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From Species Richness to Genetic Utility: A Regionally Normalized Priority Index for In- Situ Conservation of Crop Wild Relatives in a Global Biodiversity Hotspot

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From Species Richness to Genetic Utility: A Regionally Normalized Priority Index for *In-Situ* Conservation of Crop Wild Relatives in a Global Biodiversity Hotspot

The data that supports the findings of this study are available in the supplementary material of this article

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ABSTRACT

Crop wild relatives (CWRs) are key components of biodiversity and constitute an essential source of genetic diversity for crop improvement. However, conservation planning based primarily on species richness and existing protected areas may underrepresent populations occurring in environmentally marginal regions and may fail to capture agriculturally important genetic resources. We developed the Crop Wild Relative Conservation Priority Index (CCPI), a high-resolution spatial prioritization framework that integrates genetic proximity to crops, socio-economic importance, rarity, and species distribution modelling to identify priority areas for the conservation of CWR. Using the Southern Levant as a model system, we applied a three-zone climatic normalization approach to account for environmental heterogeneity and evaluated its effects on conservation prioritization across climatic gradients. The CCPI preserved 99.2% of the traditional biodiversity hierarchy while improving the representation of arid and hyper-arid environments. Regional normalization re-prioritized 796.75 km² across 3,187 grid cells and maintained the distributional continuity of key primary and secondary gene-pool taxa. The approach identified priority populations in the driest environments that were less represented under conventional methods. Incorporating land-use constraints enabled the delineation of a "Realizable Conservation Estate", providing a practical framework for translating conservation priorities into implementable conservation actions. Our findings demonstrate that effective biodiversity conservation of CWRs requires the representation of environmentally differentiated populations and intraspecific variation, rather than focusing solely on species occurrence patterns. By integrating biodiversity value, genetic utility, and environmental representation, the CCPI provides a practical tool for strengthening *in situ* conservation and safeguarding genetic resources essential for future agricultural resilience.

Keywords

conservation prioritization, crop wild relatives, genetic resources, *in-situ* conservation, species distribution modeling.

1 Introduction

Global food security faces some escalating threat from rapid human population growth and anthropogenic climate change, continuously eroding the ecological resilience of the agricultural systems (Toromade et al., 2024; Vincent et al., 2013). To adapt cultivated species to these growing environmental pressures, modern plant breeders rely, among

others, on crop wild relatives (CWRs)-undomesticated plant taxa that maintain a close genetic proximity to cultivated species, functioning as a reservoir of stress-adaptive alleles with high potential as gene donors for crop improvement (Dempewolf et al., 2017; Maxted et al., 2006). While the broad taxonomic umbrella of CWRs encompasses an array of socio-economically functional groups such as ornamental, medicinal, and aromatic herbs (Heywood et al., 2007; Maxted et al., 2006), conservation strategies must prioritize the wild progenitors of cereals, Legumes, vegetables, and fruit trees, as these directly underpin global caloric and nutritional food security (Barazani et al., 2008b). Within this agricultural framework, the Gene Pool concept dictates that taxa categorized in the primary (GP1) and secondary (GP2) gene pools hold the highest immediate conservation utility as their close genetic proximity to cultivated crops facilitates the introgression of vital stress-adaptive alleles into elite modern cultivars (Maxted et al., 2012; Yali & Mitiku, 2024)

While *ex-situ* conservation in gene banks remains an important conservation strategy, it inherently "freezes" populations in time, halting their evolutionary trajectory (Maxted et al., 2012). In addition, *ex-situ* collections typically represent only a limited subset of the natural genetic variation present within populations (Wei & Jiang, 2021; Xiao et al., 2025). To maintain the dynamic adaptive potential required under future climate change scenarios, CWRs must be therefore complementary conserved *in-situ* as actively evolving populations that continue to respond to natural environmental pressures (Wambugu & Henry, 2022).

Despite their importance, CWRs are frequently marginalized in traditional *in-situ* conservation spatial planning (Tobón-Niedfeldt et al., 2022; Tyack et al., 2020). Standard biodiversity conservation models rely mostly only on alpha-diversity (overall species richness) and the protection of rare or endemic taxa to designate formal protected reserves (Fielder et al., 2015). Although relaying on these models is effective for general nature conservation, this paradigm is not always adequate for the *in-situ* preservation of agrobiodiversity. Because the primary goal of CWR *in-situ* conservation is to secure actively evolving genetic resources for future crop improvement, a reliance only on species richness may overlook natural populations with high genetic value for agriculture (Maxted et al., 2007, 2012; Zhang et al., 2017).

Furthermore, the traditional consideration only on species richness, introduces a spatial bias when applied across regions with steep environmental gradients by favoring mesic, highly diverse environments as they naturally support a higher baseline of overall alpha-

diversity. Consequently, this bias can overlook the conservation value of species-poor arid margins, even though populations at the trailing, arid edges of a species' distribution often harbor adaptations shaped by prolonged exposure to environmental stress (Kawecki, 2008). For global food security in an era of accelerating climate change, the qualitative value of drought- and heat-tolerant traits, often outweigh the quantitative metric of total species richness (Rehm et al., 2015).

To address this tension, we suggest using the Southern Levant as a microcosm. Characterized by a steep climatic gradient that plunges from mesic Mediterranean zones to hyper-arid deserts, the region encompasses considerable environmental heterogeneity (Barazani et al., 2024). However, the Southern Levant is not only a botanical transition zone but also a recognized hotspot of CWR diversity within the Fertile Crescent, harboring wild progenitors of numerous crops of global agricultural importance, including cereals such as wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*) and wild barley (*Hordeum vulgare* subsp. *spontaneum*), as well as Legumes such as lentil (*Lens culinaris*), pea (*Pisum sativum*), and chickpea (*Cicer arietinum*) (Abbo et al., 2010; Barazani et al., 2024; Zeder, 2011; D. Zohary et al., 2012). As part of the Fertile Crescent, the region also retains a high density of GP1 and GP2 CWRs that have evolved across the steep environmental gradients and have been subjected to diverse abiotic and biotic selection pressures for millennia (Nave et al., 2019; Peleg et al., 2008), making them valuable resources for modern crop improvement (Castañeda-Álvarez et al., 2016; Dahan-Meir et al., 2024; Maxted et al., 2012).

To bridge the gap between theoretical botanical richness and practical agricultural value, while actively unmasking the genetic reservoirs of the arid south, this study presents a novel prioritization framework. We introduce the CWR Conservation Priority Index (CCPI), an integrated model that synthesizes genetic proximity to crops, socio-economic utility, and a regional climatic normalization designed to unmask and correct the mesic bias. The study aims to integrate a bio-economic model with empirical land-use constraints to create a "Realizable Conservation Estate" network that moves beyond passive species cataloging, identifying dynamic conservation hotspots capable of sustaining the evolutionary potential of the region's CWRs in the face of the Anthropocene.

2 Materials and Methods

The step-by-step methodological framework developed for this study is illustrated in Figure 1 to provide a comprehensive overview of the analytical approach.

2.1 Generation of the target taxa checklist

To establish a baseline for conservation planning, a national checklist of CWR was compiled through a multi-stakeholder consultation process involving the Israel Gene Bank (IGB), the Israel Nature and Parks Authority (INPA), and academic partners. Reflecting the region's status as part of the center of crop origin (Abbo et al., 2010; D. Zohary et al., 2012), the inventory scope extended beyond the primary gene pools of major food crops to include wild relatives of forage, herbs and spices, medicinal, industrial, and ornamental species (Barazani et al., 2008, 2017). Taxonomic nomenclature was harmonized with the Israel Gene Bank (https://igb-aro.co.il/) and the Jerusalem Botanical Garden (https://flora.org.il/) taxonomic lists. Taxa were prioritized for inclusion based on indigenous status, excluding neophytes and casual aliens, and socio-economic potential. This baseline candidate list was subsequently filtered to remove taxa with uncertain taxonomy or negligible breeding potential (table S1).

2.2 Collation and expert curation of occurrence data

Occurrence records were collated from the INPA national observation database yielding a raw dataset of 254,466 records. To address taxonomic and spatial errors inherent in historical biological databases, we employed a manual expert validation protocol overseen by a steering committee of senior botanists.

The data cleaning process involved the following criteria: (1) taxonomic and spatial verification, identifying and correcting misidentifications and spatial outliers inconsistent with known phytogeography; (2) differentiation of wild vs. cultivated populations, excluding synanthropic populations, cultivated individuals, or feral populations, e.g., *Olea europaea* **(**Barazani et al., 2016) and *Lepidium sativum* (flora.org.il); and (3) data consolidation, removing duplicate records arising from database mergers.

2.3 Species distribution modeling (SDM)

To identify potential habitats in under-sampled regions, we generated SDMs for species with sufficient unique occurrence records (≥30). We selected a suite of environmental predictors at a resolution of 500 sqm, These included five climatic variables: mean

annual precipitation (mm), mean and minimum temperature for January, and mean and maximum temperature for August (ºC), obtained from the Israel Meteorological Service, alongside topographic and edaphic variables: elevation (m.a.sl), distance from the Mediterranean Sea (m), lithology and soils derived from national geographic information system (GIS) databases and soil maps (Ravikovitch, 1992). We employed an ensemble forecasting approach to reduce the uncertainty associated with individual algorithms (Araújo & New, 2007). The ensemble integrated four distinct algorithms: BioClim (Busby, 1991), Mahalanobis (Farber & Kadmon, 2003), Domain (Carpenter et al., 1993), and Maxent (Phillips et al., 2006).

To generate the final binary presence/absence maps, a consensus rule was applied: a grid cell was considered ecologically "suitable" only if it was predicted by at least two of the four independent models. Continuous probability maps (0–1) were subsequently generated for use in the calculation of the prioritization index.

The analysis was conducted at a spatial resolution of 500 m (0.25 km²), a scale selected to align with the high-resolution national climatic and edaphic layers. This resolution retains sufficient granularity to capture extreme environmental heterogeneity and distinct landscape features, such as wadi systems and mountain ridges, which are critical for regional conservation planning in the Southern Levant (Barazani et al., 2024).

