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Review Article

Developing Countries' Challenges in Cultivating Salt-Tolerant Fodder Peas for Animal Feed

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ABSTRACT

As a result of the rapid increase in the world population, the problem of balanced and adequate nutrition has emerged, and the importance of animal production has increased even more. In this respect, to ensure sufficient and balanced nutrition of existing animals, there is a need to increase the cultivation areas of fodder crops and proper management of pastures and breeding studies. For this reason, fodder pea (*Pisum sativum* L.), which has high nutritional value and is preferred for animal consumption, is a vital fodder plant to meet this need. Fodder peas are suitable for consumption as animal feed because they contain high levels of carbohydrates and digestible substances. However, salinity, one of the abiotic stress factors, is an essential problem for fodder peas. Salinity significantly limits the development of the plant and leads to yield losses. Although the consequences of climate change vary in many parts of the world, it is predicted that the frequency and severity of conditions such as decreased precipitation, increased temperatures, floods, droughts, and increased saline areas will increase with climate change in developing countries. In addition, salt stress also affects the photosynthetic mechanism in plants and causes changes in chlorophyll, carotenoid, phenolic, and antioxidant concentrations. Since the reclamation of saline farmland is expensive and complex, it is more appropriate to grow salinity-resistant plants. Therefore, gene studies to improve the salinity tolerance of plants have gained momentum in recent years. In this review, studies conducted in the last 20 years are discussed. Salt tolerance in gene-transferred and non-transferred peas, as well as plant growth in a saline environment, were assessed by comparing proline, chlorophyll, total phenolic, and antioxidant levels. In summary, this study seeks to highlight the issues of drought, aridity, and salinity, all of which are expected to worsen as climate change progresses.

Keywords: *Abiotic stress, Secondary metabolite, Salinity, Fodder pea*

Gelişmekte Olan Ülkelerin Hayvan Beslenmesinde Tuza Toleranslı Yem Bezelyesi Yetiştirmede Karşılaştıkları Zorluklar

ÖZ

Dünya nüfusunun hızla artması sonucu dengeli ve yeterli beslenme sorunu ortaya çıkmış ve bu noktada hayvansal üretimin önemi daha da artmıştır. Bu açıdan mevcut hayvanların yeterli ve dengeli beslenmeleri için meraların doğru yönetimi ve ıslah çalışmalarının yanında yem bitkileri ekim alanlarının artırılmasına da ihtiyaç vardır. Bu nedenle beslenme değeri yüksek ve hayvanlar tarafından tüketimi tercih edilen yem bezelyesi (*Pisum sativum* L.) bu ihtiyacı gidermek için önemli bir yem bitkisidir. Yem bezelyesi, yüksek düzeyde karbonhidrat ve sindirilebilir

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maddeler içermesi nedeniyle hayvan yemi olarak tüketime uygundur. Fakat yem bezelyesi için abiyotik stres faktörlerinden tuzluluk, önemli bir problemdir. Tuzluluk, bitkinin gelişimini önemli ölçüde sınırlamakta ve verim kayıplarına yol açmaktadır. İklim değişikliğinin ortaya çıkaracağı sonuçlar dünyanın birçok yerinde farklılık göstermekle birlikte, gelişmekte olan ülkelerde de, iklim değişikliği ile birlikte, yağışların azalacağı, sıcaklıkların artacağı, sel, kuraklık, tuzlu alanların artışı gibi durumların sıklığının ve şiddetinin artacağı tahmin edilmektedir. Ayrıca tuz stresi bitkilerde fotosentetik mekanizmayı da etkileyerek klorofil, karotenoid, fenolik ve antioksidan konsantrasyonunda da değişikliğe sebep olmaktadır. Tuzlu tarım arazilerinin ıslahı pahalı ve zor olduğu için tuzluluğa dayanıklı bitkilerin yetiştirilmesi daha uygundur. Bu nedenle, son yıllarda bitkilerin tuzluluk toleranslarını geliştirmeye yönelik gen çalışmaları hız kazanmıştır. Bu derlemede, son 20 yıldır yapılan çalışmalar ele alınmıştır. Gen aktarılmış bezelyeler ve aktarılmamış bezelyelerin tuz toleransı, bitkilerin tuzlu ortamda gelişimleri prolin, klorofil, toplam fenolik ve antioksidan madde içeriği kıyaslanarak değerlendirilmiştir. Özet olarak, özellikle iklim değişikliği ile birlikte artacağı öngörülen kuraklık, çoraklık ve tuzluluk problemlerini ortaya koyulması amaçlanmaktadır. Böylece, yem bezelyesinin yetiştirilme alanlarının artırılması ve kaba yem ihtiyacı giderilmesi ve marjinal alanların üretimine kazandırılması konusuna ışık tutacaktır.

