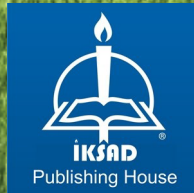


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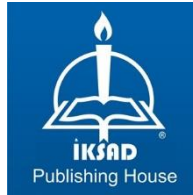
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Prof. Dr. Vecihi AKSAKAL
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Authors:

Prof. Dr. Şaziye Canan BÖLÜKBAŞI AKTAŞ
Assoc. Prof. Dr. Mahir Murat CENGİZ
Assoc. Prof. Dr. Murat GENÇ
Assoc. Prof. Dr. Yaşar ERDOĞAN
Assist. Prof. Dr. Betül GIDİK
Assist. Prof. Dr. Yasin Yahya YILMAZ
Phd.Mazhar Burak CAN
MSc Agricultural Engineer Ayşenur KANDEMİR



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TÜRKİYE TR: +90 342 606 06 75
USA: +1 631 685 0 853
E mail: iksadyayinevi@gmail.com
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PREFACE

Agriculture and animal husbandry are sectors of vital importance for the food supply and development of our country. These sectors have undertaken important economic functions in terms of producing essential goods for consumers and producers, having a constant demand for these goods, providing input to the industry and services sectors, creating employment within the sector and achieving the goal of balanced development both in sectors and regions.

The importance and indispensability of agriculture in Turkey during the epidemic period was once again revealed. While operations could not be carried out in different production areas, agricultural production was tried to be increased. The potential that Turkey has is better understood. The technological innovations that the coming years may bring are developments that have the capacity to transform the global agricultural sector. As technology is used more in production, efficiency and production value can be increased significantly. Turkey should not be left out of the possible transformation and should lead this transformation.

In this book, which is divided into 5 chapters, 1 on Crop Production; There are 4 departments related to animal husbandry. This book contains texts written by approximately 8 academics on different subjects.

This book has been prepared in detail to cover current issues and is presented to you in return for a certain amount of effort. Considering that this book will contribute significantly to the world of science, we hope that it will be useful to everyone.

Editors

Prof. Dr. Vecihi AKSAKAL

Prof. Dr. Ümmügülsüm ERDOĞAN

CHAPTER 1

EFFECTIVE FACTORS ON MILK β -CASOMORPHIN 7

Ayşenur KANDEMİR¹

Şaziye Canan BÖLÜKBAŞI AKTAŞ²

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¹ MSc Agricultural Engineer, Ayşenur KANDEMİR¹, Atatürk Üniversitesi, Ziraat Fakültesi, Zootehni Bölümü, Erzurum, Türkiye, ORCID: 0000-0002-2662-9291, aysenur.kandemir19@ogr.atauni.edu.tr

² Prof. Dr., Şaziye Canan BÖLÜKBAŞI AKTAŞ, Atatürk Üniversitesi, Ziraat Fakültesi, Zootehni Bölümü, Erzurum, Türkiye, ORCID:0000-0003-1153-3489, canan@atauni.edu.tr

INTRODUCTION

Milk and dairy products due to their high nutritional value and physiological functions are the main components of the human diet (Keating et al., 2008). Milk proteins are at the forefront of the substances necessary for the development and growth of our bodies and contain all of the essential amino acids that cannot be synthesized in the body (Şenel, 2016). Milk proteins, making up to approximately 27% of the total dry matter, are the most important basic components of milk. Milk proteins consisting of more than thirty fractions are basically classified as casein and serum proteins (Gürsoy, 2015). These proteins are positive regulators for human health as they contain critical nutritional elements and provide immunological protection (Clare and Swaisgood, 2000). Casein being the most abundant protein of the milk (~80% by weight) is the key component of milk protein both quantitatively and nutritionally (Sarode et al., 2016). Comprising four fractions, casein micelles include alpha s1- (α s1-), alpha s2- (α s2-), beta- (β -), and kappa- (κ) casein (Day 2016). Beta casein (β -Cn), with thirteen genetic variants, is the most polymorphic milk protein. A1 and A2 are the most common forms of these variants (Rahman et al., 2016).

It was determined that originally the milk was A2 and the A1 appeared at some point due to a genetic mutation (Ng-Kwai-Hang and Grosclaude, 2003). A1 milk describes milk from cows

that have been bred to produce more milk, while A2 milk describes healthier milk from non-mutated cows (Dinç, 2009). “Beta-casomorphin-7” (BCM-7) peptide is formed as a result of gastrointestinal digestion of the A1 variant of β -casein (Brooke-Taylor et al., 2017). BCM-7 is thought to be associated with diseases such as ischemic heart diseases, type-1 diabetes, atherosclerosis, sudden infant death syndrome, autism and schizophrenia (Rahman et al., 2016). The health issues attributed to A1 milk consumption are believed to arise from the production of BCM-7, whereas A2 milk is considered not to have any adverse effects on human health (Kamiński et al., 2007). A1 β -Cn is common in cattle in the Western world. While the A1 variant of β -casein is higher in Holstein milk, Asian herds (Guernsey, Jersey, sheep, goat, donkey, yaks, camel, buffalo) and human milk mostly contain A2 β -Cn (Pasin, 2017). According to reports, A1 β -Cn levels of milk obtained from local breeds grown in Turkey are quite low and A2 type healthy milk is obtained from these animals (Sarı, 2014). Factors such as animal species, breed, origin, stage of lactation, lactation number, and technological processes to which milk and its products are exposed, heredity and presence of dipeptidyl peptidase enzyme (DPP-4) affect BCM-7.

Milk proteins

Milk, an ideal food source for humans of all ages, consists of water, lactose, protein, fat, vitamins, and minerals (Smirnova et al., 2020). The main proteins in cow milk are whey (whey proteins AKA fast proteins), and caseins (AKA slow proteins) (Kollias, 2011). Casein and whey respectively account for about 80% (29.5 g/L) and 20% (6.3 g/L) of the total milk proteins (Davoodi et al., 2016). Milk protein fractions according to different mammal species are shown in Table 1.

Table 1. Protein Fractions in Different Mammalian Milks (g/100g Total Casein and g/100g Total Whey Protein) (Tamime et al., 2011)

Protein fractions (%)	Caprine	Ovine	Bovine
Caseins			
α s-casein	26-30	31-51	48-49
α s-1 casein	5	16	38
α s-2-casein	25	15	10
β -casein	50-64	39-47	33-39
k-casein	10-20	7-10	11-13
Whey proteins			
α -lactalbumin	40	25	25
β -lactoglobulin	40	51	50
Immünoglobulins	18	12	12
Proteose-peptone	9	6	13

Casein

Casein coagulates and precipitates after the reaction of milk with acid (Deeth and Bansal, 2019). Casein composed of carbon, hydrogen, oxygen, and sulfur, as the main element giving color to milk, is found in cow's milk at an average rate of 2.63%. Casein is present in milk as micelles, and each casein micelle consists of α -casein, β -casein, κ -casein and γ -casein fractions, and has a heterogeneous structure. The main protein of the casein complex is α s1-casein (38%) followed by β -casein (36%), κ -casein (13%) and α s2-casein (10%) (Bhat et al., 2016).

Beta casein (β -Cn)

β -casein constitutes approximately 25-30% of cow's milk proteins (Swinburn, 2004). Bovine and human β -casein contain 209 and 211 amino acid residues, respectively (Uniacke-Lowe and Fox, 2011). The β -Cn concentration and amino acid sequence in the total casein protein of different species are shown in Table 2.

Table 2. Concentration of β -Cn and Amino Acid Sequence of β -Cn in Total Casein Protein in human and different mammalian milks (Chianese et al., 1993; Tamime et al., 2011; *Uniacke-Lowe and Fox, 2011*; Ghnimi and Eldin, 2015;; Park, 2021).

	Camel	Cattle	Goat	Human
The percentage of β -Cn in total casein	65	36	54.8	60-70
Amino acid sequence of β -Cn	217	209	223	211

β -Cn, the second most abundant protein in cow's milk (Muhammed and Stephen, 2012), is polymorphic with 13 genetic variants (A1, A2, A3, A4, B, C, D, E, F, H1, H2, I and G). The most common ones in dairy cattle are A1 and A2, while B, A3 and C are the rarest β -Cn variants (Li and Gaunt 1972). Variants A1 and A3 originate from variant A2, while variants B and C are derived from variant A1. The A1, B, and C allelic variants differ from each other in an amino acid at position 122 (serine in A1 and C, arginine in B) and an amino acid at position 37 (glutamic acid in variants A1 and B and lysine in variant C) (Sebastiani et al., 2020).

About 5000 years ago, cows producing A1 type casein emerged as a result of genetic mutation in a herd of cattle in Europe (Chitra, 2021). A2 β -Cn, the original β -casein, was found in European herds before the mutation and formation of A1 β -Cn (Ng-Kwai-Hang and Grosclaude 2003). The A1 variant

is the only β -Cn form that has detrimental effects on human health. Upon consumption of milk from A1 gene carrying cow, β -caseins are converted into BCM-7 by enzymes in the intestine (Swinburn, 2004).

Casomorphins, which are biologically active molecules, are formed from α - and β -casein as a result of gastrointestinal digestion of milk, fermentation with proteolytic starter cultures or hydrolysis by proteolytic enzymes (Petrotos et al., 2014). Food-derived bioactive peptides could affect digestive, endocrine, immune, nervous and cardiovascular systems exerting antihypertensive, antimicrobial, lipid-lowering, immunomodulatory, mineral-binding, antithrombotic, opiate-like and anti-cariogenic effects (Moughan et al., 2014). Opioid peptides with morphine-like activities such as casomorphins exert relaxing and stimulating effect (Gobbetti et al., 2002; Séverin and Wenshui, 2005). Most milk opioid peptides are derived from β -casein and are characterized as μ -opioid ligands (Miralles et al., 2018). Major opioid peptides are β -Cn fragments called β -casomorphins (Clare and Swaisgood, 2000).

Beta Casomorphins

Beta casomorphins (BCM), with 3-7 amino acids, are released from β -casein during digestion or food processing (EFSA, 2009) (Muehlenkamp and Warthesen, 1996). These peptides with opioid and pharmacological activities, bind to μ -receptors found in the central nervous system, gastrointestinal

tract, and some immune cells. Among them, the most active ones are BCM-7 (Tyr - Pro - Phe - Pro - Gly - Pro - Ile) and β -casomorphin 5 (BCM-5) (Ul-haq et al., 2014). BCMs have been detected in various commercial cheeses, cow and human milk; however, has not yet been detected in commercial yoghurts. BCMs can occur in yogurt as well as cheese but it is thought to be degraded during processing (Nguyen et al., 2015). Jarmołowska et al. (2007) reported the presence of BCM-5 and BCM-7 in human colostrum and mature milk.

Beta-Casomorphin-7

There is histidine in the 67th (His67) position of the A1 β -Cn amino acid (aa) sequence, and proline in the 67th (Pro67) position of the A2 β -Cn amino acid sequence (Lonnerdal et al. 1990). The difference of A1 β -Cn from the A2 allele is due to the substitution of histidine amino acids with proline at the 67th position of A1 β -Cn (Mclachlan, 2001). At the 67th position of the amino acid chain in A1 β -Cn, the existence of histidine leads to the generation of BCM-7, whereas the presence of proline at the same position in A2 β -Cn hinders the formation of BCM-7 and results in the production of the BCM-9 peptide (Kostyra et al. 2004). Figure 1 shows the difference between the amino acid sequence of A1 and A2 and the amino acid sequence of the released BCM-7 (Rashidinejad et al., 2017).

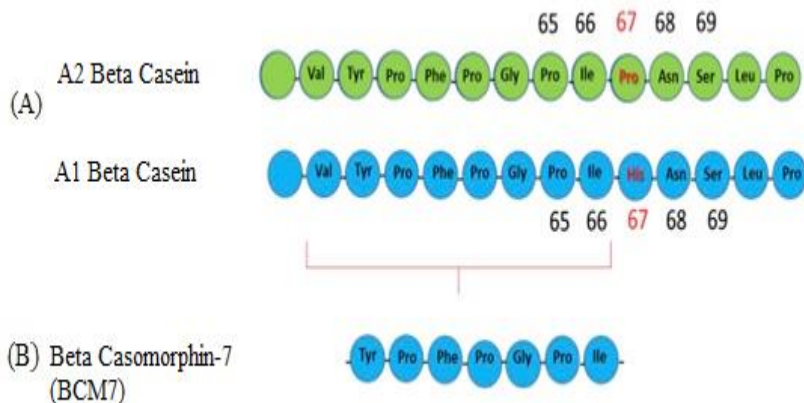


Figure 1. The Difference in amino acid sequence between A1 and A2 β -casein (A); release of β -casomorphin-7 in the human digestive system and amino acid sequence of BCM-7 (B). Figure is extracted from the study of Rashidinejad et al., 2017.

Commercially produced milk in many countries contains a mixture of A1 and A2. Thoroughbred Asian and African cattle do not have the His67 mutation. Similarly, the presence of an equivalent histidine mutation in other mammalian species, including humans, is either absent or extremely rare (Brooke-Taylor et al., 2017). Gastrointestinal proteolytic digestion of the A1 variant of β -casein leads to the formation of BCM-7 (Sodhi et al., 2012a). A1- and A2- β -Cn react differently to enzymes in the human gut, such as leucine aminopeptidase (LAP), elastase, trypsin, chymotrypsin, and pepsin. Different responses of these polypeptides is thought to be caused by a single amino acid difference originating from histidine at position 67 of A1 β -Cn

and proline at position 67 of A2 β -Cn. This difference in amino acids at position 67 causes differences in the sensitivity of the peptide bond between amino acids 66 and 67 of the A1 and A2 β -Cn amino acid sequence (Parashar and Saini, 2015).

The elastase enzyme cleaves the peptide bond between A1 β -casein 66th (isoleucine) and 67th (Histidine), releasing the carboxyl end of BCM-7; Pepsin and leucine aminopeptidase (LAP) enzymes release the amino terminus of BCM-7. In the digestion of A2 β -Cn, however, the peptide bond between the isoleucine at 66th position and proline at 67th position is not cleaved so BCM-7 is not formed (Jinsmaa and Yoshikawa, 1999). BCM-7 is hydrolyzed to BCM-5 and BCM-3 by dipeptidyl peptidase-4 (DPP-4) (Parashar and Saini, 2015). The formation of BCM-7 and other β -casomorphins with the breakdown of β -casein by enzymes during the digestion of A1 and A2 milks is shown in Figure 2 (Parashar and Saini, 2015). In sequential gastrointestinal digestion of milk containing the A1 variant of β -casein, the level of BCM-7 is 4-times higher than in A2 variant containing milk (Kaminski et al., 2007). *In-vivo* release of BCM-7 from bovine milk; depends on the protein content of milk, the ratio of A1 and A2 β -Cn, and the specific gastrointestinal conditions of the individual (Pal et al., 2015).

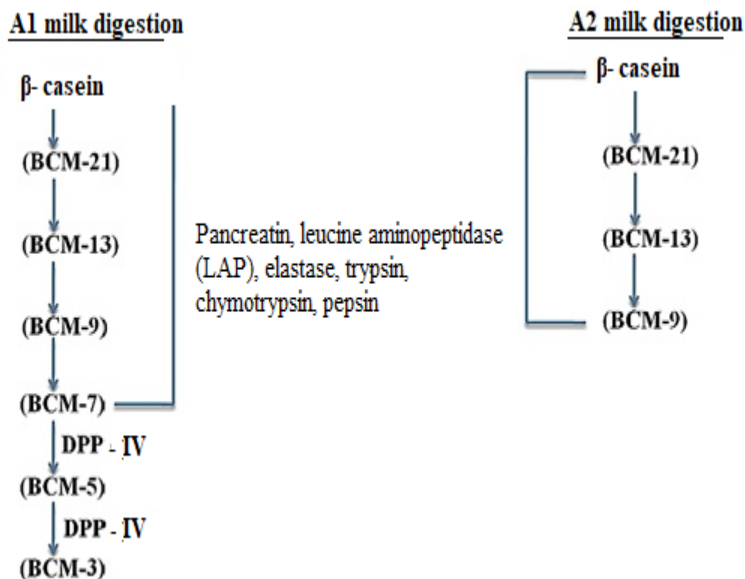


Figure 2. Cleavage of β -casein by enzymes. Figure is extracted from the study of Parashar and Saini, 2015.

PRESENCE OF B-CASOMORPHIN-7 IN MILK AND DAIRY PRODUCTS

Although it has been suggested that BCM-7 is abundant in milk containing the A1 variant, it has also been reported to be present in the A2 variant. In a study, it was observed that BCM-7 was not detected in the milk of cows with mastitis, where somatic cell concentration was high (Napoli et al. 2007). Cieślińska et al. (2012) found that BCM-7 was more abundant in the A1 variant in bovine milk samples.

There are studies showing that BCM-7 is released not only in cow's milk but also from human milk, yogurt, cheese and possibly any dairy product. In addition, BCM-7 is slightly released during cheese and yogurt making processes; however, there are also studies showing that some bacteria found in yogurt can hydrolyze BCM-7 (Pal et al., 2015). Jarmolowska and Krawczuk et al. (2012) determined that the BCM-7 level in natural and probiotic yogurt ranged between 0.86-2.45 $\mu\text{g/g}$ and this level decreased during the storage period. It has been suggested that during storage, bacterial enzymes in yogurt cause degradation of BCM-7 by digesting the peptide bonds between proline and other amino acid residues.

Nguyen et al. (2014) examined the BCM-7 level in commercial yogurt and milk as well as yogurt prepared using powdered milk in the laboratory. BCM-7 was not detected in commercially produced yogurts; however, they reported 93 ng/g and 98 ng/g BCM-7 in milk and yogurt obtained from milk powder in the laboratory, respectively. De Noni et al. (2015) investigated the amount of BCM-7 in different cheese varieties and reported that BCM-7 was present in both undigested and hydrolyzed samples of cheeses. Other studies have reported the presence of β -casomorphins in parmesan (Addeo et al., 1992), cheddar (Stepaniak et al., 1995), sharp cheddar, Swiss, blue, brie and limburger cheeses (Muehlenkamp and Warthesen, 1996).

FACTORS AFFECTING BETA CASOMORPHIN-7

In the preceding section, authors will discuss the effectual factors such as animal species, breed, origin, stage of lactation, lactation number, technological processes to which milk and its products are exposed on BCM-7.

1-Effect of heredity

Each copy of the β -Cn allele in dairy animals leads to the production of the corresponding beta casein type (A1A1, A1A2 or A2A2). A1 type milk is obtained from cows with A1A1 and A1A2 genotypes, while A2 type milk is obtained only from cows with A2A2 genotype (Beavers and Doormaal, 2016). The A1 β -Cn has the potential to release the BCM-7 opioid peptide during gastrointestinal digestion (Brooke-Taylor et al., 2017).

2-The influence of animal species and breeds

This mutation does not occur in purebred Asian and African cattle and is very rare in other mammalian species including humans (Brooke-Taylor et al., 2017). Asian herds, Guernsey, Jersey, sheep, goat, donkey, yaks, camel, buffalo, cattle and human milk mostly contain A2 β -casein (Pasin, 2017). β -casomorphins have been isolated from various milk sources such as cattle, buffalo, sheep, and humans yet not obtained from goats and camels (Xu, 2009). β -Cn in goat and camel milk is mainly found as type A2 (Zimmerman, 2016) and does not produce BCM-7 during the milk digestion process (Jung et al., 2017).

Northern European dairy cow breeds (British Shorthorn, Ayrshire Holstein Friesian) generally produce milk with high A1 β -Cn content. Dairy cow breeds from Southern France and the Channel Islands, such as Guernsey, Jersey, Simmental, Guernsey, Charolea and Limousine, and the African indigenous Zebu cattle breed produce A2 β -Cn milk (Trustwell, 2005; Kaminski et al., 2007). Indian crossbreed A1, while domestic cattle breed milks from India and other Asian countries mostly have the A2 protein variant (Priyadarshini et al., 2018). The main morphological differences between A1 and A2 dairy cattle breeds are shown in Figure 3 over Zebu and Holstein cattle breeds (Singh, 2020). Evaluating the β -Cn alleles and genotypes of 657 buffaloes from four different breeds in Brazil showed that

all animals have the A2A2 genotype but not A1 allele thus producing A2 type healthy buffalo milk (De Oliveira et al. 2021). In India, Mishra et al. (2009) and Ramesha et al. (2016) had similar results in two studies conducted on 9 different buffalo breeds.

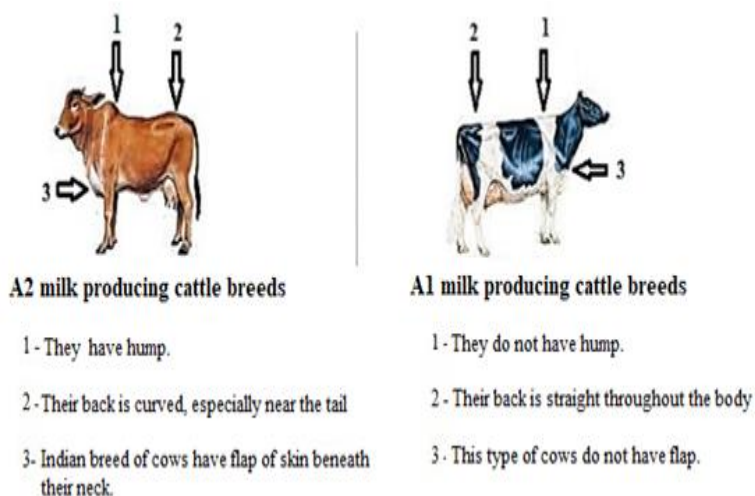


Figure 3. Morphological differences between A1 and A2 milk producing cattle breeds. Figure is extracted from the study of Singh, 2020.

The frequency of the A2 gene in the Jersey breed is higher worldwide (60-80%). The frequency of A2 is very high (>98%) in cows and stud bulls of the US/European Guernsey breed, almost equal to that of Indian hump cows. The A2 frequency of the Kerry breed from Ireland and the Spotted breed in Hungary is over 75% (Behera et al., 2018). β -Cn allele frequency values

of some western cattle breeds are shown in Table 4 (Kaminski et al., 2007).

Table 3. *The allele frequencies of β -casein gene variants in various cattle breeds and countries.*

Breed	Country	Frequency of beta-casein alleles			References
		B	A1	A2	
Guernsey	USA	0.010-0.020	0.010-0.060	0.880-0.970	Enennam et al. 1991
Jersey	Germany	0.186	0.093	0.721	Ehrmann et al. 1997
	Denmark	0.350	0.070	0.580-0.650	Bech et al. 1990
	NewZelland	-	0.123	0.591	Winkelman &Wickham 1997
	USA	0.290-0.370	0.090-0.220	0.490-0.540	Ennenam et al.1991
Brown Swedish	Germany	0.170	0.108	0.705	Ehrmann et al. 1997
	USA	0.100-0.180	0.140-0.150	0.660-0.720	Swaigood 1992
	USA	0.100-0.180	0.140-0.180	0.660-0.720	Ennenam et al. 1991
Simmental	Croatia	0.150	0.190	0.630	Curik et al. 1997
	Germany	-	0.343	0.566	Ehrmann et al. 1997
HF	USA	0.010-0.060	0.310-0.660	0.240-0.620	Swaigood 1992
	USA	0.010-0.040	0.310-0.490	0.490-0.620	Ennenam et al. 1991
	Hungary	0.107	0.418	0.470	Baranyi et al. 1997
	Germany	0.026	0.472	0.496	Ehrmann et al. 1997
	Poland	-	0.402	0.598	Kaminski et al. 2006a
	New Zealand	-	0.465	0.510	Winkelman et al. 1997
	Norway	0.010	0.400	0.490	Lien et al. 1993

Red and White	Sweden	0.008	0.460	0.531	Lunden et al. 1997
	Germany	0.020	0.573	0.366	Ehrmann et al. 1997
Ayrshire	New Zealand	-	0.432	0.527	Winkelman&Wickham 1997
	Finland	0.001	0.509	0.490	Ikonen 1997
	United Kingdom	0-0.003	0.600	0.400	Swaigood 1992
	USA	0	0.720	0.280	Swaigood 1992
Red	Denmark	0.044-0.060	0.710	0.230	Bech et al. 1990

Data is extracted from the study of Kaminski et al., 2007.