2.4 SDM verification and ground-truthing

The reliability of the SDMs was assessed through a two-tiered process. Maps were qualitatively reviewed by senior botanists to discard ecologically implausible predictions. Then, targeted field surveys were conducted over two seasons to ground-truth ‘transparent areas’-regions predicted as highly suitable by the models but poorly represented in the occurrence records.

2.5 CWR Conservation Priority Index (CCPI)

To prioritize areas for in situ conservation, we developed the CCPI (CWR Conservation Priority Index), a spatially based framework for identifying conservation priorities. This index integrates species richness with a multi-criteria valuation of genetic and economic importance, while correcting for the steep climatic gradient of the study area (Mediterranean vs. Desert).

The spatial analysis described in the following sections was executed in an ESRI ArcGIS Pro environment (v. 3.6.1). To facilitate efficient processing, custom Python scripts were developed utilizing the *arcpy* library for spatial data processing and the *SciPy* library (v. 1.14.1). Additionally, the mathematical formulation of CCPI was refined and simplified using AI-assisted drafting tools to ensure computational efficiency. All AI-generated outputs were validated, debugged, and manually tested against standard geoprocessing outputs to ensure the analytical integrity of the consensus models.

2.5.1 Species valuation and ranking

Prior to spatial analysis, a composite conservation value (W_i) was assigned to each target species. This value (ranging from 6 to 54.9) was derived from a hierarchical weighting of four key biological criteria: (1) genetic proximity to crops, following Harlan and de Wet (1971), where species in the primary Gene Pool (GP1) received the highest weight; (2) Socio-Economic importance, stratified into five tiers ranging from Cereals and Legumes (Tier 1) to Ornamental plants (Tier 5) (Barazani et al., 2008); (3) Rarity and Threat Status (Mayzlish-Gati et al., 2018), adjusted based on the local "Red Number" (https://redlist.parks.org.il/en/plants/list/); and (4) Endemism (https://flora.org.il/). GP and crop importance were weighted five times more heavily than all other criteria, resulting in food-security contribution dominating the overall score (Table S1).

2.5.2 Calculation of local weighted sum (S_j)

A strict probability threshold of $P \geq 0.75$ was applied to all verified SDMs to ensure high confidence. For every grid cell (j) in the study area, a raw weighted sum (S_j) was calculated by summing the conservation values of all species predicted to be present:

$$S_j = \sum_{i=1}^{n} (I_{ij} \times W_i)$$

Where W_i is the pre-assigned conservation value of species i. I_{ij} is an indicator function defined as:

- 1 if $P_{ij} \geq 0.75$
- 0 if $P_{ij} < 0.75$

Where P_{ij} is the probability of species i in cell j

2.5.3 Regional climatic normalization

To prevent the species-rich Mediterranean northern region from masking critical diversity in the arid and hyper-arid southern regions, the study area was segmented into three distinct biogeographical zones defined by precipitation gradients. The zones were delineated using the 200 mm isohyet and the 100 mm isohyet (Danin, 1988; M. Zohary, 1973), designated as Mediterranean, arid, and hyper-arid.

A regional normalization was applied to calculate the final index. The raw score of each cell was converted into a percentage relative to the maximum biodiversity score observed within its specific zone:

$$\mathrm{CCPI}_j = \left(\frac{S_j}{S_{max_zone}}\right) \times 100$$

Where S_j is the local weighted sum for the grid cell and S_{max_zone} is the highest recorded S value found anywhere in that zone (Mediterranean or arid or hyper-arid).

To define conservation priorities, the continuous CCPI scores were classified into 15 tiers using the Equal Interval method. Grid cells within the top 40th percentile threshold (Score > 60), were prioritized for a further analysis and defined as the National Priority Estate.

2.5.4 Validation of regional climatic normalization

To validate the necessity of the three-zones approach, a sensitivity analysis was performed comparing the regionally normalized CCPI against a "Naive" national richness model. The naive model normalized species scores against the global national maximum (S_{global_max}), treating the entire study area as a single climatic unit. The control score $\left(Naive_j\right)$ for each grid cell j was calculated as:

$$Naive_j = \left(\frac{S_j}{S_{global_max}}\right) \times 100$$

Where S_j is the local weighted sum at point j, and S_{global_max} represents the highest accumulated weighted conservation score observed across the entire country. The differential impact was quantified by calculating the score uplift ($\Delta > 0$) for arid and

hyper arid zone cells. A difference map was generated by subtracting the control model from the regional model:

$$\Delta_{Correction} = \text{CCPI}_{Regional} - \text{Model}_{Naive}$$

To evaluate the practical impact of the regional correction on national conservation planning, we quantified the absolute score uplift ($\Delta Correction$) for arid and hyper-arid grid cells. Rather than relying on null-hypothesis significance testing, which is overly sensitive to the massive sample size (n=95,672), we utilized a threshold transition analysis to measure the net area (km²) of arid sites transitioning from non-priority status under the Naive model to the top 40th percentile threshold under the regionally normalized model. Finally, we evaluated the practical impact of the regional correction on national conservation planning by quantifying the net increase in the number of arid sites exceeding the top 40th percentile threshold under the regional model compared to the Naive model. The "Rescue Magnitude" was defined as the net increase in the number of arid sites identified as national priorities:

$$Rescue_{Arid} = N_{Regional(Top40)} - N_{Naive(Top40)}$$

2.5.5 Assessment of conservation utility and efficiency

To decouple the influence of species richness ("quantity") from genetic and economic utility ("quality" e.g., Maxted et al., 2012; Vincent et al., 2013), we conducted a spatially explicit sensitivity analysis focused on the national priority estate (grid cells with a CCPI score > 60.00).

A counterfactual unweighted richness model was generated to represent botanical richness while maintaining climatic fairness. The unweighted baseline retained the three-zones climatic normalization previously established, ensuring that any divergence between models was driven strictly by species composition ("quality") rather than regional mesic bias.

The Unweighted Score (R_{cell}) for each grid cell was calculated as:

$$R_{cell} = \left(\frac{S_{obs}}{S_{max_zone}} \right) \times 100$$

Where S_{obs} is the simple species count within the cell, and S_{max_zone} is the maximum species richness recorded within the specific climatic zones (Mediterranean, arid, or hyper-arid).

To quantify the efficiency and distinctness of the Weighted CCPI Model compared to this unweighted baseline, we restricted the analysis to the intersection of priority zones (scores > 60.00) and performed a paired statistical evaluation:

Spatial congruence was quantified using the Jaccard Similarity Index (ArcGIS *SciPy*) to measure spatial overlap between priority estates identified by both models, assessing whether biological weighting altered the physical footprint of conservation targets.

Ranking stability within shared conservation hotspots was assessed using Spearman's rank correlation (*rs*) (*SciPy* v. 1.14.1). To determine the significance of the correlation independently of the large sample size (n = 47,067), a randomization approach was implemented with 999 permutations to generate a null distribution. Error probabilities were obtained by calculating the *Z* standard deviate, defined as

$$Z = \frac{|r_{obs} - \mu_{perm}|}{\sigma_{perm}}$$

Where: r_{obs} is the observed correlation coefficient, μ_{perm} is the mean of the permuted coefficients and σ_{perm} is the standard deviation of the permuted coefficients.

2.6 Conservation conflict and the realizable estate

To define the "Realizable Estate," the priority landscape was intersected with a high-resolution urban infrastructure mask (Landcover Israel 2020; https://hamaarag.org.il/). We employed a core loss classification protocol, identifying grid cells as "urban" only if the aggregate sum of built-up polygons exceeded the remaining open space. This raster-based approach was validated against a vector-based strict disturbance model to distinguish definitive land-cover conversion from edge effects.

The biological integrity of the remaining estate was assessed by comparing the median CCPI scores of 'lost' (Urban) versus 'realizable' (Open) pixels across the shared priority landscape (*N*=47,592). As massive sample sizes can inflate standard p-values in null-hypothesis significance testing, we applied a Mann–Whitney U test supplemented by a standardized effect size $r = \frac{|Z|}{\sqrt{N}}$ to quantify the actual magnitude of ecological divergence between the two estates. Furthermore, agricultural sub-habitats such as field margins and orchards were retained within the Realizable Estate and classified as Other Effective area-based Conservation Measures (OECMs), acknowledging their role in maintaining culture-dependent taxa ((IUCN WCPA Task Force on OECMs, 2019; S.

Jarvis et al., 2015; Fielder et al., 2015) and *in-situ* management tools along agricultural areas (Maxted & Kell, 2009; Vincent et al., 2022).

3. Results

The national CWR inventory: The CWR inventory was compiled at the specific and sub-specific levels (hereafter collectively referred to as taxa) based on systematic review of the national flora and identified 369 candidate species with potential value for crop improvement. Following the application of strict filtration criteria-excluding neophytes, casual aliens, and taxa with negligible socio-economic utility, the final target checklist was refined to 321 priority CWR taxa (Table S1). This inventory encompasses 72 families and 187 genera, representing a broad spectrum of agricultural utility. The inventory is dominated by the *Fabaceae* (66 species), *Labiatae* (*Lamiaceae*; 27 species) and *Gramineae* (*Poaceae*; 26 species) families. About 37% of these taxa are categorized within the primary gene pool (GP1) and 14% are categorized within the secondary gene pool (GP2), representing the most accessible genetic resources for immediate utilization in breeding programs. The remaining taxa are categorized as GP3 (9%), comprising distantly related species that require advanced biotechnologies for successful gene transfer; and wild-harvested species or those with undetermined gene pool affiliations (40%).

