New Uses of Common Vetch for Sustainable Agriculture

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Common vetch (*Vicia sativa* L.) is a grain legume used in animal feed. It is rich in protein, fatty acid and minerals content, therefore is a very suitable component for feed enrichment. Furthermore, important pharmacological properties in humans have been described. Like other legumes, common vetch has the ability to fix atmospheric nitrogen, an important characteristic in sustainable agricultural systems. These characteristics enhance the usage of vetch as a cover crop and its use in intercropping systems. In addition, several studies have highlighted the potential of vetch in the phytoremediation of polluted soils. These features make common vetch an appropriate crop to address for various potential improvements. Comparative analyzes have allowed the identification of varieties with different flowering time, shattering resistance, yield, nutrient content and composition, drought response, rhizobacteria associations, nitrogen fixation capacity, and other agronomically relevant traits.

Vicia sativa   common vetch   breeding

1. Introduction

The common vetch (*Vicia sativa* L., Tribe *Viciae,* Family *Fabaceae*) is one of the world's most economically important annual grain legumes, used as animal feed, as forage (grain, hay, and for silage production) or as grain legume as a cheap and rich source of protein and minerals of high digestibility and high energy content [1][2]. Additionally, vetch fixes atmospheric nitrogen through its symbiotic interactions with rhizobia soil bacteria, which could improve the soil fertility significantly, making its cultivation appropriate in sustainable agriculture, as a main crop, as an element of rainfed rotation, as a cover crop, or in rotation with cereals [3] by decreasing the use of fertilizers and reducing CO_2 emissions and other pollutants [4]. The main bottleneck of this species is the presence of antinutritional factors in various parts of the plant, but the enormous dependence on proteins of vegetable origin for animal feed and the interest in the EU for the use of species of environmental value make the use of this crop a relevant agricultural option with an essential role in the implementation of environmental measures such as From Farm to Fork Strategy and the new Common Agricultural Policy (CAP) directive.

2. Taxonomy

The botanical tribe Viceae, from the subfamily *Papilioboideae*, of the family *Fabaceae,* includes some genus of agricultural interest such as *Lens*, *Cicer, Pisum, Lathyrus*, and *Vicia* [5]. The genus *Vicia*, whose center of origin and diversification has been placed in the Mediterranean and Irano-Turanian regions [6], includes a number of species ranged between 150 [7] and 210 [8], from which 34 are cultivated. The genus is, nowadays, distributed in temperate regions of the northern hemisphere in Asia, Europe, and North America, and also in the non-tropical region South America [9]. This genus has an enormous phenotypic variation [10]; in fact, there has been a big number of taxonomic revisions made over the genus, more than 20 since the original classification presented by Linneo (1735–1770) in the 18th century, following for those of Jaaska and other authors [9][11][12][13][14][15]. In a focus on *V. sativa* section *Vicia*, which includes the most important agricultural species, one of the last classifications was proposed by Van der Wouw et al. [16] after several studies focus on *Vicia L*. series *Vicia*, who presented a classification of this series in four species: *V. babazitae* Ten&Guss., *V. incisa* M.Bieb., *V. pyrenaica* Pourr., and *V. sativa*, which includes six subspecies: *nigra* (L.) Ehrh., *segetalis* (Thuill) Čelak., *amphicarpa* L.Batt, *macrocarpa* (Moris) Arcang., *cordata* (Wulfen ex Hoppe) Batt., and *sativa.* This group of forms is named the *V. sativa* aggregate.

Commercially vetch includes, in addition to *V. sativa, V. villosa* Roth. (winter vetch, hairy vetch) and other species of similar local importance such as *V. pannonica* L. in Turkey, *V. pannonica*, *V. ervilia* L. and *V. articulata* Hormen in Spain, and *V. benghalensis* L. in Australia; the same term, vetch, has been used for different species such as *Lathyrus sativus* L. and other *Lathyrus* species in Africa [17].

3. A Historical Crop

The common vetch, similar to other species of the *Fabaceae* family, has been cultivated together with cereals since the beginning of agriculture. Archaeological evidences indicate the Mediterranean Basis as the center of origin and primary diversification of this species [18][19].

Some authors indicate that the first archaeological references to vetch seeds date back to the Neolithic Periodic and the Bronze Age. This point is not clearly established because these seeds could also belong to wild species, associated with the crops. Additionally, others authors such as Zohary [20] disagree with this approach, dating the use of vetch into the agricultural systems in the Roman Empire, at a time when the use of vetch as a fodder species as already been reported, together with others species such as alfalfa and lupin or fenugreek, also associated with cereals and others grain legumes [21]. Columela, an ancient Roman scientist and writer who lived in the first century B.C. cited the use of vetch for poultry (hens and pigeons) feeding and as a fodder and green manure, together with other legumes such as alfalfa and fenugreek [22]. In the same time period, Plinius The Elder (First century B.C.) said that their use would improve soil fertility, giving indications about the sowing times in the function to the final use, including the use as fallow [23]. This author mentioned that vetch was the best feed for the bullocks. In the 4th century, Paladio described the use of a mixture of lupin and vetch as a soil improver when cutting in green, and they also made mention of the differences in the sowing date of the function of the final use. Isidore of Seville, who lived between the 6th–7th century, highlighted the scarce production of seed of vetch compared with other legumes [24]. In the Middle Age (11th and 12th century), vetch was a minority crop in Europe [25], even if the Andalusian author Abü l-Jayr indicated names such as *Umda* or *Amank* to identify different forms of vetches [26].

In the 16th century, Juan de Járava wrote that this species could be found among cereals and that it could be eaten as lentils, although it did not taste good [27]. In this century, vetch traveled to the New World, adapting perfectly to the local conditions of America, to the point that some escapees from cultivated vetches came to grow wild in the new environmental conditions [25]. Thus, in the 19th century, vetch was introduced to Argentina by Italian immigrants (settlers) establishing it as a well-known fodder [28]. To conclude this historical revision, a book from the 18th century used several names for cultivated and wild vetches and mentioned that they were a well-known crop in Europe, and that they could have reached Spain from the east by crossing France. Here, also, its uses as grain, green manure, and as a flour component to make bread in times of scarcity are mentioned [29].

4. Worldwide Vetch Cultivation

Due to its economic and ecological advantages, vetch is now widespread throughout many parts of the world. **Figure 1**A shows, based on data by FAOSTAT and the Spanish Ministry of Agriculture, Fisheries and Food [30], the surface and production of this crop from 1961 to 2021 are shown in **Figure 1**A. In the agricultural season of 2020–2021, the main producers were Ethiopia, the Russian Federation, Spain, Mexico, and Australia (**Figure 1**B,C).