In a study conducted in Brazil, it was reported that β -casein A2 allele frequencies of Gir and Guzera cattle breeds were 98% and 97%, respectively. Authors reported 0.96 and 0.93 values for A2A2 genotype frequencies, respectively (Rangel et al., 2017). In a study conducted in India, A1A2, A2A2, A1A1 genotypes in Frieswal crosses were 51.5%, 31% and 17.5%, respectively. The frequency for β -Cn A2 allele was 56.8% (Kumar et al., 2019). Genotype frequencies of A1A1, A2A2 and A1A2 in Indian Vrindavani crosses were 12.3%, 39.6% and 48.1%, respectively. β -Cn A1 and A2 allele frequencies were 0.364 and 0.636 (Kumar et al., 2021). Kumar et al. (2019) attributed the predominance of the A2 allele despite years of crossbreeding to the high A2A2 genotype frequency of the Indian domestic cattle breed used in the crossbreeding

program. Due to the low A1 β -Cn levels of milk obtained from local breeds grown in Turkey, BCM-7 formation does not occur and A2 type original healthy milk is obtained (Sarı, 2014). A1 and A2 β -Cn allele and genotype frequencies detected in domestic cattle breeds raised in Turkey are shown in Table 5 (Dinç, 2009) and (Şahin et al., 2020).

Table 4. Genotype and allele frequencies of the β -casein variants in Turkish Native Cattle Breeds

Breed	Number of animals	Allelic frequency		Genotype frequency			References
		A1	A2	A1A1	A1A2	A2A2	
East Anatolian Red	25	0,080	0,880	0	0,160	0,760	Dinç, 2009
	100	0,195	0,805	0,070	0,250	0,680	Şahin, 2020
South Anatolian Red	30	0,117	0,766	0	0,233	0,534	Dinç, 2009
	87	0,190	0,810	0	0,380	0,620	Şahin, 2020
Native Black	16	0,125	0,781	0,062	0,125	0,625	Dinç, 2009
	100	0,200	0,800	0,020	0,360	0,620	Şahin, 2020
Gray Steppe	34	0,426	0,544	0,235	0,382	0,324	Dinç, 2009
	87	0,201	0,799	0,020	0,360	0,620	Şahin, 2020

Data is extracted from the study of Dinç,2009 and Şahin, 2020.

3-The influence of origin

Studies have shown that A1/A2 frequencies are not species-specific, but are specific to the region and geography. For example, the incidence of the A1 variant in Holstein Friesen (HF) cows in North America and Northern Europe was >90%, while the incidence of the A2 variant (97%) was higher in German HF cows. In other countries, the incidence of A1 frequency in HF cows varies between 40-65% (Behera et al., 2018). Frequency β -Cn A2 allele 60%, A1 frequency 30% in Italian Holstein Friesian cattle population; genotype frequencies were determined as A2/A2 (36.96%), A1A2 (35.79%), A1A1 (9.88%) (Sebastiani et al., 2020). A1 and A2 allele frequencies in Czech Holsteins were 0.45 and 0.55, respectively; while genotype frequencies are reported as A1A1 (0.20), A1A2 (0.51) A2A2 (0.29) (Manga and Dvorak 2010), β -Cn A1 and A2 alleles are 0.396 and 0.604, respectively, in Serbian Holstein-Friesian population; genotype frequencies were reported as A1A1 (12.26%), A1A2 (54.72%) and A2A2 (33.02%) (Ristanic et al., 2020). In Chinese Holstein cattle, the β -Cn A1/A2 alleles were 0.432 and 0.459, respectively; genotype frequencies were determined as A2A2 (0.226), A1A2 (0.353), A1A1 (0.203) (Dai et al. 2016). In a study conducted in India, β -Cn A1A1, A1A2 and A2A2 ales in HF cows were found to be 0.216, 0.451 and 0.333, respectively; genotype frequencies were found as A2 (0.559) and A1 (0.441) (Sodhi et al., 2012a). Gholami et al. (2016) reported Iranian HF β -Cn A1 and A2 allele frequencies

as 0.50, while Dinç et al. (2013) reported Turkish HF β -Cn allele frequencies as A1 (0.485) and A2 (0.456).

4-Effect of lactation number and stage

Nguyen et al. (2019) examined raw milk samples from animals of different breeds, ages, and lactation periods in terms of β -casomorphin-7 (Table 6). They suggested that there were significant differences in the amount of BCM-7 in milk samples, and that this difference was caused by the breed, age, and lactation period of the animals. The amount of BCM-7 in milk is lower as age increases in Holstein Fresian animals. In the Jersey breed, the BCM-7 level in the milk of the animal in the first lactation was found to be considerably higher than that in the second lactation. The number of peptides is higher in the first week of lactation and decreases in later stages of lactation.

Table 5. BCM-7 Level by Different breed, Age and Lactation Period

Breed	Lactation cycle	Lactation stage	BCM-7 (ng/g)
Holstein Fresian	1	Mid	-
	1	Early	29,5
	1	Early	37,94

	5	Late	-
	2	Late	22,99
	2	Late	78,27
	6	Early	-
	3	Early	56,40
	7	Late	22,05
Jersey	1	Early	242,19
	2	Early	65,11

Data is extracted from the study of Nguyen et al., 2019.

Cieřslińska et al. (2012) included Holstein Friesian A1A1, A2A2 and A1A2 cows in the first lactation. Samples were collected on the 30th, 100th and 200th days of lactation, hydrolyzed with different enzymes and examined for BCM-7 levels (Table 7). In the study, the lowest BCM-7 values were found in raw milk, and the highest in the milk of A1 variant cows hydrolyzed with pepsin+trypsin+elastase. They reported that BCM-7 value was the lowest in A2 variant cow's milk in all periods. They suggested that the presence of β -casomorphin-7 in milk obtained from cows with the A2 variant is probably the result of acid hydrolysis during digestion of β -casein with

pepsin. In the same study, it was reported that high temperature processing of raw milk (pasteurized and sterilized) increased BCM-7 values in both A1A1, A1A2 and A2A2 variants.

Table 6. BCM-7 level in raw and hydrolyzed milk in different stages of the cow lactation (ng/ml)

Periods of the lactation (day)	Genotype	Milk		
		Raw	Hydrolyzed by enzyme pepsin	Hydrolyzed by enzymes pepsin+ Trypsin +Elastase
30th	A1A1	2,0	25,0	544
	A1A2	1,8	21,0	357
	A2A2	1,2	8,0	47
100th	A1A1	2,1	22	596
	A1A2	1,9	18	469
	A2A2	1,1	7,0	45
200th	A1A1	2,1	23	683
	A1A2	2,0	19	479
	A2A2	1,2	6	59

Data is extracted from the study of Cie'sli 'nska et al., 2012.

Jarmołowska et al. (2007) examined BCM-5 and BCM-7 levels by taking 3 different milk samples from 30 breastfeeding mothers immediately after birth (colostrum), 1 and 4 months after birth. At the end of the study, they reported that the level of BCM-7 found in colostrum was 8- and 9-times higher than in

milk taken 1 and 4 months after birth, respectively. The highest concentrations of β -casomorphin-8 immunoreactive substance in female plasma were found between the second and sixth days postpartum.

5-Effect of technological processes to which milk is exposed

De Noni (2008) investigated β -casomorphine levels by hydrolyzing milk samples obtained from Holstein-Friesian and Jersey cows with pepsin. BCM-7 was only present in A1 type milk. β - β -Casein types (A1A1, A1A2, and A2A2) have been detected in the dairy of Karan Fries (KF) cattle, which are carriers of the A1 and A2 alleles with high milk yields and stimulated using in-vitro proteolytic enzymes in India. The level of BCM-7 from the A1A1 variant was nearly 3.2 times greater than that from the A1A2 variant of β -casein; nevertheless, it has been reported that BCM-7 is not released from the A2A2 variant of β -casein (Haq et al., 2015).

Cie'sli 'nska et al. (2007) defined two genotypes, A1/A1 and A2/A2, in their study on ten Polish Holstein-Friesian cows. The researchers selected all cows from a herd and milked them in the same season and lactation stage to minimize the impact of the environment on milk characteristics, including the amount of BCM-7. They reported traces of BCM-7 in unhydrolyzed raw

milk. As a result of hydrolysis of milk protein extracts with pepsin, they detected 2.87 µg/mg in A2/A2 samples and 11.59 µg/mg BCM-7 in A1/A1 samples. As a result of the research, they reported that BCM-7 was formed in A2 milk by hydrolysis of raw milk, although not as much as in A1 milk.

Asledottir et al. (2018) quantified the amount of BCM-7 released after ex-vivo digestion of Danish Holstein cow milk for different β-casomorphine variants (A1, A2, I and F) representing variants containing both proline and histidine at position 67 of the sequence. In the study, each milk sample was exposed to 60 min gastric + 5 min duodenal and 60 min gastric + 120 min duodenal digestion. At the end of the study, the highest BCM-7 level was in the A1 variant in both periods; they also found that with the increase of duodenal digestion time, the level of BCM-7 increased in the A1 variant and decreased in the A2 variant. A serving of milk (200 mL) after 5 minutes of duodenal digestion contained 1.15 mg and 0.05 mg of BCM-7 in A1 and A2 variants respectively. More of BCM-7 was detected after 120 minutes of duodenal digestion (3.71 mg and 0.02 mg in A1 and A2 variants). Nguyen et al. (2021) investigated the effect of thermal processing on βCM-7. Milk samples were subjected to *in-vitro* gastrointestinal digestion following different thermal processing conditions (73°C for 20 seconds, 85°C for 5 minutes, and 121°C for 12 minutes). Although βCM-7 was not secreted in milk with A2A2 phenotype, it was detected at the level of 127.25 to 198.10

ng/mL (4.94–7.70 ng/mg protein) in heated milk with A1A1 phenotype.

6-Effect of presence of dipeptidyl peptidase-4 enzyme

Dipeptidyl Peptidase-4 (DPP-4) is an important enzyme effective on glucose metabolism, nutrition, gastrointestinal, reproductive and immune system functions and is associated with the treatment of many diseases such as diabetes, cancer, inflammatory bowel disease and multiple sclerosis (Leventerler et al., 2019). The DPP-4 enzyme has a key role in the modification, processing, and inactivation of peptides (Wasilewska et al., 2011) and is the primary degrading enzyme of BCM-7. BCM-7 is hydrolyzed to form BCM-5 and BCM-3 through the action of DPP-4 enzymes present on enterocyte surfaces and within the blood. In the absence of DPP-4 enzyme activity, BCM-7 crosses the blood-brain barrier from the intestine and reaches μ (MOP) receptors in the brain (Parashar and Saini, 2015). The presence of DPP-4 enzyme is an important factor determining the biological activity of BCM-7 in the human body. BCM-7 is thought to modulate the immune response by affecting DPP-4 gene expression (Fiedorowicz et al., 2014).

There are studies showing that infants with ALTE syndrome (life-threatening events: sudden infant death syndrome, apnea) have higher BCM-7 concentrations and lower levels of DPP4 enzyme compared to healthy infants. This

suggests that infants at risk lack the ability to produce sufficient amounts of DPP-4, the only enzyme that can break it down (Woodford 2011). The effect of insufficient DPP-4 enzyme activity on casein protein and the transition process of BCM-7 from gut to brain are shown in Figure 4 (Parashar and Saini, 2015).

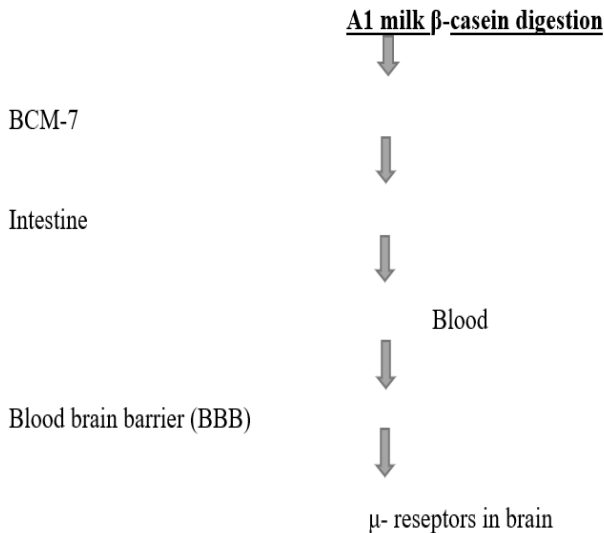


Figure 4. Digestion of β -casein A1 variant and transition of BCM-7 from intestine to brain in DPP-4 enzyme deficiency. Figure is extracted from the study of Parashar and Saini, 2015.

CONCLUSION

Milk is one of the basic foods that has an important role in human nutrition. It is suggested that milks called A1 and A2 have different effects on human health. Negative effect of β -casomorphin-7 opioid peptide on human health has recently been suggested. Studies have shown that some diseases such as heart diseases, neurological disorders, intestinal diseases and sudden infant death syndrome are associated with A1 milk consumption and BCM-7 level. It has been understood that studies on this subject have not reached a sufficient level yet, and the importance of genetic, breeding, and feeding studies that can prevent and/or minimize BCM-7 formation has emerged. For this reason, A1 β -casein levels are quite low and can produce A2 type healthy milk, but the number of indigenous breeds that have decreased and is on the verge of disappearing, should be accelerated, and studies should be accelerated to increase their numbers, and besides issues such as lactation period and order, which are effective on BCM-7, Studies should focus on investigating the relationship between feeding and BCM-7. As a result, it has been observed that many factors affect β -casomorphin-7 from studies conducted to date. It was concluded that more studies should be done on the subject in order to better understand the mechanism of the factors affecting BCM-7

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REFERENCES

- Addeo, F.L., Chianese, A., Sachi, R., Cappucino, U., Ferranti, P. and Malorni, A. (1992). Characterization of the 12% trichloroacetic acidsoluble oligopeptides of Parmigiano-Reggiano cheese, *Journal of Dairy Research*, 59 (3), 401-411.
- Asledottir, T., Leb, T.T., Poulsen, N.A., Devold, T.G., Larsen, L.B. and Vegarud, G.E. (2018). Release of b-casomorphin-7 from bovine milk of different b-casein variants after ex vivo gastrointestinal digestion, *International Dairy Journal*, 81, 8-11.
- Beavers, L. and Van Doormaal, B. (2016). Beta casein, A2 milk and genetics. *Canadian Dairy*, <http://www.cdn.ca/document.php?id=461>
- Behera, R., Sahu, A., Mandal, A., Rai, S., Karunakaran, M. and Dutta T. (2018). A1 versus A2 milk - impact on human health, *International Journal of Livestock Research*, 8(4), 1-7.
- Bhat, M.Y., Dar, T.A. and Singh, L.R. (2016). Casein Proteins: Structural and Functional Aspects. Isabel Gigli (Ed.), *Milk Proteins-From Structure to Biological Properties and Health Aspects* (pp. 3-15). Published by InTech, Croatia.

- Brooke-Taylor, S., Dwyer, K., Woodford, K. and Kost, N. (2017). Systematic review of the gastrointestinal effects of A1 compared with A2 β -casein, *Advances in Nutrition*, 8, 739–748.
- Chianese, L., Garro, G., Nicolai, M.A., Mauriello, R., Ferrani, P., Pizzano, R., Cappuccio, L.P., Addeo, F., Ramunno, L., Rando, A. and Rubino, R. (1993). The nature of β -casein heterogeneity in caprine milk, *Lait*, 73, 533-547.
- Chitra, P. (2021). Bovine milk: A1 and A2 beta casein milk proteins and their impact on human health: a review, *Agricultural Reviews*, 43(3), 374-378. doi: 10.18805/ag.
- Cieślińska, A., Kostyra, E., Kostyra, H., Oleński, K., Fiedorowicz, E. and Kamiński, S. (2012). Milk from cows of different β -casein genotypes as a source of β -caso-morphin-7. *International Journal Food Science Nutrition*, 63(4), 426–430.
- Clare, D. and Swaisgood, H. (2000). Bioactive milk peptides: a prospectus. *Journal of Dairy Science*, 83(6), 1187-1195.
- Dai, R., Fang, Y., Zhao, W., Liu, S., Ding, J., Xu, K., Yang, L., He, C., Ding, F. and Meng, H. (2016). Identification of alleles and genotypes of beta-casein with DNA

- sequencing analysis in Chinese Holstein cow, *Journal of Dairy Research*, 83(3), 312-316.
- Davoodi, S.H., Shahbazic, R., Esmaeilid, S., Sohrabvandid, S., Mortazaviane, A.M., Jazayerie, S. and Taslimi, A. (2016). Health-related aspects of milk protein. *Iranian Journal of Pharmaceutical Research*, 15(3), 573-591.
- Day, L. (2016). Protein: Food Sources. Encyclopedia of Dairy Sciences, Ed: Caballero, B., Finglas, P.M., Toldrá, F. *Academic Press*, 530-537.
- Deeth, H.C. and Bansal, N. (2019). Whey Proteins: From Milk to Medicine. *Academicpress*, 746 p, London, UK.
- De Noni, I. (2008). Release of β -casomorphins 5 and 7 during simulated gastro - intestinal digestion of bovine β -casein variants and milk-based infant formulas, *Food Chemistry*, 110 (4), 897–903.
- De Noni, I., Stuknytė, M. and Cattaneo, S. (2015). Identification of β -casomorphins 3 to 7 in cheeses and in their in vitro gastrointestinal digestates, *LWT-Food Science and Technology*, 63 (1), 550–555.
- De Oliveira, L.S.M., Alves, J.S., Bastos, M.S., Rocha da Cruz, V.A., Pinto, L.F.B., Tonhati, H., Costa, R.B. and Ferreira de Camargo, G.M. (2021). Water buffaloes (*Bubalus bubalis*) only have A2A2 genotype for beta-casein, *Tropical Animal Health and Production*, 53, 145.

- Dinç, H. (2009). Genotyping of Beta-casein, Kappa-casein and Beta-lactoglobulin Genes in Turkish native cattle breeds and efforts to delineate BCM-7 on human PBMC. PhD Thesis, Graduate School of Natural and Applied Sciencs, Middle East Technical University, Ankara, Turkey.
- Dinç H., Özkan, E., Koban, E. and Togan, İ. (2013). Beta - casein A1/A2, kappa-casein and beta-lactoglobulin polymorphisms in Turkish cattle breeds, *Archives Animal Breeding*, 56,650-657.
- EFSA, 2009. Review of the Potential Health Impact of β -Casomorphins and Related Peptides Peptides, *European Food Safety Authority Scientific Report*, 231,1-107.
- Fiedorowicz, E., Kaczmarek, M., Cieslinska, A., Szłapka, E.S., Jarmołowska, B., Chwała, B. and Kostyra, E. (2014). β -casomorphin-7 alters – opioid receptor and dipeptidyl peptidase IV genes expression in children with atopic dermatitis, *Peptides*, 62, 144–149.
- Ghnimi, S. and Eldin, A.K. (2015). Casein variants and challenges in the valorization of camel milk as a healthy alternative to cow milk, *Journal of Bioequivalency and Bioavailability*, 7(4), 1-2.
- Gholami, M., Hafezian, S.H., Rahimi, G., Farhadi, A., Rahimi, Z., Kahrizi, D., Kiani, S., Karim, H., Vaziri, S., Mohammadi, S., Veisi, F., Ghadiri, K., Shetabi, H. and Zargooshi J. (2016). Allele specific-PCR and melting

curve analysis showed relatively high frequency of β -casein gene A1 allele in Iranian Holstein, Simmental and native cows, *Cell and Molecular Biology*, 62 (12), 138-143.

Gobbetti, M., Stepaniak, L., De Angelis, M., Corsetti, A. and Di Cagno R. (2002). Latent bio- active peptides in milk proteins: proteolytic activation and significance in dairy processing, *Critical rev. Critical reviews in food science & nutrition.*, 42 (3), 223 - 39.

Gürsoy, A. (2015). Composition and properties of milk. <http://cv.ankara.edu.tr/duzenleme/kişi/sel/dosyalar/06012015013030.pdf>. 26.05.2021

Haq, M.R.U., Kapila, R. and Kapila S. (2015). Release of β -casomorphin-7/5 during simulated gastrointestinal digestion of milk β -casein variants from Indian crossbred cattle (Karan Fries), *Food Chemistry*, 168, 70–79.

Jarmolowska, B. and Krawczuk, S. (2012). The influence of storage on contents of selected antagonist and agonist opioid peptides in fermented milk drinks, *Milchwissenschaft*, 67(2), 130-133.

Jinsmaa, Y. and Yoshikawa M. (1999). Enzymatic release of neocasomorphin and beta- caso morphin from bovine beta-casein, *Peptides*, 20 (8), 957-962.

- Jung, T. H., Hwang, H.J., Yun, S.S., Lee, W.J., Kim, J.W, Ahn, J.Y., Jeon, W.M. and Han K.S. (2017). Hypoallergenic and physicochemical properties of the A2 β -Casein fraction of goat milk, *Korean Journal of Food Science Animal Resource*, 37(6), 940-947.
- Kaminski, S., Cieslinska, A. and Kostyra E. (2007). Polymorphism of bovine betacasein and it's potential effect on human healt, *Journal of Applied Genetics*, 48(3): 189-198.
- Keating, A., Smith, T., Ross, R. and Cairns, M. (2008). A note on the evaluation of a beta-casein variant in bovine breeds by allele - specific PCR and relevance to β -casomorphin, *Irish Journal of Agricultural and Food Research*, 47, 99-104.
- Kollias, H. (2011). Research review: Fast vs. slow whey for protein synthesis. <https://www.precisionnutrition.com/whey-vs-casein>. (12.03.2021).
- Kostyra, E., Szłapka, E.S., Jarmołowska, B., Krawczuk, S. and Kostyra, H. (2004). Opioid peptides derived from milk proteins. *Polish Journal of Food and Nutrition Science*, 13/54 (1), 25-35.
- Kumar, A., Singh, R.V, Chauhan, A., Ilayakumar, K., Kumar, S., Kumar, A., Kumar, S., Sonwane, A., Panigrahi, M.

- and Bhushan, B. (2019). Genetic association analysis reveals significant effect of β -casein A1/A2 loci on production & reproduction traits in frieswal crossbred cows, *Biological Rhythm Research*, 51(8), 1259-1272.
- Kumar, A., Kumar, S., Singh ,R.V., Chauhan, A., Kumar, A., Sonwane, A., Ilayakumar, K. and Singh, R. (2021). Investigation of genetic polymorphism at β -casein A1 / A2 loci and association analysis with production & reproduction traits in Vrindavani crossbred cows, *Animal Biotechnology*, 33(7),1562-1570.
- Leventerler, H., Ürünsak, İ.F. and Dikmen N. (2019). Biochemical approach to dipeptidyl peptidase-4 enzyme, *Archives Medical Review Journal*, 28(1), 41-50.
- Li, F.H. and Gaunt, S.N. (1972). A Study of genetic polymorphisms of milk β - lactoglobulin, α s₁-casein, β - casein, and κ -casein in five dairy breeds, *Biochemical Genetics*, 6(1), 9-20.
- Lonnerdal, B., Bergstrom, S., Andersson, Y., Hjalmarsson, K., Sundqvist, A.K. and Hernell, O. (1990). Cloning and sequencing of a DNA encoding human milk beta – casein, *FEBS Letters*, 269 (1),153-156.
- Manga, I. and Dvorák, J. (2010). TaqMan allelic discrimination assay for A1 and A2 alleles of the bovine CSN2 gene, *Czech Journal of Animal Science*, 55(8), 307–312.