Robustness of Species Distribution Models. Of the priority checklist, 233 species possessed sufficient unique occurrence points ($N \geq 30$) to generate statistically reliable SDMs. The remaining species, primarily rare or highly localized taxa, were excluded from the spatial prioritization analysis to ensure the statistical robustness. The ensemble forecasting approach reduced uncertainty associated with individual algorithms by requiring agreement among at least two of four models (BioClim, Mahalanobis, Domain, and MaxEnt). Expert review identified cases in which individual algorithms produced predictions that were inconsistent with known ecological conditions. For example, the BioClim model occasionally predicted suitable habitat for *Origanum syriacum* in areas characterized by unsuitable soil conditions, whereas predictions supported by multiple algorithms were more consistent with known distributions. Following expert review and targeted field validation, 176 species were retained for analysis. The final distribution models achieved a mean Area Under the Curve (AUC) greater than 0.85, indicating sufficient predictive performance

The CWR Conservation Priority Index (CCPI): The application of the CCPI effectively decouples conservation value from simple species richness by synthesizing bio-economic utility and eco-geographic saturation into a single metric. Prior to regional normalization, the raw summation of species conservation weights (*Sj*) reached a global national maximum (*Sglobal_max*) of 4,194.60 points in the densest Mediterranean grid cells. In contrast, the maximum raw scores achievable in the Arid and Hyper-Arid zones dropped precipitously to 2,834.69 (67.6% of the national maximum) and 728.86 (17.4% of the national maximum), respectively. To standardize this across fundamentally different climatic zones and prevent this massive northern baseline from statistically obscuring the less species-dense desert margins, the final CCPI is expressed on a continuous normalized scale from 0 to 100, representing the percentage realization of a specific region's theoretical genetic carrying capacity.

When sensitivity analysis evaluated a Naive national model (Figure 2A) where scores were unadjusted and normalized solely against the global national maximum (4,194.60), high-value conservation zones were identified almost exclusively in the Mediterranean zone, north of the 200 mm isohyet. In this unadjusted model, arid and hyper-arid zones are systematically undervalued due to their naturally lower alpha-diversity, creating a 'masking effect' behind the high-density biomass centers of the north.

The implementation of a three-zones climatic normalization, segmented along the 100- and 200-mm isohyets, successfully corrected this spatial bias without distorting the internal conservation hierarchy of the desert regions (Figure 2B). A Spearman’s rank correlation between the naive and regional models yielded a perfect correlation (rs =1.000, p<0.001) across both the Arid (n=18,613) and Hyper-Arid (n=33,884) zones (combined n=52,497). This monotonic relationship suggests that the regional normalization process functions as a scalar transformation, reducing the 'masking effect' of the Mediterranean baseline without artificially altering the biological hierarchy of desert ecosystems.

However, while internal rankings remained strictly stable, the absolute conservation values shifted significantly (Table 1), demonstrating that the masking effect is more significant in extreme environments. Prior to normalization, the unadjusted Naive model systematically assigned low priority scores to desert-margin areas, with conditionally rescued cells in the Hyper-Arid zone yielding a mean priority score of

11.88 points (constrained by the zone's absolute mathematical ceiling of 17.4%). Regional normalization actively corrected this bias, generating a massive mean score uplift (Δ) of +56.49 points in the Hyper-Arid zone, more than double the correction observed in the Arid zone (+23.68 points). This tangible 'rescue effect' successfully elevated these marginal sites to a mean Regional CCPI score of 68.37, pushing them firmly into the National Priority Estate solely based on their relative ecological potential (Figure 2B1-3; Figure 2C).

Overall, the regional normalization re-prioritized 796.75 km² (3,187 grid cells) across the Arid and Hyper-Arid zones of the Southern Levant, securing 6.1% of the southern desert landscape, including 11.8% of the Arid ecological unit and 2.9% of the Hyper-Arid unit. This approach highlighted desert regions often overlooked in broad-scale assessments despite their importance as reservoirs of stress-tolerant CWRs for future crop adaptation.

Analysis of Cereal and legume CWRs prioritized by the CCPI within the Arid (100-200 mm) and Hyper-Arid (<100 mm) zones indicated the preservation of distributional continuity from the Mediterranean region into drier environments for several taxa. These included the GP1 species *Triticum dicoccoides*, *Avena barbata*, *Avena sterilis*, and *Hordeum spontaneum*, as well as the GP2 species *Aegilops bicornis Aegilops kotschyi* (Table S2).

Similarly, continuity between the Mediterranean and Arid zones was maintained for *Elytrigia elongata*, *Cicer judaicum*, *Pisum fulvum*, *Aegilops peregrina*, *Hordeum bulbosum*, and *Lens ervoides*.

In contrast, *Aegilops geniculata*, a GP2 relative of wheat, was prioritized only within the Arid and Hyper-Arid zones and does not occur in the Mediterranean region. Likewise, *Aegilops vavilovii* was prioritized exclusively within the Hyper-Arid zone. Consequently, populations of these species in the driest environments would have received limited representation under the unnormalized prioritization framework.

Assessment of Conservation Utility and Precision When evaluated against the unweighted richness baseline (based solely on species richness count), the weighted CCPI model (based on a hierarchical weighting of genetic, economic, and ecological criteria) revealed high spatial and hierarchical congruence. The analysis yielded a Jaccard Similarity Index of 0.97 across the national priority estate and a near-perfect Spearman's rank correlation within the shared priority estate (n = 47,067 grid cells; r_s

= 0.9922). A permutation test (n = 999) confirmed the significance of this correlation (Z-score = 211.65, $p < 0.001$). The weighted CCPI model preserved 99.2% of the traditional biodiversity hierarchy, maintaining the geographic footprint of overall CWR biomass represented by the "core consensus" (Figure 3, dark grey points).

Rather than indicating broad spatial reconfiguration, the model's refinement reduced the national priority estate by a net 228 grid cells (57.00 km²), reflecting two complementary filtering processes. First, 753 "generalist" grid cells (188.25 km²) characterized by high overall species richness but lacking taxa with close genetic affinity to priority crops (e.g., dominated by tertiary gene pool taxa or species of minor socio-economic importance) were excluded ("efficiency gain," Figure 3, red points). Second, 525 "genetic anchor" sites (131.25 km²) that did not meet raw richness thresholds were included due to their high concentrations of critical primary gene pool (GP1) resources ("utility-driven rescue," Figure 3, blue points). This shift demonstrates a transition toward precision conservation, whereby areas with high alpha-diversity but limited breeding potential are excluded in favor of sites maximizing targeted agrobiodiversity value.

A subsequent spatial intersection of these transitioning grid cells with the regional climatic zones revealed a pronounced geographical dichotomy in how the genetic weighting operated. The filtration of generalists (efficiency gain) was concentrated at the extreme environmental margins. Of the 753 excluded grid cells, 82.0% (n = 617) were located in the hyper arid (<100 mm isohyet), while only 13.1% (n = 99) and 4.9% (n = 37) were located in the Mediterranean North (>200 mm) and arid (100-200 mm) zones, respectively. The utility-driven rescue effect was highly concentrated in the saturated mesic core. Of the 525 genetic anchor sites elevated into the priority estate, 76.2% (n = 400) were situated in the Mediterranean North, with the hyper-arid and arid zones accounting for 22.3% (n = 117) and 1.5% (n = 8) of the rescued sites, respectively.

Quantification of Habitat Attrition The biological model initially identified 11,897.25 km² of high-priority land (Score > 60.0) as possessing the necessary attributes to support the *in-situ* conservation of CWR, forming the theoretical CWR priority landscape (Figure 4A). However, spatial overlay analysis reveals that 1,506.25 km² (12.7%) of this extent has been converted to built-up infrastructure. By applying an anthropogenic urban filter to mask out these areas of core loss, the analysis delineates the actionable conservation landscape. Consequently, the remaining 10,391.00 km² constitutes the "Realizable Conservation Estate" (Figure 4B). This confirms that despite

urbanization pressures, approximately 87.3% of the country's primary genetic reservoirs remain-situated in open spaces, comprising potentially compatible land uses such as agricultural lands, nature reserves, and other open spaces, that are physically accessible for different *in-situ* conservation management.

Differential Habitat Attrition: the vulnerability of high-value sites. While the net spatial attrition across the total priority landscape was moderate (12.7%), a stratified analysis of the six priority tiers reveals a structural bias: habitat conversion is not uniformly distributed but is skewed toward the landscape's primary genetic reservoirs (Table 2). The higher tier, defined by CCPI scores >93.33, experienced the highest reduction, losing 35.4% (107.25 km²) of their theoretical extent to infrastructure. This attrition rate is nearly triple the global priority landscape average (12.7%) and is significantly higher than the 6.2% loss observed in the lowest priority tier. A Spearman's rank correlation analysis confirmed a monotonic relationship between conservation priority and the intensity of habitat loss ($r_s = 1.000, p < 0.001$). This confirms that anthropogenic pressure in the Southern Levant is non-random, with development intensity rising in tandem with ecological value, resulting in the direct physical elimination of critical CWR genetic reservoirs.

Despite the disproportionate attrition in the top tiers, the "Realizable Conservation Estate" retains high biological integrity. An analysis comparing the biological value of 'lost' (Urban) sites (n=6,025) against 'realizable' (Open) sites (n=41,567) within the priority landscape confirmed that the 'lost' estate possessed a higher median genetic value (CCPI = 84.99) than the remaining estate (CCPI = 80.89).

However, while a Mann-Whitney U test indicated this difference was statistically significant (Z=−34.73, p<0.001), the absolute difference was only 4.10 CCPI points. Furthermore, the calculated effect size was not significant (r=0.159), stating that this divergence represents a minor ecological shift. Therefore, this difference does not indicate a collapse in the quality of open spaces. The median score of the realizable estate remains well above the high-priority threshold.

Discussion

From species richness to genetic affinity: refining conservation

The potential contribution of beneficial traits from CWRs for priority crops has an estimated value of $120 billion (PwC, 2013), with global estimates indicating that CWRs already contribute approximately $115 billion per year worldwide in increasing crop yields (Cockel et al., 2022; Pimentel et al., 1997), reinforcing that the *in-situ* conservation of these regional progenitors is a global economic imperative.

Global assessments have made significant strides in defining priorities for CWR conservation. Spatial frameworks, such as the global gap analysis by Castañeda-Álvarez et al. (2016), have successfully established conservation priorities by modeling the distribution of wild relatives across numerous major crop genepools. Building on these approaches, recent studies have utilized advanced ensemble species distribution modeling (ESDM) to project the impacts of climate change on specific agricultural groups, such as global rice wild relatives (Lin et al., 2024). Broadening this scope, the global model by Vincent et al. (2019) successfully identified 150 macro-hotspots for *in -situ* conservation by modeling 1,261 CWR species and employing Ecogeographic Land Characterization (ELC) as a proxy to maximize the inclusion of intra-specific genetic diversity and unique adaptive scenarios.