Anahtar Kelimeler: *Abiyotik stres, Sekonder metabolit, Tuzluluk, Yem bezelyesi*

I. INTRODUCTION

As a result of the rapid increase in the world population, the problem of balanced and adequate nutrition has emerged, which has further increased the importance of agricultural land and animal production. The development of people's eating habits and the continuous progress in the direction of health and safety have led to an increase in the global demand for food products of animal origin, including meat, eggs and milk [1]. These demands and challenges have further increased the importance of the forage crops market for farmers, especially to produce better quality animal products and improve animal productivity [2]. In addition, the importance of food safety has increased as a result of the "Mad Cow Disease" in Europe in 1989, the "Salmonella" cases in the USA in 1993 and 2008, and the "Tainted Milk Powder" incident in China in 2008. These events have also increased awareness of animal production. [1]. Forage crop agriculture is the most important way of producing continuous and safe forage. Quality roughage has a special place in ruminant nutrition. In animal nutrition, quality roughages should be a must for being an economic source, rich in protein, cellulose, fat, vitamins and minerals, increasing meat and milk yield, preventing metabolic diseases related to feeding and obtaining high quality animal products [3], [4]. Livestock breeding is also very important for the development of developing countries, increasing export potential, supplying raw materials to industry, preventing unemployment in rural areas and providing new employment [5], [6], [7], [8]. In addition, it is the best insurance against drought, famine and other natural disasters [5].

In countries with developed livestock breeding, the proportion of forage crops cultivated constitutes 25% of the total agricultural land in the UK, 30% in Italy, 31% in the Netherlands, 36% in Germany, 71% in Brazil and 13% in Turkey [9], [10], [11]. According to FAO and national statistical sources, there are approximately 137 million hectares of forage crop cultivated area in Latin America and the Caribbean region, followed by 12 million hectares in South and Southeast Asia, 6.5 million hectares in Central-West Asia and North Africa, and 14.6 hectares in Turkey [10], [12], [13].

Among fodder crops, fodder pea *Pisum sativum* L. is a legume rich in protein, vitamins, minerals and bioactive compounds used for both human and animal nutrition [14], [15]. The country with the highest production in the world is Canada, followed by China, Russia and India [15].

When the growing conditions of forage crops are evaluated, biotic and abiotic stress factors significantly limit plant growth and cause great yield losses in agriculture [16], [17]. Especially abiotic stress factors prevent the survival of plants. Due to global climate change, the majority of agricultural land is exposed to stress conditions and abiotic stress reduces agricultural yields by up to 60% [18], [19], [20]. Among abiotic stressors, salinity is the primary factor that will directly affect crop yields today and in the future [16], [21], [22], [23]. Today, more than 6% of the world's land area and 20% of the world's irrigated land is affected by salinity. Even in well-watered soils, salinity causes water deficit by reducing the osmotic potential of solutes in the soil, thus making it difficult for roots to draw water from the surrounding environment (soil solution) [24], [25]. According to the Food and Agriculture Organization of the United Nations (FAO, 2018), the area of saline soils in the world continues to increase steadily, suggesting that 50% will face salinity problems by 2050 [14], [21], [26].