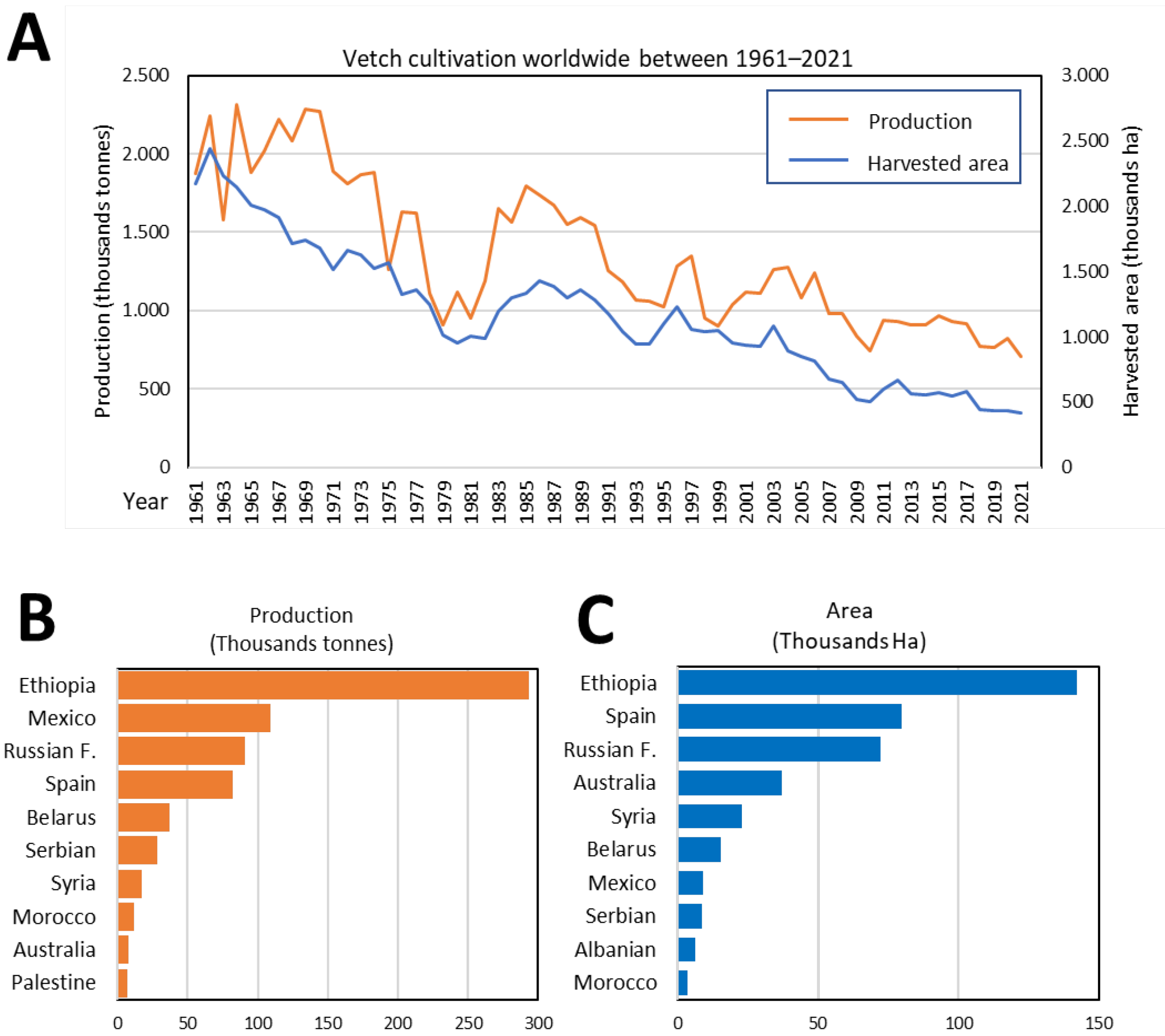

Figure 1. Worldwide *V. sativa* cultivation. (**A**) Production data and cultivated area of vetch worldwide during the last 60 years. Main producers according to cultivated area (**B**) or production (**C**) during the year 2021.

According to FAO data from FAOSTAT, the economic value of the agricultural gross production of vetches worldwide was USD 139,237,000. This value was clearly well below the economic value of other legumes, partly due to its low production. Comparing its production worldwide with that of other legumes (average of last 5 years, 2017–2021), vetch production was 8 times less than lentil production or 18 times less than the production of chickpeas [30][31]. One of the reasons for this reduced production was the presence of antinutritional factors (ANFs) present in the grains.

5. Nutritional and Pharmacological Properties

The nutritional value of the common vetch as a livestock feedstuff has been analyzed in different studies that have recently been reviewed [2][31]. The main conclusions of different works agree with the potential of common vetch grain, despite of the well-known deficit in sulfur amino acids (methionine and cysteine), as a rich source of proteins, minerals, and other nutrients, while being cheaper than other alternatives. The average crude protein values range from 21 to 39% (dry matter) and crude fat ranges from 9% to 38%, with high levels of palmitic and linoleic acids. The main essential and non-essential amino acids are leucine and glutamic acid, respectively. The seeds have high caloric content and are highly digestible [2]. These characteristics make vetch a potential nutrient-rich resource to be incorporated into animal diets and are very suitable to replace soy or a large proportion of cereals in certain feeds, maintaining their energy content. The nutritional content of the vetch seeds has been analyzed, and great differences in protein content, fatty acid composition, and mineral composition, including iron, were observed between accessions from different geographical origins. Although these studies have been carried out on a small scale, these data support the use of the variability of genetic resources from the gene banks of *V. sativa* for breeding purposes [32]. Remarkably, the large variation in crude protein and mineral content between different cultivars is much greater even than that due to climatic conditions [2][33][34]. This fact must be considered when selecting varieties with better nutritional conditions.

The medical uses of *V. sativa* have been also explored [35]. The seed flour and plant extract are traditionally used as an anti-poison and antiseptic [36][37], as an anti-asthmatic and respiratory stimulant in bronchitis [38], and as rheumatism treatment and an antipyretic [39]. Anti-acne [40] and antibacterial activity has been also validated [41]. However, most of the phytopharmacological mechanisms of action remain to be unraveled.