- McLachlan, C.N.S. (2001). Beta - casein A1, ischaemic heart disease mortality and other illnesses, *Medical Hypotheses*, 56(2), 262–272.
- Miralles, B., Hernández-Ledesma, B., Fernández-Tomé, S., Amigo, L. and Recio I. (2018). Health-Related Functional Value of Dairy Proteins and Peptides. *Proteins in Food Processing*, 2nd., Ed: Yada, Y.R., Woodhead Publishing, 523-568.
- Mishra, B. P., Mukesh, M., Parakash, B., Bujarbaruah, K.M., Sodhi, M., Kapila, R., Kishore, A. and Bhaseen, V. (2009). Status of milk protein, β -casein variants among Indian milch animals, *The Indian Journal of Animal Sciences*, 79(7): 722-725.
- Moughan, P.J., Rutherford, S.M., Montoya, C. and Dave L. (2014). Food-derived bio-active peptides a new paradigm, *Nutrition Research Reviews*, 27(1), 16–20.
- Muchlenkamp, M.R. and Warthesen, J.J. (1996). B-Casomorphins: analysis in cheese and susceptibility to proteolytic enzymes from *Lactococcus lactis* ssp. *Cremoris*, *Journal Dairy Science*, 79(1), 20-26.
- Muhammed, E.M. and Stephen, M. (2012). Betacasein A1A2 polymorphism and milk yield in Vechur, Kasargode dwarf and crossbred cattle, *Journal of Indian Veterinary Association Kerala*, 10(3), 5-9.

- Napoli, A., Aiello, D., Di Donna, L., Prendushi, H. and Sindona G. (2007). Exploitation of endogenous protease activity in raw mastitic milk by MALDI-TOF/TOF, *Analytical Chemistry*, 15: 5941–5948.
- Ng-Kwai-Hang, K. and Grosclaude F. (2003). Genetic Polymorphism of Milk Proteins. *Advanced Dairy Chemistry-1 Proteins*, Ed: P.F. Fox P.L.H. McSweeney, Springer, Boston, MA., 739-816.
- Nguyen, D.D., Solah, V.A., Johnson, S.K., Charrois, J.W. and Buseti, F. (2014). Isotope dilution liquid chromatography-tandem mass spectrometry for simultaneous identification and quantification of beta-casomorphin 5 and beta-casomorphin 7 in yoghurt, *Food Chemistry*, 146, 345–352.
- Nguyen, D.D., Johnson, S.K., Buseti, F. and Solah, A.S. (2015). Formation and degradation of beta-casomorphins in dairy processing, *Critical Reviews Food Science and Nutrition*, 55(14): 1955-67.
- Nguyen, D.D., Solah, V.A., Johnson, S.K., Nguyen, H.A., Nguyen, T.L.D., Tran, T.L.H., Mai, T.K. and Buseti, F. (2019). Identification and quantification of beta-casomorphin peptides naturally yielded in raw milk by liquid chromatography-tandem mass spectrometry, *LWT*, 111, 465–469.

- Nguyen, D.D., Buseti, F., Johnson, G.S.S.K. and Solah, V.A. (2021). Release of beta-casomorphins during in-vitro gastrointestinal digestion of reconstituted milk after heat treatment, *LWT*, 136(1), 110312.
- Nowier, A.M. and Ramadan, S.I. (2020). Association of β -casein gene polymorphism with milk composition traits of Egyptian Maghrebi camels (*Camelus dromedarius*). *Archives Animal Breeding*, 63, 493–500.
- Pal, S., Woodford, K., Kukuljan, S. and Ho, S. (2015). Milk intolerance, beta-casein and lactose. *Nutritions*, 7(9), 7285-97.
- Parashar, A. and Saini, R. (2015). A milk and it's controversy- a review, *International Journal of Bioassays*, 4, 4611-4619.
- Park, Y. (2021). A2 Milk and CMPA. <https://encyclopedia.pub/10268>.
- Pasin, G. (2017). A2 milk facts: what is A2 milk ? <https://cdrf.org/2017/02/09/a2-milk-facts/>
- Petrotos, K., Tsakali, E., Goulas, P. and D'Alessandro A.G. (2014). Casein and Whey Proteins in Human Health. Milk and Dairy Products as Functional Foods Ed: Kanekanian, A., John Wiley & Sons, Ltd. Published, 94-146.

- Priyadarshini, P., Mishra, C., Mishra, B., Swain, K., Rout, M. and Mishra S.P. (2018). Impact of milk protein on human health: A1 verses A2. *IJCS*, 6, 531 – 535.
- Rahman, S.M., Islam, A., Alam, Md., Hossain, Md.K., Alim, Md.A., Salimmullah, Md. and Alam, J. (2016). Analysis of Beta-casein gene variants of milk in cattle. Conference: *Proceedings of the 3rd International Exhibition on Dairy Aqua and Pet organized by AHCAB*, February 2016. Bangladesh, Dhaka.
- Ramesha, K. P., Rao, A., Basavaraju, M., Alex, R., Kataktalware, M.A., Jeyakumar, S. and Varalakshmi, S. (2016). Genetic variants of β -casein in cattle and buffalo breeding bulls in Karnataka state of India, *Indian Journal of Biotechnology*, 15(2), 178-181.
- Rangel, A.H.N., Zaros, L.G., Lima, T.C., Borba, L.H.F., Novaes, L.P., Mota, L.F.M. and Silva M.S. (2017). Polymorphism in the beta casein gene and analysis of milk characteristics in Gir and Guzera dairy cattle, *Genetics and Molecular Research*, 16 (2), gmr16029592.
- Rashidinejad, A., Bremer, P., Birch, E.J. and Oey, I. (2017). Nutrients in Cheese And Their Effect on Health And Disease. Part 14, Nutrients in Dairy and Their Implications For Health and Disease, Ed: Watson, R.R., Collier, R.J., Preedy, V.R., *Academic Press*, 177-192.

- Ristanic, M., Glavinic, U., Vejnovic, B., Maletic, M., Kirovski, D., Teodorovic, V. and Stanimirovic, Z. (2020). Beta-casein gene polymorphism in Serbian holstein-friesian cows and its relationship with milk production traits. *Acta Veterenaria Beograd*, 70(4), 497-510.
- Sarı, B. (2014). Indigenous cattle breeds of Turkey and healthy milk. <http://bilalsari.com/yerli-sigirirklarimiz-ve-saglikli-sut/> (03.01.2021).
- Sarode, A.R., Sawale, P.D., Khedkar, C.D., Kalyankar, S.D. and Pawshe, R.D. (2016). Casein and Caseinate: Methods of Manufacture. Encyclopedia of Food and Health, Ed: Caballero, B., Finglas, P.M., Toldra, F., *Encyclopedia of Food and Health*, 676-682. DOI: 10.1016/B978-0-12-384947-2.00122-7
- Sebastiani, C., Arcangeli, C., Ciullo, M., Torricelli, M., Cinti, G., Fisichella, S. and Biagetti M. (2020). Frequencies evaluation of β -Casein gene polymorphisms in dairy cows reared in central Italy, *Animals* (Basel), 10(2), 252.
- Séverin, S. and Wenshui, X. (2005). Milk biologicaliy active components as nutraceuticals review, *Critical Reviews in Food Science and Nutrition*, 45(7-8), 645-56.

- Singh, R. (2020). A2 milk: a healthier choice. <https://www.pashudhanpraharee.com/a2-milk-a-healthier-choice/>
- Smirnova, A., Konoplev, G., Mukhin, N., Stepanova, O. and Steinmann, U. (2020). Milk as a complex multiphase polydisperse system: approaches for the quantitative and qualitative analysis, *Journal of Composites Science*, 4(4), 151.
- Sodhi, M., Mukesh, M., Mishra, B.P, Kishore, A., Prakash, B., Kapil, R., Khate, K., Kataria, R.S. and Joshi B.K. (2012a). Screening of taurine and crossbred breeding bulls for A1/A2 variants of β -casein gene, *Indian Journal of Animal Sciences*, 82 (2), 183–186.
- Sodhi, M., Mukesh, M., Kataria, R.S., Mishra, B. P. and Joshii, B.K. (2012b). Milk proteins proteins and human health: A1/A2 milk hypothesis, *Indian Journal Endocrinology Metabolism*, 16(5), 856.
- Stepaniak, L., Foxi, P.F, Sorhang, T. and Grabska, J. (1995). Effect of peptides from the sequence 58±72 of b-casein on the activity of endopeptidase, aminopeptidase and X-propyl-dipeptidyl aminopeptidase from *Lactococcus lactis* MG 1363, *Journal of Agricultural and Food Chemistry*, 43(3), 849-853.

- Swinburn, B. (2004). Beta casein A1 and A2 in Milk and Human Health . Report to New Zealand Food Safety Authority. <http://biochemie-crashkurs.de/wp-content/uploads/2014/08/Betacasein.pdf>
- Şahin, Ö. (2020). Determination of Polymorphic Structure on Exon 7 of Beta-Cn Gene (CSN2) and A1/A2 Milk Production Potentiality in Some Domestic and Crossbreed Cattle Breeds Reared in Turkey. (Ph.D Thesis, Graduate School of Natural and Applied Sciences of Selçuk University, Konya.Turkey.
- Şenel, E (2016). Part 4: Milk proteins. <https://docplayer.biz.tr/12515538-4-bolum-sut-proteinleri-doc-dr-ebru-senel-ankara-universitesi-ziraat-fakultesi-sut-teknolojisi-bolum-u.html> (20.12.2020)
- Tamime, A.Y., Wszolek, M., Božanić, R. and Özer, B. (2011). Popular ovine and caprine fermented milks, *Small Ruminant Research*, 101(1-3), 2-16.
- Trustwell, A.S. (2005). The A2 milk case: a critical review, *European Journal of Clinical Nutrition*, 59(5), 623–631.
- Ul Haq, M.R., Kapila, R., Shandilya, U.K. and Kapila, S. (2014). Impact of milk derived β -casomorphins on physiological functions and trends in research: a review, *International Journal of Food Properties*, 17(8), 1726-1741.

- Uniacke-Lowe, T. and Fox, P. F. (2011). Equid milk. In J. W. Fuquay, P. F. Fox, & P. L. H. McSweeney (Eds.) (2nd ed.). *Encyclopedia of Dairy Sciences*, Vol. 3 (pp.518e529) San Diego, CA, USA: Academic Press
- Wasilewska, J., Sienkiewicz, - Szlapka, E., Kuzbida, E., Jarmolowska, B., Kaczmarek, M. and Kostyra, E. (2011). The exogenous opioid peptides and DPPIV serum activity in infants with apnoea expressed as apparent life-threatening events (ALTE), *Neuropeptides*, 45(3), 189-195.
- Woodford, K. (2008). A1 Beta-casein, Type 1 Diabetes and Links to Other Modern Illnesses. (IDF) International Diabetes Federation Western Pacific Congress, Wellington, New Zealand.
- Woodford, K. (2011). BCM-7 and sudden infant death syndrome <https://keithwoodford.wordpress.com/2011/04/10/bcm7-and-sudden-infant-death-syndrome/> (23.12.2020)
- Xu, R. J. (2009). Bioactive peptides in milk and their biological and health implications, *Food Reviews International*, 14(1), 1–16.

Zimmerman, K. A. (2016). Camel milk: nutrition facts, risks & benefits.
<https://www.livescience.com/53579-camel-milk.html>
(04.05.2021).

CHAPTER 2

HONEYBEE BREEDING

Mahir Murat CENGİZ¹

Murat GENÇ²

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¹ Assoc. Prof. Dr. Mahir Murat CENGİZ, Atatürk University, Vocational School of Technical Sciences, Department of Plant and Animal Production, Erzurum, Turkey. mahirmuradcengiz@gmail.com, Orcid ID: 0000-0002-9844-4229

² Assoc. Prof. Dr. Murat GENÇ, Atatürk University, Faculty of Veterinary Medicine, Department of Animal Science and Animal Nutrition, Erzurum, Turkey. vet.murat.genc@gmail.com, Orcid ID: 0000-0002-9565-0887

INTRODUCTION

In all living things, new individuals are more similar to their parents and siblings than to other individuals. In other words, heredity is essential for all the characters that every living species has and will have in the future. However, the similarity of individuals with a common ancestor is not absolute. In fact, there is no absolute similarity between any two individuals, and there are some differences even in identical twins. These differences between individuals with common origins are called genetic variation. Accordingly, genetics is a science that investigates how and to what extent variation can be controlled through heredity.

Research in this field has revealed many genetic principles and laws. Observable variations in existing individuals constitute a prelude to genetic principles and rules that may emerge in the future. So genetics is a dynamic issue. Characters seen in parents may change in offspring.

The genes that determine the characters are localized at certain points of the chromosomes in the cell. Genes are capable of reproducing themselves in cell generations. However, sometimes the chemical composition of a gene can change and thus create a different structure and activity. Sometimes it can even reveal a new character. Such a change is called mutation. Then, genetics can be defined as a branch of science that

examines the principles of transferring the characters of parents to offspring through genes.

In general, there are two main ways to increase the productivity of animals. The first of these is to manage the herd in the best, most accurate and flawless way by streamlining the maintenance and feeding works, in short, to improve the environmental conditions; The second is to raise superior animals with higher productivity, that is, to correct the hereditary structure.

All of the work carried out to raise the average productivity of the herd to a higher level in future generations by obtaining individuals with superior productivity abilities within the current herd is called breeding. Breeding studies consist of selection and breeding methods. These two elements of correction are both interconnected and complementary to each other. Selecting highly productive individuals in each generation and separating them for breeding is defined as selection. All honeybee species in nature have been subjected to constant selection since their existence. This works in two ways: natural selection and artificial selection.

In natural selection, individuals that can withstand harsh environmental conditions survive and reproduce, while individuals that cannot adapt to natural conditions cannot survive and disappear. Artificial selection, on the other hand, is

a selection applied by human beings and aims to eliminate individuals from the herd that do not benefit them and do not suit the breeding purposes. Since human breeding purposes are often different from the selection pressure created by environmental conditions, there is a big difference between these two types of selection. Artificial selection is a matter of emphasis and importance in terms of breeding in breeding.

1.1. Inbreeding in Honey Bee Colonies

Queen bee breeders and some researchers state that there is no difference between queen bees obtained from breeding material (eggs) taken from the same colony. However, the unique mating behavior of the queen bee causes her to form groups of individuals with different genetic structures in the colony.

In order for there to be no genetic variation among the offspring of the queen bee, mating must be with only one drone bee, that is, the offspring must be one mother and one father. However, queen bees mate with more than one (8-18) drone bees and store the sperm cells they receive from them in their spermathecae and use them to fertilize their eggs, which serve as a source for female individuals throughout their lives. This situation affects the degree of kinship in the colony, creating a very complex kinship phenomenon between individuals of the same colony.

The queen bee is the mother of all colony individuals, but also their parent. Because although drone bees have a haploid chromosome structure; Female individuals are diploid and naturally become second generation individuals. Drones within the colony are not the fathers of any individual in the colony. Moreover, they carry the queen bee's own gametes. In other words, drone bees themselves do not have a father, as they develop from the infertile eggs of the queen bee that do not unite with sperm; but they have maternal grandparents.

The mating of the queen bee with more than one drone causes most of the female offspring in the colony to have a mother and separate sisters. Therefore, in order to fully shed light on the issue, it is necessary to examine the mating alternatives that the queen bee can engage in practically or theoretically. These are summarized below.

1.1.1. Queen Bee Mating with Only One Drone

Theoretically, a queen bee mating with only one drone bee can happen very rarely in practice. However, it is always possible to achieve this through artificial insemination under laboratory conditions. In this case, since the queen's eggs will be fertilized by sperm from the same drone bee, the female offspring are super sisters with the same mother and father (Figure 1.1). The situation is different for drone offspring.

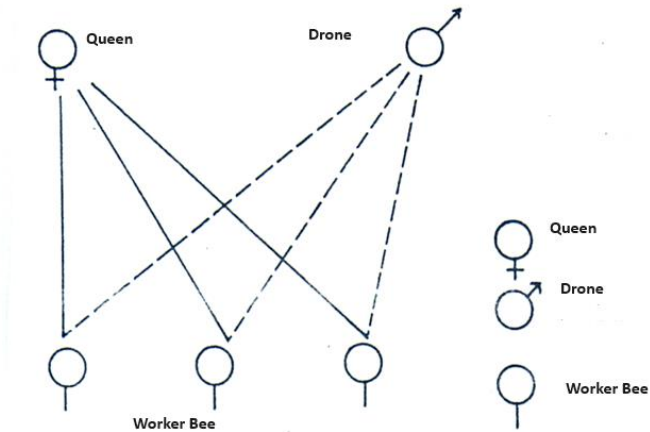


Figure. 1.1 Mating of a queen bee with a drone

In order to understand the kinship relationship between colony individuals in such a mating, it is necessary to know how the inheritance mechanism works. Whereas genetic material is transferred to female offspring through both eggs and sperm; In drone offspring, this is achieved only through the egg.

Since drones are haploid, they have the same genotypic structure. However, since the transfer of allele genes to the egg cell, which is the source of female offspring, depends on chance, genetic variation also occurs among the female offspring of the queen bee that mates with a single drone. However, there is no genetic variation among the gametes obtained from the father.

This mode of inheritance has very important consequences for breeding studies.

The fact that the drone gives gametes with the same genetic structure increases the degree of kinship between the sisters to 75%, enabling the formation of super sisters. On the other hand, a single gamete of the queen bee that turns into a drone bee enables this drone to produce 8-10 million gametes with the same genetic structure. Since drone bees are haploid, F2 generation cannot be obtained. Because the F2 generation can only be obtained from two F1 individuals that are hybrids themselves, and drone bees cannot be hybrids. This situation poses a disadvantage in terms of breeding.

1.1.2. Mating of the Queen Bee with Drones from Different Colonies

Under natural conditions, the queen bee mates with several drones from different colonies, and their sperm cells are stored in the queen bee's spermatheca. As a result, offspring with the same father may occur in the colony, as well as offspring with different fathers.

As seen in Figure 1.2, the queen bee mating with drone number 1 creates population A; Mating with drones numbered 2, 3 and 4 results in the formation of B, C and D populations, respectively. Worker bees belonging to population A are super sisters consisting of the same parents and the degree of

relatedness between them is 75%. Likewise, worker bees in populations B, C and D are super sisters among themselves within the population. Each of these populations is a family group or subfamily with parents. Members of two different subfamilies are half sisters because they have different mothers and fathers.

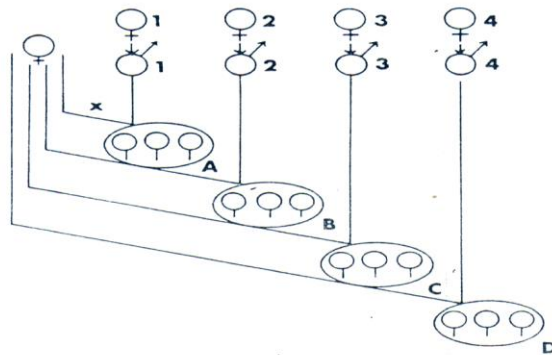


Figure 1.2. Mating of the queen bee with several drones from different colonies.

The degree of consanguinity between half-sisters is 25%. In this type of mating, there is no chance of forming a full sister with a 50% degree of kinship between them. So, under normal conditions, a colony is practically the sum of its super sister groups. Although each group is a super sister within itself, there is a half-sister relationship between the groups. Within the colony, subfamilies are formed as many as the number of drones with which the queen mates. The colony itself is a superfamily formed by these subfamilies.

1.1.3. Mating of the Queen Bee with Several Drones from the Same Colony

Since the queen bee must mate outdoors, the chance of mating with several drones from the same queen (colony) is extremely limited under natural conditions. However, such mating is possible with artificial insemination under laboratory conditions. The drones used in such a mating are haploid individuals that develop from the unfertilized eggs of the same queen and are also hereditary representatives of their queens. Therefore, this type of mating means genetically mating two queen bees.

As seen in Figure 1.3, a subfamily (A, B, C,...) is formed in the colony for each drone bee that is the offspring of the same queen and mates with the fertile queen. Worker bees within a subfamily are super sisters with a 75% degree of relatedness among themselves. However, there is sisterhood between worker bees belonging to two different subfamilies and the degree of relatedness between them is 50%. Worker bees belonging to different subfamilies have the same mothers but different fathers. However, the fathers are haploid offspring of the same queen. Therefore, the kinship relationship or degree is slightly different here.

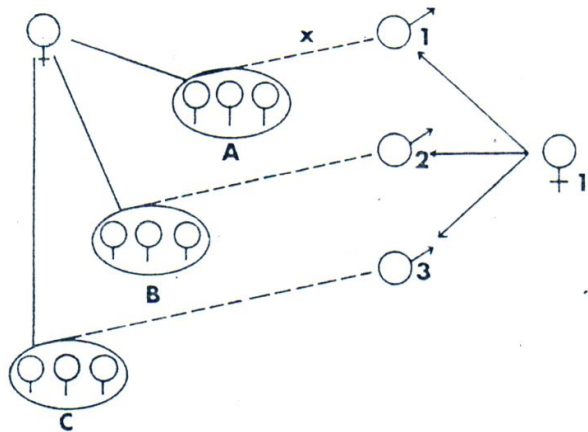


Figure 1.3. Mating of a queen bee with drone bees from the same colony.

1.1.4. Mating of a Queen Bee with Several Drones, Some from the Same Colony

A queen bee mates with 8-18 drones under natural conditions, and sometimes several of them can be offspring of the same queen. In this way, the kinship relationships mentioned under the last two headings are formed between the individuals in the colony formed by a mated queen bee. In other words, all three of the super sisterhood, full sisterhood and half sisterhood situations exist among the colony individuals.

As seen in Figure 1.4, in a situation where the queen bee mates with three separate drones, two of which are from the same colony, a subfamily (A, B, C) is formed for each drone within the colony. Worker bees within the same subfamily are

supersisters. However, there is full sisterhood between the worker bees of subfamily A and worker bees of subfamily B, even though they come from different fathers. Because these drones numbered 1 and 2 developed from the haploid gametes of the same queen bee. Between worker bees belonging to subfamilies A or B and C, a half-sister relationship is valid because their mothers are the same but their fathers are different. Thus, it is possible to see all half-sisters, full-sisters and supersisters with a degree of kinship of 25%, 50% and 75% in the same colony.

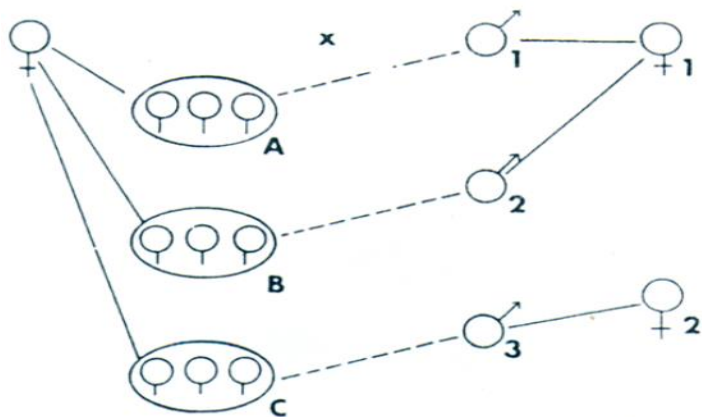


Figure 1.4. Mating of a Queen Bee with Several Drones, Some from the Same Colony

Even if they do not know the details of the system and how it works, beekeepers have noticed that there are different-looking bees in the same colony from time to time. It is natural

for the queen bee to produce sometimes dark and sometimes light colored female offspring, depending on the genetic characteristics of the drone bees that mate with her. Depending on the characteristics of these drone bees, individuals in the colony can be seen to exhibit different behaviors at different times of the year. This ensures that the drones that mate with her become as important as the queen bee in bee breeding.

If the queen bees are not through artificial insemination; If it is to be inseminated through natural mating, then it is necessary to use isolated areas closed to the entry of foreign bees in queen bee breeding. Otherwise, it is not possible to hold the qualities of the queen bees raised to a standard.

1.2. Selection

In scientific terms, selection is to remove from the herd individuals whose phenotypes are undesirable and inadequate in terms of the characters emphasized in a population, and to provide high-yield individuals with a higher chance of survival and reproduction. When selection is applied to increase the average productivity of any herd, individuals whose productivity is below the herd average are first selected and excluded from the herd. In addition, there is a decrease in the herd every year due to various reasons such as death and disease. In order to maintain the herd population, it is necessary to add the best of the new generation to the herd every year, equal to the number

of those removed from the herd and those who leave it. Therefore, artificial selection is applied on the animals in the existing herd, on the one hand, and on the other hand, it is carried out to select new breeders among the offspring obtained in order to keep the herd size constant.