Despite these major advances, an important challenge remains unresolved. Global conservation frameworks are highly effective at identifying broad geographical priorities and maximizing representation of CWR diversity, yet they generally rely on species occurrence, complementarity, or richness-based approaches that implicitly treat all taxa as having equal conservation value (Castañeda-Álvarez et al., 2016; Maxted et al., 2007; Vincent et al., 2019). In practice, however, CWR species differ substantially in their immediate utility for crop improvement, reflecting variation in genetic affinity to cultivated crops and their relevance to global food security. Furthermore, when species richness is evaluated across regions characterized by strong environmental gradients, conservation priorities may become strongly influenced by underlying climatic and productivity patterns rather than by the distribution of the most valuable genetic resources. As recognized in broader conservation planning theory, priorities based solely on species counts often fail to effectively capture specific subsets of biodiversity or particular conservation objectives (Bonn et al., 2002; Margules & Pressey, 2000).

Our results demonstrate that these limitations generate a dual masking effect in CWR conservation. First, botanical quantity can obscure genetic quality. Sites dominated by common taxa or species with limited breeding relevance may achieve high conservation

rankings, while areas containing comparatively few but highly valuable primary and secondary gene pool taxa remain statistically overshadowed. Second, comparisons based on absolute richness across steep environmental gradients create a spatial masking effect in which species-rich mesic regions dominate conservation priorities, thereby obscuring climatically marginal environments that support sparse but evolutionarily significant populations adapted to extreme conditions (Kawecki, 2008; Rehm et al., 2015). By combining hierarchical genetic weighting with regional climatic normalization, the CCPI framework addressed both dimensions of this priority diversity.

By prioritizing primary and secondary gene pool taxa of major cereals and legumes, our framework shifts conservation efforts from a focus on botanical quantity toward agricultural utility. Important cereals and legumes form the foundation of global food and nutritional security, supplying most of the world's caloric and plant-derived protein intake (Foyer et al., 2016; Shiferaw et al., 2013; Smýkal et al., 2018). Because primary gene pool species can readily cross with cultivated crops and produce fertile offspring (Harlan & de Wet, 1971), they represent the most immediately accessible genetic resources for crop improvement. Consequently, conserving wild populations of these globally important crops is likely to provide far greater returns for future agricultural resilience than broadly protecting numerous taxa with limited breeding value (Maxted & Kell, 2009).

The importance of climatic normalization is particularly evident in the Southern Levant, a globally significant center of CWR diversity characterized by environmental heterogeneity and a steep gradient extending from mesic Mediterranean ecosystems to hyper-arid desert environments (Barazani et al., 2008, 2024; Danin, 1988; Schaffer & Levin, 2014). Standard richness-based approaches create a structural mesic bias that favors biologically dense regions while masking the conservation value of arid and semi-arid margins. Yet these species-poor environments frequently function as evolutionary driven systems in which populations have developed adaptive mechanisms under long-term exposure to severe biotic and abiotic stress (Kawecki, 2008). Such trailing-edge populations often contain unique alleles such as heat and drought tolerance that may prove essential for future crop adaptation under climate change (Hampe & Petit, 2005; Nevo & Chen, 2010; Peleg et al., 2008; Rehm et al., 2015). By accounting for regional climatic context, the CCPI effectively unmasks these

marginal environments and highlights genetic resources that would otherwise remain overlooked.

The model's ability to preserve the distributional continuity of key CWRs across the climatic gradient, from Mediterranean environments to the Arid and Hyper-Arid zones, highlights an important consideration in agrobiodiversity conservation: the need to represent intraspecific genetic and trait variation rather than focusing solely on species occurrence (Fielder et al., 2015; Maxted et al., 2012). Previous studies have shown that populations of wild emmer wheat (*Triticum dicoccoides*) and wild barley (*Hordeum spontaneum*) exhibit genetic and phenotypic differentiation along aridity gradients, reflecting adaptation to local environmental conditions (Nevo & Chen, 2010; Peleg et al., 2008; Volis et al., 2002). Conservation strategies centered primarily on mesic core distributions may underrepresent variation occurring at the drier margins of species ranges, where distinct adaptive traits may be present (Bontrager et al., 2020; Hampe & Petit, 2005; Kawecki, 2008; Rehm et al., 2015). In this study, the CCPI framework prioritized populations of several GP1 and GP2 taxa, across multiple climatic zones, while also identifying priority populations within the most arid environments. These suggest that regional normalization can improve the representation of populations distributed across broad environmental gradients, thereby supporting the conservation of adaptive traits relevant to future crop improvement (Maxted & Magos Brehm, 2023; Van Deurs et al., 2025).

Based on our spatial distribution analysis, the interaction between genetic weighting and climatic normalization reveals a marked geographical dichotomy in conservation prioritization. Our results illustrate two distinct spatial phenomena across the landscape rather than a uniform national shift. First, within arid and hyper-arid regions, we found that climatic normalization alone risks over-correcting by elevating sites containing relatively high concentrations of common desert taxa, including tertiary gene pools or species associated with minor crops. In these environments, our model demonstrates that hierarchical weighting acts as a stringent quality-control mechanism, ensuring resources are directed exclusively toward genuine refugia for high-value primary and secondary gene pool (GP1 and GP2) resources of important food-security taxa. This phenomenon of filtering out botanical noise occurred almost exclusively at the desert margins. Most of the 'Generalist' sites (over 80%) excised by the model for lacking sufficient genetic utility were located in the hyper-arid extreme south.

On the other hand, our findings reveal that in the botanically rich mesic core, genetic weighting functions as a utility-driven rescue mechanism. Because richness thresholds are naturally elevated in highly diverse mesic environments, sites supporting moderate overall species richness but high concentrations of valuable crop progenitors are frequently overlooked. By incorporating genetic importance, the CCPI successfully uncovered these critical agrobiodiversity anchors despite the dense botanical background surrounding them. This rescue phenomenon was distinctly concentrated in our spatial results: over three-quarters of all Utility driven (quality) sites locations that failed standard unweighted richness criteria but were salvaged due to their high primary gene pool concentrations, were recovered directly from the mesic Mediterranean north. Overall, these contrasting phenomena, derived from our modeling outputs, demonstrate that effective conservation across strong environmental gradients requires both spatial equity through climatic normalization and agricultural relevance through utility weighting.

Despite its advantages, the CCPI framework possesses an important limitation regarding the treatment of climatic boundaries. By segmenting continuous environmental gradients into zones defined by specific isohyets, the model creates artificial boundaries. Analysis of ecotones between Mediterranean, arid, and hyper-arid zones revealed a tendency for populations beyond these thresholds to be underrepresented in hotspot identification. This limitation is important to acknowledge, and future developments should therefore move beyond rigid regional thresholds by incorporating continuous environmental surfaces, ecotone modeling, or boundary-buffering approaches that more accurately capture populations occupying these climatically sensitive transition areas.

Strategic Conservation in a Crowded Landscape. A constraint of conservation in the Southern Levant is the acute scarcity of land. With a population density of approximately 445 people per km² (CBS, 2025) and intensifying development pressures on open landscapes (Rotem-Mindali et al., 2024), the allocation of land for "passive" nature conservation is becoming politically and spatially unfeasible. Therefore, to secure the remaining CWR diversity, conservation strategies must shift from a binary model-Nature vs. Urban, to a multi-functional model that reconciles infrastructure development with the maintenance of genetic connectivity.

In this highly competitive spatial context, the CCPI framework provides an administrative advantage. By prioritizing conservation areas based on their direct utility to global food security rather than abstract botanical richness, the CCPI supplies a powerful socio-economic justification for land protection (Maxted et al., 2012). As recent global assessments highlight, conservation efforts that bridge biodiversity protection with essential ecosystem services-such as agricultural resilience and human food provisioning, are significantly more likely to garner the necessary political will, stakeholder support, and limited financial resources required for statutory implementation (Obiar et al., 2025).

Establishing this socio-economic justification is underscored by our finding that historical urbanization has driven a non-random attrition of the region's most valuable landscapes, leading to the extirpation of high-priority conservation areas and the erosion of critical genetic resources beyond the loss of physical habitat alone (Khoury et al., 2022; van de Wouw et al., 2009).

By applying the CCPI framework, our analysis indicates that historical development has disproportionately affected areas of high agrobiodiversity value, including many of the highest-priority conservation areas ("Mega-Hotspots"). Although development has affected a considerable proportion of these high-value areas, the remaining fragments retain characteristics comparable to those of the lost sites. Moreover, because infrastructure expansion has not completely disrupted landscape connectivity, the model suggests that these remaining top-tier areas continue to represent a highly valuable conservation estate deserving of statutory protection.

However, conservation of this genetic resource diversity cannot rely solely on the existing protected area network (Hunter et al., 2012), as isolated reserves may not adequately maintain the connectivity required for long-term gene flow and metapopulation dynamics. Ecological corridors and complementary areas beyond formal protected boundaries are needed to reduce the risks of genetic isolation, inbreeding, and genetic drift (Ervin et al., 2010; Khoury et al., 2022). This challenge is particularly relevant in densely populated regions such as the Southern Levant, where limited conservation land and ongoing development pressures constrain the capacity of formal protected areas to capture the full breadth of CWR diversity (CBS, 2025). Conservation planning should therefore extend beyond traditional reserves to incorporate complementary areas within the wider multi-functional landscape, for

improving the representation and persistence of agrobiodiversity (Perfecto & Vandermeer, 2010; Vincent et al., 2019).

The Agricultural Matrix as an Active Conservation Framework for CWRs

Conservation planning has traditionally treated agricultural landscapes as a primary threat, emphasizing the protection of relatively undisturbed habitats within formal reserves (Maxted et al., 2012; Maxwell et al., 2016; Vincent et al., 2019). However, many CWRs are associated with disturbed and early-successional habitats rather than stable climax communities (Jain, 1975; Maxted et al., 1997). Reflecting this ecological affinity, our framework incorporates agricultural landscapes into the spatial prioritization process. Arable lands, orchards, and traditional farming systems can support diverse CWR populations by providing suitable microhabitats, including field margins, boundaries, and orchard understories (Al-Atawneh et al., 2007; S. Jarvis et al., 2015). Consequently, the "Realizable Conservation Estate" includes 6,018 km² of agricultural land as complementary areas for *in situ* conservation beyond formal protected areas, improving the representation of CWR diversity across the broader landscape.