As described in other grain legumes, common vetch seeds contain a variety of antinutritional factors (ANFs), such as vicine, convicine, tannins, phenolic compounds, trypsin inhibitors, and cyano-alanines. Although some of these elements, such as polyphenols, have been studied as a source of antioxidants [42], these ANFs have partially limited the use of the seeds in food and/or feedstuffs, especially in the diets of monogastric animals [43]. However, the inclusion of a high proportion of common vetch seeds in the diet of ruminants does not produce relevant negative effects on their health [44][45][46][47][48][49]. The levels of anti-nutritional factors such as tannins, trypsin inhibitors, and hydrogen cyanide nutrients show huge variations between different accessions conserved in gene banks [32]. These variations have permitted the selection of low vicianine levels in common vetch accessions and have allowed the production of cultivars such as *Blanchefluer* without vicianine [50][51], extensively growing in Australia as a substitute for red lentils, although its consumption in humans is residual [17]. Last year, the molecular bases that regulate the hydrogen cyanide (HCN) synthesis from these cyanogenic glycosides have been unraveled in common vetch. Transcriptomic assays at different seed developmental stages enlighten important information about the regulatory network of this pathway. Eighteen key regulatory genes that are involved in HCN biosynthesis have been identified. These genes would be crucial as molecular markers for the selection and breeding of low HCN levelled vetch germplasm [52]. In any case, and especially for non-ruminant diets, it seems that these ANFs present in common vetch seeds need to be reduced or partially inactivated by adequate grain processing methods. A practical approach would be the selective breeding of varieties with a lower content of these antinutrients, but also the processing by soaking, chemical treatment, dehulling heat treatment, or germination. These treatments not only reduce the ANF content, but also improve the digestibility, palatability, and availability of the nutrients [34][53][54].

6. Environmental Benefits

The multiple benefits of common vetch for the farm as a versatile crop have been reviewed [2][31]. Plants need relatively large amounts of nitrogen for proper growth and development. The largest input of N into the terrestrial environment occurs through the process of biological nitrogen fixation (BNF). Therefore, BNF has great agricultural and ecological relevance, since N is often a limiting nutrient in many ecosystems [55]. The reduction of synthetic nitrogen fertilizers through the use of legumes not only has a decrease in environmental impact but also an economic one, due to the prices of these fertilizers, whose synthesis involves a large energy cost [56].

Rhizobia from legume-symbiotic systems make use of its nitrogenase enzyme to catalyze the conversion of atmospheric nitrogen (N_2) to ammonia (NH_3), which is a plant assimilable nitrogenous compound. This process utilizes energy produced by the legume photosynthesis and takes place in the symbiotic nodules of the legume roots. As other species of the *Vicia* genus, common vetch forms indeterminate-type root nodules through symbiosis with rhizobia to promote nitrogen fixation (**Figure 2**C). The interaction between the bacteria and host legume is so intricate that many rhizobial species nodulate in a host-specific manner despite the fact that the same symbiotic bacteria can infect different species, and even different genera, of legume. *Rhizobium leguminosarum* biovar *viciae* (Rlv) is the most common symbiont of *V. sativa* in which effective nitrogen fixation has been validated [55]. Furthermore, different strains of the *Mesorhizobium* and *Bradyrhizobium* genus have been isolated from *V. sativa* nodules, although there are no data about their ability to fix nitrogen [57]. Specific rhizobial nodule establishment in the plant host not only depends on the strain abundance in soil but also their nodulation competitiveness. *R. leguminosarum* biovar *viciae* establishes symbiosis with several legume genera, and genomics studies reveal plant preferences between specific rhizobial genotypes and the host *V. sativa* [58]. The complexity of these symbiotic associations and their specificity have been extensively addressed. These interactions present differences between *V. sativa* cultivars and wild relatives and are also affected by environmental conditions [57]. Moreover, the analysis of symbiotic genes of *R. leguminosarum* isolated from *V. sativa* from different geographical locations reveals a common phylogenetic origin, suggesting a close coevolution among symbiotic genes and legume host in this *Rhizobium*-*Vicia* symbiosis [59]. Symbiosis within *V. sativa* and *Rlv* has also been chosen as a model system to analyze different bacterial compounds, mainly oligosaccharides, and the plant-produced *nod* gene inducers (NodD protein activating compounds) involved in the establishment of the effective symbiosis with its host plant and the requirements for the host-plant specificity [60][61][62][63]. The bacterial nodulation genes (*nod*) are activated by flavonoids excreted by the common vetch roots [64], and, subsequently, the plant responds with the development of the root nodule [65]. Several physiological, biochemical, and transcriptomic analyses support an increase in drought tolerance in nodulated vetch plants compared to non-nodulated ones. Transcriptomic analysis has helped to discover specific drought pathways that are specifically activated in nodulated *V. sativa* plants, improving the understanding of the impact of the symbiosis-associated genetic pathways on the plant abiotic stress response [66].