Until recently, there were almost no studies on bee breeding. There was no human influence on the new colonies formed by swarming; these colonies were only affected by natural selection. In other words, colonies that could not adapt to the environment and survive in adverse environmental conditions were spontaneously selected. After the development of the Doolittle method in queen bee breeding, artificial selection carried out by humans began to be effective in detecting new generations, apart from natural selection.

Yapay seleksiyonun amacı, arzu edilen özellikleri aynı ırk veya hatta bir araya getirirken, istenmeyen özellikleri ayıklamaktır. İşçi arıların kısır dişiler olması ve erkek arıların ise ana arının kalıtsal temsilcisi durumunda bulunmaları ıslah çalışmalarının ana arı üzerinde planlanmasını gerektirmektedir. Because the only individual that can be selected in a colony is the queen.

In artificial selection, it is possible to predict the performance of an individual from the phenotype of himself, his parents, his siblings or his offspring. Focusing selection studies

on the queen bee provides some benefits, but it also brings some drawbacks. Because if a limited number of colonies with high performance are used as the source of new offspring, all colonies will become highly related to each other in a short time. This time, the drawbacks of inbreeding are encountered. One of the two basic elements of breeding is selection and the other is breeding methods.

1.2.1. Factors Affecting Success in Selection

1. Correct determination of the purpose: Researches carried out for the purpose of breeding and selection of bees appear as studies based on defining the existing genotype in terms of morphological, physiological and behavioral characteristics, comparing it with other genotypes and improving it in terms of various characteristics, and creating a line to meet a certain need.

The applied selection program must have a concrete purpose and appropriate methods must be used to achieve this purpose. Targeting more than one unrelated goal in selection makes it difficult and often impossible to obtain results. On the other hand, the determined goal should remain constant and should not be changed frequently. For example, while a selection program is being implemented to increase honey yield, giving up on this and choosing to reduce aggressiveness or increase resistance to diseases dooms the selection to failure.

2. Using breeders suitable for environmental conditions: Breeders apply selection to improve a character in their herd that will benefit them. However, new breeders subjected to selection should not be expected to be successful in all environmental conditions. Because colonies that achieve good results in a certain environment in terms of the character emphasized cannot maintain the same productivity level when environmental conditions change. In other words, it is not possible to create a herd that will be successful in all environmental conditions. A highly productive genotype can only demonstrate its superior productivity under suitable environmental conditions.

Since beekeepers use different ecologies throughout the year due to migratory beekeeping, while they get good results in one region, they experience disappointment in another region. For example, the Caucasian bee is the bee of high altitude and cold climate zones, and the Italian bee is the bee of the warm Mediterranean zone. High yields should not be expected with the Caucasian bee in hot coastal regions and with the Italian bee in Eastern Anatolia conditions.

For this reason, the environment suitable for the genotype or the genotype suitable for the environment should be preferred. If there is no genotype-environment compatibility, it may not be possible to keep colonies alive, let alone get high yields. Pure

Caucasian breed breeders have been marketed to producers for years in our country, and these pure breeders are expected to be successful both in Eastern Anatolia conditions and in the Muğla, Antalya, Adana and Mersin climate zones by using them in nomadic beekeeping. This mistake should be abandoned and genotypes suitable for different ecological regions should be developed and beekeepers should be provided with breeders suitable for the region in which they grow. F1 hybrids should be preferred rather than using pure genotypes in breeding.

3. Status of the starting herd: In order for selection or breeding selection to be made accurately, the phenotypic differences seen between the colonies in the current flock in terms of the character used as a basis for selection must be based on the genotype, that is, there must be a genotypic variation in the population.

If the phenotypic variation in the herd, that is, the difference between colonies, is due to environmental conditions, the population is pure line since there is no genotypic variation. No success can be achieved by selection in such a population.

Turkey is a bridge connecting the continents of Europe, Africa and Asia (Middle East), the homeland of the honey bee, and the natural distribution areas of the world's important honey bee races. With its geographical location, our country is an

important gene bank of the world in terms of honeybee populations.

Turkey is surrounded by the natural distribution areas or homelands of the world's important honeybee races. Therefore, it is possible to see the genetic effects of Italian bees in the Aegean Region, Carniolan bees in Thrace, Caucasian bees in Northeastern Anatolia, Iranian and Armenian bees in Eastern Anatolia, and Syrian bees in Southeastern Anatolia. In its current state, Anatolia is a gene pool where many important honey bee races and ecotypes in the world mix and blend together. It is possible to encounter other races in a region where one race is thought to exist. In a large part of Turkey centered in Central Anatolia, the Anatolian bee (*Apis mellifera anatoliaca*), a distinct and very valuable race unique to Anatolia, and its various ecotypes are dominant.

There is an extremely high genetic variation in honeybee populations in Turkey. Different ecotypes of the Anatolian bee are breedable raw materials. These are not just for Türkiye; It is a biological wealth that is very important for the development of world beekeeping and must be evaluated.

To date, no systematic breeding program has been implemented on the honeybee population of our country. Due to the high genetic variation in our country's bee population, it is much easier to obtain successful results with selection programs

than in indoor-bred populations with increased homogeneity. However, due to migratory beekeeping, which is becoming increasingly common in our country and is done unconsciously, the ecotypes we have are mixing with each other, losing their identities and degenerating.

4. Number and nature of characters considered:

Breeding and selection studies should always be based on characters that are economically important and determined by a very limited number of gene pairs that do not have a negative correlation between them. As the number of characters considered increases, it will become difficult to find a sufficient number of breeders that meet all the desired characteristics in the herd and larger herds will be needed. In such a case, the breeding program will cease to be feasible and economical.

If half of the herd is sought after for only one character, $\frac{1}{4}$ of it for two characters, $\frac{1}{6}$ for three characters, $\frac{1}{8}$ for four characters and $\frac{1}{2n}$ for n number of characters will be sought after.

In breeding programs, progress is often made by increasing the frequency of genes that determine the characteristics emphasized in the herd, in other words, by increasing the number of individuals with the desired characteristics. Although progress is easier and faster in characters determined by only one gene pair, progress slows

down as the number of genes effective on the character desired to be improved increases. For this reason, while progress is very rapid in quantitative characters determined by a small number (1-2) gene pairs; Improving the qualitative characters determined by a large number of genes is quite difficult and time-consuming.

If there is a genetic and physiological interaction or linkage between the characters to be discussed, the selection made for one character will also be valid for the other character and thus the selection effect will be multiplied.

For example, as the queen's egg-laying rate increases, the colony population grows and more honey is obtained from strong colonies. In other words, these characters change together and there is a positive correlation between them; Healing and reforming one will lead to the reformation of others.

In cases where more than one character is considered together and improved, there should be no negative correlation between these characters. Otherwise, with the selection made to improve one of the two characters that have a negative relationship between them, the herd will go backwards in terms of the other character.

For example, if it is determined that the pugnacious colonies in the herd have higher honey yield and these two

characters are considered together, in a selection to improve the undesirable pugnacity trait, the honey yield will be negatively affected and the progress in the selection will slow down. Such interactions between characters must be corrected by gene crossing over.

In the selection made for characters whose effects on the phenotype are opposite to each other, at the point when one of the characters is sufficiently improved, selection for this character is abandoned and breeding selection is made based on the other character that has declined.

5. Heritability: In studies aiming to improve various productivity traits of existing honeybee populations through selection, the heritability of the traits emphasized must be known. When determining the characters that are the basis for selection, those with high heritability are preferred. Because the variation displayed by the herd in terms of a character with a high heritability degree is due to genotypic differences rather than environmental factors. So in this case, the phenotypic value of the character is very close to its genotypic value. Since only genotypic variation is passed on to offspring, progress through selection is extremely limited in pure-line herds where there is little or no genotypic variation.

In addition, the methods to be used in breeder selection (such as performance testing, progeny control) are determined

based on the degree of heredity. In selection for characters with high heritability, it is possible to make breeding selection based on phenotypic values. However, for a character with low heritability, selection should be made based on the phenotypic values of parents, siblings or offspring, instead of basing the selection of breeders on phenotypic variation.

In cases where more than one character is considered at the same time, breeding stock selection should be made according to the selection index. To calculate the selection index, the heritability of the characters to be included in the index must be known.

In herds with increased homogeneity, if the phenotypic value of the character in question is desired to be further improved, it is necessary to add blood from other herds of the same race, where the phenotypic value of this character is much higher, or to increase the variation by crossbreeding with other breeds.

6. Efficiency level: In herds with very low productivity levels, the initial progress achieved through selection will be high. However, in future generations, as the herd average and productivity level increases, the rate of progress in selection slows down. Because as the productivity level increases for the character considered, the phenotypic value of this character approaches the upper limit allowed by the genotype.

7. Herd size: The larger the starting flock, the more effective the selection. Because as the herd size increases, it will become easier to find more colonies with the desired productivity level to be reserved for breeding.

8. Year/season effect: It should always be taken into consideration that there may be a year/season effect in studies conducted on subjects such as breeding of honeybees, their physiological and behavioral characteristics, bee diseases, parasites and pests, pollination and biological activities of products obtained from beekeeping, etc. Because the phenotypic values of the traits examined in such studies are determined by the joint effect of genotype and environmental factors. In other words, the variation present in the herd in terms of character is not just the hereditary structure; The year/season effect shaped by environmental factors such as topographic structure, altitude, vegetation, temperature, humidity, wind and precipitation regime, etc. in the research conditions is also responsible. This effect should not be expected to be the same in every season, every year or every repetition of the research, and it should not be expected to affect the phenotypic value in the same direction and to the same extent under all conditions.

In order to increase success in selection and make a more accurate breeding selection, the year/season effect should be eliminated. To ensure this, phenotypic value measurements that

may depend on the year or season should be repeated in successive years or seasons.

9. Dependence on chance: All conditions must be the same for individuals/colonies in different treatment groups and competed or compared with each other in the herds to be selected. During the selection program, conditions must be equal in terms of issues such as queen bee, race, hive type, climate characteristics, care-feeding, disease control, water supply, etc., which may cause stress for each individual or colony and change the phenotypic value to be obtained in terms of the character in question. . In other words, the breeders of future generations should be selected among individuals/colonies with high phenotypic values kept under equal conditions. If there is no dependence on chance, it will not be possible to make an accurate selection.

10. Breeding system: To increase success in selection, an appropriate breeding system should be used. Since variation increases in herds where distance breeding system is applied, the selection effect is high. However, as inbreeding homozygosity increases, the effect of selection on the character in the herd will be less.

Another negative effect of the inbreeding system on selection occurs when colonies become homozygous for one or two undesirable recessive genes, and these homozygous

recessive genes have an epistatic effect against the genes that determine the desired traits. In this case, the genotypic effect of the desired genes is obscured due to epistasis and is not reflected in the phenotype. Thus, individuals/colonies that are in good condition in terms of the desired genes cannot be allocated to breeding due to their low phenotypic values and are expelled from the herd. In other words, the rate of progress slows down because the selection works incorrectly.

Despite all this, the relative amounts of desired genes in herds where selection is applied are gradually increasing compared to the whole population in future generations. In addition, selection ensures that the desired genes create new combinations and that the gametes with these new gene combinations increase proportionally. These two genetic effects are the most important results of selection.

1.2.2. Genotypic Progress and Selection Superiority Achieved in Selection

The efficiency level of a selection program is generally measured by the annual progress that that program will make. The difference between the phenotypic average of the herd and the genotypic average of the offspring of individuals selected from this herd is called "Genotypic Progress Achieved in Selection (R)". The genotypic progress that will occur in a generation through selection in terms of a quantitative character

emphasized in a herd is determined by selection superiority and the degree of heritability.

Selection superiority (S) is defined as the difference between the phenotypic average of individuals allocated for breeding in a generation and the phenotypic average of the herd in that generation. Heritability (h^2) expresses to what extent the phenotypic superiority of the selected ones corresponds to the genotypic superiority. That is, heritability is the share of the genotype in the phenotype. According to this;

Genotypic progress achieved by selection is defined as (R)
$$R = h^2 \times S.$$

For example; For honey yield, if $h^2 = 0.25$, average honey yield of the parent herd = 20 kg/colony and average honey yield of the colonies allocated to breeding = 24 kg/colony;

Since $S = 24 - 20 = 4$ kg and $R = 0.25 \times 4 = 1.0$ kg/colony;

Honey yield of the offspring (next generation) should be expected as $= 20 + 1.0 = 21.0$ kg/colony.

There is a positive correlation between the genotypic progress (R) achieved in selection and the heritability (h^2) and selection superiority (S). In other words, as the heritability and selection superiority increases, the progress made in selection also increases.

In animal breeding, the genetic progress achieved in a year rather than a generation is considered more important as a measure of efficiency of selection programs;

Annual Genotypic Progress is shown as $(R) = S \times h^2/y$.

In the formula, y defines the time between generations (generation interval). The generation interval is considered as the average parental age of the animals allocated for breeding when they give birth. The average age of drone and female breeders gives the average age of the herd; This value is close to the generation range. There is a negative correlation between intergenerational time and genetic progress. In other words, as the time between generations shortens, genetic progress increases.

It is extremely important to shorten this period in breeding programs. Just as the generation interval varies between animal species; It can also vary between different races of the same species and even herds of the same race.

1.2.3. Selection Pressure

Selection pressure is the proportion of individuals excluded from breeding in each generation. It is also referred to as sorting. The population of a herd can only be maintained by separating as many individuals for breeding as the number of

individuals selected. Therefore, as the number of individuals leaving the herd increases, a larger portion of the individuals of a generation will be reserved for breeding. Selection pressure or selection is the opposite of selection and means removing the bad ones from the herd. As selection pressure increases in a herd, selection advantage will decrease.

Selection pressure should be reduced by improving care, feeding and health protection services in the herd. In herds where selection pressure is low, the duration of breeding and therefore the average age increases and the generation interval increases. Therefore, in herds where a selection program is applied, a selection pressure must be applied to keep the genetic progress achieved in selection above a certain level.

1.2.4. Character Average

The character average is obtained by dividing the sum of the phenotypic values of the colonies in terms of characteristics that are repeatedly measured during the season, such as the number of frames with bees, the number of frames with brood, brood production and egg-laying rate of the queen bee, by the number of measurements.

For example; The average bee frame of colony A is the ratio of the total number of bee frames of this colony throughout the season and on different dates to the number of measurements

made. Phenotypic values of colonies, such as nectar collecting tendency, honey yield, viability and wintering ability, are directly used as the average of these characteristics of that colony.

Character average is a very important value that will be used to determine the superiority of colonies belonging to a flock and raced under the same conditions in terms of character and to select the breeders of the next generation. Colonies, which will be compared with each other by calculating the character average for any character under consideration, should be balanced at the beginning of the season in terms of factors such as hive type, queen age, race, food stock, presence of bees and offspring.

On the other hand, there should not be any different treatment between colonies throughout the season in terms of feeding, spraying, pasture and the type of comb provided, etc. Among the colonies competed under equal conditions in this way, those that swarm, those that lose or renew their queen, those that contract any disease or die out should not be taken into account for subsequent measurements and processes and excluded from evaluation.

1.2.5. Character Index

Selection of new breeders can be made based on a single character, or more than one character can be considered at the same time. In cases where more than one character is tried to be improved at the same time, the index must be calculated for each character. The sum of the character indices calculated for each colony gives the colony index.

When calculating the character index, a certain score, such as 5 or 10, is taken as basis for each characteristic of each colony. For a character, the unit value obtained by dividing the highest phenotypic value measured in the herd that year by this score is accepted as 1, and the character index is calculated by dividing it by the average unit value of this character.

Let's try to explain the subject again with a simple example: Let's evaluate each feature of the colonies out of 5 points. If the highest honey yield among the colonies in the herd/apiary is 60 kg and the honey yield of colony A is 15 kg, our unit value will be $60 \text{ kg} : 5 = 12 \text{ kg}$ and the honey yield index for colony A in that year will be $= 15 \text{ kg} : 12 \text{ kg} = 1.25$. Accordingly, the index value found for any character will be between 0 and 5.

If there is a character among the characters under consideration whose phenotypic value in the herd is planned to

be reduced, the index value to be found for this character should be defined with a negative sign. For example, the tendency to be irritable is such a trait, and the index value to be found for this character should be used with a (-) sign when calculating the colony index.

1.2.6. Colony Index

The colony index is the sum of the index values calculated for each of the characters considered for each colony in the flock. For example; Let's say that a program that aims to improve 6 different characters in the swarm at the same time, including the number of frames with bees, the number of frames with brood, pugnaciousness tendency, nectar collecting tendency, honey yield and wintering ability, is implemented. If colony A's bee frame index = 2.50, brood frame index = 2.00, pugnacity index = -3.00, nectar collection tendency index = 2.50, honey yield index = 4.50 and wintering ability index = 4.00; colony index = $(2.50 + 2.00 + 2.50 + 4.50 + 4.00) - 3.00 = 12.50$. Accordingly, the colony index of a colony will be a value between 0 and 25.

Colonies are ranked every year according to their colony index values, and a certain number of colonies with the highest index are selected as breeders for the next generation. The queen bees to be raised by using an equal number of larvae and semen/drones from each of the breeding colonies and the queen

bees of the colonies in the entire flock are renewed, and this process is repeated every year until the planned goal (yield value) is reached in terms of the characters emphasized.

1.2.7. Selection Methods

1.2.7.1. Mass Selection

When breeding selection is made taking into account the phenotypic value of the individual, it is defined as Mass selection, Individual selection or Phenotypic selection. In other words, mass selection is a selection made according to individuals' own phenotypic values. In this selection, the selection of breeders is made entirely by looking at the phenotypes of the individuals, that is, their appearance and performance, and success depends on the share of the genotype in the phenotype. The most important measure of this is the heritability of the character considered in selection.

Individuals with low genotypic values can show high performance under suitable environmental conditions, and in this case, mass selection fails. In other words, mass selection is ineffective in selection for characters with low heritability, that is, characters that are more affected by environmental conditions. Selection according to the individual's efficiency (phenotype) is an accurate selection model for characters with a heritability greater than 0.50. Selection based on phenotypic

values can only provide satisfactory genetic progress if the heritability of the character in question is high.

In mass selection, the individuals/colonies in the herd are ranked according to their phenotypic values by calculating the character average, character index and colony index in terms of the characters emphasized, and then, starting from the top in this order, a predetermined number of individuals are reserved for breeding. However, since the heritability of the quantitative traits that are being tried to be bred is generally low, mass selection is not applied in breeder selection.

With individual selection, it is possible to raise some characters with low phenotypic value (yield) in the herd to a certain level. However, it is not possible to increase the efficiency above this value by taking the selection further. Therefore, after the efficiency reaches a certain level, it is necessary to use other methods.

For example, if selection is to be made to increase honey yield, mass selection is not a correct selection model. Because the heritability of honey yield is low, an individual with a low genotypic structure can exhibit a phenotypically high performance in an environment where environmental conditions are very suitable. In this case, the selection applied may lead to the selection of an undesirable genotype and produce unsuccessful results. In order to avoid making such a wrong

choice, the performances of individuals' relatives should also be evaluated; In other words, pedigree selection should be made. Naturally, this practice reduces the individual selection intensity.

1.2.7.2. Pedigree Selection

Pedigree is the fertility records of an individual's parents and grandparents. The basis of breeder selection according to pedigree is to separate the descendants of highly productive individuals for breeding. By looking at the pedigree, it can be determined how valuable an individual's ancestors are in terms of the character emphasized. Because highly productive individuals have a high ability to transfer these characteristics to their offspring through their genes. When using pedigree, yield records should be reliable and not go back beyond the second generation.

Breeder selection according to pedigree means that any female individual (queen and worker bees) receives half of her genotype from her mother and the other half from her father; It is based on the principle that the genotype of drone bees comes entirely from the mother. However, since queen bees are heterozygous, they produce two types of gametes; It is not possible to predict which genetic half of the queen bee passes to each egg and which of the drone bees that have mated with the queen bee is the father of a fertile egg. In other words, just

because an individual's parents have good fertility records does not necessarily mean that the individual will also be highly productive.

In beekeeping, even if the queen bee of the population forming the colony is known, if artificial insemination is not used, it is not possible to determine how many and which drones of which colonies she mates with. For this reason, the pedigree of these colonies may be misleading when choosing the colonies from which breeding larvae will be provided. Despite some of the inadequacies of pedigree records in breeding selection, they are necessary for preliminary breeding selection until more reliable selection criteria (individual yield values) are obtained. In breeding selection, pedigree is an accurate selection method for characters with low heritability.

Selection based on pedigree or productivity records of relatives can be applied as Family selection, Combined selection and Selection based on offspring and sibling productivity.

In family selection, since the family averages are more genotypic, all individuals of the families with high productivity in terms of phenotypic values are allocated for breeding within the family groups created.

In order to make the right breeder selection through family selection, there must be no different treatment or environmental

differences between families and the number of individuals in the family must be sufficient. Otherwise, environmental differences between family groups will reduce the degree to which family averages reflect the genotype and the expected benefit from selection will not be achieved. On the other hand, as the number of individuals in a family increases, the phenotypic average of that family approaches the genotypic average.

In family selection, high-productive individuals of a family with a low average productivity are excluded from breeding; Low-yielding individuals in a high-yielding family are separated for breeding. This drawback of family selection is eliminated in combined selection, which is a special form of family selection. Because, in combined selection, only a sufficient number of individuals with high phenotypic values from families with superior average productivity are allocated for breeding. Thus, in combined selection, the average productivity of both the individual and the family to which it belongs is taken into account. Combined selection always produces greater genetic improvement than mass selection.

To determine the phenotype of a colony, which is a genotypic structure, phenotypic measurements of some characteristics (nectar and pollen collecting ability, docileness, etc.) are made. However, if the trait being studied is directly

related to the queen itself (such as lifespan, structural state), then the queen bee's own phenotype must be determined. However, most of the time, the feature emphasized is the joint effect of both the queen bee and her offspring. For example, brood production depends neither entirely on the queen nor on the worker bees. In this case, the egg-laying ability of the queen bee and the propensity of the worker bees to raise offspring are limiting factors and together determine the phenotype of the colony.

Although selection based on fertility (Progeny Testing) is mostly used in the selection of drone breeders, it can also be applied to female breeders. Progeny testing, that is, evaluating the offspring according to their productivity, is more suitable for selection for characters with low heritability. The progeny testing method can double the progress made in selection when used in conjunction with individuals' own phenotypic yields. However, for characters with high heritability, it is more accurate to use only individual yield values.

Since drone bees do not have a phenotypic image in terms of characteristics such as nectar collection tendency, honey yield, brood production, honeycomb processing tendency, propolis collection tendency and pugnacity tendency, etc., in the selection of breeding colonies that will be encouraged to raise drone bees to be used as the father line, the female relatives of

these colonies should be considered. Phenotypic values of (parent, sibling, offspring) are used.

Pedigree records are also an important tool in the selection of female breeders (queens). Since the queen bee's own phenotypic value cannot be mentioned for traits such as nectar collection tendency, honey yield, comb processing tendency, propolis collection tendency and pugnacity tendency, etc., her breeding value for such characteristics is determined by the female offspring (worker bees) in the colony. In this way, it is decided in advance whether the individual will be a good breeder or not, and individuals without breeding potential are disposed of as soon as possible.

Selection according to sibling productivity is based on the principle of separating individuals with superior sibling productivity for breeding. Characters such as the number of ovarioles, spermatheca diameter and spermatozoid stock of queen bees can only be measured by killing the queen bees. In such cases, sibling yields are taken into account. In this selection, the family average is calculated only based on the phenotypic values of the queen bees killed for measurement. On the other hand, in the selection of breeding colonies to be used as sire lines, the phenotypic yield averages of their parents and sister queen groups are taken into account.

1.2.7.3. Selection Between Related Lines

Inbreeding is simply a form of breeding that involves mating individuals who are more related to each other than the average degree of relatedness of the population. For this purpose, different forms of inbreeding can be applied, such as mother-daughter mating, sister mating or backbreeding with parents, etc.

Whichever system is applied, the aim of inbreeding is to limit variations in future generations in terms of desired traits or to create a suitable line by activating homozygosity. However, advanced inbreeding should be avoided in order not to reduce selection effectiveness. Otherwise, genotypic variation will decrease in a short time and the chance of success in selection will weaken.