Regional assessments across the Levant demonstrate that agricultural boundary support numerous CWR taxa of conservation importance, highlighting their contribution to the persistence of CWR diversity outside formal protected areas. Within these environments, traditional viticultural systems have been shown to support populations of wild grapevine (*Vitis vinifera* subsp. *sylvestris*) that retain distinct regional genetic signatures (Sivan et al., 2021). Similarly, the Dryland Agrobiodiversity Project in the Levant reported the occurance of CWRs of wheat, barley, lentil, pea, and bean within modern apple orchards (Al-Atawneh et al., 2007). In the intensively cultivated Beqaa Valley of Lebanon, populations of rare CWRs have been recorded along formerly cultivated terraces and roadside habitats (Al-Atawneh et al., 2007). Likewise, in Jordan, CWR species such as wild lettuce (*Lactuca aculeata* and *L. orientalis*) have been documented in disturbed habitats, including neglected agricultural areas and transportation verges (Maxted et al., 2024). Patterns of this kind have also been reported for wild fruit trees. For example, wild Syrian pear (*Pyrus syriaca*) is encountered as scattered individuals within traditional agricultural landscapes rather than as components of large continuous populations (Al-Atawneh et al., 2007).

Similar observations have been reported from other regions. A national assessment in the United Kingdom found that priority food crop CWRs were frequently associated with cropped and weedy habitats and commonly occurred along hedgerows, field margins, and transportation verges (S. Jarvis et al., 2015). Likewise, in traditional African agricultural systems, wild relatives of crops such as yam (*Dioscorea* spp.) in West Africa and enset (*Ensete ventricosum*) in Ethiopia are often retained within or along cultivated fields (FAO, 2010).

The contribution of agricultural landscapes to CWR conservation extends beyond habitat provision. Semi-natural elements such as field margins, orchards, and other boundary features can facilitate connectivity among populations across fragmented landscapes, thereby supporting gene flow and metapopulation processes (Kawecki, 2008). Agricultural landscapes may, therefore, complement formal protected areas and could be considered within broader site-based conservation frameworks, including Other Effective area-based Conservation Measures (OECMs) (IUCN-WCPA Task Force on OECMs, 2019).

Global Implications: Exposing the Incongruence in Conservation Planning

The broader relevance of the CCPI framework is supported by evidence from multiple global regions. In the United States, assessments of approximately 600 native CWR taxa revealed that overall diversity is concentrated in temperate northeastern, midwestern, and northwestern regions, whereas species-poor desert borderlands contain unique wild relatives of Legumes, roots, tubers, and fiber crops (Khoury et al., 2020). Conservation strategies based solely on richness metrics would therefore prioritize high-biomass regions while overlooking these genetically important desert refugia. Similar patterns have been documented in South Africa, where threatened endemic relatives of globally significant crops, including rye (*Secale*), yams (*Dioscorea*), and sweet potatoes (*Ipomoea*), remain outside protected area networks because they do not coincide with conventionally defined biodiversity hotspots (Holness et al., 2019).

If conservation planning continues to rely on simple measures of botanical richness, critical components of global agrobiodiversity will remain vulnerable. Predictive models suggest that 16-22% of wild relatives of crops such as peanuts, potatoes, and cowpeas could face extinction by the middle of the twenty first century under projected environmental change (A. Jarvis et al., 2008). By explicitly integrating genetic utility

with climatic context, the CCPI framework provides a practical pathway for identifying and safeguarding the stress-adapted alleles and evolutionarily significant populations that will be essential for maintaining agricultural resilience under future climates.

Figure 1. The CWR Conservation Priority Index (CCPI) methodological framework. This workflow illustrates the methodology designed in this manuscript to shift from traditional species-richness models to a targeted, utility-driven conservation strategy. By systematically integrating genetic value and regional climatic corrections, the model actively unmasks critical CWR resource that are statistically obscured in standard assessments, ultimately applying real-world infrastructure constraints to delineate a pragmatic and actionable "Realizable Conservation Estate".

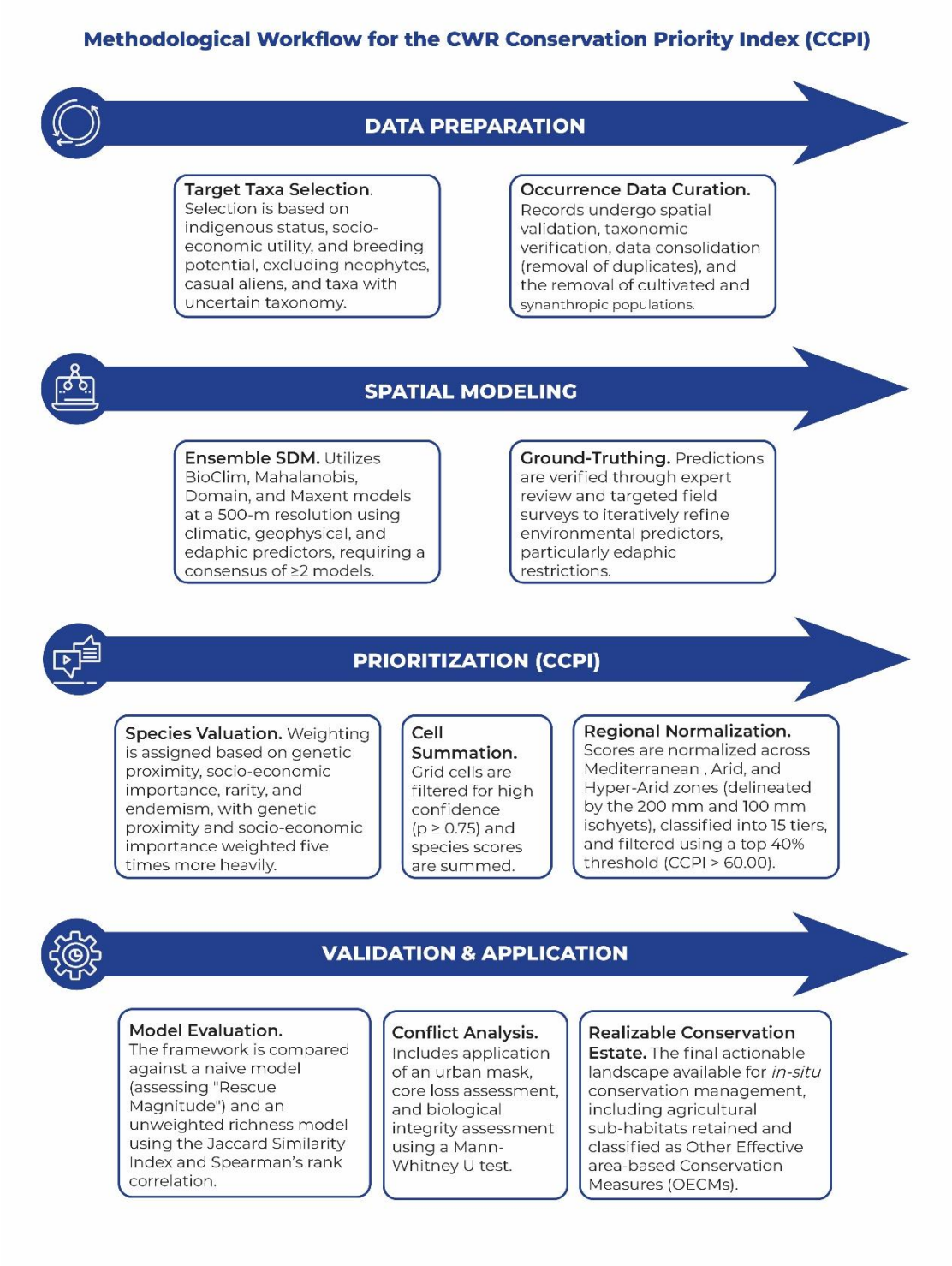

Figure 2. Effect of Regional Normalization on Biodiversity Prioritization Across Mediterranean, Arid, and Hyper-Arid Zones. *Lines in all panels denote the 200 mm (purple) and 100 mm (blue) isohyets, marking the climatic transitions between the Mediterranean, Arid, and Hyper-Arid zones.*

(A) **Naive National Model**: Spatial prioritization calculated by normalizing composite values against the national maximum (S_{global_max} = 4,194.60), treating the study area as a single climatic unit. High priority scores are concentrated in the Mediterranean zone, whereas arid and hyper-arid zones receive comparatively lower scores, reflecting differences in overall diversity patterns. (B) **Regionally Normalized CCPI**: Final Conservation Priority Index after dividing the study area into three biogeographical zones. Scores within the Arid and Hyper-Arid zones were normalized relative to their respective regional maxima, resulting in the identification of priority areas within desert regions that received lower scores in the national model. Panels B1-B3 provide enlarged views of selected priority areas in the Arid (B1) and Hyper-Arid (B2-B3) zones. (C) **Differential Analysis (Δ)**: Difference map showing the change in conservation scores following regional normalization. The blue gradient indicates areas where normalization increased prioritization scores, with some desert locations gaining up to 82 points relative to the national-scale model.

Note: The West Bank region is partially masked in all panels because of insufficient botanical and occurrence data for these areas.