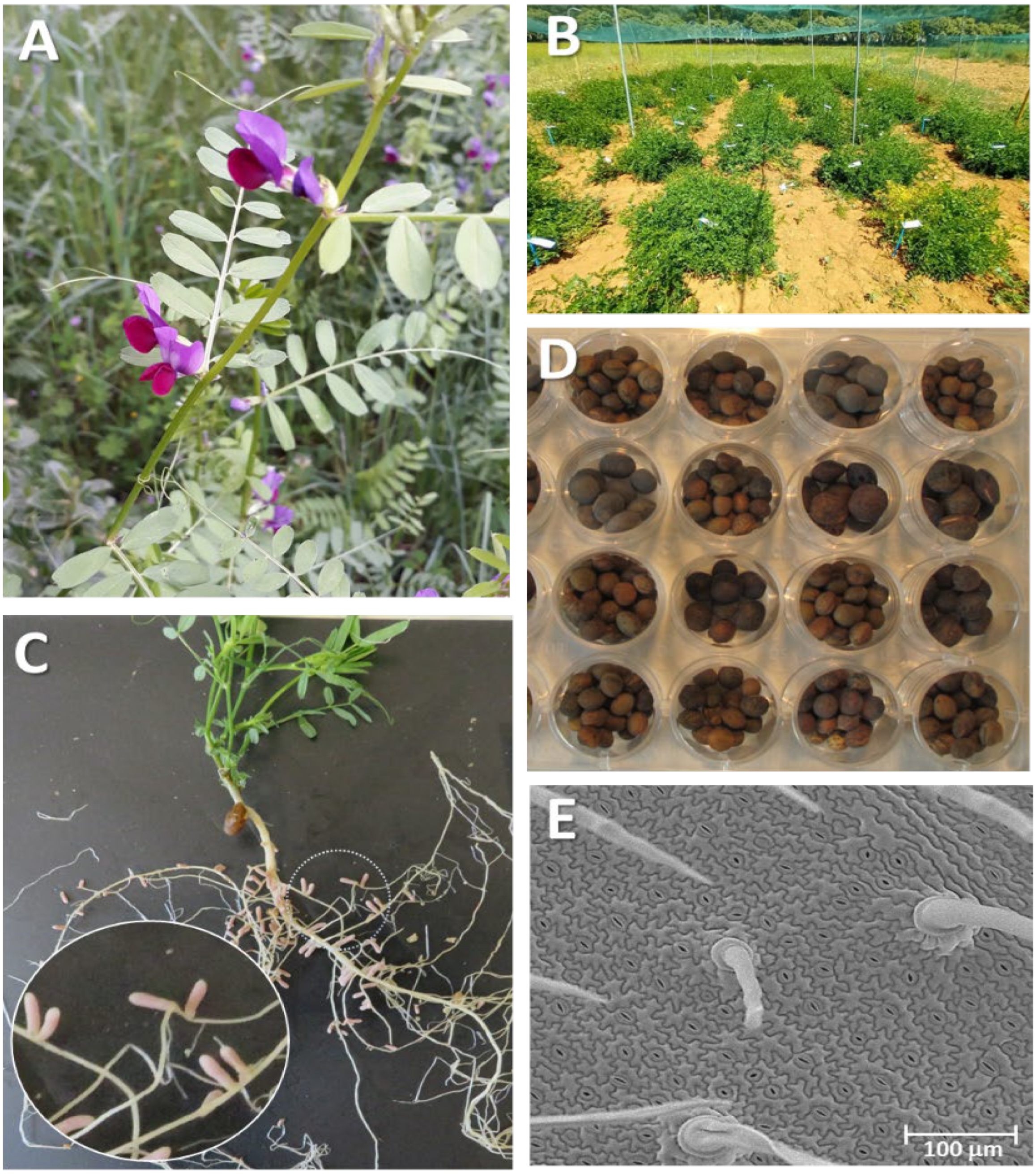

Figure 2. *V. sativa* plants showing different tissues and growing stages. (**A**) Wild-growing common vetch at "Sierra Norte"-Madrid (Spain). (**B**) Field evaluation assay of different accessions (CRF-INIA/CSIC gene bank). (**C**) Indeterminate *Rhizobium* nodules of a common vetch root. (**D**) Diversity of size, shape, and color observed in seeds from different accessions from a CRF core collection. (**E**) Abaxial leaf surface, showing trichomes, stomas, and epidermal cells.

Crop systems in which legumes intercropped with cereals have traditionally been used in preference to legume or cereal monocultures, as it will result in higher forage yields and minimize synthetic fertilizers due to the nitrogen fixation ability of the legumes. The intercropping system of spring wheat (*Triticum aestivum* L.) with common vetch had a significant advantage on grain yield, beneficial effects on root development on both crops, and less N and P fertilizer requirements [67]. The use of vetch in the rotation of maize (*Zea mays* L.) and wheat helped to reduce the N deficiency, the increase in N concentration in the soil during next growing season, and the reduction in N losses by leaching [68]. Systems of oats (*Avena sativa* L.) or ryegrass (*Lolium multiflorum* Lam.) intercropped with common vetch have also proven to be especially profitable on dairy farms in central Mexico for silage cow feeding [69]. Finger millet *(Eleusine coracana L.)* is a widely grown cereal crop in some arid and semiarid areas in Africa, such as Ethiopia. Field assays in which ringer millet was intercropped with three vetch species, including *V. sativa,* concluded a general improving of the total dry matter yield and the quality of the intercrops [70][71][72]. Although the most well-characterized intercropped systems are those of legume cereal, other systems have been documented as intercropping with rapeseed (*Brassica napus* L.), which require higher levels of N fertilizers [72]. Additionally, the use of *V. sativa* in kiwifruit orchards increases the microbial community, moisture, and nutrients in the soil, activating plant growth [73].

Cover crops play an essential role in agroecosystems. They are unharvested plants grown in the gap between crops or integrated into rotations, which improve soil health, reduce erosion, enhance water availability, promote nutrient capture, are useful for controlling pests, weeds, and other diseases, and promote additional benefits for agriculture [74][75][76]. The use of legumes such as *V. sativa* as a cover crop allows the fixation of atmospheric nitrogen in the rhizobia symbiosis nodules, then the plant residue decomposes and remains available in the soil for the next harvest, acting as green manure by reducing the amount of inorganic fertilizer and reducing CO_2 emissions [76][77]. It has recently been observed that *V. sativa* helps prevent water losses and soil erosion in vineyards (*Vitis vinifera* L.) [78]. In the USA, *V. sativa* is the most widely used legume cover crop [75]. In Argentina, *V. sativa* and *V. villosa* are the most important cultivated cover crop [79]. In Central Spain, the use of vetch as a cover crop in maize planted in the summer and autumn ensured the good production of principal crops and significant biomasses and N contents in the next following spring [80].

In recent years, environmental problems derived from soil and water contamination have begun to gain importance. In this context, the role that cover crops can have in phytoremediation is of great relevance [81]. *V. sativa*, together with *V. faba*, is the species of *Vicia* genus most frequently used in phytoremediation studies against inorganic and organic pollutants [82]. Different studies of phytoremediation, tolerance, and accumulation of inorganic and organic pollutants on *V. sativa* are summarized in **Table 1**. The relevance of *V. sativa* for the remediation of saline soils has recently been revealed. The phytodesalination process implies a high capacity of the plant to tolerate, absorb, and accumulate sodium in harvestable tissues [83]. Regarding the detoxification of organic compounds on *V. sativa*, the effect of the herbicide sulfosulfuron was evaluated without relevant effects on root or shoot growth parameters [84]. Similar studies assessed the effect of phenol and mepiquat chloride on seed yield and yield components in *V. sativa* plants, without drastic damages [85][86][87]. The growth, nodulation nitrogen fixation activity and *V. sativa* were less negatively affected by high concentrations of phenolics than in other tested legumes [88]. Wider studies on phytoremediation of diesel-fuel-contaminated soil were also developed in common vetch. The assays showed a greater tolerance of the vetch in diesel-contaminated soils and a greater capacity for decontamination of the soils compared to other crops [89]. Although *V. sativa* cannot be considered a hyperaccumulating plant capable of storing high concentrations of metals, copper tolerance has been described for germinative seeds [90][91]. Molecular mechanisms responsible for this tolerance remain to be explored, although it has been shown that vetch may prevent oxidative damage in the presence of some pollutants such as phenol by increasing the activity of lipid kinase and phosphatidic acid avoiding its toxicity [85][92]. *V. sativa* plants can also accumulate and concentrate different heavy metals. Curiously, these plants accumulate mercury (Hg) in the roots [93] but concentrate cadmium (Cd), lead (Pb), zinc (Zn), and nickel (Ni) in the aerial parts [94][95][96][97]. The tolerance of *V. sativa* to Cd seems to be related to antioxidant enzymes [98]. Phytochelatin synthases (PCS) and γ-Glutamylcysteine synthetase (γ-ECS) are directly involved in metal detoxification in plants. Ectopic overexpression of *V. sativa* PCS (*VsPCS1*) and γ-ECS (*Vsγ-ECS*) genes, which are Cd-inducible genes, are capable of increasing the tolerance to cadmium and the triggering of the detoxification pathway in Arabidopsis [99][100]. These results support the potential biotechnological use of these plants in phytoremediation processes against metal contamination.

Table 1. Summary of studies of phytoremediation, tolerance, and accumulation of inorganic and organic pollutants on *V. sativa*.