The objective of this paper is to review and evaluate the current evidence on the extent of forage crops and forage peas cultivated in the world and the abiotic stressors of salt stress. This study is organized in 2 parts; (i) to determine the current area and production characteristics of forage crops cultivated in the world and (ii) to determine the extent of *Pisum sativum* L., a globally important forage crop, and to review the available evidence on salt stress in forage crops, especially forage peas. Our geographical focus covers all of Latin America and the Caribbean except the southern cone countries of South America (Argentina, Chile, Paraguay and Uruguay), developing countries in Asia except China, Mongolia and North Korea, Africa and Turkey.

II. FEED PLANTS

Livestock production is socioeconomically very important for developing countries and the continuous increase in per capita income leads to an increase in the demand for livestock products [27]. At this point, since feed production is of primary importance for livestock/poultry productivity, it is very important to examine agricultural production for developing countries [28]. At this point, when forage crop cultivation is evaluated, forage crops in developing countries include many species. These include tropical grasses such as *Brachiaria spp.* and *Panicum maximum* as well as legumes such as *Stylosanthes spp*., *Leucaena leucocephala* and *Vigna unguiculata*. *Brachiaria spp.* of African origin is the most widely cultivated forage species and accounts for a significant proportion of the area in Latin America. *Trifolium alexandrinum* is the dominant species in Egypt and *Medicago sativa* is widely used in North Africa. Today, more than 600 grass species are used for grazing and animal feeding [10].

In Brazil, 80 percent of cultivated pastures (80 million hectares) are covered by *Brachiaria spp.* and it is estimated that *B. brizantha cv. marandu* alone covers 40 million hectares. *Brachiaria spp.* are native to East and Central Africa, where they are an important component of the pioneer species of open grasslands (*B. decumbens*), humid savannas (*B. humidicola*), stream banks (*B. mutica*) and cleared rainforests (*B. ruziziensis*) [29], [30].

African grasslands represent the most important source of genetic material for grasses such as *Brachiaria*, *Pennisetum* and *Panicum*, while Latin America represents the most important source of genetic material for forage legumes and shrubs such as *Stylosanthes spp., Arachis pintoi, Leucaena leucocephala, Gliricidia sepium* and *Cratylia argentea* [30].

Annual clovers (*Medicago spp.*) and subterranean clover (*Trifolium subterraneum*) from the Mediterranean basin are common in Mediterranean-type climate zones such as South Africa. Several tropical pasture grasses grown on a fairly large scale are propagated vegetatively, usually in areas with reliable rainfall. These are usually stoloniferous and the most important are Giant Star Grass *Cynodon aethiopicus*, *Cynodon nlemfuensis*, Pangola Grass *Digitaria eriantha subsp. pentzii*, formerly *D. decumbens* and *Pará Grass Brachiaria mutica*. These African grasses have been widely used in Latin America for many years [30], [31].

Forage cereals include oats (*Avena sativa* and *A. strigosa*), maize (*Zea mays*), sorghum (*Sorghum bicolor*), pearl millet (*Pennisetum americanum*), barley (*Hordeum sativum*), rye (*Secale cereale*), proso millet (*Panicum miliaceum*) and finger millet (*Eleusine coracana*). *Saccharum officinarum* is also used as feed. Federizzi and Mundstock (2004) reported that in 2003, more than two million hectares of fodder oats were grown in Argentina and Uruguay and more than three million hectares in Brazil [30].