On the other hand, the evaluation of an inbred line is based on the performance of the hybrid combinations of this line. For this purpose, various crosses are made between 3-4 inbred lines and these are tested for performance under different conditions. Those whose performance is appropriate in terms of the trait emphasized, that is, a few of the hybrids that show superior performance under the same conditions, are kept. By repeating the method followed for the resulting superior performance hybrid combination every season, it is possible to raise consistently superior performance breeders.

1.2.7.4. Recurrent Selection

The purpose of inbreeding is to obtain hybrid individuals or lines that are superior to their parents. But the superiority gained cannot be transferred to future generations. In other words, the purpose of inbreeding is to benefit from heterosis (hybrid abundance). When related lines are mated, heterosis sometimes does not occur in the offspring, and even undesirable results may occur. To avoid such a situation, it should be known that honeybees are extremely sensitive to inbreeding and the degree of inbreeding should be kept at a certain level.

Recurrent selection is used to eliminate the problems caused by inbreeding and to create the desired gene combinations. For this purpose, the line whose special combination ability is desired to be developed is continuously mated with a highly inbred line or with a population of a certain genotype, and the selection of the parents is continued according to the performance of the hybrid offspring to be obtained.

There are different models of recurrent selection that can be applied for various purposes. Among these, the selection model that is suitable for the purpose is applied. However, since it would not be economical to preserve a large number of inbred lines, it is necessary to implement a model that minimizes inbreeding and at the same time provides sufficient selection

opportunity in developing lines. In this case, the breeder should apply the "Reciprocal Recurrent Selection" model.

In reciprocal selection, new generations are obtained by crossing these pure lines (for example, two lines) with each other. The best of both lines are mated with each other and breeder selection for the new generation is made through hybrids. In other words, this selection is aimed at taking advantage of the superior dominance advantage between races or lines. For this purpose, the best female and drone individuals in pure breeds or lines are determined and the best of both sides are mated with each other. Thus, it is possible to improve the traits with high heritability (additive gene effect) and then benefit from the heterosis (hybrid overgrowth) that occurs due to non-additive gene effect by crossbreeding these improved races or lines.

1.2.7.5. Indirect Selection

Indirect selection is a selection model that makes use of the correlation between phenotypic and genotypic values of various characters in a population, allowing breeding selection to be made earlier and without waiting for individuals' own yield values. In indirect selection, selection for a trait is made against another character that is related to that trait, has a high heritability, and can be measured accurately at an earlier stage.

For example, the brood production of colonies is a feature that develops depending on the egg-laying rate of the queen. In other words, as the queen's egg-laying rate increases, brood production also increases. Brood production supports the number of adult bees in the colony, and there is a positive relationship ($r = +0.922$) between brood production and adult bee development of the colony. On the other hand, there is a positive and high correlation ($r = +0.83-0.85$) between the number of offspring of the colonies in the spring and their honey yield.

In this case, colonies with a high queen laying rate (incubation production ability) from the beginning of spring create larger populations, and colonies with larger populations have higher honey yields at the end of the season. In other words, the selection of new breeders to increase honey yield can be made accurately, without waiting for the honey harvest, and by taking into account the egg-laying rate of the queen bee, the brood production of the colonies in the spring and the population size.

1.2. Mating (Breeding) Methods

The aim of bee breeding programs is to create desired gene combinations, collect them in certain races or lines, and eliminate genes that determine undesirable traits. The main economic reason for the interest in honeybees is the honey yield of the colonies. The joint effect of a wide variety of individual

and group characteristics determines honey yield. These are closely related features such as the size of the colony population, the egg-laying rate of the queen bee, the propensity of worker bees to raise offspring, the viability of the offspring and the longevity of worker bees. In addition, characteristics such as pugnaciousness, tendency to swarm, tendency to process honeycombs, tendency to collect propolis and resistance to diseases, etc. can also be taken into consideration.

Most of the economic characteristics in honeybees are quantitative. These characteristics usually develop depending on more than one gene pair and are affected to one degree or another by environmental conditions. Therefore, the breeding of quantitative traits depends on the combination of genes effective on them in a particular breed or line.

In order to keep the desired genes in the same line, it is necessary to create homozygous gene pairs, that is, to apply an inbreeding program. Thus, desired gene combinations can be created and at the same time genes that determine undesirable traits can be eliminated. The basis of the mating methods used are given below.

1.3.1. Random Mating

In random mating, all individuals in the swarm have the same chance of producing offspring and any queen bee has an

equal chance of mating with any drone bee. In fact, the mating type that honeybees have been subject to since their existence on earth is random mating. There is no outbreeding in bees. The queen bee mates outdoors, during flight, under completely natural conditions and with multiple (8-18) drones. In other words, since only natural selection and random mating were valid for honeybees until the recent past, the genetic balance in honeybee populations has been preserved and their genetic resources have survived until today.

Random mating does not affect the genetic variation in the population, that is, it does not increase homozygosity. It ensures the preservation of allele genes present in the herd and desired but low frequency gene pairs.

There is a special form of random mating called selective random mating. In this process, firstly, female and drone breeders are raised and selected, and then the selected sire line of the selected queen bees is ensured to mate naturally with the drone bees of the colonies in isolated mating areas. Random mating with selection can always be successfully implemented by creating isolated mating zones.

In beekeeping, the only way to fully control the mating of queen bees is artificial insemination. Since artificial insemination requires a special apparatus, some tools and equipment, and expertise in this field, it should never be

considered for mass (commercial) queen bee production. However, artificial insemination is an indispensable tool that universities and breeding institutions should use for the improvement of existing honeybee genotypes and controlled mating.

1.3.2. Pure Breeding

Pure breeding is based on the principle of selecting the best female and drone breeders of each generation and mating them with each other in a closed herd consisting of individuals/colonies belonging to the same race or sub-race. Selection is an important issue in herds where pure breeding is practiced. In order for selection to be successful, the genetic variation in the herd must be sufficient in terms of the character considered and the heritability of the character must be high. If there is no genetic variation in the current herd, the variation should be increased by adding external blood to the herd.

If a business constantly selects its breeders from its own herd, the herd becomes a closed herd that is raised pure within itself. In herds that are closed to the outside, selection efficiency decreases as inbreeding increases in future generations. Increasing genotypic similarity in the herd makes the phenotypic values of individuals increasingly similar to each other. However, indoor breeding is a way to obtain a new breed by stabilizing the characters. Locking out herds that have reached

the desired productivity level does not create a problem. In this case, it is even possible to not apply any selection until a regression in productivity is observed. In inbreeding degeneration in herds that are closed to the outside, it is more likely to occur in cases where the herd size is small and for characters with low heritability.

Due to the unique mating biology of queen bees, in our country's conditions, even in remote mountain villages surrounded by natural boundaries and where no other beekeepers can enter, complete indoor farming cannot be considered unless artificial insemination techniques are used.

1.3.3. Inbreeding

Inbreeding is a form of breeding between relatives in which pure breeding is practiced much more intensively. In biological terms, kinship is the state of having at least one common ancestor between individuals. Accordingly, any two individuals of a race are related to each other to some extent because they have at least one common ancestor. However, a weak relationship at this level is almost completely meaningless in terms of genetics. As the kinship between individuals in the herd increases, the genetic structures of the individuals become more similar.

In terms of breeding, individuals who have at least one common ancestor in 4-6 generations are called relatives, and matings between them are called inbreeding. From the moment the swarm is closed to outside bee access, it comes under inbreeding pressure.

Inbreeding can be divided into two types: Close breeding and Line breeding, depending on the degree of kinship between mated individuals. Inbreeding is rearing between father and daughter, mother and son, and full siblings who share a common parent in the second generation backwards. Distant inbreeding, on the other hand, is a form of mating in which inbreeding is broader, more intensive and more moderate, between half-siblings, siblings' children, grandparents and grandchildren, uncles and nephews, and between individuals with more distant kinship ties.

Related individuals show certain levels of genetic similarity, depending on the degree of relatedness between them. Genetic similarity (homozygosity) increases in offspring obtained from mating of relatives. The effect of inbreeding on increasing homozygosity in future generations is much higher for characters with high heritability.

Inbreeding enables obtaining a uniform herd by increasing the genetic purity (homozygosity) in the herd and therefore the ability of the individual to transmit their characters to their

offspring (prepotence), removing unwanted recessive genes from the herd by making them homozygous, and obtaining new lines by selection by separating a heterogeneous genetic material into many homogeneous gene complexes.

In herds where inbreeding is practiced, homozygous gene pairs increase proportionally and genetic similarity (purification) occurs. With accurate selection applied in parallel with inbreeding, the uniformity of the herd should be increased in terms of desired characters.

Inbreeding increases prepotency, which is the ability of individuals in the herd to transmit their characters to their offspring. Thus, the desired gene combinations in terms of desired characters are preserved and the expansions are reduced in future generations. With inbreeding, phenotypic and genotypic expansions and new gene combinations occur. In other words, in a heterogeneous population where inbreeding is applied, distinct and homogeneous gene complexes occur more quickly than with other breeding methods. Thus, it is possible to create the desired genotype.

With inbreeding, when homozygosity in the herd exceeds a certain limit, the additivity between the genes that determine the characters disappears and a non-additive gene effect is observed. In other words, when inbreeding is taken too far, it can also lead to some negativities called inbreeding degeneration.

As the rate of homozygous genes increases in inbreeding herds, the progress made in selection slows down. With inbreeding, recessive genes with an epistatic effect in the herd can become homozygous and cover the effects of dominant or homozygous recessive genes of high economic importance, and this situation prevents accurate selection by causing individuals who are thought not to have the desired genes to be excluded from breeding.

As homozygosity increases in the herd through inbreeding, there may be a regression in terms of characteristics such as environmental adaptability, disease resistance and viability, etc. For these reasons, when homozygosity reaches a sufficient level in the herd, blood must be added to the herd, as no further genetic progress can be achieved through selection and inbreeding.

The main inbreeding methods that can be applied in beekeeping are given below. Inbreeding is generally not possible in situations where artificial insemination is not applied and mating occurs in its natural course, as queens mate outdoors, in flight, and with multiple drones. However, inbreeding programs can be implemented at all levels using artificial insemination techniques.

1.3.3.1. Mother-Daughter Mating

As seen in Figure 1.5A, queen number one (Q1) is mated with the drone of queen number two (Q2) to obtain queen number three (Q3). Queen bee number three (Q3) is then mated with the drone of its own queen to obtain queen bee number four (Q4). This mating method is not actually mating siblings, but mother-daughter mating. Because Q3's eggs were fertilized by Q1, his mother's son. Thus, Q1 was used in both the mother and father cases.

1.3.3.2. Mating of Sisters

This mating method is based on mating infertile queen bees with their sister's drone offspring. Thus, the sisters are actually mated (Figure 3.5B). If queen number one (Q1) is mated with a drone of queen number two (Q2), queens number three and four (Q3 and Q4) become sisters and are very similar to each other. Because the eggs that formed Q3 and Q4, which are highly related, were fertilized by the sperm cells of the same drone bee.

1.3.3.3. Mating of Cousins

Yakın kuzenlerin çiftleştirilmesi yöntemi Şekil 3.5 C'de gösterilmiştir. Ancak kuzenlerin çiftleştirilmesi yoluyla yüksek verimli hatlar elde etmek çok güç olduğu için, akrabalı yetiştiricilikte bu çiftleştirme yöntemi pek kullanılmaz.

1.3.3.4. Mother-Son Mating

This mating method, known as self-fertilization, can be easily implemented under laboratory conditions. For this purpose, the fertile queen bee is made to lay eggs by giving CO₂ gas. CO₂ is an anesthetic agent. However, it also causes rapid maturation in the queen's ovaries, causing egg laying to begin early. Since all the eggs obtained in this way will be infertile, they develop into drone bees. Mother-son mating is achieved by applying artificial insemination to the queen bee in the laboratory with sperm cells taken from these drone bees.

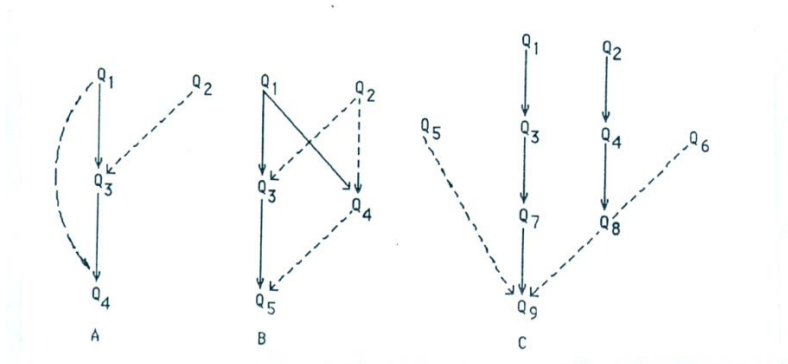


Figure 1.5. Mating methods (A: Mother-daughter mating, B: Sister mating, C: Cousin mating).

1.3.3.5. Line-Breeding

The distant inbreeding program applied to maintain the kinship of any individual (usually the father) with high productivity ability within the herd throughout the generations, that is, to intensify the blood, is called Line-breeding. Although line breeding can be done very easily in animal species with a high reproductive rate, such as pigs, rabbits, chickens and bees, it is much more difficult in species with a slow reproductive rate, such as horses, cattle and even sheep.

Although inbreeding and line breeding are similar in terms of increasing homozygosity in the herd; In inbreeding, kinship originates from more than one common ancestor, whereas in line breeding, the kinship of individuals is based on a selected qualified individual. In line breeding, the female offspring of a qualified sire selected for any character are combined with the drone offspring of another selected qualified sire throughout successive generations. Line breeding based on ancestry is maintained over generations through reciprocal repeated selection.

Line breeding is a special form of inbreeding. Distant inbreeding is a mating system in which parents who are related to each other are mated, but no special effort is made to increase the degree of relatedness of the offspring resulting from this mating. However, in line breeding, the kinship of individuals

with a certain lineage is tried to be preserved as much as possible in future generations. It even increases the likelihood of the ancestral genes on which line breeding is based to be found in the offspring. In other words, in line breeding, the possibility of the desired and undesirable harmful recessive genes of the ancestors being present in the offspring in the heterozygous state is higher.

To date, many line breeding programs have been implemented in many countries, aiming to reduce the tendency of bees to be aggressive and swarm, to increase their resistance to some microbial diseases and parasites, and to increase their effectiveness in pollinating certain plants, and very successful results have been obtained. In recent years, similar studies have been carried out by various universities in our country.

1.3.4. Crossbreeding

Crossbreeding is the mating between individuals with theoretically different genotypes. According to this definition, matings between all individuals, except identical twins, should be defined as crossbreeding. In practice, matings between individuals of different races and ecotypes are called crossbreeding. Crossbreeding requires good selection, as it will increase heterozygosity in the herd and lead to expansion in future generations.

Crossbreeding causes heterosis (hybrid overgrowth) in the new offspring obtained in this way. Heterosis is the superiority of the new offspring, especially F1 hybrids, obtained from matings between different races and ecotypes, than the parent and paternal lines in terms of some characters. This occurs due to increased homozygosity for several dominant genes, sometimes when dominant homozygous genes present in the mother and father are passed on to the offspring in a way that inhibits the effects of the recessive alleles and enhances each other's effects.

Offspring with heterosis may be superior to both parents in terms of some characters (brood production, honey yield, resistance to diseases etc.). However, heterosis cannot be used for breeding purposes. Because when the resulting F1 generation is mated among themselves, they cannot pass on their superior characteristics to their offspring. For this reason, in order to continue to benefit from heterosis, new hybrid offspring are tried to be obtained by new crosses by keeping the parental lines.

For example, if the honey yield averages of genotypes A and B crossed with each other are 30 kg/colony and 40 kg/colony, respectively; In some hybrid colonies, the yield is more than 40 kg, which is heterosis. That is, if the honey yield of a hybrid colony with heterosis is determined as 50 kg, more than the parental average ($30 + 40 = 70/2 = 35$ kg and $50 - 35 =$

15 kg) is the result of heterosis. If the yield increase achieved by heterosis is more than that of the high-yield parent ($50 - 40 = 10$ kg), it is defined as beneficial heterosis.

The ability of hybrid individuals to adapt to environmental conditions, performance, resistance to diseases, survival power and maternal ability are higher than their pure parents. In short, as a result of heterosis, new and superior characteristics that are not seen in the parents appear in hybrid individuals.

Depending on the purpose of breeding, the crossbreeding can be in the form of breeding crossbreeding, conversion crossbreeding, combination crossbreeding and utilization crossbreeding.

a. Breeding Crossbreeding: Crossbreeding made for a temporary period in order to correct, develop and improve any feature of the existing race that is not suitable for the purpose of breeding by using breeders from another race with a superior genotype in terms of the same feature is called breeding crossbreeding. The progeny that have the desired productivity level (F1) in the first generation obtained by hybridization are mated with each other, while those that cannot reach this level are backcrossed with the breeding breed.

In order to prevent any changes in the other characteristics of the breed being tried to be bred, it is necessary to know all the

characteristics of the breeds to be crossed and to make careful selection. Otherwise, some characters of the race planned to be improved may go backwards. If the breeding breed and the breeders selected from this breed are chosen correctly, crossbreeding is stopped and the herd is closed outside. Then, the planned goal is tried to be achieved through accurate selection on the hybrid offspring.

Caucasian bees have long been used as gene material to improve the said characteristics of other races in breeding studies carried out abroad due to their long tongue, docileness and low tendency to swarm.

b. Inversion Crossbreeding: Inversion crossbreeding is the crossbreeding of any breed that needs to be improved with drone individuals of another improved breed for generations (5-6 generations). In each generation, female breeders (queen bees) are mated with the drones of the breeding race's paternal line, and the genetic structure of the current race is largely transformed into a breeding race. F1 hybrid drones obtained in conversion crossbreeding are not used in breeding. After the conversion process is completed (after 5-6 generations), the drone and female breeders obtained in each generation are subjected to selection and mated with each other.

When performing inversion crossbreeding, it is necessary to focus on a very limited number of traits, to know the

characteristics of the breeds to be crossed and to apply careful selection. In addition, environmental conditions such as climate, vegetation, altitude, etc. in the distribution area of the breed to be improved must meet the demands of the breeder.

Inversion hybridization means the extinction of existing breeds with undesirable characteristics in the long term. Therefore it is necessary to be very careful. Marketing Caucasian queen bees to our country's beekeepers for years makes it difficult to protect our genetic resources, causes degeneration and even poses the danger of extinction.

c. Combination Crossbreeding: Double, triple or multiple crossbreeding to obtain a new breed by combining the superior characteristics of more than one breed in the same genotype is called combination crossbreeding. For this purpose, first the characteristics of the new race to be obtained are determined, healing races with these features are selected and then crossbreeding begins. The determined characteristics of breeding breeds are tried to be fixed in the hybrid offspring of each generation. The hybridization process continues until a herd containing a sufficient number of male and female individuals with the desired character combination is obtained. Once the desired type is obtained, hybridization is terminated.

d.Exploitation Crossbreeding: Crossbreeding made to obtain hybrid individuals/colonies by taking advantage of

heterosis is called exploitation crossbreeding. F1 offspring obtained by crossing two pure breeds are superior to both parents in terms of some characters. However, when the F1 generation is mated with each other, a gap occurs and they cannot pass on these superior features to their offspring. For this reason, F1 hybrids are not used as breeding. In order to obtain new hybrid individuals, pure breeds must be kept. This application is mostly possible for species with high reproductive rates such as bees, chickens, pigs and sheep. The broad form of exploitation hybridization between species is not possible in beekeeping.

REFERENCES

- Arıtürk, E. (1983). Evcil Hayvanların Genetiği. Ank. Üniv. Veteriner Fak. Yay.:394, Ders Kitabı, Ank. Üniv. Basımevi, Ankara, 1983, 356s.
- Bıyıkoglu, K. (1973). Genel Zootečni. Atatürk Üni. Yay. No:231, Ziraat Fak. Yay. No: 117, Ders Kitapları Serisi No: 15, Atatürk Üniv. Basımevi, Erzurum, 1973, 316s.
- Du, M., Bernstein, R., & Hoppe, A. (2023). The Potential of Instrumental Insemination for Sustainable Honeybee Breeding. *Genes*, 14(9), 1799.
- Emsen, H. (1992). Hayvan Yetiştirme İlkeleri. Atatürk Üniversitesi Yayınları no: 720, Ziraat Fakültesi no: 310, Ders Kitapları Serisi no: 62, Atatürk Üniversitesi Ziraat Fakültesi Ofset Tesisi, Erzurum-1992, 231s.
- Cengiz, M. M., Diler, A. & Yazıcı, K. (2022). Structural Status of Beekeepers and Beekeeping Enterprises in Ardahan. *Arı ve Arıcılık Teknolojileri Dergisi*, 1(1), 19-28.
- Cengiz, M. M., Diler, A. (2022). Ardahanda Arıcıların Üretim Dönemindeki Uygulama Eğilimlerinin

Belirlenmesi, Ardahan Değerlemeleri-4: Potansiyeller ve Yaklaşımlar (323-339. ss.), İ. KURTBAŞ (Ed.), Nobel Akademik Yayıncılık, Ankara.

Genç, F., Dodoloğlu, A. (2011). Arıcılığın Temel Esasları. Atatürk Üniversitesi yayınları no: 931, Ziraat Fakültesi yayınları no: 341, ders kitapları serisi: 88, Atatürk Üniversitesi Ziraat Fakültesi Ofset Tesisi, Erzurum-2011, 386s.

Guzman-Novoa, Ernesto. (2007). Elemental Genetics and Breeding for the Honeybee. First Edition, Published by the Ontario Beekeepers Association, Printed in Canada, ISBN 978-0-9782166-1-0, 50p.

İncekara, F. (1970). Genetik. Ege Üniv. Zir. Fak. Yay No:166, Ders Kitabı, Ege Üniv. Matbaası, Bornova-İzmir, 1970, 273s.

Kistler, T., Basso, B., & Phocas, F. (2021). A simulation study of a honeybee breeding scheme accounting for polyandry, direct and maternal effects on colony performance. *Genetics Selection Evolution*, 53(1), 1-16.

- Meixner, M. D., Costa, C., Kryger, P., Hatjina, F., Bouga, M., Ivanova, E., & Büchler, R. (2010). Conserving diversity and vitality for honey bee breeding. *Journal of Apicultural Research*, 49(1), 85-92.
- Niño, E. L., & Jasper, W. C. (2015). Improving the future of honey bee breeding programs by employing recent scientific advances. *Current Opinion in Insect Science*, 10, 163-169.
- Obšteter, J., Strachan, L. K., Bubnič, J., Prešern, J., & Gorjanc, G. (2023). SIMplyBee: an R package to simulate honeybee populations and breeding programs. *Genetics Selection Evolution*, 55(1), 1-17.
- Oxley, P. R., & Oldroyd, B. P. (2010). The genetic architecture of honeybee breeding. In *Advances in Insect Physiology* (Vol. 39, pp. 83-118). Academic Press.
- Page Jr, R. E., & Laidlaw Jr, H. H. (1982). Closed population honeybee breeding. 1. Population genetics of sex determination. *Journal of Apicultural Research*, 21(1), 30-37.
- Plate, M., Bernstein, R., Hoppe, A., & Bienefeld, K. (2019). The importance of controlled mating in honeybee breeding. *Genetics Selection Evolution*, 51(1), 1-14.

- Root, A.I. (1983). The ABC and ZYZ of Bee Culture. Published by A. I. Root Company, Medina, Ohio, U.S.A., 712p.
- Rothenbuhler, W. C. (1958). Genetics and breeding of the honey bee. Annual Review of Entomology, 3(1), 161-180.
- Soysal, M., İ. (2000). Hayvan Islahının Genetik Prensipleri. Trakya Üniv., Tekirdağ Zir. Fak., Yayın No:48, Ders Notu No: 40, Tekirdağ, 323s.
- Tüzemen, N., Yanar, M., Akbulut, Ö. (2006). Hayvan Islahı (Düzeltilmiş İkinci Baskı), Atatürk Üniversitesi Ziraat Fakültesi Ders Yayınları No: 230, Atatürk Üniversitesi Ziraat Fakültesi Ofset Tesisi, Erzurum-2006, 428s.