Pollutant	Developed Assay	References
Cd	Cd tolerance. Oxidative damage accumulation.	[95]
Cd and Zn	Zn and Cd accumulation in different tissues	[94]
Zn	Zn tolerance	[97]
Cu	Cu tolerance	[90][91]
Salt	Tolerance to salt. Na and K accumulation	[83]
Hg	Hg accumulation in different tissues	[93][99]
Ni	Ni accumulation. Oxidative damage accumulation.	[96]
Sulfosulfuron herbicide	Tolerance to sulfosulfuron	[84]
Diesel fuel	Tolerance to diesel	[89]
Phenol derivatives	Polychlorinated biphenyl (PCB) dissipation	[86]

Pollutant	Developed Assay	References
Phenolics	Tolerance to phenolics. Effects on biomass, nodulation and nitrogen fixation activity	[88]
Mepiquat	Tolerance to mepiquat	[87]

It has recently been shown that the rhizosphere microorganisms associated with the vetch roots can synergistically increase the decontamination potential by maximizing the efficiency of the process [101][102][103]. However, it is necessary to analyze the possible synergies or antagonisms derived from symbiosis to improve their efficiency in phytoremediation. On some occasions, bacterial strains tolerant to different pollutants do not show this activity when they are in symbiosis with *V. sativa* [82].

References

1. Parissi, Z.; Irakli, M.; Tigka, E.; Papastylianou, P.; Dordas, C.; Tani, E.; Abraham, E.M.; Theodoropoulos, A.; Kargiotidou, A.; Kougiteas, L.; et al. Analysis of Genotypic and Environmental Effects on Biomass Yield, Nutritional and Antinutritional Factors in Common Vetch. Agronomy 2022, 12, 1678.
2. Huang, Y.F.; Gao, X.L.; Nan, Z.B.; Zhang, Z.X. Potential value of the common vetch (Vicia sativa L.) as an animal feedstuff: A review. J. Anim. Physiol. Anim. Nutr. 2017, 101, 807–823.
3. Lithourgidis, A.; Dordas, C.; Damalas, C.A.; Vlachostergios, D.N. Annual intercrops: An alternative pathway for sustainable agriculture. Aust. J. Crop Sci. 2011, 5, 396–410.
4. Dalias, P.; Neocleous, D. Comparative Analysis of the Nitrogen Effect of Common Agricultural Practices and Rotation Systems in a Rainfed Mediterranean Environment. Plants 2017, 6, 61.
5. Maxted, N. An ecogeographical study of Vicia subgenus Vicia. In Systematic and Ecogeographic Studies on Crop Genepools; IPGRI: Rome, Italy, 1995; Volume 8, p. 184.
6. Maxted, N. A phenetic investigation of Vicia L. subgenus Vicia (Leguminosae, Vicieae). Bot. J. Linn. Soc. 1993, 111, 155–182.
7. Hanelt, P.; Mettin, D. Biosystematics of the Genus Vicia L. (Leguminosae). Annu. Rev. Ecol. Syst. 1989, 20, 199–223.
8. Kupicha, F.K. The infrageneric structure of Vicia. Notes R. Bot. Gard. Edinb. 1976, 34, 287–326.
9. Leht, M. Phylogenetics of Vicia (Fabaceae) based on morphological data. Feddes Repert. 2009, 120, 379–393.
10. Tate, M.; Ennerking, D. Vetches: From feed to food? Grain Legumes 2006, 47, 12–13.
11. Potokina, E. Vicia sativa L. aggregate (Fabaceae) in the flora of former USSR. Genet. Resour. Crop Evol. 1997, 44, 199–209.

12. Jaaska, V. Isoenzyme diversity and phylogenetic affinities in Vicia subgenus Vicia (Fabaceae). Genet. Resour. Crop Evol. 1997, 44, 557–574.

13. Jaaska, V. Isozyme Variation and Phylogenetic Relationships in Vicia subgenus Cracca (Fabaceae). Ann. Bot. 2005, 96, 1085–1096.

14. van de Wouw, M.; Maxted, N.; Chabane, K.; Ford-Lloyd, B.V. Molecular taxonomy of Vicia ser. Vicia based on Amplified Fragment Length Polymorphisms. Plant Syst. Evol. 2001, 229, 91–105.

15. Yeater, K.M.; Bollero, G.; Bullock, D.; Rayburn, A.L. Flow cytometric analysis for ploidy level differentiation of 45 hairy vetch accessions. Ann. Appl. Biol. 2004, 145, 123–127.

16. van de Wouw, M.; Maxted, N.I.; Ford-Lloyd, B.V. A multivariate and cladistic study of Vicia L. ser. Vicia (Fabaceae) based on analysis of morphological characters. Plant Syst. Evol. 2003, 237, 19–39.

17. Ennerking, D.; Tate, M. Global vetch production. Grain Legumes 2006, 47, 14–15.

18. Zohary, D.; Hopf, M. Domestication of Plants in the Old World: The Origin and Spread of Cultivated Plants in West Asia, Europe and the Nile Valley (No. Ed. 3); Oxford University Press: Oxford, UK, 2000.

19. Maxted, N.; Bennett, S. Plant Genetic Resources of Legumes in the Mediterranean; Springer Science & Business Media: Berlin/Heidelberg, Germany, 2001; Volume 39.

20. Zohary, D.; Hopf, M.; Weiss, E. Domestication of Plants in the Old World: The Origin and Spread of Domesticated Plants in Southwest Asia, Europe, and the Mediterranean Basin; Oxford University Press: Oxford, UK, 2012.

21. Varron, M. Rerum Rusticarum: Libri III; Cubero-Salmeron, J.I., Translator; Consejería de Agricultura y Pesca, Junta de Andalucía: Seville, Spain, 2010; 1st century BC.

22. Holgado-Redondo, A.; Columela, L.J.M. (1st Century)-Translation; “De re Rustica”: De los Trabajos de Campo; Holgado-Redondo, A., Translator; Ministerio de Agricultura: Madrid, Spain, 1988; 339p, ISBN 84-323-0622-3.

23. Hernandez, L.; Huerta, J. Secundus Plinius The Elder (1st Century) Historia Natural; UNAM-Universidad Nacional Autónoma de Mexico: Mexico City, Mexico, 1976; Hernandez, L. (books 1–25), Huerta, J. (books 26–37).

24. Oroz-Reta, J.; Marcos-Casquero., M.A. Isidore of Seville (6–7th Century)-Translation “Etymologiae” Etimologias; Oroz-Reta, J.; Marcos-Casquero, M.A., Translators; BAC: Madrid, Spain, 1982; Volume 15.