Table 1. *Fodder crop varieties and cultivation areas in developing countries according to the International Agricultural Research Advisory Group [3], [10].*

Country or region	Feed types	Cultivation areas between 2010-2015 (hectares)
Brazil	*Brachiaria spp.*	5.000
Andean Countries	*Brachiaria spp.*	3.357
Central America	*Brachiaria spp.*	1.560
India	*Stylosanthes*	250
Thailand	*Stylosanthes*	300
West Africa	*Stylosanthes*	36
West Africa	*Vigna ungiculata*	1.615
East Africa	*Calliandra spp.*	186
Turkey	*Pisum sativum spp.*	24.319
Turkey	*Medicago sativa*	662.888

In Turkey, *Medicago sativa* has the highest share in the cultivation area with 662,888 hectares. In Thailand and India, *Stylosanthes* cultivation areas are 300 and 250 hectares, respectively. *Brachiaria spp.* in Central America and *Vigna ungiculata* in West Africa have an area of 1,560 and 1,615 hectares, respectively (Table 1).

Forage crops are generally divided into two groups as cool season wheatgrass and cool season legume forage crops according to their climate requirements (Table 2).

Table 2. *Cool season wheatgrass and legume forage crops [32], [33].*

Cool Season Forage Crops	
Wheatgrass Group	Legume Group
Lolium perenne L.	*Vicia pannonica* L.
Lolium multiflorum L.	*Lotus corniculatus* L.
Phalaris aquatica L.	*Lotus pedunculatus* L.
Cynodon dactylon	
Agropyron elongatum L.	*Lathyrus saivus* L.
Bromus inermis L.	*Pisum sativum* L.
Dactlylis glomerata L.	*Trifolium alexandrinum* L.
Festuca arundinacea L.	*Trifolium meneghinianum* L.
Elytrigia elongata	*Trifolium resupinatum* L.
Puccinellia ciliata	*Medicago* sp.

Cool season forage crops are generally resistant to hot and arid climates. Especially *Agropyron elongatum* L. and *Festuca arundinacea* L. have high salt tolerance. In addition, *Festuca arundinacea* L. has a high tolerance to extreme temperatures.

Cool season legume forage crops are also very cold tolerant. *Vicia pannonica* L. can withstand temperatures down to -16°C, especially in conditions without snow cover. *Lathyrus saivus* L. and *Trifolium meneghinianum* L. are among the most drought tolerant forage crops. At the same time, *Trifolium meneghinianum* L. and *Lotus corniculatus* L. have high salt tolerance while *Pisum sativum* L. has low salt tolerance [32].

A summary of forage plant researches and analyses on protein sources, which is one of the most important nutrients in animal nutrition, is presented in Table 3.

Table 3. *Some nutritional value ratios of some forage crops (%)*

Forage crops	**Nutrient content**	**Rate (%)**	**Reference**
Medicago sativa	Protein	8.034-8.042	[34]
	Fiber	5.883	
Medicago sativa	Protein	32	[35]
Medicago sativa	Protein	8,7-13,9	[36]
	NDF	39,6-54,3	
	ADF	30,6-41,8	
Trifolium alexandrinum L.	Protein	3.102-3.105	[34]
	Fiber	4.867	
Avena sativa L.	Protein	4.114-4.116	[34]
	Fiber	12.35	
Zea mays L.	Protein	5.13-5.19	[34]
	Fiber	4.867	
Zea mays L.	Protein	6.5-6.9	[37]
	NDF	49.1-50.0	
	ADF	29.4-29.6	
Sorgum L.	Protein	3.90-5.64	[38]
Lolium perenne	Protein	6-34	[35]
	NDF	34-62	
	ADF	4-42	
	Dry matter	11-37	
Lolium multiflorum	Protein	6-28	[35]
	ADF	2-35	
Trifolium repens	Protein	32	[35]
Agropyron cristatum	Protein	8-36	[35]
Leucaena leucocephala	Dry matter	24-93	[35]
Panicum maximum	Dry matter	22-91	[35]