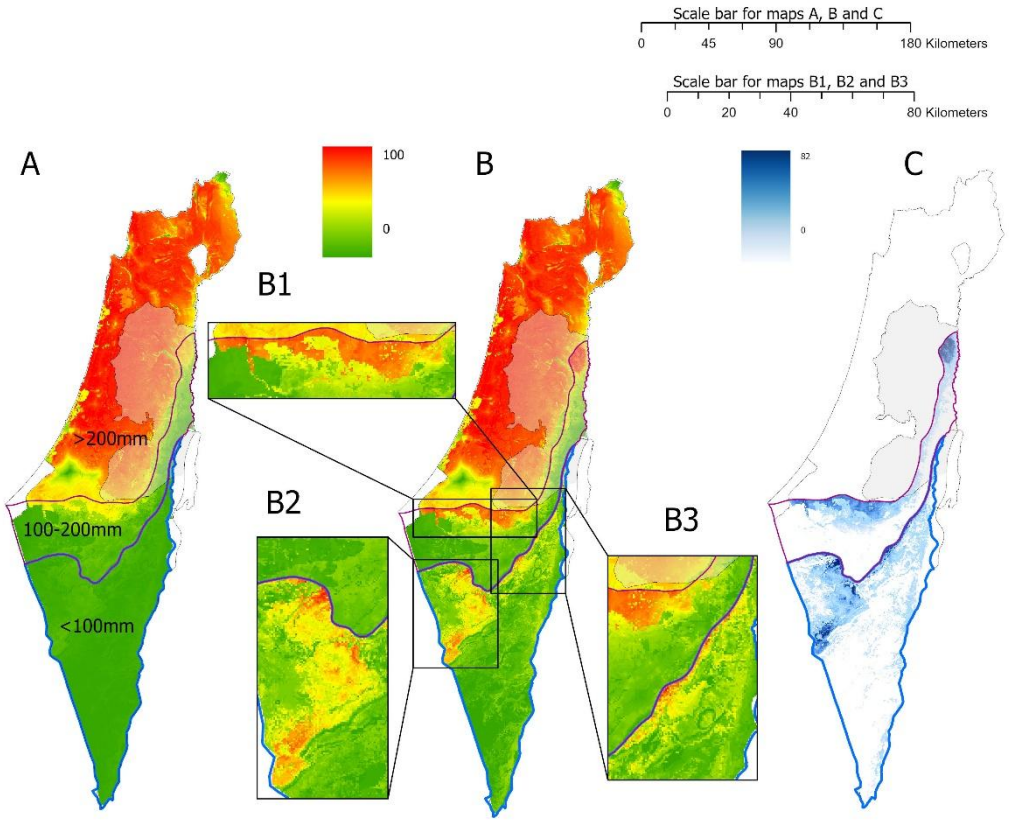

Figure 3. Comparison of Unweighted Species Richness and Weighted CCPI Prioritization. Bivariate scatter plot of 500 × 500 m grid cells comparing Unweighted Species Richness ("Quantity") and Weighted CCPI scores ("Quality"). Both axes represent regionally normalized values, such that broad climatic differences among zones are accounted for in both models. Dashed lines indicate the conservation priority threshold (Score > 60.0). **Non-Priority Cells (light grey circles):** Grid cells scoring below the conservation threshold in both models. **Consensus Priority Areas (dark grey circles):** Grid cells exceeding the conservation threshold in both the unweighted and weighted models. **Richness-Priority Cells (red circles; N = 753):** Grid cells prioritized by the unweighted richness model but not by the weighted CCPI model, representing 188.25 km². **CCPI-Priority Cells (blue circles; N = 525):** Grid cells prioritized by the weighted CCPI model but not by the unweighted richness model, representing 131.25 km². These sites are characterized by high concentrations of primary gene pool resources of important agriculture species despite comparatively lower species richness.

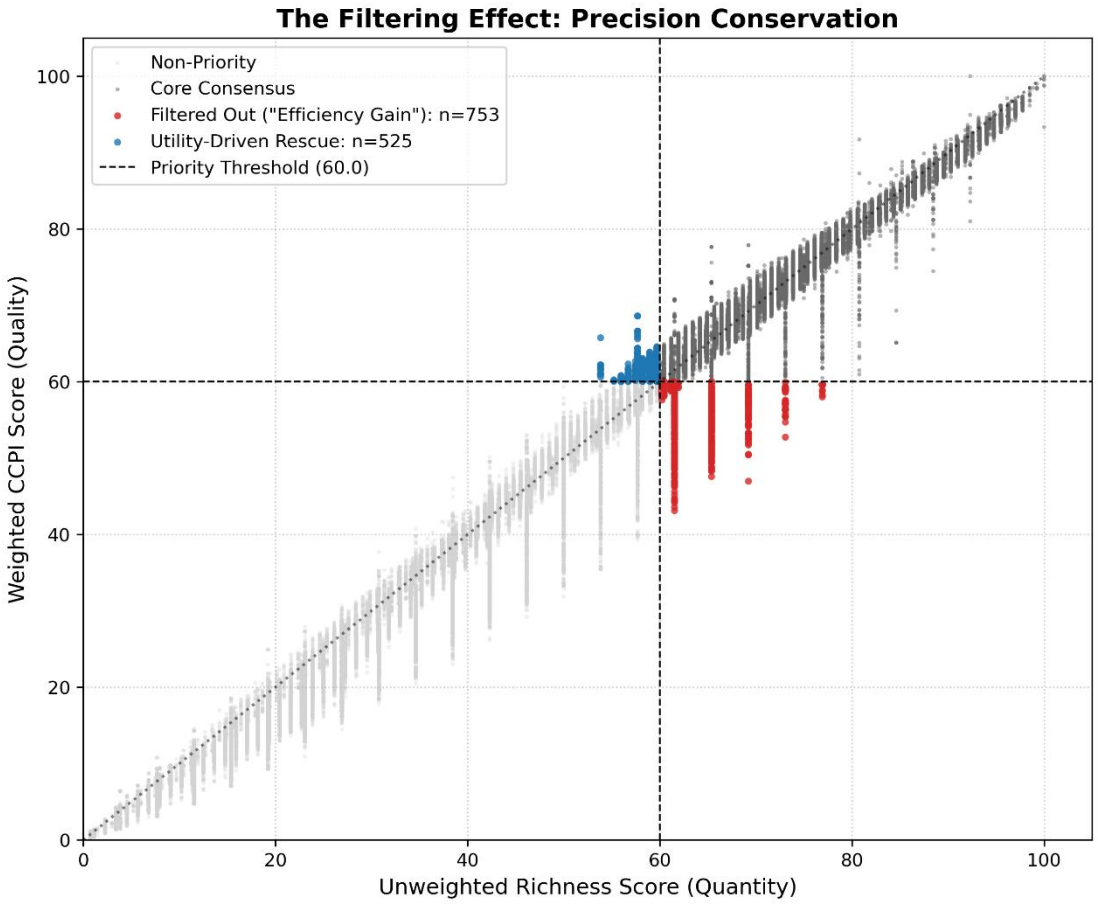

Figure 4. From Theoretical Potential to Realizable Estate. (A) Theoretical CWR Priority Landscape: The biological baseline derived from the regionally normalized CCPI, displaying all grid cells exceeding the national conservation threshold of > 60.00 points. Warmer colors (red) indicate primary genetic reservoirs and "Mega-Hotspots" of high genetic saturation (Scores > 90.0). (B) Realizable Conservation Estate: The actionable conservation landscape following the application of the anthropogenic urban filter. Areas classified as "Core Loss" (built-up infrastructure and impervious surfaces) have been masked out (rendered blank/white), while potentially compatible land uses remain visible. This represents the 10,391.00 km² of priority land functionally available for *in-situ* implementation. *Note: The West Bank region is partially masked in all panels due to insufficient botanical and occurrence data in these areas.*

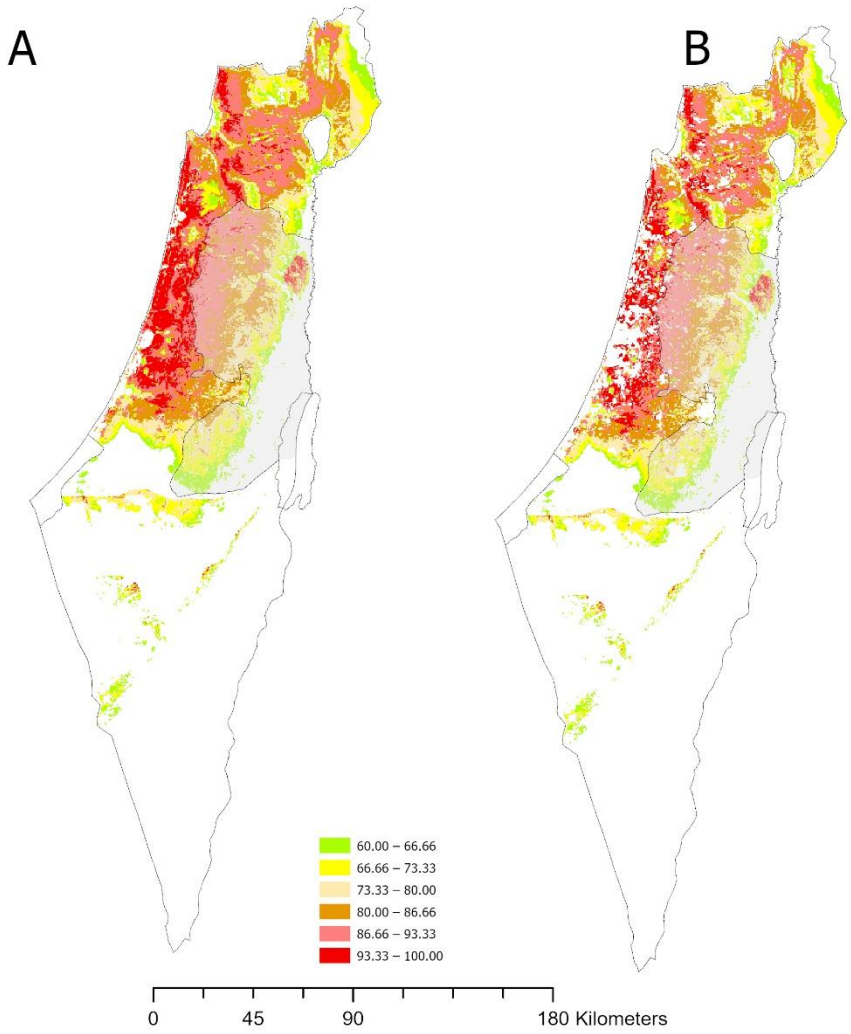

Table 1. The "Rescue Effect": Impact of Regional Climatic Normalization on the prioritization of arid and hyper-arid conservation sites. A summary of the comparative spatial analysis between the unadjusted "Naive" National Model and the three-zones CCPI model. Score uplift (Δ) represents the mean increase in the conservation value assigned to each grid cell (500 × 500 m resolution) after accounting for regional climatic gradients. "Rescued" sites are defined as grid cells that scored strictly below the priority threshold (< 60.00) in the Naive model but were successfully elevated to the National Priority Estate (≥ 60.00) once normalized against their specific regional climatic potential.