25. Cubero, J.I. Historia General de la Agricultura; Guadalmazán: Córdoba, Spain, 2018; ISBN 9788494155239. p. 840.

26. Carabaza-Bravo, J.M.; L-Jayr, A.; Al-Filāḥa, K. Tratado de Agricultura; (11st–12nd Century) Translation; Carabaza-Bravo, J.M., Ed.; Instituto de Cooperación con el Mundo Arabe: Madrid, Spain, 1991.
27. Jarava, J. “Historia de las Yerbas y Plantas” (from Dioscoride Anazarbeo); Gorda, L.G., Ed.; Heirs of A. Byrcman: Antwerp, Belgium, 1557.
28. Weber, L.H.; Schifino-Wittmann, M.T. The Vicia sativa L. aggregate (Fabaceae) in southern Brazil: Karyotypes, phenology and qualitative morphology. Genet. Resour. Crop Evol. 1999, 46, 207–211.
29. Gomez-Ortega, C. Continuacion de la Flora Española, ó Historia de las Plantas de España, Que Escribía Don Joseph Quer. Ibarra, J.: Madrid, Spain, 1784; Volume V–VI.
30. Faostat. 2023. Available online: https://www.fao.org (accessed on 15 February 2023).
31. Nguyen, V.; Riley, S.; Nagel, S.; Fisk, I.; Searle, I.R. Common Vetch: A Drought Tolerant, High Protein Neglected Leguminous Crop With Potential as a Sustainable Food Source. Front. Plant Sci. 2020, 11, 818.
32. Grela, E.R.; Samolinska, W.; Rybinski, W.; Kiczorowska, B.; Kowalczuk-Vasilev, E.; Matras, J.; Wesolowska, S. Nutritional and Anti-Nutritional Factors in Vicia sativa L. Seeds and the Variability of Phenotypic and Morphological Characteristics of Some Vetch Accessions Cultivated in European Countries. Animals 2021, 11, 44.
33. Larbi, A.; El-Moneim, A.M.A.; Nakkoul, H.; Jammal, B.; Hassan, S. Intra-species variations in yield and quality determinants in Vicia species: 3. Common vetch (Vicia sativa ssp. sativa L.). Anim. Feed Sci. Technol. 2011, 164, 241–251.
34. Huang, Y.F.; Matthew, C.; Li, F.; Nan, Z.B. Common vetch varietal differences in hay nutritive value, ruminal fermentation, nutrient digestibility and performance of fattening lambs. Animal 2021, 15, 100244.
35. Salehi, B.; Abu-Reidah, I.M.; Sharopov, F.; Karazhan, N.; Sharifi-Rad, J.; Akram, M.; Daniyal, M.; Khan, F.S.; Abbaass, W.; Zainab, R.; et al. Vicia plants—A comprehensive review on chemical composition and phytopharmacology. Phytother. Res. 2021, 35, 790–809.
36. Abbasi, A.M.; Shah, M.H.; Li, T.; Fu, X.; Guo, X.; Liu, R.H. Ethnomedicinal values, phenolic contents and antioxidant properties of wild culinary vegetables. J. Ethnopharmacol. 2015, 162, 333–345.
37. Shinwari, M.I.; Khan, M.A. Folk use of medicinal herbs of Margalla Hills National Park, Islamabad. J. Ethnopharmacol. 2000, 69, 45–56.
38. Prabhu, S.; Vijayakumar, S.; Yabesh, J.E.; Ravichandran, K.; Sakthivel, B. Documentation and quantitative analysis of the local knowledge on medicinal plants in Kalrayan hills of Villupuram

district, Tamil Nadu, India. J. Ethnopharmacol. 2014, 157, 7–20.

39. Marc, E.; Nellya, A.; Annick, D.D.; Frederic, D. Plants used as remedies antirheumatic and antineuralgic in the traditional medicine of Lebanon. J. Ethnopharmacol. 2008, 120, 315–334.
40. Nelson, K.; Lyles, J.T.; Li, T.; Saitta, A.; Addie-Noye, E.; Tyler, P.; Quave, C.L. Anti-Acne Activity of Italian Medicinal Plants Used for Skin Infection. Front. Pharmacol. 2016, 7, 425.
41. Saleem, M.; Karim, M.; Qadir, M.; Ahmed, B.; Rafiq, M.; Ahmad, B. In vitro antibacterial activity and phytochemical analysis of hexane extract of Vicia sativa. Bangladesh J. Pharmacol. 2014, 9, 189–193.
42. Megías, C.; Pastor-Cavada, E.; Torres-Fuentes, C.; Girón-Calle, J.; Barragán, M.A.; Juan, R.; Pastor, J.E.; Vioque, J. Chelating, antioxidant and antiproliferative activity of Vicia sativa polyphenol extracts. Eur. Food Res. Technol. 2009, 230, 353–359.
43. Ford, R. Vetch pod rupture associated with unrelated streak-inducing viruses of peas. Phytopathology 1965, 55, 935.
44. Mao, Z.; Fu, H.; Nan, Z.; Wan, C. Fatty acid, amino acid, and mineral composition of four common vetch seeds on Qinghai-Tibetan plateau. Food Chem. 2015, 171, 13–18.
45. Fırıncıoğlu, H.K.; Ünal, S.; Erbektaş, E.; Doğruyol, L. Relationships between seed yield and yield components in common vetch (Vicia sativa ssp. sativa) populations sown in spring and autumn in central Turkey. Field Crops Res. 2010, 116, 30–37.
46. Firincioğlu, H.K.; Tate, M.; Ünal, S.; Doğruyol, L.; Özcan, İ. A Selection Strategy for Low Toxin Vetches (Vicia sativa spp.). Turk. J. Agric. For. 2007, 31, 303–311.
47. Matić, R.; Nagel, S.; Robertson, S.; Young, I.; Mihailović, V.; Mikić, A.; Kirby, G. Vetch (Vicia spp) expansion and use in Australia. Biotechnol. Anim. Husb. 2005, 21, 203–207.
48. Daryanto, S.; Wang, L.; Jacinthe, P.A. Global Synthesis of Drought Effects on Food Legume Production. PLoS ONE 2015, 10, e0127401.
49. Koumas, A.; Economides, S. Replacement of Soybean Meal by Broad Bean or Common Vetch Seed in Lamb and Kid Fattening Diets. Tech. Bull. 1987, 88, 1–5.
50. Delaere, I. The Chemistry of Vivia sativa L. Selection; University of Adelaide, Department of Plant Science: Adelaide, Australia, 1996.
51. Rathjen, J.M. The Potential for Vicia sativa L. as a Grain Legume for South Australia/Thesis Jane Mary Rathjen. Ph.D. Thesis, The University of Adelaide, Adelaide, Australia, 1997.
52. Li, M.; Zhao, L.; Zhou, Q.; Fang, L.; Luo, D.; Liu, W.; Searle, I.R.; Liu, Z. Transcriptome and Coexpression Network Analyses Provide In-Sights into the Molecular Mechanisms of Hydrogen

Cyanide Synthesis during Seed Development in Common Vetch (Vicia sativa L.). Int. J. Mol. Sci. 2022, 23, 2275.