CHAPTER 3

CLIMATE CHANGE AND BEEKEEPING

Yaşar ERDOĞAN

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Assoc. Prof. Dr. Yaşar ERDOĞAN, Bayburt University, Demirözü Vocational School, Department of Veterinary Medicine, Bayburt, Türkiye, ORCID ID: 0000-0001-6154-7008, E-mail: yasarerdogan@bayburt.edu.tr

INTRODUCTION

Average weather conditions that do not change over many years within a fairly large region are called climate. Climate is an extremely important factor for the activity and productivity of honeybee (*Apis mellifera*) (Le Conte & Navajas, 2008). The greenhouse effect caused by the release of gases into the atmosphere resulting from human and agricultural activities is gradually increasing in temperature. If the necessary steps are not taken, it will continue to rise. (Köknaroğlu & Akünal, 2010; Sağlam, Düzgüneş, Balık, & Sciences, 2008).

Climate change affects our lives more and more day by day. As a result of climate change, living things may leave the regions they live in, and new species that do not belong there may settle in the same regions (Doğan, Özçelik, Dolu, & Erman, 2010). Climate change is considered the main threat of the future due to its consequences on all living organisms, including flowering plants and pollinators (Yoruk & Sahinler, 2013). Today, many climacteric changes have emerged that affect the life and behavior of bees. Honey bee survival is affected not only by climacteric conditions, but also by the microclimate inside the hive, hive volume and the egg-laying capacity of the queen.

However, due to the high adaptation capacity of honeybees, they have adapted to very different climatic conditions and have spread almost all over the world (Figure

1). Different honeybee ecotypes have adapted to deserts, mountains, tundra and even rainforests (Ruttner, 2013). Predictions regarding climate change predict that deserts will expand in different regions of the world in future, glaciers will melt, precipitation regimes will change, and more extreme and harsh climate events will occur. The genetic diversity of the honey bees is very important in terms of its adaptation, and this diversity must be protected. Additionally, honeybee colonies will need to adjust to new predators, parasites and pathogens in the case of climate change. The fact that honeybees have different genetic structures is important for their adaptation, and these different genetic structures must be protected. Additionally, honeybee colonies will need to adjust to new predators, parasites and pathogens in case of global warming. A consequence of climate change, not only will the parasites that bees encounter change, but they will also have to confront with new stressors resulting from the transmission of pathogens introduced through trade.

In other words, global warming may create new opportunities for honeybees to live even in unimaginable regions or habitats.

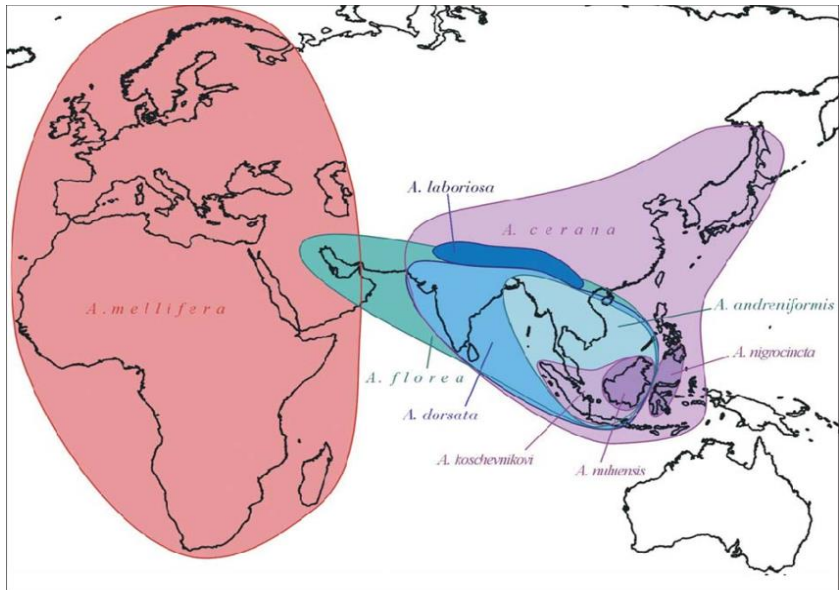


Figure.1. Regions where *Apis* species live in the world (Franck, Garnery, Solignac, & Cornuet, 2000).

Honeybees

The long-term survival of crop production and therefore farming all over the world depends on pollinator insects. In monetary terms, the annual contribution of pollinator insects to the economy is estimated at \$117 billion. 84% of cultivated plants need pollinator insects. Honeybees (*Apis mellifera*) are the most effective pollinators of agricultural crops all around the world (Johnson, Resources, & Division, 2007). Many plants other than grains are insect pollinated, that is, they depend on insects. Approximately 73% of plants are pollinated by

honeybees, 19% by flies, 5% by wasps and 6.5% by bats. In other words, 5 percent of plants are pollinated by insects, 4 percent by birds, and 4 percent by butterflies and moths (Abrol, 2009).

Bats, birds and honeybees are the most effective pollinators globally, affecting 35 percent of agricultural production and increasing the production of 87 of the most important food crops (FAO, 2014).

Honey bees are also very important for preserving biodiversity. Because they enable pollination of many species of plant (Allen-Wardell et al., 1998; Michener, 2000). Climate changes will change plant phenology, especially the flowering period. The bioclimatic and economic balance created by global warming will also affect the distribution of all plant species (Thuiller, Lavorel, Araújo, Sykes and Prentice, 2005). Global warming may destabilize the relationships between flowering plants and pollinators, and pollinators, which are vital for economic and ecological balance, will need to be protected to make ensure pollination. There are 25 subspecies or races of the domestic honey bee (Fig. 2) (*Apis mellifera*) identified by morphometry and molecular analysis. *Apis mellifera* is the most commonly found honey bee worldwide due to its huge honey collecting potential. Each bee race is defined by its morphological, behavioral, physiological and ecological

characteristics and has evolved to suit its own climate and environmental conditions.



Figure.2. Honeybee (<https://www.treehugger.com/honeybees-live-shorter-lives-50-years-ago-6830135>).

1. How are honeybees affected by climate changes?

Honeybees are affected by climate changes at different levels. It is certain the biggest impact will be on the behavior and physiological characteristics of honey bees. It can change the quality of the flower environment. It can increase or decrease the pollen and nectar collection capacity and development of colonies.

As a result of climate changes, honeybee races may change their distribution areas, which may cause them to encounter new bee pests and parasites to which they are not

accustomed. Beekeepers will also have to change their beekeeping methods and techniques. They will choose to move their hives to new apiaries or import bee races they are not used to.

1.1. How is the behavior, physiology and distribution of honeybees affected?

European honeybees (*Apis mellifera*) are very well adapted to hot climates. For example, *Apis mellifera sahariensis* is the North African subspecies of *Apis mellifera* species. This species has adapted to the flowering periods of plants in the region and to extremely high temperatures, and is found in the Sahara region (Ruttner, 2013).

Honey bees need large amounts of water to raise offspring, balance the incubation temperature between 34°C - 35°C, in short, to survive.

In deserts, the temperature is quite high and the flowers of the plants in these regions may not meet the water needs of honeybees and this may lead to their death. It is thought that climate change will further increase drought in deserts, resulting in the destruction of oases and honeybees. *Apis mellifera sahariensis*, which has adapted to deserts, cannot migrate between oases that will disappear due to drought, because their structures are not suitable for long migrations. For this reason, it

is very important to move them to suitable areas to prevent the extinction of this race, which is very important for biodiversity.

Climate changes can also affect the development cycle of honeybees. Because it is accepted that each honey bee race develops at its own pace (J. Louveaux, Albisetti, Delangue, & Theurkauff, 1966). Therefore, any climate change or transfer of a honey bee race from one geographical area to another will have certain consequences. Honeybees spend the winter cold in clusters. They provide the energy they need to keep alive until spring by eating the honey they have stored. As the weather begins to warm up in spring, the queen bee initiates egg laying, strengthens the colony and increases the worker population. When the weather gets cold and they cannot go on nectar and pollen collection flights, honey bees use the pollen and nectar stocks they have stored, but if this period is prolonged, the stores will not be enough and the colony may disappear. However, since local ecotypes adapt to the regional climate, they can adjust their stock amounts and development speed very well and are not affected by these negativities. Therefore, a distinction must be made between local ecotypes that can adapt their development and food stocks to the climate and hybrid breeds obtained as a result of crossbreeding. These hybrid breeds were not developed for storing food; The queen cannot regulate the egg laying period and the worker bees cannot regulate the larval

rearing period; As a result, bees cannot survive without the help of a beekeeper (Sugar syrup, vitamins) (J. Louveaux et al. 1966).

Honeybees adjust their behavior according to the weather. For example, while they do not leave the hive when it rains a lot, they carry a lot of water to cool the colony in extreme heat.

1.2. Climate change affects the living conditions of honey bees due to the change in vegetation.

Climate affects the development of flowering plants, the amount of nectar and pollen production of flowers, the flight efficiency of the colony and colony development (Winston, 1987). Honeybees need to create sufficient honey stores to survive the winter. Worker honeybees need to consume pollen in order to feed the baby bees with the royal jelly they secrete from the hypopharyngeal glands. Climate change also changes the distribution of flower species that are the food source of honey bees (Winston, 1987).

Will the plants be able to withstand extreme drought or, conversely, constant rain? If they can survive, will they be able to produce the pollen and nectar needed for honeybees? Although the effects of these factors on honey bees are not fully known, it is known that environmental factors have effects.

The changes have a direct impact on honey bee development. We know the effect of rain on bees collecting nectar. In rainy weather, the nectar produced by plants is too watery and bees do not prefer it. In extremely dry weather, nectar production stops and even the colony may die of starvation if additional feeding is not done. Insect nectar production also depends strictly on climate. Again, food scarcity is the biggest problem today, resulting from an extremely dry climate that reduces pollen production and reduces nutritional quality (Stokstad, 2007). The pollen shortage seen in autumn will strain the bees in winter, weaken the immune system and make them more susceptible to diseases and pests. The lifespan of honeybees is also shortened.

As a result of climate change, droughts may occur in tropical climate regions. It may turn into more distinct seasons. For this reason, Asian honey bees will need to rapidly change their honey collection strategies to store sufficient amounts of honey and pollen to survive flowerless periods. Or bees of the genus *Apis* may need to develop a migration strategy like the giant honey bee *Apis dorsata* (Figure 3). *Apis dorsata* migrate easily if the seasons and flowering patterns are disrupted. They can migrate hundreds of kilometers to escape hunger or predators. What will happen to non-migratory honey bee species? If large-scale natural swarming occurs, these species may be driven to more favorable areas and leave their areas of

origin. The Landes ecotype, found in France, thrives with heather flowers, which are the main natural source for. Landes ecotype adapted its development to the heather plant. (J. J. B. W. Louveaux, 1973).



Figure 3: *Apis dorsata* (Giant Bee)

(https://www.flickr.com/photos/nico_bees_wasps/).

2. Results regarding the geographical distribution of *Apis mellifera mellifera* and other races.

As with other arthropods, climate change will cause the areas available to honey bees to decrease or increase (Chown, Slabber, McGeoch, Janion, & Leinaas, 2007). Bees will leave the arid areas and migrate towards the edges of these areas. Conversely, they will migrate towards areas that are too cold for honeybees and establish these as habitats. Africanized

honeybees, which have developed adaptations for arid regions, are a good example.

Africanized honey bee; It is a hybrid honey bee. *Apis ellifera scutellata* (Figure 4); It was formed by hybridization with European honey bee species such as the Italian honey bee (*Apis mellifera ligustica*) (Figure 5) and the Iberian honey bee (*Apis mellifera ibirensis*) (Figure 6). The geographical distribution of the African honey bee extends to and ends in Argentina and the United States (Diniz, Soares, Sheppard, Del Lama, & Biology, 2003; Pinto, Rubink, Patton, Coulson, & Johnston, 2005). This is because the climate conditions are too cold for the African honey bee. Therefore, global warming is helping the bee to move beyond its current distribution range. Moreover, African honeybees are less susceptible to Varroa mites than European honeybees (Martin & Medina, 2004).



Figure 4: *Apis ellifera scutellata* (<https://phys.org/news/2014-04-east-african-honeybees-safe-invasive.html>)



Figure 5: *Apis mellifera ligustica*
(<https://observation.org/photos/31307638/>)



Figure 6: Iber honeybee (*Apis mellifera ibirensis*)
<https://www.erbel.eus/fr/2023/01/31/protection-de-labeille-locale-apis-mellifera-iberiensis/>)

It is predicted that beekeepers will change their migration period from winter to summer and move from arid regions to relatively humid regions. They will likely begin importing queens of different breeds to test their potential in adapting to new climates. Although these introduced queen bees will increase genetic diversity, they will also serve as hosts for the introduction of new pathogens or new bee haplotypes with different benefits, as in the past. Crossbreeding imported bees with local breeds can facilitate a genetic mix with a high ability to survive against adverse conditions, but will also tend to destroy local ecotypes and pure breeds through genetic pollution.

3. Adaptation potential and genetic diversity

Apis mellifera is a species with high adaptability, spread all over the world. Imported to America by beekeepers, this species has spread throughout the continent with the help of humans. Since the biodiversity of the species is quite high, it can be assumed that it can use its genetic diversity to adapt to the climate. In contrast, Asian species will be vulnerable if they remain in Asia, as their ability to adapt to climate changes is weak.

Apis mellifera has much higher adaptability than Asian species, whose productive capacity and migration ability are quite low.

Human beings, who have been living with honeybees for hundreds of years, will definitely be decisive in helping honeybees survive in unsuitable environments and preserving the biodiversity of these regions. Bee trade is carried out between countries and continents all over the world. Hybrids between bee races produced by queen bees fertilized by artificial insemination can produce much more honey than the European black honeybee (*Apis mellifera mellifera*) (Fresnaye, Lavie, and Boesiger, 1974). For the production of different bee products, studies are carried out with different honeybee races (Prost & Le Conte, 2005). However, honeybee races obtained as a result of hybridizations are less adaptable to changes in environmental factors than local bee races, and are also more sensitive to bee diseases and pests. A great genetic diversity has occurred due to reasons such as the continued import of hybrid bee races and the deterioration of the genetic structure of local honey bee races.

Companies that engage in large-scale queen bee breeding produce queen bees from the best colonies they have selected. This results in the development of breeds that are more susceptible to all diseases. From a global warming perspective, the more genetic diversity a region has, the more adaptive potential it has. For example, the detection of honeybee colonies in France that survived for years without any treatment against the Varroa mite is important to consider the spontaneous emergence of Varroa-resistant honeybee races (Le Conte et al.,

2007). However, in countries that restrict honey bee imports (Germany, USA), resistance to Varroa mite has not yet been detected in honey bees.

CONCLUSION

The widespread mortality rate of the honey bee (*Apis mellifera*) worldwide and the fact that environmental conditions are becoming harsher day by day reveal the difficulties that this species will face in the future. Factors causing this situation are pesticide use, new diseases and stress. As a result, climate change will disrupt the balance between plant structure, honeybees and diseases. Honey bees have made great progress in colonization. The genetic diversity of bees will make it easier for them to adapt to climate change. However, climate-induced stress is thought to further increase various factors that endanger species in the future. By changing the living environments of honeybees, human beings must also protect the rich genetic diversity of honeybees.

Basic research is necessary to understand the factors causing honey bee extinction.

REFERENCES

- Abrol, D. J. J. o. P. (2009). Plant-pollinator interactions in the context of climate change-an endangered mutualism. 45, 1-25.
- Allen-Wardell, G., Bernhardt, P., Bitner, R., Burquez, A., Buchmann, S., Cane, J., .Ingram, M. J. C. b. (1998). The potential consequences of pollinator declines on the conservation of biodiversity and stability of food crop yields. 8-17.
- Chown, S. L., Slabber, S., McGeoch, M. A., Janion, C., & Leinaas, H. P. J. P. o. t. R. S. B. B. S. (2007). Phenotypic plasticity mediates climate change responses among invasive and indigenous arthropods. 274(1625), 2531-2537.
- Diniz, N. M., Soares, A. E. E., Sheppard, W. S., Del Lama, M. A. J. G., & Biology, M. (2003). Genetic structure of honeybee populations from southern Brazil and Uruguay. 26, 47-52.
- Doğan, S., Özçelik, S., Dolu, Ö., & Erman, O. J. İ. D. v. Ç. (2010). Küresel ısınma ve biyolojik çeşitlilik. 3, 63-88
- FAO. (2014). *Agriculture Organization of the United Nations. Fisheries Department. The state of world fisheries and*

aquaculture: Food and Agriculture Organization of the United Nations.

Franck, P., Garnery, L., Solignac, M., & Cornuet, J.-M. J. A. (2000). Molecular confirmation of a fourth lineage in honeybees from the Near East. *31*(2), 167-180.

Fresnaye, J., Lavie, P., & Boesiger, E. J. A. (1974). La variabilité de la production du miel chez l'abeille de race noire (*Apis mellifica* L.) et chez quelques hybrides interraciaux. *5*(1), 1-20.

Johnson, R., Resources, S., & Division, I. (2007). *Recent honey bee colony declines*: Congressional Research Service.

Köknaroğlu, H., & Akünel, T. J. Z. F. D. (2010). Küresel Isınmada Hayvancılığın Payı ve Zooteknist Olarak Bizim Rolümüz. *5*(1), 67-75.

Le Conte, Y., De Vaublanc, G., Crauser, D., Jeanne, F., Rousselle, J.-C., & Bécard, J.-M. J. A. (2007). Honey bee colonies that have survived *Varroa destructor*. *38*(6), 566-572.

Le Conte, Y., & Navajas, M. J. R. S. e. T.-O. I. d. E. (2008). Climate change: impact on honey bee populations and diseases. *27*(2), 499-510.

- Louveaux, J., Albisetti, M., Delangue, M., & Theurkauff, M. J. L. a. d. l. a. (1966). Les modalités de l'adaptation des abeilles (*Apis mellifica* L.) au milieu naturel. 9(4), 323-350.
- Louveaux, J. J. B. W. (1973). The acclimatization of bees to a heather region. 54(3), 105-111.
- Martin, S. J., & Medina, L. M. J. T. i. P. (2004). Africanized honeybees have unique tolerance to Varroa mites. 20(3), 112-114.
- Michener, C. D. (2000). *The bees of the world* (Vol. 1): JHU press.
- Pinto, M. A., Rubink, W. L., Patton, J. C., Coulson, R. N., & Johnston, J. S. J. G. (2005). Africanization in the United States: replacement of feral European honeybees (*Apis mellifera* L.) by an African hybrid swarm. 170(4), 1653-1665.
- Prost, J., & Le Conte, Y. J. L., paris. (2005). Apiculture: connaître l'abeille, conduire le rucher. 382.
- Ruttner, F. (2013). *Biogeography and taxonomy of honeybees*: Springer Science & Business Media.

Sağlam, N. E., Düzgüneş, E., BALIK, İ. J. E. J. o. F., & Sciences, A. (2008). Küresel Isınma ve İklim Değişikliği. 25(1), 89-94.

Stokstad, E. J. S. (2007). The case of the empty hives. 316(5827), 970-972.

Thuiller, W., Lavorel, S., Araújo, M. B., Sykes, M. T., & Prentice, I. C. J. P. o. t. N. A. o. S. (2005). Climate change threats to plant diversity in Europe. 102(23), 8245-8250.

Winston, M. L. (1987). *The biology of the honey bee*: harvard university press.

Yoruk, A., & Sahinler, N. J. U. B. J. (2013). Potential effects of global warming on the honey bee. 13(2), 79-87.

CHAPTER 4

MEDICINAL AROMATIC PLANTS GROWING AND USAGE AREAS IN TÜRKİYE

Betül GIDİK

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Assist. Prof. Dr. Betül GIDİK, Bayburt University, Faculty of Applied
Sciences, Department of Organic Agricultural Management, Bayburt,
Türkiye. betulgidik@bayburt.edu.tr, ORCID ID: 0000-0002-3617-899X

INTRODUCTION

Medicinal Plants

Medicinal plants are those that have chemicals that may be extracted from different parts of the plant and are used internally or externally to treat illnesses. In addition to being used to heal illnesses, these plants are now utilized in phytotherapy, pharmacy, cuisine, spices, cosmetics, colors, and agriculture. Raw, processed, and herbal goods are the three categories of herbal remedies derived from aromatic and medicinal plants. These plants are quite useful; we may classify them based on their families, the organs they are utilized in, the active substances they contain, how they are used, consumed, and their pharmacological effects (Gül, 2014; Hakverdi and Yiğit, 2017).

The active components and usage area of aromatic and medicinal plants differ greatly. Because of this, they can be broadly grouped based on their families, the active compounds they contain, their intake and use patterns, the organs they are employed in, and their pharmacological effects, even though there isn't a set grouping for them yet. Herbal and fragrant plants are utilized in cuisine, cosmetics, paint, textiles, medicine, and farming, among other industries. The degree of development of a country influences the use of plants for medicinal purposes. In poor nations, herbal remedies are used to cure 80% of the population. Türkiye is home to a wide variety of plant species

and a lush flora. In Türkiye, there are over 11,000 different plant species, and 500 of those are utilized in complementary medicine (Ceylan, 1995; Acıbuca and Budak, 2018; Bayraktar et al., 2017).

Türkiye's Floristic Structure and Herbal Drugs

Medicinal aromatic plant combinations and herbal beverages are expected to be the key concept in the herbal products market. The increasing consumption of medicinal aromatic plants also supports this idea (Ferrier et al., 2006).

The "Flora of Turkey and The East Aegean Islands" states that there are about 12,000 species and subspecies taxa in Türkiye, along with 1251 genera that belong to 174 families. This makes Türkiye's botany highly rich. Of these taxa, 234 are imported or cultivated plants, and the remaining taxa are plants that are found naturally across Türkiye. Given that there are about 12,000 plant species on the European continent, Türkiye has an abundance of plant (Davis 1985, Güner et. al., 2000; Erik and Tarıkahya, 2004).

Thyme, bay leaf, cumin, anise, and sage are the most often exported aromatic and medicinal plants from Türkiye in terms of quantity in recent years. If we look at the quantity of aromatic and therapeutic plants that Türkiye has imported recently, black pepper comes in first. Ginger, cumin, black cumin, anise,

cinnamon, bay leaf, thyme, and sage come next (Bayraktar et al. 2017).

Certain fragrant and therapeutic plants are harvested from nature, while others are grown. Türkiye is the home of several plant cultivations, including thyme (Figure 1), cumin (Figure 2), anise, fennel, sage, black cumin, coriander, fenugreek, mint, poppy, and hops. Certain plants, such rosemary, linden, mahleb, sage, and laurel, are harvested from the natural world. Furthermore, some 347 plant species are traded in Türkiye both domestically and internationally, of which about 139 are exported (Özgüven et al., 2005; Bayraktar et al. 2017).



Figure 1. *Thymus vulgaris* L. (Anonymous, 2011)

Although approximately 200 medicinal plant species used for medicinal purposes in Türkiye have export potential, only 70-100 species are exported (Başer 2000).

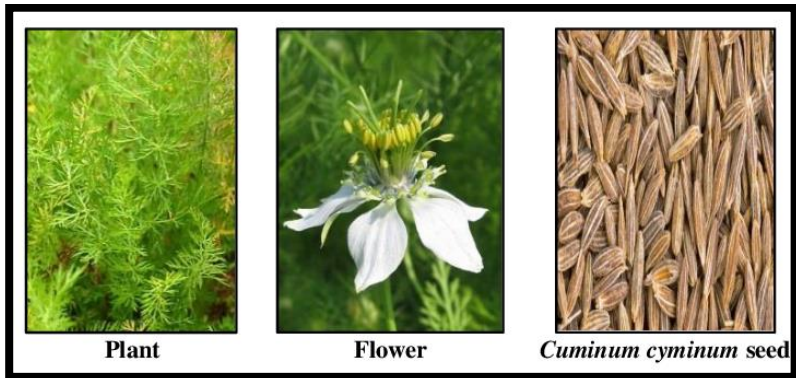


Figure 2. Cumin (*Cuminum cyminum*) (Agarwal et al., 2017)

Türkiye has not been able to raise the volume and value of exports to the necessary levels, despite being one of the most significant producers and exporters of aromatic and medicinal plants in the world. Examining international trade data reveals that some of the aromatic and medicinal plants exported are also among the imported goods, despite the fact that the amounts vary from year to year. Of course, the main cause of this is the profit-driven inclinations of middlemen and businesses involved in the industry, but there are other factors as well, such as Türkiye's processing of aromatic and medicinal plants and the way their goods are packaged for retail (Başer 2000; Bayraktar et al. 2017).