Metric	*Arid Zone (100–200 mm)*	*Hyper-Arid Zone (<100 mm)*
Total Analyzed Cells (n)	18,613	33,884
Mean Naive Score (Unadjusted)	49.36 points	11.88 points
Mean Regional CCPI Score (Adjusted)	73.04 points	68.37 points
Mean Score Uplift (Δ)	+23.68 points	+56.49 points
Rescued Priority Sites	2,189 cells	998 cells
Rescued Priority Area	547.25 km²	249.50 km²

Table 2. Differential impact of urbanization on CWR conservation priority tiers within the National Priority Estate. The data highlights a perfect monotonic correlation between genetic value and threat ($r_s = 1.000, p < 0.001$), with the highest priority sites (Tier 15) disappearing at nearly triple the national priority average rate (35.4% vs. 12.7%). *Note: "Theoretical Area" represents the total high-priority landscape (Score > 60.00) identified by the Regional CCPI model, comprising both the currently Realizable Estate and the area Lost to existing urbanization.*

PRIORITY TIER	*CCPI SCORE RANGE*	*THEORETICAL AREA (KM²)*	*REALIZABLE AREA (KM²)*	*AREA LOST (KM²)*	*% LOSS*
TIER 15 (MEGA-HOTSPOTS)	93.33 – 100.00	303.00	195.75	107.25	35.4%
TIER 14	86.66 – 93.33	2,401.75	1,887.75	514.00	21.4%
TIER 13	80.00 – 86.66	3,910.25	3,497.00	413.25	10.6%
TIER 12	73.33 – 80.00	2,660.25	2,386.50	273.75	10.3%
TIER 11	66.66 – 73.33	1,594.75	1,460.00	134.75	8.4%
TIER 10 (LOWEST PRIORITY)	60.00 – 66.66	1,027.25	964.00	63.25	6.2%
TOTAL	> 60.00	11,897.25	10,391.00	1,506.25	12.7%

References

Abbo, S., Lev-Yadun, S., & Gopher, A. (2010). Agricultural origins: centers and noncenters; a Near Eastern reappraisal. *Critical Reviews in Plant Sciences*, 29, 317–328.

Al-Atawneh, N., Amri, A., Assi, R., & Maxted, N. (2007). Management plans for promoting in situ conservation of local agrobiodiversity in the West Asia centre of plant diversity. In N. Maxted, B.V. Ford-Lloyd, S.P. Kell, J. Iriondo, E. Dulloo, & J. Turok (Eds.), *Crop wild relative conservation and use* (pp. 340–363). Wallingford: CAB International.

Araújo, M. B., & New, M. (2007). Ensemble forecasting of species distributions. Trends in Ecology & Evolution, 22 (1), 42-47.

Barazani, O., Lifshitz, D., & Mayzlish-Gati, E. (2024). Conservation of plant genetic resources in the southern Levant. *Scientia Horticulturae*, 331, 113124. https://doi.org/10.1016/j.scienta.2024.113124

Barazani, O., Mayzlish-Gati, E., Lifshitz, D., Hadas, R., Keren-Keiserman, A., Golan, S., Faraj, T., Singer, A., Beerman, A., & Perevolotsky, A. (2017). Strategies and priorities in field collections for ex situ conservation: the case of the Israel Plant Gene Bank. *Genetic Resources and Crop Evolution*, 64, 1–5.

Barazani, O., Keren-Keiserman, A., Westberg, E., Hanin, N., Dag, A., Ben-Ari, G., Fragman-Sapir, O., Tugendhaft, Y., Kerem, Z., & Kadereit, J. W. (2016). Genetic variation of naturally growing olive trees in Israel: from abandoned groves to feral and wild? BMC Plant Biology, 16, 261. https://doi.org/10.1186/s12870-016-0947-5

Barazani, O., Perevolotsky, A., & Hadas, R. (2008). A problem of the rich: Prioritizing local plant genetic resources for ex situ conservation in Israel. *Biological Conservation*, 141 (2), 596–600.

Bonn, A., Rodrigues, A. S. L., & Gaston, K. J. (2002). Threatened and endemic species: are they good indicators of patterns of biodiversity on a national scale? Ecology Letters, 5, 733-741.

Bontrager, M., Angert, A. L., & Ågren, J. (2020). Adaptation at range edges. Annual Review of Ecology, Evolution, and Systematics, 51 (1), 341-362.

Busby, J. R. (1991). BIOCLIM-a bioclimate analysis and prediction system. Plant and Animal Environmental Analysis, 64-68.

Carpenter, G., Gillison, A. N., & Winter, J. (1993). DOMAIN: A flexible modelling procedure for mapping potential distributions of plants and animals. *Biodiversity & Conservation*, 2 (6), 667–680.

Castañeda-Álvarez, N. P., Khoury, C. K., Achicanoy, H. A., Bernau, V., Dempewolf, H., Eastwood, R. J., Guarino, L., Harker, R. H., Jarvis, A., Maxted, N., Müller, J. V., Ramirez-Villegas, J., Sosa, C. C., Struik, P. C., Vincent, H., & Toll, J. (2016). Global conservation priorities for crop wild relatives. *Nature Plants*, 2, 16022. https://doi.org/10.1038/nplants.2016.22

CBS. (2025). *Statistical abstract of Israel 2025*. Jerusalem: Central Bureau of Statistics.

Cockel, C. P., Guzzon, F., Gianella, M., & Müller, J. V. (2022). The importance of conserving crop wild relatives in preparing agriculture for climate change. *CABI Reviews*.

Dahan-Meir, T., Ellis, T. J., Mafessoni, F., Sela, H., Rudich, O., Manisterski, J., Avivi-Ragolsky, N., Raz, A., Feldman, M., Anikster, Y., & Nordborg, M. (2024). 36-year study reveals stability of a wild wheat population across microhabitats. *Molecular Ecology*, 33 (19), e17512.

Danin, A. (1988). Flora and vegetation of Israel and adjacent areas. In Y. Yom-Tov & E. Tchernov (Eds.), *The zoogeography of Israel* (pp. 129–159). Dordrecht: Dr. W. Junk Publishers.

Dempewolf, H., Baute, G., Anderson, J., Kilian, B., Smith, C., & Guarino, L. (2017). Past and future use of wild relatives in crop breeding. *Crop Science*, 57 (3), 1070–1082. https://doi.org/10.2135/cropsci2016.10.0885

Ervin, J., Mulongoy, K. J., Lawrence, K., Game, E., Sheppard, D., Bridgewater, P., Bennett, G., Gidda, S. B., & Bos, P. (2010). *Making protected areas relevant: A guide to integrating protected areas into wider landscapes, seascapes and sectoral plans and strategies* (CBD Technical Series No. 44). Montreal: Secretariat of the Convention on Biological Diversity.

FAO. (2010). *The second report on the state of the world's plant genetic resources for food and agriculture*. Rome: Food and Agriculture Organization of the United Nations.

Farber, O., & Kadmon, R. (2003). Assessment of alternative approaches for bioclimatic modeling with special emphasis on the Mahalanobis distance. *Ecological Modelling*, 160 (1–2), 115–130.

Fielder, H., Brotherton, P., Hosking, J., Hopkins, J. J., Ford-Lloyd, B. V., & Maxted, N. (2015). Enhancing the conservation of crop wild relatives in England. *PLoS ONE*, 10 (6), e0130804. https://doi.org/10.1371/journal.pone.0130804

Foyer, C. H., Lam, H. M., Nguyen, H. T., Siddique, K. H., Varshney, R. K., Colmer, T. D., Cowling, W., Bramley, H., Mori, T. A., Hodgson, J. M., & Cooper, J. W. (2016). Neglecting legumes has compromised human health and sustainable food production. *Nature Plants*, 2, 16112.

Hampe, A., & Petit, R. J. (2005). Conserving biodiversity under climate change: The rear edge matters. *Ecology Letters*, 8, 461–467.

Harlan, J. R., & de Wet, J. M. J. (1971). Toward a rational classification of cultivated plants. *Taxon*, 20 (4), 509–517. https://doi.org/10.2307/1218252

Heywood, V. H., Casas, A., Ford-Lloyd, B. V., Kell, S. P., & Maxted, N. (2007). Conservation and sustainable use of crop wild relatives. *Agriculture, Ecosystems & Environment*, 121 (3), 245–255. https://doi.org/10.1016/j.agee.2006.12.014

Holness, S., Hamer, M., Brehm, J. M., & Raimondo, D. (2019). Priority areas for the *in-situ* conservation of crop wild relatives in South Africa. *Plant Genetic Resources*, 17 (2), 115-127.

Hunter, D., Maxted, N., Heywood, V., Kell, S., & Borelli, T. (2012). Protected areas and the challenge of conserving crop wild relatives. *Parks*, 18 (1), 87–98.

IUCN-WCPA Task Force on OECMs. (2019). Recognising and reporting other effective area-based conservation measures. *IUCN Gland Switzerland*.

Jain, S. K. (1975). Genetic reserves. In O. H. Frankel & J. G. Hawkes (Eds.), *Crop genetic resources for today and tomorrow* (pp. 379–396). Cambridge: Cambridge University Press.

Jarvis, A., Lane, A., & Hijmans, R. J. (2008). The effect of climate change on crop wild relatives. *Agriculture, Ecosystems & Environment*, 126, 13–23.

Jarvis, S., Fielder, H., Brotherton, P., Hopkins, J. J., Maxted, N., & Smart, S. (2015). Distribution of crop wild relatives of conservation priority in the UK landscape. *Biological Conservation*, 191, 444–451. https://doi.org/10.1016/j.biocon.2015.07.039

Kawecki, T. J. (2008). Adaptation to marginal habitats. *Annual Review of Ecology, Evolution, and Systematics*, 39, 321–342.

Khoury, C. K., Brush, S., Costich, D. E., Curry, H. A., de Haan, S., Engels, J. M. M., Guarino, L., Hoban, S., Mercer, K. L., Miller, A. J., Nabhan, G. P., Perales, H. R., Richards, C., Riggins, C., & Thormann, I. (2022). Crop genetic erosion:

Understanding and responding to loss of crop diversity. *New Phytologist*, 233 (1), 84–118. https://doi.org/10.1111/nph.17733

Khoury, C. K., Greene, S., Wiersema, J., Maxted, N., Jarvis, A., & Struik, P. C. (2020). Crop wild relatives of the United States require urgent conservation action. *Proceedings of the National Academy of Sciences*, 117 (52), 33351–33357. https://doi.org/10.1073/pnas.2007029117

Lin, Y., Chen, Y., Wang, H., Hong, J., Yang, R., Cao, Y., Yan, S., & Fang, W (2024). Global potential distributions and conservation status of rice wild relatives. *Plants, People, Planet*.