53. Akande, K.E.; Fabiyi, E.F. Effect of Processing Methods on Some Antinutritional Factors in Legume Seeds for Poultry Feeding. Int. J. Poult. Sci. 2010, 9, 996–1001.
54. Lambein, F.; Kuo, Y.H.; Ikegami, F.; Kusama-Eguchi, K.; Enneking, D. Grain legumes and human health. In Food Legumes for Nutritional Security and Sustainable Agriculture, Proceedings of the 4th International Food Legumes Research Conference, New Delhi, India, 18–22 October 2005; Indian Society of Genetics and Plant Breeding: New Delhi, India, 2009; pp. 422–432.
55. Ampomah, O.; Huss-Danell, K. Genetic diversity of rhizobia nodulating native Vicia spp. in Sweden. Syst. Appl. Microbiol. 2016, 39, 203–210.
56. Daramola, D.A.; Hatzell, M.C. Energy Demand of Nitrogen and Phosphorus Based Fertilizers and Approaches to Circularity. ACS Energy Lett. 2003, 8, 1493–1501.
57. Lei, X.; Wang, E.T.; Chen, W.F.; Sui, X.H.; Chen, W.X. Diverse bacteria isolated from root nodules of wild Vicia species grown in temperate region of China. Arch. Microbiol. 2008, 190, 657–671.
58. Jorrin, B.; Imperial, J. Population Genomics Analysis of Legume Host Preference for Specific Rhizobial Genotypes in the Rhizobium leguminosarum bv. Viciae Symbioses. Mol. Plant Microbe Interact. 2015, 28, 310–318.
59. Alvarez-Martinez, E.R.; Valverde, A.; Ramirez-Bahena, M.H.; Garcia-Fraile, P.; Tejedor, C.; Mateos, P.F.; Santillana, N.; Zuniga, D.; Peix, A.; Velazquez, E. The analysis of core and symbiotic genes of rhizobia nodulating Vicia from different continents reveals their common phylogenetic origin and suggests the distribution of Rhizobium leguminosarum strains together with Vicia seeds. Arch. Microbiol. 2009, 191, 659–668.
60. Laus, M.C.; van Brussel, A.A.; Kijne, J.W. Exopolysaccharide structure is not a determinant of host-plant specificity in nodulation of Vicia sativa roots. Mol. Plant Microbe Interact. 2005, 18, 1123–1129.
61. Laus, M.C.; van Brussel, A.A.; Kijne, J.W. Role of cellulose fibrils and exopolysaccharides of Rhizobium leguminosarum in attachment to and infection of Vicia sativa root hairs. Mol. Plant Microbe Interact. 2005, 18, 533–538.
62. Muszynski, A.; Laus, M.; Kijne, J.W.; Carlson, R.W. Structures of the lipopolysaccharides from Rhizobium leguminosarum RBL5523 and its UDP-glucose dehydrogenase mutant (exo5). Glycobiology 2011, 21, 55–68.
63. Tak, T.; van Spronsen, P.C.; Kijne, J.W.; van Brussel, A.A.; Boot, K.J. Accumulation of lipochitin oligosaccharides and NodD-activating compounds in an efficient plant--Rhizobium nodulation assay. Mol. Plant Microbe Interact. 2004, 17, 816–823.

64. Recourt, K.; Schripsema, J.; Kijne, J.W.; van Brussel, A.A.; Lugtenberg, B.J. Inoculation of Vicia sativa subsp. nigra roots with Rhizobium leguminosarum biovar Viciae results in release of nod gene activating flavanones and chalcones. Plant Mol. Biol. 1991, 16, 841–852.
65. Göttfert, M. Regulation and function of rhizobial nodulation genes. FEMS Microbiol. Rev. 1993, 10, 39–63.
66. Álvarez-Aragón, R.; Manuel Palacios, J.M.; Ramirez-Parra, E. Rhizobial symbiosis promotes drought tolerance in Vicia sativa and Pisum sativum. Environ. Exp. Bot. 2023, 208, 105268.
67. Zhang, E.; Li, L.; Huang, G.; Huang, P.; Chai, Q. Regulation of fertilizer application on yield and root growth of spring wheat-faba bean intercropping system. Ying Yong Sheng Tai Xue Bao J. Appl. Ecol. 2002, 13, 939–942.
68. Allende-Montalbán, R.; Martín-Lammerding, D.; del Mar Delgado, M.; Porcel, M.A.; Gabriel, J.L. Nitrate Leaching in Maize (Zea mays L.) and Wheat (Triticum aestivum L.) Irrigated Cropping Systems under Nitrification Inhibitor and/or Intercropping Effects. Agriculture 2022, 12, 478.
69. Garduno-Castro, Y.; Espinoza-Ortega, A.; Gonzalez-Esquivel, C.E.; Mateo-Salazar, B.; Arriaga-Jordan, C.M. Intercropped oats (Avena sativa)—common vetch (Vicia sativa) silage in the dry season for small-scale dairy systems in the highlands of central Mexico. Trop. Anim. Health Prod. 2009, 41, 827–834.
70. Keba, W.; Tolemariam, T.; Mohammed, A. Straw dry matter yield and quality of finger millet intercropped with selected vetch species at different seeding ratios in western Oromia, Ethiopia. Heliyon 2022, 8, e10433.
71. Hontoria, C.; Garcia-Gonzalez, I.; Quemada, M.; Roldan, A.; Alguacil, M.M. The cover crop determines the AMF community composition in soil and in roots of maize after a ten-year continuous crop rotation. Sci. Total Environ. 2019, 660, 913–922.
72. Genard, T.; Etienne, P.; Laine, P.; Yvin, J.C.; Diquelou, S. Nitrogen transfer from Lupinus albus L., Trifolium incarnatum L. and Vicia sativa L. contribute differently to rapeseed (Brassica napus L.) nitrogen nutrition. Heliyon 2016, 2, e00150.
73. Wang, Q.; Zhang, C.; Li, J.; Wu, X.; Long, Y.; Su, Y. Intercropping Vicia sativa L. Improves the Moisture, Microbial Community, Enzyme Activity and Nutrient in Rhizosphere Soils of Young Kiwifruit Plants and Enhances Plant Growth. Horticulturae 2021, 7, 335.
74. Ogilvie, C.M.; Ashiq, W.; Vasava, H.B.; Biswas, A. Quantifying Root-Soil Interactions in Cover Crop Systems: A Review. Agriculture 2021, 11, 218.
75. Baldwin, K.; Creamer, N. Cover Crops for Organic Farms; Center for Enviromental Farming Systems, NCSU-NCA&TSU-NCDA&CS; North Carolina Cooperative Extension Service: Raleigh, NC, USA, 2006; pp. 1–22.