Table 3 (cont). *Some nutritional value ratios of some forage crops (%)*

Cynodon nlemfuensis	Dry matter	97	[35]
Pisum sativum L.	Protein	17.6-21.2	[39]
Pisum sativum L.	Protein	17.73-27.17	[40]
Pisum sativum L.	Protein	16.25-18.69	[41]
	NDF	38.40-42.82	
	ADF	28.5	
Pisum sativum L.	Protein	16,8-19,9	[42]
	NDF	38,6-42,8	
	ADF	29,0-34,4	
Pisum sativum L.	Protein	18,1-23,9	[43]
	NDF	33,2-38,3	
	ADF	27,9-30,2	
Vicia sativa L.	Protein	8.1-12.4	[44]
	NDF	42.0-51.4	
	ADF	29.5-37.3	
Vicia sativa L.	Protein	5.1-15.4	[45]
	NDF	37.4-48.1	
	ADF	28,1-31.2	

In order to reveal the nutritive value of fodder plants, the protein ratio of *Medicago sativa* is 8-32%, Lolium perenne 6-34%, *Agropyron cristatum* 8-36%. The protein ratio of *Pisum sativum* L. varies between 16-27% (Table 3). When these ratios are evaluated, *Pisum sativum* L. fodder peas show less variation in protein ratio in different growing areas. This situation makes fodder peas valuable in terms of nutrition.

A. FORAGE PEA (*Pisum sativum L.)*

Our geographical focus covers all of Latin America and the Caribbean except the southern cone countries of South America (Argentina, Chile, Paraguay and Uruguay), developing countries in Asia except China, Mongolia and North Korea, Africa and Turkey.

Pisum sativum L. is one of the important grain legume crops grown worldwide. In many developing countries such as Latin America, Africa and Turkey, it is also used for feeding ruminants in the form of fresh feed, feed dry matter, feed meal, silage and hay [46]. Legumes account for about 30% of the world's agricultural production. Legume residues provide soil organic matter balance. In years of irregular rainfall distribution (temperate climates) or rainfall deficiency (Southern European climatic conditions), when mineral nitrogen uptake is poor, legumes have a particularly positive effect on the soil. The decomposition of *Fabaceae* plant residues in soil provides forms of nitrogen to both successional plants and soil microorganisms through biological nitrogen sorption [47], [48]. Accordingly, the "European Green Deal" policy aims to reduce fertilizer consumption by at least 20% by 2030 while maintaining soil fertility. In order to achieve these targets, peas are important for providing nitrogen to the soil in the process of nitrogen fixation. Increasing pea cultivation will reduce the use of nitrogen from mineral fertilizers and maximize biological nitrogen use [49].

In addition, the inclusion of legumes in crop rotation has an important place in global agriculture as it contributes to the reduction of weed, pest and disease populations [47], [48]. When cereals and legumes are grown in rotation, they increase soil fertility by altering physical and chemical properties and counteracting soil erosion. Thanks to the well-developed root systems of legumes, they also provide soil aeration. Another important feature of legumes is that they positively affect sustainable agriculture by eliminating the need for fertilizer by binding atmospheric nitrogen to the soil as a result of symbiotic effect with *Rhizobium* spp. bacteria [48]. Pea, one of the most important plants in the *Fabaceae* family, has a protein content of 21-32%. It is rich in lysine, an essential amino acid important for nutrition, and low in sulfur-containing amino acids. It also has low allergenicity [47], [48].

Forage pea (*Pisum sativum* L.) is one of the high quality forage resources from the legume forage crops group. In terms of nutrient composition, forage peas contain proportionally higher crude protein (21-25%), starch from carbohydrates and dietary fiber from digestible substances (86-87%) than other roughages and have high antioxidant activity [4], [44], [47], [50], [51]. Forage peas, which are important in terms of containing essential amino acids, are used in the nutrition of slaughter, dairy and laying animals without affecting production and fattening performance. In many countries of the world, forage pea cultivation is given importance in terms of replacing high-cost soybean meal in terms of protein value [39], [47], [48]. For this reason, forage pea (*Pisum sativum* L.), which has high nutritional value and is preferred for consumption by animals, is an important fodder plant in terms of closing the roughage deficit. Fodder pea, whose grains, green and dry grass are used as forage plant, is preferred both as a pasture plant and as a green fertilizer plant [14], [32], [52]. In addition, forage peas grown as silage for animal nutrition have high nutritional value and taste preferred by animals [53]. In addition to minerals such as phosphorus and calcium, it also contains vitamins A and D [50], [52], [54]. In addition to these advantages, since it is affected by biotic-abiotic stress conditions, the cultivation rate is relatively low [48].