Margules, C. R., & Pressey, R. L. (2000). Systematic conservation planning. *Nature*, 405, 243–253.

Maxted, N., Ford-Lloyd, B. V., & Hawkes, J. G. (1997). *Plant genetic conservation: The in situ approach*. London: Chapman & Hall.

Maxted, N., Ford-Lloyd, B. V., Jury, S. L., Kell, S. P., & Scholten, M. A. (2006). Towards a definition of a crop wild relative. *Biodiversity and Conservation*, 15 (8), 2673–2685. https://doi.org/10.1007/s10531-005-5409-6

Maxted, N., Scholten, M., Codd, R., & Ford-Lloyd, B. V. (2007). Creation and use of a national inventory of crop wild relatives. *Biological Conservation*, 140 (1–2), 142–159. https://doi.org/10.1016/j.biocon.2007.08.006

Maxted, N., & Kell, S. P. (2009). *Establishment of a global network for the in situ conservation of crop wild relatives: Status and needs*. Rome: Food and Agriculture Organisation of the United Nations (FAO).

Maxted, N., Kell, S., Ford-Lloyd, B., Dulloo, E., & Toledo, Á. (2012). Toward the systematic conservation of global crop wild relative diversity. *Crop Science*, 52 (2), 774–785. https://doi.org/10.2135/cropsci2011.08.0415

Maxted, N., & Magos Brehm, J. (2023). Maximizing the crop wild relative resources available to plant breeders for crop improvement. *Frontiers in Sustainable Food Systems*, 7, 1010204. https://doi.org/10.3389/fsufs.2023.1010204

Maxted, N., Magos Brehm, J., Abulaila, K., Al-Zein, M. S., Kehel, Z., & Yazbek, M. (2024). Review of crop wild relative conservation and use in West Asia and North Africa. *Plants*, 13 (10), 1343. https://doi.org/10.3390/plants13101343

Maxwell, S. L., Fuller, R. A., Brooks, T. M., & Watson, J. E. M. (2016). The ravages of guns, nets and bulldozers. *Nature*, 536, 145–146.

Mayzlish-Gati, E., Walczak, M., Singer, A., Faraj, T., Golan, S., Lifshitz, D., Bar, D., Ur, Y., Carmeli, D., & Lotan, R. (2018). Ex situ conservation strategies for endangered plants in the Israel Gene Bank. *Israel Journal of Plant Sciences*, 65, 121–128.

Nave, M., Avni, R., Çakır, E., Portnoy, V., Sela, H., Pourkheirandish, M., Ozkan, H., Hale, I., Komatsuda, T., & Dvorak, J. (2019). Wheat domestication in light of haplotype analyses of the Brittle rachis 1 genes (BTR1-A and BTR1-B). *Plant Science*, 285, 193–199.

Nevo, E., & Chen, G. (2010). Drought and salt tolerances in wild relatives for wheat and barley improvement. *Plant, Cell & Environment*, 33 (4), 670–685. https://doi.org/10.1111/j.1365-3040.2009.02107.x

Obiar, N., Eckert, I., Baker, J., Moerman, D., & Pollock, L. J. (2025). Bridging biodiversity and ecosystem services through useful plant species. *Plants, People, Planet*, 7 (5), 1498–1509.

Peleg, Z., Saranga, Y., Krugman, T., Abbo, S., Nevo, E., & Fahima, T. (2008). Allelic diversity associated with aridity gradient in wild emmer wheat populations. *Plant, Cell & Environment*, 31 (1), 39–49.

Perfecto, I., & Vandermeer, J. (2010). The agroecological matrix as alternative to the land-sparing/agriculture intensification model. *Proceedings of the National Academy of Sciences*, 107, 5786–5791.

Phillips, S. J., Anderson, R. P., & Schapire, R. E. (2006). Maximum entropy modelling of species geographic distributions. *Ecological Modelling*, 190 (3–4), 231–259.

Pimentel, D., Wilson, C., McCullum, C., Huang, R., Dwen, P., Flack, J., Tran, Q., Saltman, T., & Cliff, B. (1997). Economic and environmental benefits of biodiversity. *BioScience*, 47 (11), 747–757.

PwC. (2013). *Crop wild relatives: A valuable resource for crop development*. PricewaterhouseCoopers.

Ravikovitch, S. (1992). *The soils of Israel*. Tel Aviv: Hakibbutz Hameuchad.

Rehm, E. M., Olivas, P., Stroud, J., & Feeley, K. J. (2015). Losing your edge: Climate change and the conservation value of range-edge populations. *Ecology and Evolution*, 5 (19), 4315–4326. https://doi.org/10.1002/ece3.1645

Rotem-Mindali, O., Katzir, N., & Perez, O. (2024). Identifying regulatory barriers in the management of ecological corridors in an increasingly congested space. *Land*, 13 (10), 1552.

Schaffer, G., & Levin, N. (2014). Mapping human induced landscape changes in Israel between the end of the 19th century and the beginning of the 21th century. *Journal of Landscape Ecology*, 7 (1). https://doi.org/10.2478/jlecol-2014-0012

Shiferaw, B., Smale, M., Braun, H.-J., Duveiller, E., Reynolds, M., & Muricho, G. (2013). Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. *Food Security*, 5, 291–317.

Sivan, A., Rahimi, O., Lavi, B., Salmon-Divon, M., Weiss, E., Drori, E., & Hübner, S. (2021). Genomic evidence supports an independent history of Levantine and Eurasian grapevines. *Plants, People, Planet*, 3 (4), 414–427. https://doi.org/10.1002/ppp3.10197

Smýkal, P., Nelson, M. N., Berger, J. D., & von Wettberg, E. J. B. (2018). The impact of genetic changes during crop domestication. *Agronomy*, 8 (7), 119.

Tobón-Niedfeldt, W., Mastretta-Yanes, A., Urquiza-Haas, T., Goettsch, B., Cuervo-Robayo, A.P., Urquiza-Haas, E., ... & Koleff, P. (2022). Incorporating evolutionary and threat processes into crop wild relatives conservation. *Nature Communications*, 13 (1), 6254.

Toromade, A. S., Soyombo, D. A., Kupa, E., & Ijomah, T. I. (2024). Reviewing the impact of climate change on global food security: Challenges and solutions. *International Journal of Applied Research in Social Sciences*, 6 (7), 1403–1416.

Tyack, N., Dempewolf, H., & Khoury, C. K. (2020). The potential of payment for ecosystem services for crop wild relative conservation. *Plants*, 9 (10), 1305.

Van Deurs, S., Reutimann, O., Luqman, H., Lifshitz, D., Mayzlish-Gati, E., Alexander, J., & Fior, S. (2025). Genomic signatures of adaptation across a precipitation gradient from niche centre to niche edge. *Molecular Ecology*, 34 (6), e17696.

van de Wouw, M., Kik, C., van Hintum, T., van Treuren, R., & Visser, B. (2009). Genetic erosion in crops: Concept, research results and challenges. *Plant Genetic Resources: Characterization and Utilization*, 8 (1), 1–15.

Vincent, H., Amri, A., Castañeda-Álvarez, N. P., Dempewolf, H., Dulloo, E., Guarino, L., Hole, D., Mba, C., Toledo, A., & Maxted, N. (2019). Modeling of crop wild

relative species identifies areas globally for *in situ* conservation. *Communications Biology*, 2, 136. https://doi.org/10.1038/s42003-019-0372-z

Vincent, H., Hole, D., & Maxted, N. (2022). Congruence between global crop wild relative hotspots and biodiversity hotspots. *Biological Conservation*, 265, 109432. https://doi.org/10.1016/j.biocon.2021.109432

Vincent, H., Wiersema, J., Kell, S. P., Fielder, H., Dobbie, S., Castañeda-Álvarez, N. P., Guarino, L., Eastwood, R., León, B., & Maxted, N. (2013). A prioritized crop wild relative inventory to help underpin global food security. *Biological Conservation*, 167, 265–275. https://doi.org/10.1016/j.biocon.2013.08.011

Volis, S., Mendlinger, S., Turuspekov, Y., & Esnazarov, U. (2002). Phenotypic and allozyme variation in Mediterranean and desert populations of wild barley, *Hordeum spontaneum* Koch. *Evolution*, 56 (7), 1403–1415.

Wambugu, P. W., & Henry, R. (2022). Supporting *in situ* conservation of the genetic diversity of crop wild relatives using genomic technologies. *Molecular Ecology*, 31, 2207–2222. https://doi.org/10.1111/mec.16402

Wei, X., & Jiang, M. (2021). Meta-analysis of genetic representativeness of plant populations under *ex situ* conservation in contrast to wild source populations. *Conservation Biology*, 35 (1), 12–23.

Xiao, Z., Liu, H., Huang, G., Wu, D., Qiu, L., Wu, J., Wei, X. and Jiang, M. (2025). Spatially biased collections and the failure to cover all wild genetic clusters in plant populations under *ex situ* conservation. *Plant Diversity*.

Yali, W., & Mitiku, T. (2024). Gene pool, classification and its importance in modern crop improvement program. *International Journal of Agricultural Science and Food Technology*, 10 (2), 068–073.

Zeder, M. A. (2011). The origins of agriculture in the Near East. *Current Anthropology*, 52 (S4), S221–S235.

Zhang, H., Mittal, N., Leamy, L. J., Barazani, O., & Song, B. H. (2017). Back into the wild—Apply untapped genetic diversity of wild relatives for crop improvement. *Evolutionary Applications*, 10 (1), 5–24. https://doi.org/10.1111/eva.12434

Zohary, D., Hopf, M., & Weiss, E. (2012). *Domestication of plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin*. Oxford: Oxford University Press.

Zohary, M. (1973). *Geobotanical foundations of the Middle East*. Stuttgart: Gustav Fischer Verlag.

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