agreed to comply with procedures described and any conditions imposed by the World Intellectual Property Organization (WIPO), Geneva, with regards to research on Indigenous Peoples and/or Traditional Knowledge.

Principal Investigator: Bal Krishna Joshi

Date: 07/16/2023

Declaration by Head of the Organization/Research Committee

I have read this application and am satisfied that the study does not involve capturing and collection of data or information of the Indigenous Community's cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices. The study fully complies with the legislation and the general principles of the World Intellectual Property Organization (WIPO), Geneva.

Head of the Organization/Research Committee

Date: 07/16/2023

Chief
SELF-DECLARATION FORM
Research on Indigenous Peoples and/or Traditional Knowledge

The nature and extent of community engagement should be determined jointly by the researcher and the relevant community or collective, taking into account the characteristics and protocols of the community and the nature of the research.

If your research involved/involves the Indigenous Peoples as participants or respondents, you should fill in and upload this Self-Declaration and/or Prior Informed Consent (PIC) from the Indigenous Peoples. [Please read carefully https://grassrootsjournals.org/credibility-compliance.php#Research-Ethics]

1. Conditions of the Research

1.1 Was or will the research (be) conducted on (an) Indigenous land, including reserve, settlement, and land governed under a self-government rule/agreement or?

No

1.2 Did/does any of the criteria for participation include membership in an Indigenous community, group of communities, or organization, including urban Indigenous populations?

Yes

1.3 Did/does the research seek inputs from participants (members of the Indigenous community) regarding a community’s cultural heritage, artifacts, traditional knowledge, biocultural or biological resources or unique characteristics/practices?

Yes

1.4 Did/will Aboriginal identity or membership in an Indigenous community used or be used as a variable for the purposes of analysis?

No

2. Community Engagement

2.1 If you answered “Yes” to questions 1.1, 1.2, 1.3 or 1.4, have you initiated or do you intend to initiate an engagement process with the Indigenous collective, community or communities for this study?

Yes

2.2 If you answered “Yes” to question 2.1, describe the process that you have followed or will follow with respect to community engagement. Include any documentation of
consultations (i.e., formal research agreement, letter of approval, PIC, email communications, etc.) and the role or position of those consulted, including their names if appropriate:

First questionnaires were developed and community members were consulted for discussion and questions answers. Verbal agreement was done for information use and analysis.

3. No Community Consultation or Engagement

If you answered “No” to question 2.1, briefly describe why community engagement will not be sought and how you can conduct a study that respects Aboriginal/Indigenous communities and participants in the absence of community engagement.

Not Applicable

Name of Principal Researcher: Bal Krishna Joshi
Affiliation of Principal Researcher:
1. Senior Scientist (S-4), National Agriculture Genetic Resources Center, Nepal Agricultural Research Council, Nepal

Signature:

Date: 7/16/2023

Declaration: Submitting this note by email to any journal published by The Grassroots Institute is your confirmation that the information declared above is correct and devoid of any manipulation.
INFORMATION AND CONSENT FORM FROM RESPONDENTS
(Non-Indigenous or Indigenous Respondents)
*This form was translated into local language for the respondents*

Title of the Research: The drivers of changes in the state of agrobiodiversity

Principal Researcher: Bal Krishna Joshi
National Agriculture Genetic Resources Center (Genebank)
Nepal Agricultural Research Council (NARC)

Research Supervisor: Self

A) INFORMATION TO PARTICIPANTS

1. Objectives of the research
To measure the key drivers that affect the genetic diversity in the farming areas of Nepal.

2. Participation in research
The researcher will ask you several pertinent questions. This interview will be recorded in written form and should last about 50-60 minutes. The location and timing of the interview will be determined by you, depending on your availability and convenience.

3. Risks and disadvantages
There is no particular risk involved in this project. You may, however, refuse to answer any question at any time or even terminate the interview.

4. Advantages and benefits
You will receive intangible benefits even if you refuse to answer some questions or decide to terminate the interview.

5. Confidentiality
Personal information you give us will be kept confidential. No information identifying you in any way will be published. In addition, each participant in the research will be assigned a code and only the researcher will know your identity.