III. SALT STRESS

Agricultural areas in developing countries face salt stress [24]. For example, in Turkey, 32 million hectares of the approximately 1.5 million hectares of agricultural land are under salinity stress. Of the 230 million hectares of irrigated land, 45 million hectares are affected by salt stress. Salt problems of this magnitude are thought to cause great economic losses in parallel with the loss in crop yield and quality [22], [55]. Salinity occurs naturally in arid and semi-arid climatic zones, and insufficient rainfall and high evaporation, poor drainage, improper agricultural practices and soil characteristics increase the salinity problem [26], [56], [57]. When salt tolerance is evaluated in terms of forage crops, they are classified as partially sensitive, partially resistant and resistant to salinity (Table 4).

Table 4. *Classification of forage crops in terms of salinity tolerance [19].*

Partially Sensitive to Salinity	**Partially Resistant to Salinity**	**Resistant to Salinity**
Medicago sativa	*Lolium perenne* L.	*Agropyron cristatum*
Vicia sativa	*Lolium multiflorum* L.	*Elymus junceus*
Pisum sativum L.	*Sorghum*	*Cynodon dactylon*
Trifolium repens	*Agropyron intermedium*	*Agropyron elongatum*
Trifolium pratense	*Lotus corniculatus*	
Phleum pratense	*Melilotus albus*	
Trifolium alexandrinum	*Melilotus officinalis*	
Zea mays		

Salinity is one of the most serious environmental factors limiting the productivity of forage crops due to the high concentrations of salinity-sensitive Agricultural plants show a range of responses to salt stress. Salinity reduces the agricultural production of most crops and also affects the physicochemical properties of the soil and the ecology-based balance of the region. Average yields for all major crops are only one-quarter to one-half of record yields; some of these losses are due to soil salinity [58].

High salinity causes both ionic and osmotic stresses, leading to secondary stresses such as oxidative stress and nutritional disorders. Furthermore, with increasing salt concentration in the soil, plant water uptake becomes difficult and plant growth slows down due to deterioration of soil structure [19], [22]. Orcan and Orcan (2024) examined the effect of different types of salts on *Oryza sativa* L. plant. Plant seeds were exposed to different concentrations of NaCl, $CaCl_2$ and $MgCl_2$ salts (0, 30 mM, 90 mM) in hormone-free and salt-free MS medium. As a result, a reduction in nutrients was observed for all three salt types [59]. Nedjimi et al. (2020) determined the salinity tolerance index of different salts (NaCl, Na_2SO_4, $CaCl_2$ and $MgCl_2$) on *M. vulgare* plants at four salinity levels (0, 50, 100 and 150 mM) as Na2SO4 < MgCl2 < CaCl2 < NaCl [60].

Exposure of plants to high salt conditions results in changes in gene expression and transcription factors. These genes and transcription factors are grouped as follows: (I) ion transport or homeostasis (e.g. *SOS*, *NHX1*, *HKT1* and *H+- ATPase* genes), (II) senescence-related genes (e.g. *SAG*), (III) molecular chaperone proteins (e.g. *HSP*) and (IV) dehydration-related genes (e.g. *DREB*). The expression of these genes increases or decreases according to stress conditions [22], [61], [62].