76. Trenton, R.; Carrie, O.; Kelsey, H.; Hannah, W.; Tyler, D. Understanding cover crops. Agric. Nat. Resour. 2018, FS2156, 1–8.
77. Wiesmeier, M.; Lungu, M.; Hübner, R.; Cerbari, V. Remediation of degraded arable steppe soils in Moldova using vetch as green manure. Solid Earth 2015, 6, 609–620.
78. Rodrigo-Comino, J.; Terol, E.; Mora, G.; Giménez-Morera, A.; Cerdà, A. Vicia sativa Roth. Can Reduce Soil and Water Losses in Recently Planted Vineyards (Vitis vinifera L.). Earth Syst. Environ. 2020, 4, 827–842.
79. Renzi, J. Efecto de la estructura de cultivo y grado de madurez a cosecha sobre el rendimiento y la calidad de semillas de Vicia sativa L. y Vicia. villosa Roth., bajo riego. MSc. Thesis, Universidad nacional del Sur, Bahia Blanca, Argentina, 2009.
80. Alonso-Ayuso, M.; Gabriel, J.L.; Pancorbo, J.L.; Quemada, M. Interseeding cover crops into maize: Characterization of species performance under Mediterranean conditions. Field Crops Res. 2020, 249, 107762.
81. Ali, H.; Khan, E.; Sajad, M.A. Phytoremediation of heavy metals-Concepts and applications. Chemosphere 2013, 91, 869–881.
82. Ibañez, S.; Medina, M.I.; Agostini, E. Vicia: A green bridge to clean up polluted environments. Appl. Microbiol. Biotechnol. 2020, 104, 13–21.
83. Lastiri-Hernández, M.A.; Alvarez-Bernal, D.; Bermúdez-Torres, K.; Cárdenas, G.C.; Ceja-Torres, L.F. Phytodesalination of a moderately saline soil combined with two inorganic amendments. Bragantia 2019, 78, 579–586.
84. Alonso-Prados, J.L.; Hernández-Sevillano, E.; Llanos, S.; Villarroya, M.; García-Baudín, J.M. Effects of sulfosulfuron soil residues on barley (Hordeum vulgare), sunflower (Helianthus annuus) and common vetch (Vicia sativa). Crop Prot. 2002, 21, 1061–1066.
85. Ibanez, S.G.; Sosa Alderete, L.G.; Medina, M.I.; Agostini, E. Phytoremediation of phenol using Vicia sativa L. plants and its antioxidative response. Environ. Sci. Pollut. Res. 2012, 19, 1555–1562.
86. Halfadji, A.; Portet-Koltalo, F.; Touabet, A.; Le Derf, F.; Morin, C.; Merlet-Machour, N. Phytoremediation of PCB: Contaminated Algerian soils using native agronomics plants. Environ. Geochem. Health 2022, 44, 117–132.
87. Tan, M.; Temel, S. Effect of mepiquat chloride, a growth retardant, on seed yield and yield components in common vetch (Vicia sativa). Indian J. Agric. Sci. 2005, 75, 160–161.
88. Machrafi, Y.; Prévost, D.; Beauchamp, C.J. Toxicity of phenolic compounds extracted from bark residues of different ages. J. Chem. Ecol. 2006, 32, 2595–2615.

89. Adam, G.; Duncan, H. The effect of diesel fuel on common vetch (Vicia sativa L.) plants. Environ. Geochem. Health 2003, 25, 123–130.
90. Muccifora, S.; Bellani, L.M. Effects of copper on germination and reserve mobilization in Vicia sativa L. seeds. Environ. Pollut. 2013, 179, 68–74.
91. Bellani, L.M.; Muccifora, S.; Giorgetti, L. Response to copper bromide exposure in Vicia sativa L. seeds: Analysis of genotoxicity, nucleolar activity and mineral profile. Ecotoxicol. Environ. Saf. 2014, 107, 245–250.
92. Ibañez, S.G.; Villasuso, A.L.; Racagni, G.E.; Agostini, E.; Medina, M.I. Phenol modulates lipid kinase activities in Vicia sativa plants. Environ. Exp. Bot. 2016, 122, 109–114.
93. Sierra, M.J.; Millán, R.; Esteban, E.; Cardona, A.I.; Schmid, T. Evaluation of mercury uptake and distribution in Vicia sativa L. applying two different study scales: Greenhouse conditions and lysimeter experiments. J. Geochem. Explor. 2008, 96, 203–209.
94. Bogatu, C.; Masu, S.; Lazarovici, M. Metals extraction from polluted soils by using of pillared zeolite and Vicia sativa. In Proceedings of the 14th Symposium on Analytical and Environmental Problems, Szeged, Hungary, 24 September 2007.
95. Rui, H.; Zhang, X.; Shinwari, K.I.; Zheng, L.; Shen, Z. Comparative transcriptomic analysis of two Vicia sativa L. varieties with contrasting responses to cadmium stress reveals the important role of metal transporters in cadmium tolerance. Plant Soil 2018, 423, 241–255.
96. Ivanishchev, V.V.; Abramova, E.A. Accumulation of nickel ions in seedlings of Vicia sativa L. and manifestations of oxidative stress. Environ. Sci. Pollut. Res. 2015, 22, 7897–7905.
97. Masu, S.; Lixandru, B.; Bogatu, C. Zinc extraction from polluted soils by using zeolite and Vicia sativa plant. In Proceedings of the 3rd International Conference on Life Cycle Management, Zurich, Switzerland, 27–29 August 2007.
98. Zhang, F.; Zhang, H.; Wang, G.; Xu, L.; Shen, Z. Cadmium-induced accumulation of hydrogen peroxide in the leaf apoplast of Phaseolus aureus and Vicia sativa and the roles of different antioxidant enzymes. J. Hazard. Mater. 2009, 168, 76–84.
99. Zhang, X.; Zhang, L.; Chen, L.; Lu, Y.; An, Y. Ectopic expression gamma-glutamylcysteine synthetase of Vicia sativa increased cadmium tolerance in Arabidopsis. Gene 2022, 823, 146358.
100. Zhang, X.; Rui, H.; Zhang, F.; Hu, Z.; Xia, Y.; Shen, Z. Overexpression of a Functional Vicia sativa PCS1 Homolog Increases Cadmium Tolerance and Phytochelatins Synthesis in Arabidopsis. Front. Plant Sci. 2018, 9, 107.
101. Ibañez, S.G.; Merini, L.J.; Barros, G.G.; Medina, M.I.; Agostini, E. Vicia sativa-Rhizospheric bacteria interactions to improve phenol remediation. Int. J. Environ. Sci. Technol. 2014, 11, 1679–1690.

102. Anderson, T.A.; Guthrie, E.A.; Walton, B.T. Bioremediation in the rhizosphere. Environ. Sci. Technol. 1993, 27, 2630–2636.

103. Ibañéz, S.G.; Oller, A.L.W.; Paisio, C.E.; Alderete, L.G.S.; González, P.S.; Medina, M.I.; Agostini, E. The challenges of remediating metals using phytotechnologies. In Heavy Metals in the Environment: Microorganisms and Bioremediation; CRC Press: Boca Raton, FL, USA, 2018; pp. 173–191.