6. Right of withdrawal
Your participation in this project is entirely voluntary and you can at any time withdraw from the research on simple verbal notice and without having to justify your decision, without consequence to you. If you decide to opt out of the research, please contact the researcher at the telephone number or email listed below. At your request, all information concerning you can also be destroyed. However, after the outbreak of the publishing process, it is impossible to destroy the analyses and results on the data collected.

B) CONSENT
Declaration of the participant

⇒ I understand that I can take some time to think before agreeing or not to participate in the research.
⇒ I can ask the research team questions and ask for satisfactory answers.
⇒ I understand that by participating in this research project, I do not relinquish any of my rights, including my right to terminate the interview at any time.
⇒ I have read this information and consent form and agree to participate in the research project.
⇒ I agree that the interviews be recorded in written form by the researcher: Yes (   ) No (   )

Signature of the participant : ____________________  Date : ____________________

Surname : ________________________________  First name : ________________________________

Researcher engagement

I explained to the participant the conditions for participation in the research project. I answered to the best of my knowledge the questions asked and I made sure of the participant's understanding. I, along with the research team, agree to abide by what was agreed to in this information and consent form.

Signature of the researcher: ______________________  Date : 07-11-2023

Surname: Joshi  First name: Bal  Middle name: Krishna

⇒ Should you have any questions regarding this study, or to withdraw from the research, please contact to Krishna Hari Ghimire by e-mail joshibalak@yahoo.com

⇒ If you have any concerns about your rights or about the responsibilities of researchers concerning your participation in this project, you can contact to National Agriculture Genetic Resources Center, Nepal Agricultural Research Council by email narc.genebank@gmail.com
Aim & Scope

The objective of our journal "Agrobiodiversity & Agroecology" is to explore variety of concepts, practices and implications in emerging scientific fields within combined and integrated domain of Agrobiodiversity (or Agricultural Biodiversity) and Agroecology. This journal aims at creating an opportunity for presenting different research from all parts of the world that facilitate the dialogue across different disciplines and various actors for capitalizing on different kind of knowledges.

What is Agrobiodiversity?
As described by UN Convention on Biological Diversity (CBD), "the Agricultural biodiversity is a broad term that includes all components of biological diversity of relevance to food and agriculture, and all components of biological diversity that constitute the agricultural ecosystems. also named agro-ecosystems; the variety and variability of animals, plants and micro-organisms, at the genetic, species and ecosystem levels, which are necessary to sustain key functions of the agro-ecosystem, its structure and processes." Agricultural biodiversity is the outcome of the interactions among genetic resources, the environment and the management systems and practices used by farmers. This is the result of both natural selection and human inventive developed over millennia. CBD expands the following dimensions of agricultural biodiversity:

1) Genetic resources for food and agriculture
2) Components of biodiversity that support ecosystem services
3) A biotic factors
4) Socio-economic and cultural dimensions.

What is Agroecology?
Agroecology is an applied science that studies ecological processes applied to agricultural production systems. Bringing ecological principles to bear can suggest new management approaches in agroecosystems. Agroecologists study a variety of agroecosystems. The field of agroecology is not associated with any one particular method of farming, whether it be organic, regenerative, integrated, or conventional, intensive or extensive, although some use the name specifically for alternative agriculture. Agroecology is defined by the OECD as "the study of the relation of agricultural crops and environment." Agroecology is a holistic approach that seeks to reconcile agriculture and local communities with natural processes for the common benefit of nature and livelihoods. Agroecology is inherently multi-disciplinary, including sciences such as agronomy, ecology, environmental science, sociology, economics, history and others. Agroecology uses different sciences to understand elements of ecosystems such as soil properties and plant-insect interactions, as well as using social sciences to understand the effects of farming practices on rural communities, economic constraints to developing new production methods, or cultural factors determining farming practices. The system properties of agroecosystems studied may include productivity, stability, sustain ability and equatability.

Exclusive Features of the Journal

This journal would be inclusive by giving the opportunity to:

- researcher from the South to publish in a journal without any fees for the open-access
- farmers' organizations and NGO to be represented as co-authors with researchers for presenting together their viewpoints on the research.

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