Krasensky and Jonak (2012) examined the expression patterns of stress-related genes under drought, high temperature and salinity conditions. They stated that changes in the expression of genes involved in plant signaling associated with environmental stresses such as salicylic acid, jasmonic acid, abscisic acid and calcium ion at initial, final and intermediate times provide information about the growth status of a plant under stress. Research on the expression information of a gene in different tissues under different environmental conditions and developmental stages reveals that it provides information about the growth status of a plant under stress at the molecular level [63].

SOS (salt overly sensitive) gene contributes to the development of salt stress tolerance in plants by controlling the flow of Na^+ ion in the cytosol [26]. Liu et al. (2015) revealed that salt stress is also controlled with the increase in the expression of *SOS1* gene [64]. *SOS (Salt Overly Sensitive)* genes regulate the *SOS* signaling pathway and control the Na^+ and K^+ ion balance [65]. *SOS* signaling pathway is activated as a result of an increase in the amount of Na^+. In terms of molecular structure of *SOS* genes, *SOS3* gene encodes a calcium binding protein, *SOS2* gene encodes a serine/threonine protein kinase, *SOS1* gene encodes a plasma membrane Na^+ /H^+ antiporter. *SOS1*, *SOS2* and *SOS3* function linearly [61]. *SOS3* interacts with *SOS2* and activates it. *SOS2* and *SOS3* activate *SOS1* and control the expression level of *SOS1*. As a result, activation of *SOS1* ensures ion balance and salt tolerance under salinity conditions [66].

Dehydration-related gene products such as *LEA* (*late embryogenesis abundant*) and *DREB* (*dehydration response element binding*) also elicit a response to salt stress and regulate signal transduction, protecting cellular structures and promoting salt tolerance [67]. *LEA* proteins are located in the cytoplasm and protect cellular structures during stress. Under stress conditions, hydrophilic and soluble *LEA* proteins are expressed by *LEA* genes and bind water. In this way, they play a role in protecting cellular membrane and protein/enzyme structures from water deficiency during salt stress [66]. In addition, the expression of *DREB* genes also increased under abiotic stress conditions. The expression of genes such as *AtDREB1*, *DREB2A*, *DREB2B*, *AtDREB2A*, *OsDREB2A* also increases rapidly under high salinity conditions. The expression of a large number of genes during salt stress suggests that these genes can be used to develop salt tolerant plants [26], [66].

It has been revealed that the expression of *Osmyb4* gene isolated from *Oryza sativa* activates cold-induced promoters such as PAL2, ScD9, SAD and COR15a. As a result of overexpression of this gene, it is reported that more than 250 genes are activated, a significant portion of which are also associated with abiotic and biotic stress [17]. Aydın et al. (2014) obtained transgenic potato plants expressing *Osmyb4* gene in a study they conducted. It was revealed that these potato plants in which *Osmyb4* gene was transferred showed better development compared to those in which the gene was not transferred [68]. Vannini et al. (2006) showed that 50% of the *Arabidopsis* plants in which *Osmyb4* gene was transferred survived after 300 mM NaCl treatment, whereas *Arabidopsis* plants in which the gene was not transferred completely disappeared [69]. On the other hand, plants increase intracellular osmotic pressure by producing osmoregulatory proteins such as proline in their cells against the stress caused by high salt concentration. Because most of the eukaryotic cells cannot tolerate salts such as NaCl because they disrupt the structure of enzymes. In plants, in order to prevent this situation, the cell produces many osmoregulatory substances such as proline proteins that do not disrupt the structure of enzymes [23], [70], [71]. There are also different plant mechanisms against salt stress such as osmotic effect, ion excretion and tissue tolerance. Osmotic effect decreases the water availability of plants as a result of increased salt concentration in the soil. The ion excretion mechanism reduces the accumulation of toxic salt in the leaves. Tissue tolerance is the growth retardation observed in plants in the face of salt stress [19], [26], [56].