In order to increase Türkiye's market share in medicinal plant exports, it is necessary to grow plants with high economic value and to improve such plants. The number of registered

varieties among plants grown in Türkiye is quite low. In recent years, registration procedures for plant varieties such as flax (Figure 3), poppy, anise, coriander (Figure 4), fenugreek, thyme, sage, basil, cress and arugula have been completed or registration efforts are continuing (Arslan et al. 2005; Yücer and Altıntaş 2012).



Figure 3. Flax (*Linum usitatissimum*) seeds and flowers (Younis, 2015)

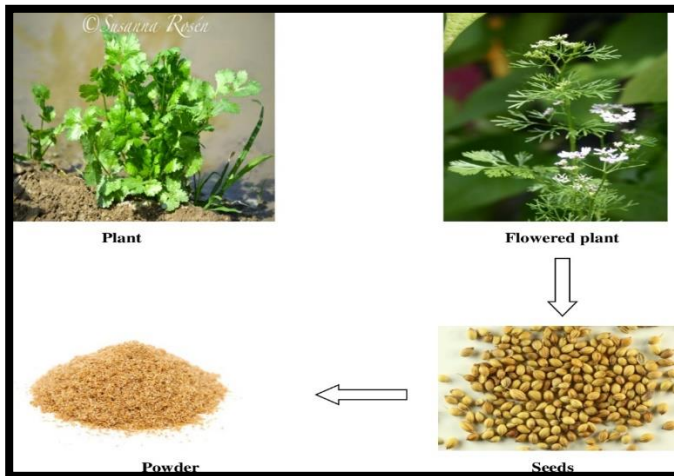


Figure 4. Coriander (*Coriandrum sativum*) (Dharamatti, 2017)

Like in many other regions of the world, Türkiye's climate and biological features allow for the growth or collection of a wide variety of fragrant and medicinal plants from the wild. Natural materials such as laurel, mahleb, linden blossom, sage (Figure 5), rosemary, licorice root, and juniper bark are gathered (TUİK,2009).



Figure 5. Leaf and flower view of *Salvia fruticosa* Mill (Bahadırılı, 2020)

Continuous collection of plants from nature unconsciously may lead to the deterioration of natural vegetation, the extinction of rare and endemic plant species, and the increase of erosion, which is a very important problem, so the collection process should not be done unconsciously (Özhatay and Atay, 1997).

Uses of Medicinal and Aromatic Plants in Turkey

Collecting plants from nature for nutritional purposes has an important history in Türkiye. The people meet their needs by

collecting food from the surrounding mountains and forests. This tradition still continues in rural areas. The aerial parts or roots of many wild plants are used as vegetables. They are consumed raw or raw, or dried, pickled or in the form of tours. Although it is known that there is a "herb culture" in our country, parallel to the rich vegetation in the Aegean and Black Sea regions, it cannot be said that this culture has been researched very well (Baytop, 1994; Bulut, 2005).

Medicinal aromatic plants have been used for medicinal purposes in the treatment of various diseases for centuries. Since essential oils are complex mixtures with different components, they also differ in terms of their biological effects. They also contain various active substances and many essential oil plants; It has antimicrobial, carminative, choleric, sedative, diuretic and antispasmodic effects (Maksimović et al., 2005).

CONCLUSION

Although medicinal aromatic plants have been used for many different purposes since ancient times, they have not yet been sufficiently elucidated. Many different studies have been conducted in this field, but much more comprehensive studies are needed. It is of great importance to conduct many enlightening studies, such as determining the adaptation abilities, active ingredient contents, antioxidant activities,

antimicrobial activities and bioactive properties of these plants, especially those that grow wild in nature.

In addition, deficiencies in the legislation regarding the collection and production of medicinal and aromatic plants from nature should be eliminated and training should be provided to collectors in order to prevent the destruction of nature and the endangerment of medicinal plant species. Apart from these, agricultural economists, agronomists, medical doctors and pharmacists should work together in the field of medicinal aromatic plants in order to solve the problems of the sector and move it forward and to obtain more effective results. Additionally; Especially plant species with high economic value should be cultivated and natural farming of these plants should be started.

Records should be maintained on a regular basis for the production, export, and/or gathering of aromatic and medicinal plants. To conduct safe research on these plants, statistics on trade, export, and production volumes particularly the proportion of production derived from field production and the remainder from natural collections must be tracked.

The demand for and use of therapeutic aromatic plants have grown significantly in recent years as consumers shift away from artificial, chemical-filled items and toward more natural, healthful options. Numerous studies in the literature demonstrate

how these plants have been utilized throughout human history in all spheres of life. Owing to growing requirements, controlled methods of gathering, drying, storing, and using these naturally occurring plants should be followed in order to avoid destruction. The main industries that use medicinal and aromatic plants are biofuel, pharmaceutical, food, fragrance, and cosmetics. These particular plants are primarily utilized for tea and cosmetics. Studies on this subject emphasize the importance of medicinal and aromatic plants.

In order for medicinal and aromatic plants to contribute more effectively to the economic development of Türkiye and to ensure that our country, which has a rich flora in terms of plant species, can benefit more efficiently from these resources, these plants should be protected, sustainable. Production activities should be carried out, controlled collection from nature should be carried out, and most importantly, legal practices should be implemented is required.

REFERENCES

- Acıbuca V. and Budak, D.B. (2018). Dünya’da ve Türkiye’de Tıbbi ve Aromatik Bitkilerin Yeri ve Önemi, Çukurova Tarım ve Gıda Bilimleri Dergisi., vol. 33, no. 1, p. 37-44.
- Agarwal, U.S., Pathak, D.P., Kapoor, G., Bhutani, R., Roper, R., Gupta, V., & Kant, R. (2017). on *Cuminum Cyminum* – Nature’s Magical Seeds.
- Anonymous, (2011). Echappees sauvages. Thym-*Thymus vulgaris* L. <http://www.mauvaisesherb.org/t1251-thym-thymus-vulgaris-l>
- Arslan N., Baydar H., Süleyman K., Karık Ü., Şekeroğlu N. ve Gümüştü A., 2015. Tıbbi Aromatik Bitkiler Üretiminde Değişimler ve Yeni Arayışlar, Türkiye Ziraat Mühendisliği VIII. Teknik Kongresi, 12-16 Ocak 2015, Ankara, s. 483-507.
- Bahadır N.P., (2020). Economically Important Sage Species from Turkey: *Salvia fruticosa* Mill. and *S. aramiensis* Rech fil. Curr. Pers. MAPs, (2020); 3(1): 31-42.
- Başer K.H.C., (2000). Sustainable Wild Harvesting of Medicinal and Aromatic Plants: An Educational Approach,

Harvesting On Non-Wood Forest Products, Seminar Proceedings, Menemenİzmir, Turkey

Bayraktar Ö.V., Öztürk G., and Arslan D. (2017). Türkiye’de Bazı Tıbbi ve Aromatik Bitkilerin Üretimi ve Pazarlamasındaki Gelişmelerin Değerlendirilmesi, Tarla Bitkileri Merkez Araştırma Enstitüsü Dergisi., vol. 26, no. 2, p. 216-229.

Baytop, T.1990. Anadolu’da Bitkisel Drog Ticaretinin Tarihi. Tarım Orman ve Köyişleri Bakanlığı Dergisi, Sayı: 53:6.

Bulut, G. 2005. Narman (Erzurum) ve Köylerinde Halk İlacı Olarak Kullanılan Bitkiler, Yüksek Lisans Tezi, Atatürk Üniversitesi Sağlık Bilimleri Enstitüsü.

Ceylan A., (1995). Tıbbi Bitkiler I. E.Ü. Ziraat Fakültesi Yayınları III. Basım No:312. Bornova/İzmir.

Davis, P.H. (1965)-1985. Flora of Turkey and the East Aegean Islands. Vol. 1-9. Edinburgh: Edinburgh University Press.

Dharamatti, V.U. (2017). Cultivation of Coriander (*Coriandrum sativum* L.): A Review Article. International Journal of Pure & Applied Bioscience, 5, 796-802.

- Erik, S., Tarıkahya, B. (2004). Türkiye Florası Üzerine. Kebikeç İnsan Bilimleri için Kaynak Araştırmaları Dergisi, Alp Matbaası, Ankara, 17, 139-163.
- Ferrier G.K.L., L.A. Thwaites, P.R. Rea, M. Raftery, (2006). US Consumer Herbal & Herbal Botanical Supplement Sales. Nutr. Business J. nbj.stores.yahoo.net/nbsubure20pr.html.
- Gül V. (2014). Rize Yöresine Ait Tıbbi ve Aromatik Bitkilere Genel Bir Bakış, Iğdır Üniversitesi Fen Bilimleri Enstitüsü Dergisi., vol. 4, no. 4 97-107.
- Güner A., Özhatay, N., Ekim, T., Baer, K.H.C. (2000). Flora of Turkey, Volume 11, Edinburgh University Press. Edinburgh.
- Hakverdi A. E. and N. Yiğit, (2017). Yozgat-Akdağmadeni Yöresinde Bulunan Bazı Tıbbi ve Aromatik Bitkiler, Bartın Orman Fakültesi Dergisi., vol. 19, no. 2, p. 82-87.
- Maksimovic, Z.A., Dordevic, S., Mraovic, M. (2005). Antimicrobial Activity of *Chenopodium botrys* Essential Oil. Fitoterapia. 76: 112-114.
- Özgüven M., Sekin S., Gürbüz B., Şekeroğlu N., Ayanoğlu F. ve Ekren S., (2005). Tütün, tıbbi ve aromatik bitkiler

retimi ve ticareti. Trkiye Ziraat Mhendislięi VI. Teknik Kongresi, 1, s.481-501.

zhatay, N., Atay, S. (1997). Kekik in Trade in Turkey, Proceeding of the XI World Forestry Congress, Vol:3:234-237, 13-22 October, Antalya.

TUİK, (2009). Trkiye İstatistik Kurumu Verileri. <http://www.tuik.gov.tr/jsp/duyuru/upload/vt/vt.htm>.

Younis, P.Y. (2015). Seed Properties And Fatty Acid Composition of Flaxseed Oil (*Linum usitatissimum*). Agricultural and Food Sciences. CorpusID:212453764.

Ycer A. ve Altıntaş G., (2012). Trkiye'nin Tıbbi ve Aromatik Bitkiler Dıř Ticareti, Tıbbı ve Aromatik Bitkiler Sempozyumu 13-15 Eyll 2012 Tokat, s.55-63

CHAPTER 5

FORAGE CROPS AND LIVESTOCK SECTOR IN BAYBURT PROVINCE

Mazhar Burak CAN¹
Yasin Yahya YILMAZ²

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¹Phd. Mazhar Burak CAN, Bayburt Provincial Directorate of Agriculture and Forestry, Animal Health Breeding and Aquaculture Branch Directorate, Bayburt, Türkiye. ORCID ID: 0000-0001-5248-1369, E-mail: drmazharburakcan@gmail.com

²Assist. Prof. Dr. Yasin Yahya YILMAZ, Bayburt University, Demirözü Vocational School, Department of Veterinary Medicine, Bayburt, Türkiye, ORCID ID: 0000-0001-6154-7008, E-mail: yasarerdogan@bayburt.edu.tr

1. INTRODUCTION

In parallel with the problems in food supply in the world and in our country, the strategic importance of the agriculture and livestock sector is increasing (Thornton and Gerber, 2010). Crop and animal production has become indispensable in terms of economic resources, regardless of the development level of societies. Although the contribution of agricultural activities to gross domestic product (GDP) has decreased in recent years, it still remains an important sector. For this reason, it is necessary to evaluate the problems experienced in the sector and the rational changes needed as a whole and to produce appropriate solutions.

Within the agricultural sector, animal products are used as raw materials in many industries (such as clothing, cosmetics and pharmaceuticals) and products such as red meat, white meat, milk and eggs meet people's need for animal-based protein (Alao et al., 2017; Potter and Hotchkiss, 2012; Reese, 2018). At the same time, the livestock sector has a critical socio-economic importance especially in rural areas due to reasons such as reducing unemployment, increasing rural development and preventing rural-urban migration (Upton, 2004; Goenenc and Tanrıvermiş, 2008). Turkey, which is one of the world's leading countries in agricultural production, is experiencing significant problems in the livestock sector. Although the increase in the rate of mechanization in the 1950s had a positive impact on the

agricultural sector, the livestock sector was not similarly affected (Sungur, 2016). However, since changes in the livestock sector are reflected positively or negatively on nutrition, raw materials, GDP and rural development, changes in this sector need to be taken under control. Although the current livestock stock in our country is above the level to meet the need, this is not the case in animal production. One of the primary reasons for this is the lack of sufficient amount of quality and cheap roughage. In a 2018 study, it was calculated that the amount of roughage produced in Turkey meets approximately 35% of the current animal wealth (Acar et al., 2020).

Since livestock activities were based on traditional primitive methods in the past, they were negatively affected by the slightest change, creating insecurity in the sector. In the last twenty years, especially with state-supported private sector investments and developments in agriculture, Turkey has taken the first place among European countries in terms of cattle and sheep stock. By aiming to benefit from these investments, especially large-scale enterprises, it is aimed to prevent imports and to make the prices of products accessible with the increase in yield in animal products. Since the livestock products obtained in our country are now processed and offered for consumption instead of being consumed raw, both the income from the sector and employment in this field have increased. However, the pressure of large companies in animal production

and their efforts to dominate the sector cause the share of producers living in rural and urban areas to decrease. As a result, private sector investments combined with many factors such as input costs and social status differences lead to unemployment, rural-urban migration and economic contraction in rural areas.

2. Demographic Structure and Socio-economic Characteristics

Bayburt province is one of the smallest provinces in Turkey with a surface area of 3739 km² (Anonymous, 2023). It ranks 74th in terms of area. It is located in a region bordered by Erzurum in the east, Erzincan in the south, Gümüşhane in the west, Trabzon and Rize in the north. Bayburt plain, which consists of 4 important sections, namely Mörmuş plain, Aydıntepe plain, Düzeker plain and Keçevi plain, has an area of approximately 900 km². The failure to achieve the expected progress in the trade and industry sectors has led the people's livelihood to agriculture and animal husbandry. Bayburt's population is generally small-scale and has a rural structure. Between 2008 and 2022, the general population of the province increased by approximately 10% to 84,241. However, due to internal migration during this period, the population growth rate between rural and urban population moved in the opposite direction. In Bayburt, which generally has a young population, the proportion of young and working age individuals is higher than other age groups. Bayburt's economy is generally based on

traditional sectors such as agriculture, animal husbandry and forestry. However, the economic structure may change over time in the province, which has the potential for urbanization trend. The population distribution in Bayburt between 2008 and 2022 is shown in Figure 1 (TÜİK, 2023a).

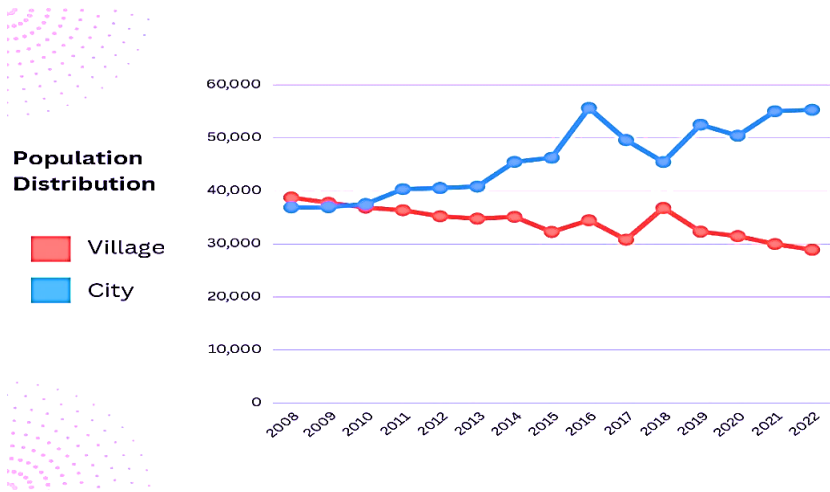


Figure 1. Urban and rural population distribution in Bayburt province between 2008-2022

3. Crop Production, Land Structure, Status of Meadow and Pasture Areas

Bayburt province has a total of 374,697 hectares of land. Although the mountainous and hilly terrain of Bayburt brings certain difficulties in plant production, various plant production activities are carried out throughout the province. The climate and land conditions of the province are suitable for the growth

of certain plant species. Agricultural products are grown in 10,457 hectares of agricultural land, which covers 30% of the province's surface area, and fruit and vegetable products are grown in 45 hectares. While meadow and pasture areas have a share of 18% in our country, this rate is 57.87% in Bayburt province (Figure 2) (Anonymous, 2023). As fruit products, species such as apple, pear and cherry are grown. Orchards are generally located in regions of the province with suitable land conditions. Vegetable crops such as spinach, cabbage and potatoes are grown. Vegetable production activities are generally carried out by small-scale family businesses. Due to climatic conditions, greenhouse activities can be carried out in Bayburt to a limited extent. Therefore, it is possible to grow certain vegetables with certain projects and farmer initiatives related to greenhouse cultivation. Bayburt's vegetable production activities face certain challenges given the climate and land conditions. However, growers generally try to sustain their production by selecting plant species suitable for these challenges and using modern agricultural techniques.

Meadow and pasture areas in Bayburt are generally limited due to its mountainous and hilly terrain. However, there are large natural pasture and meadow areas in certain regions of the province. These areas are important for grazing animals and utilizing natural feed resources. Cold temperatures and snowfalls in winter months negatively affect grazing and animal

feeding processes. Breeders engaged in livestock activities need to plan their animal feeding strategies in order to make the most efficient use of pasture and meadow areas.

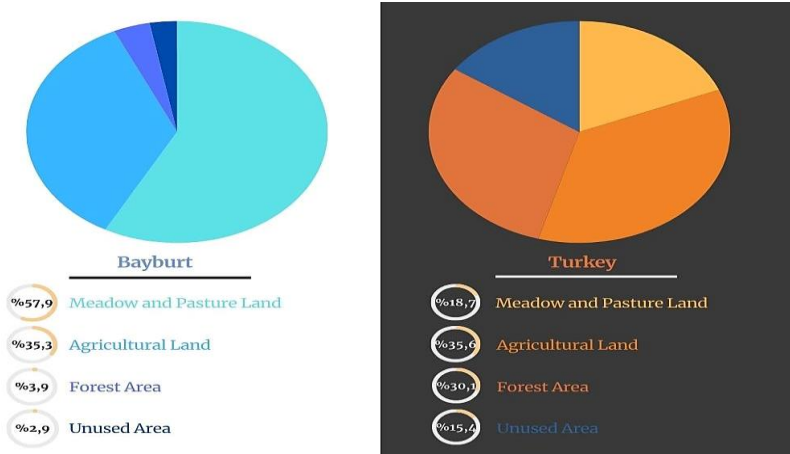


Figure 2. Land distribution in Turkey and Bayburt province, %

Bayburt has a rich land structure in terms of plant production activities. However, when we look at the diversity of agricultural products, the fact that fodder crops stand out intensively shows that the livelihood of the people consists of animal husbandry activities. Among agricultural products, alfalfa, oats and sainfoin are in the first three places in terms of cultivation area and production amount, respectively. The cultivation areas (da) and production amounts (tons) of the priority crops in agricultural activities in Bayburt province in 2022 are presented in Figure 3 (TÜİK, 2023b).

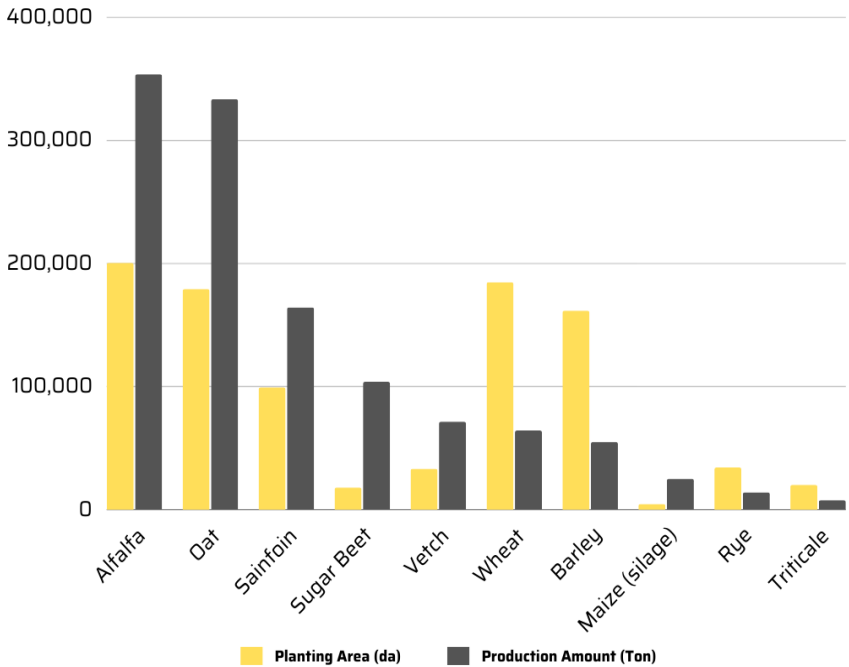


Figure 3. Planting areas (da) and production amounts (tons) of priority crops preferred in agricultural activities in Bayburt province in 2022.

4. Bovine and Ovine Livestock

According to 2022 statistics, Turkey has 17,023,791 cattle and 56,265,750 sheep. In the last ten years, the number of bovine and ovine animals increased by 17.1% and 46.1%, respectively. However, in this period, the number of bovine and ovine animals in Bayburt reached 78,568 with an increase of 2.2% and 80,514 with an increase of 13.4%, respectively. Although livestock farming in Bayburt is mostly done by small-scale family

businesses, the land structure of the province has suitable potential for cattle and sheep breeding. Both types of animal husbandry contribute to Bayburt's agriculture and economy. In recent years, the support provided to livestock enterprises in Bayburt, increasing rainfall due to the effect of climate change and the spread of modern techniques used in animal husbandry have had a positive impact on the number of animals. The number of bovine and ovine animals in Turkey and Bayburt province between 2013-2022 is shown in Table 1 (TÜİK, 2023c).

Table 1: Number of bovine and ovine animals in Turkey and Bayburt between 2013-2022

Years	Turkey		Bayburt	
	Number of Bovine Animals	Number of Ovine Animals	Number of Bovine Animals	Number of Ovine Animals
2013	14.532.848	38.509.795	76.804	70.983
2014	14.345.223	41.485.180	67.045	53.283
2015	14.127.837	41.924.100	85.459	55.282
2016	14.222.228	41.329.232	87.032	48.200
2017	16.105.025	44.312.308	78.931	45.317
2018	17.220.903	46.117.399	97.975	48.797
2019	17.872.331	48.481.479	100.026	39.951
2020	18.157.971	54.112.626	87.182	50.668
2021	18.036.117	57.519.204	79.647	70.464
2022	17.023.791	56.265.750	78.568	80.514

5. Forage Crops Grown in Bayburt Province

The production of fodder crops within agricultural activities plays a locomotive role in meeting the need for roughage and sustaining animal production. Forage crops reduce damage caused by overgrazing, drought and erosion in meadows and pasture areas. Some of the products obtained from agricultural lands are used in animal feeding and transformed into animal products (Soya et al. 2004). Since livestock farming activities in our country are mainly based on a pasture-based extensive farming approach, the desired productivity level cannot be achieved because animals raised in pastures with reduced forage potential cannot be fed well and balanced. Failure to obtain sufficient yield from meadow and pasture areas leads to an increase in the pressure on the cultivation and production of fodder crops. In case of an increase in the production of fodder crops, the opportunity will be given to renew the meadow and pasture areas that have deteriorated or are about to deteriorate (Yolcu and Tan, 2008).