Salt stress negatively affects the photosynthetic mechanism, which is one of the most important metabolic processes in plants, causing stomatal closure and changes in chlorophyll structure [57], [72]. Taffouo et al. (2010) reported that the total chlorophyll concentration of tomato (*Lycopersicum esculentum* L.) leaves under salt stress decreased significantly [73]. Shahid et al. (2011) reported that chlorophyll content decreased in different pea genotypes under salt stress [74]. Taibi et al. (2016) revealed that photosynthetic pigments of *Phaseolus vulgaris* L. decreased in the face of increasing salt concentration [75]. Kaymak and Acar (2020) determined that the amount of chlorophyll a, chlorophyll b and carotenoid in the leaves of forest clover (*Bituminaria bituminosa* L.) decreased with increasing salt concentration [76]. Loudari et al. (2020) revealed a significant decrease in chlorophyll content of tomato plants (*Lycopersicum esculentum* L.) as a result of salt application [72].

Plants produce secondary metabolites as a defense mechanism against pathogens and insects. The formation of these metabolites is also possible under different environmental stress conditions (e.g. salinity) and it is this group of metabolites that constitutes the majority of plant antioxidants. Phenolic compounds are one of the secondary metabolites produced in plant tissues to scavenge free radicals and/or inhibit their production through hydroperoxide decomposition [16], [77]. Many studies have revealed that peroxidase and polyphenoloxidase enzymes involved in the synthesis of phenolic compounds increase under biotic and abiotic stress conditions [78]. Kıpçak et al. (2019) found that the total phenolic matter content in the green parts of bean genotypes treated with different concentrations of salt decreased significantly compared to control plants [79]. In addition, reactive oxygen species are formed in plants under oxidative stress in saline conditions. These reactive oxygen species cause serious problems in plants such as inactivation of proteins and enzymes, injury to plant metabolism, change in the structure of photosynthetic components, and lipid peroxidation [80]. Phenolic compounds neutralize these reactive oxygen species thanks to their antioxidant activities [79]. Boughalleb et al. (2020)

revealed that the total phenolic and antioxidant content of Polygonum equisetiforme plants under different salt concentrations increased especially up to 300 mM salt concentration [77].

Since reclamation of saline agricultural lands is expensive and difficult, it is more appropriate to grow salinity-tolerant plants to increase yields in these areas. Therefore, studies to improve the salinity tolerance of plants have gained momentum in recent years [14]. In this context, studies in the field of molecular biology, biotechnology and genetic engineering have increased in recent years to overcome yield problems in agricultural fields. The productivity achieved through classical breeding studies, especially in the agricultural field, cannot meet the food needs of the growing world population due to the limitations in arable land.

IV. CONCLUSION

Especially for developing countries, it is very important to increase forage crops cultivation areas with proper management of pastures and breeding studies in order to ensure adequate and balanced nutrition of existing animals. For this reason, the forage pea (*Pisum sativum* L.), which has high nutritional value and is preferred by animals, is an important fodder plant in animal nutrition. However, salinity is an important problem, especially for forage peas. Among abiotic stress factors, salinity is the primary factor that will directly affect crop yields today and in the future. As a result of exposure of plants to salt, changes in gene expression and transcription factors occur. With gene studies, salinity genes in the plant are found, characterized, isolated and transferred to the target cell to obtain transgenic plants. The aim here is to provide salinity tolerance as a deficiency in the plant. This also contributes to plant breeding methods. Today, crops are grown in this way on 3.7% of the world's agricultural land, and according to statistics from the International Service for the Acquisition of Agricultural Biotechnology Applications (ISAAA), global biotech crop coverage reaches 170.3 million hectares. Since 2014, transgenic crops have been grown in the US, Brazil, Argentina, India and Canada. This study shows that the usable agricultural areas can be increased in the future with the suggestions put forward by the researchers for the elimination of the salinity problem in feed crops, which is an important problem for livestock in developing countries.

V. REFERENCES

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