High quality roughage is a basic necessity for the continuity of livestock farms consisting of healthy and high-yielding breeds (Kaya and Bilgen, 1995; Alçiçek et al., 1999). For this reason, the most important step to be taken to increase the contribution from the sector among agricultural and livestock policies in developing and underdeveloped countries should be activities that encourage the production of forage

crops. In our country, alfalfa, silage corn, sainfoin, oats and vetch are the most commonly grown forage crops (Özkan, 2020). When the crop production amounts in Bayburt are evaluated, it is seen that priority is given to alfalfa, oats, sainfoin, vetch and sugar beet agriculture (TÜİK, 2023b).

5.1. Alfalfa

Alfalfa (*Medicago sativa* L.), a perennial forage crop, has a privileged position among the forage crops grown in the world and in our country (Tucak et al., 2021). Characteristically, it is resistant to drought and cold, has high grass yield, can be harvested many times during the vegetation period, wide adaptability and longevity make it stand out against other forage crops (Lane et al., 2000). Although alfalfa silage consumption has become widespread recently, it can also be consumed dry and green (Zhao et al., 2021). There is approximately 16-17% crude protein in dry alfalfa grass and 22% crude protein in green alfalfa grass. Alfalfa is a source of high quality protein. However, when it is used in the form of alfalfa grass or silage, it meets the energy requirement (Albrecht and Beauchemin, 2003). It also contains minerals such as calcium, phosphorus, magnesium and vitamins such as A, D and E to support the development of animals. Alfalfa grass is an important food source in animal nutrition. It is often preferred for dairy cattle because it is tasty and contains high energy and protein.

However, direct grazing should be prevented before it is mowed and withered so that it can be consumed as green. Otherwise, excessive consumption of green clover grass causes sudden bloating (tympani) and death (Artan and Polat, 2019).

Although the cultivation area of alfalfa decreased by 3% between 2015 and 2022 in our country, the production amount increased by 36% to approximately 5 million tons (Figure 4). In Bayburt province, the cultivation area of alfalfa increased by 17% to 200,556 decares and the production amount increased by 12% to 353,691 tons (Figure 5). The cultivation areas (hectares) and production amounts (tons) of alfalfa in Turkey and Bayburt province between 2015-2022 are presented in Figures 4 and 5 (TÜİK, 2023b).

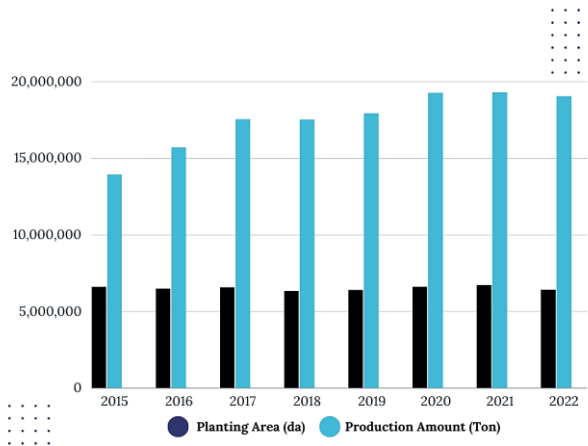


Figure 4. Planting area (da) and production (tons) of alfalfa in Turkey between 2015 and 2022

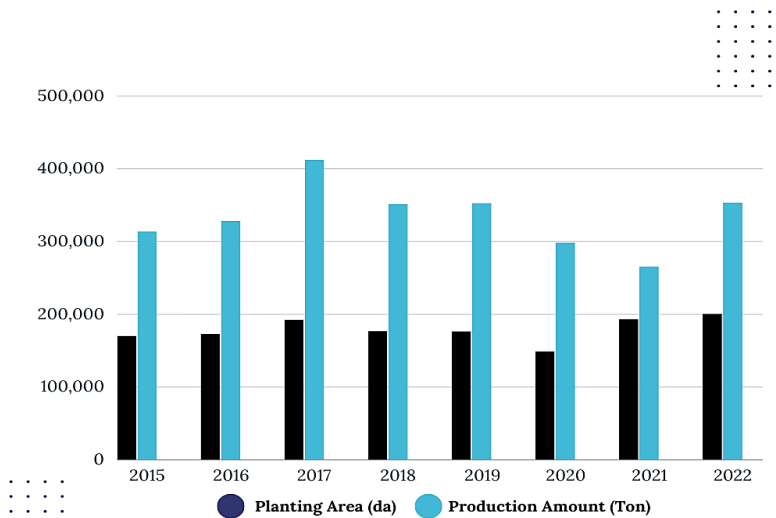


Figure 4. Planting area (da) and production (tons) of alfalfa in Bayburt between 2015 and 2022

5.2. Oat

Oat (*Avena sativa* L.) is one of the main forage crops grown in the world and is an annual cereal plant (Ahmad et al., 2014). Thanks to the nodules in its roots, it increases soil fertility by binding nitrogen in the air and bringing it into the soil. Temperate is not picky about the soil in which it is grown. However, more yield is obtained in well-drained soils. Its ability to be used in many different ways for grain and plants has enabled it to play an important role in the agricultural sector. Its high fiber content and quality make it preferred as human food because it lowers blood sugar and cholesterol (Mut et al., 2017).

The fact that oats, which find a place among the dietary habits of people, have the opportunity to be used in the industrial field, especially in the pharmaceutical and cosmetic sector, has led to an increase in the production area and quantity. In addition to being utilized in human food and non-food products, oats are also frequently used in animal nutrition as animal feed for cattle and sheep, especially horses. Oat contains 80% globulin or legume-like avenalin as a storage protein (Singh et al., 2013). The dehulled oat grain has a high crude protein content ranging from 15-20% (Peterson and Brinegar, 1986). It also has a good balance of amino acids and contains an important concentration of essential amino acids such as lysine. It is rich in oleic and linoleic acids and has a high fat content (Youngs and Püskülcü, 1976). It is also rich in oat-specific tocopherols, tocotrienols, phenolic acids, flavonoids, sterols and phytic acid antioxidants (Andersson and Hellstrand, 2012; Robards et al., 2009). The high protein content and the avenin substance in the grain give it the potential to be a valuable raw material in fattening and growth feeds used in the nutrition of young ruminants (Dumlupınar, 2010). The crude oil content in oat grain, which can be up to 6.5%, adds flavor to the feed and makes the animals consume it with appetite. Oats are generally not preferred in poultry diets because they contain beta-glucan polysaccharide which causes digestive problems in monogastric animals (Akyıldız, 1967; Ergün et al., 2001).

In recent years, there has been a remarkable increase in the cultivation area and production amount of oat, which has gained an important place among forage crops. In the last 6 years, the cultivation area has increased by 339% to 3.607.194 decares and the production amount has reached 4.649.051 tons with an increase of 264%. However, although oat cultivation area in Bayburt province reached 179,265 decares with an increase of 145% and 333,472 tons of production with an increase of 136%, it remained behind the average of Turkey. Oat cultivation area (hectares) and production amounts (tons) in Turkey and Bayburt between 2017-2022 are presented in Figure 6 (TÜİK, 2023b).

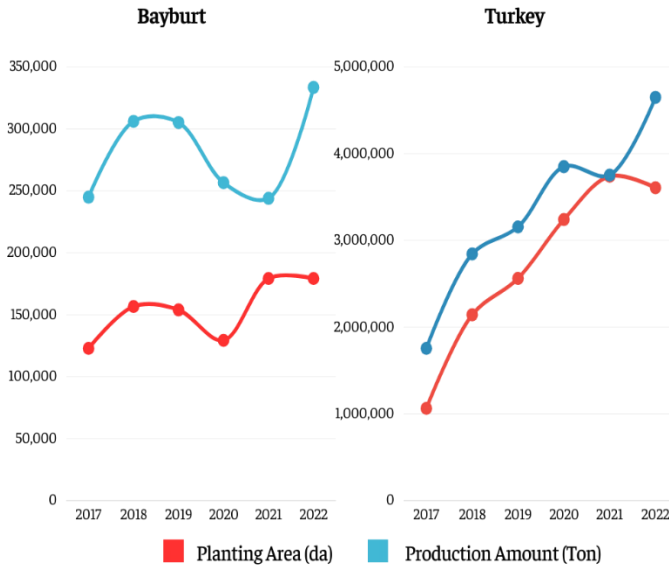


Figure 6. Oat cultivation area (da) and production (tons) in Turkey and Bayburt between 2017-2022

5.3. Sainfoin

Sainfoin (*Onobrychis viciifolia*) is a perennial forage plant in the legume family and can be harvested from the field in the same way for 5-6 years without deterioration (Carbonero, 2011). It is also a good pasture plant as it is resistant to grazing. It is used as an alternative to forage crops where the desired yield cannot be obtained in cold and arid climatic conditions because high yields can be obtained (Açıkgöz, 2021). It is an indispensable forage plant for dry areas as it can produce better yields compared to alfalfa in areas where irrigated agriculture is not possible. Today, it is used in animal feeding by making green, dry or silage. Sainfoin has high nutritional value and is rich in crude oil, crude protein, calcium, phosphorus and other minerals (Er, 2008). Thanks to the condensed tannins it contains, it reduces parasites in the ruminant digestive system and contributes positively to the environment by reducing methane emission (Bhattarai vd., 2018; Hoste et al., 2012). Since crude cellulose (HS) and crude ash (AC) rates are low and digestible dry matter (DM) rates are high, tympani (swelling) cases are not encountered in ruminant nutrition (Manga, 1977; McMahon et al., 1999; Wang et al., 2006). Besides being a valuable animal feed for ruminants, it is also a valuable source of pollen and nectar for honey bees (Dubbs, 1968; Deveci et al., 2012).

Compared to other forage crops, sainfoin cultivation did not develop in the same way in our country between 2016 and 2022; on the contrary, it is seen that there is a decrease in cultivation areas and production amounts (Figure 7). However, it is not possible to talk about this negative picture for Bayburt province. In the last 7 years in our country, sainfoin production areas decreased by 17% to 1,618,249 decares and production amount decreased by 10% to 1,786,207 tons. In Bayburt, sowing area increased by 10% to 99,347 decares and production increased by 18% to 164,437 tons. The area under sainfoin cultivation (da) and production (tons) in Turkey and Bayburt between 2016 and 2022 are shown in Figure 7 (TÜİK, 2023b).



Years	Bayburt		Turkey	
	Planting Area (da)	Production Amount (Ton)	Planting Area (da)	Production Amount (Ton)
2016	89.915	139.006	1.936.940	1.982.047
2017	128.084	194.687	1.961.808	2.001.379
2018	106.306	175.913	1.817.338	1.934.847
2019	92.818	148.509	1.752.763	1.781.789
2020	80.293	128.469	1.744.949	1.934.697
2021	100.051	122.546	1.814.737	1.546.641
2022	99.347	164.437	1.618.249	1.786.207

Figure 7. Area under sainfoin cultivation (da) and production (tons) in Turkey and Bayburt between 2017-2022

5.4. Sugar Beet

The fact that sugar beet is basically an industrial plant makes it a prominent agricultural policy in many countries. Its ability to decompose into by-products such as ethanol, molasses and bagasse makes it strategically important (Mustafa et al., 2020). Sugar beet, a biennial plant, forms the root body in the first year and then produces seeds in the second year (Wu et al., 1976). Although sugar beet is primarily grown for sugar production, excess production is used as animal feed (Vladu et al., 2021). Sugar beet itself, its pulp, leaves and molasses obtained during sugar production are used in animal feed (Muir, 2022). The increase in the rate of sugary substances in the feed enables animals to consume it with appetite (Avena et al., 2012). Sugar beet contains 22-25% dry matter (DM), 4.8% crude protein (HP), 4.8% crude cellulose (HS), 0.4% crude fat (CF), 1.9% crude ash (CA) (Ergün et al., 2002). It contains high amounts of acetate, which helps increase milk fat and yield in ruminants (Goyal and Kaur, 2022). It is used as wet, dry and silage in animal nutrition. However, since it may cause gas formation in ruminants due to its high content of easily soluble carbohydrates, it should be allowed to be consumed in small amounts mixed with feeds such as hay, alfalfa and dry grass. The head of sugar beet has a higher nutrient content than the leaves (Ak and Uzatici, 2001). For this reason, the head parts remaining between the leaves during harvesting increase the nutritional

value. However, since oxalic acid and saponins in the structure of sugar beet leaves limit calcium intake in animals, diarrhea cases are encountered in case of excessive consumption (Govindan, 2021). It is recommended that sugar beet should be ensiled within 1-2 days after harvest before it spoils (Kupryś-Caruk and Podlaski 2019). Since sugar beet leaves are rich in carbohydrates, silage can be easily made. Sugar beet pulp is a highly digestible and cheap feed source (Habeeb et al., 2017). Since it is recommended to be consumed fresh, it is more suitable to be utilized by making silage.

Although the cultivation areas of sugar beet decreased by approximately 8% between 2016 and 2022 in our country, the amount of production did not change (Figure 8). In Bayburt, it is seen that there is an increase in yield in sugar beet cultivation due to the increase in irrigation opportunities in some regions. Sugar beet cultivation area increased 5-fold to 18,076 decares and the production amount increased 6-fold to 103,880 tons. The cultivation area (da) and production amount (tons) of sainfoin in Turkey and Bayburt between 2016-2022 are shown in Figure 8 (TÜİK, 2023b).

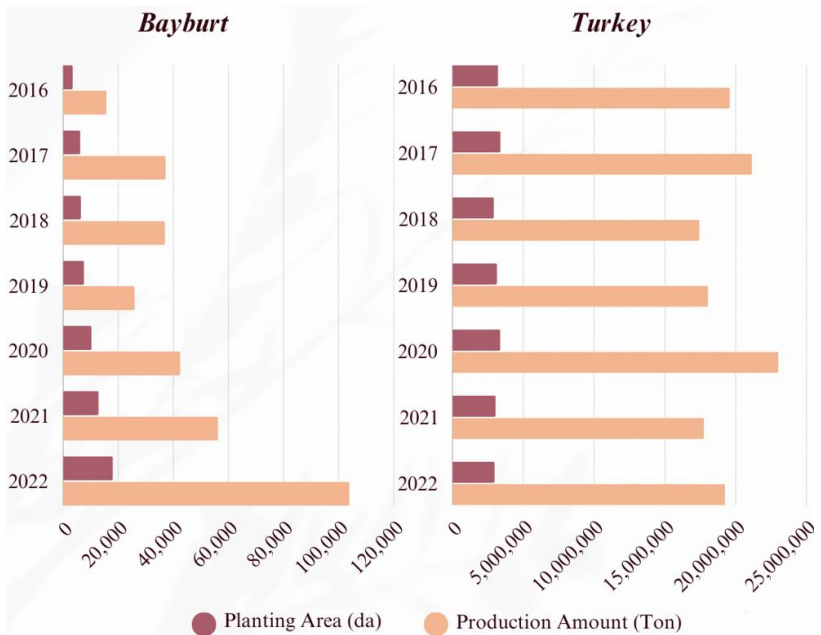


Figure 8. Sugar beet planting area (da) and production (tons) in Turkey and Bayburt between 2017-2022

5.5. Vetch

Vetch, which has about 150 species in the world, is an annual legume forage plant and becomes bitter towards the end of flowering (Shaeffer et al., 2017). Among the vetch species grown in the world and in our country, common vetch (*Vicia sativa* L.) takes the first place (Dong et al., 2019). It is used in temperate climate regions to increase the productivity of soil and animals because it provides high nutritional value and high grass yield (Huang et al., 2017). In regions with mild winters, it is

sown in the fall for winter and in spring for summer where winters are cold (Aydoğdu and Açıkgöz, 1995). Since it is resistant to cold and drought, it is easily grown in semi-arid regions (Dong et al., 2017; Huang et al., 2017; Nan et al., 2006). However, excessive drought causes a decrease in yield. The vetch plant grown in our country is utilized as green or dry grass, grain feed, pasture plant and silage plant. The fact that vetch plant, which is among the legumes, is rich in mineral substances, protein and vitamins, has high adaptability, and is easy to cultivate, stands out in meeting the quality roughage deficit in animal nutrition (Kuşvuran et al., 2011). Vetch is generally used in feed mix formulations in combination with other feed crops (Jilani et al., 2018).

Although legumes are frequently among the consumption preferences for humans, vetch cannot be used as human food due to antinutritional factors such as phytic acid, phenolics, raffinose and dense tannins. Substances called vicin and vicianin in vetch combine with the enzyme to form glycosides that cause the formation of cyanic acid glycosides and cause bitterness in the seed. For this reason, excessive consumption of vetch should be allowed in limited amounts as it causes bitter milk in ruminants and colic in horses. In order to eliminate the effect of antinutritional factors, it should be subjected to processes such as boiling, soaking, autoclaving and hulling. Compared to other legume grain feeds, the crude protein ratio is high (25-30%) and

a significant portion of the protein is composed of nitrogenous substances such as betaine and choline.

Between 2017 and 2022, it is observed that the cultivation area and production amounts decreased in Turkey and Bayburt due to the increase in the production of other fodder crops in the agricultural crop pattern (Figure 9) (TÜİK, 2023b).

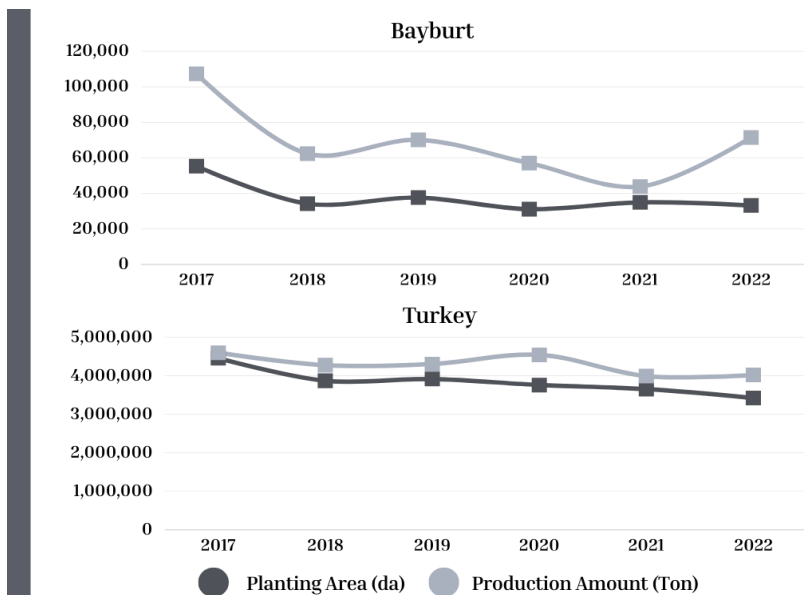


Figure 9. Area under vetch cultivation (da) and production (tons) in Turkey and Bayburt between 2017-2022

6. Conclusion

Adequate production and consumption of animal products are among the most important indicators of the development level of societies. The high nutritional values contained in these products contribute significantly to the quality and balanced nutrition of human beings. However, the increase in the amount of animal products is possible with care, feeding and genetic improvement studies. The fact that genetic improvement studies are long and costly increases the importance of care and feeding. Our meadow and pasture areas are significantly damaged due to excessive, early or late grazing. For this reason, ideas are being developed to increase the contribution of intensive and semi-intensive breeding methods to the economy. The most important step in this regard is to ensure that the nutrients needed by animals in terms of efficiency are met and that they can be fed with sufficient quality roughage. However, it should not be forgotten that the most important cost of livestock enterprises is feed expenses. Fodder crops production is an important agricultural activity carried out to support livestock activities. It is possible to reduce the need for feed-derived protein by increasing the feed utilization rate in animals and the value of the nutritional components in the feed. In this way, it will be possible to use existing resources more efficiently.

In recent years, there have been significant developments in the production of forage crops and in the livestock sector in

our country. There has been an increase in the cultivation areas of many plants, especially forage crops cultivated in irrigable areas. Although this picture is positive for the sector, increasing the cultivation areas of fodder crops, which are resistant to drought and cold, will ensure the continuity of the economic animal husbandry model.

Agriculture and animal husbandry have an important place in Bayburt's economy. Forage crops grown in Bayburt and large meadow-pasture areas meet an important part of animal husbandry activities. Increasing the quantity and quality of fodder crops grown in the province, especially alfalfa, oats and sainfoin, makes a significant contribution to the increase in livestock production. However, productivity levels should be increased through breeding and management studies to be carried out in these areas. Farmers should be informed about the cultivation of fodder crops and the use of certified seeds in cooperation with the public and private sectors and the results should be shared to set an example. In this way, efficiency losses from unit area in the use of existing resources will be prevented.

REFERENCES

- Acar, Z., Tan, M., Ayan, İ., Onal Aşçı, Ö., Mut, H., Başaran, U., Gülümser, E., Can, M., & Kaymak, G. (2020). Türkiye’de Yem Bitkileri Tarımının Durumu ve Geliştirme Olanakları. Türkiye Ziraat Mühendisliği IX. Teknik Kongresi Bildiriler Kitabı-1, Yay. Haz. TMMOB Ziraat Mühendisleri Odası, (s. 529-553), Ankara.
- Açıkgöz, E. (2021). Yem Bitkileri (Cilt 1). Tarım ve Orman Bakanlığı Bitkisel Üretim Müdürlüğü Yayınları, Ankara.
- Ahmad, M., Dar, Z. A., & Habib, M. (2014). A review on oat (*Avena sativa* L.) as a dual-purpose crop. *Scientific Research and Essays*, 9(4), 52-59.
- Ak, İ., & Uzatici, A. (2001). Şeker pancarı yapraklarının hayvan beslemede kullanımı. *Atatürk Üniversitesi Ziraat Fakültesi Dergisi*, 32(1), 95-99.
- Akyıldız, R. (1967). Türkiye Yem Maddeleri, A. Ü. Ziraat Fakültesi Yayınları no:293, A.Ü. Basımevi Ankara.
- Alao, B. O., Falowo, A. B., Chulayo, A., & Muchenje, V. (2017). The potential of animal by-products in food systems: Production, prospects and challenges. *Sustainability*, 9(7), 1089.

- Albrecht, K. A., & Beauchemin, K. A. (2003). Alfalfa and other perennial legume silage. *Silage science and technology*, 42, 633-664.
- Alçiçek, A., Tarhan, F., Özkan, K., & Adışen, F. (1999). İzmir İli ve Civarında Bazı Süt Sığırcılığı İşletmelerinde Yapılan Silo Yemlerinin Besin Madde İçeriği ve Silaj Kalitesinin Saptanması Üzerine Bir Araştırma. *Hayvansal Üretim*, 39-40: 54-63.
- Andersson, K. E., & Hellstrand, P. (2012). Dietary oats and modulation of atherogenic pathways. *Molecular nutrition & food research*, 56(7), 1003-1013.
- Anonymous, 2023. Coğrafi yapı. <http://www.bayburt.gov.tr/cografi-yapi>. Erişim Tarihi: 11.11.2023
- Artan, H., & Polat, T. (2019). Şanlıurfa sulu koşullarında bazı çok yıllık sıcak mevsim buğdaygil yem bitkisi türleriyle yoncanın saf ve karışık ekimlerinde yem kalite değerlerinin belirlenmesi. *Harran Üniversitesi Veteriner Fakültesi Dergisi*, 8(1), 85-92.
- Avena, N. M., Bocarsly, M. E., & Hoebel, B. G. (2012). Animal models of sugar and fat bingeing: relationship to food

addiction and increased body weight. Psychiatric disorders: Methods and protocols, 351-365.

Aydoğdu, L., & Açıkgöz, E. (1995). Effect of seeding rate on seed and hay yield in common vetch (*Vicia sativa* L.). *Journal of Agronomy and Crop Science*, 174(3), 181-187.

Bhattarai, S., Coulman, B., & Biligetu, B. (2016). Sainfoin (*Onobrychis viciifolia* Scop.): Renewed interest as a forage legume for Western Canada. *Canadian Journal of Plant Science*, 96(5): 748–756.

Carbonero, C. H. (2011). Sainfoin (*Onobrychis viciifolia*), a forage legume with great potential for sustainable agriculture, an insight on its morphological, agronomical, cytological and genetic characterisation. The University of Manchester (United Kingdom).

Deveci, M., Sıralı, R., & Cımbırtoğlu, Ş. (2012). Korunga (*onobrychis* sp.) yetiştiriciliğinin arıcılık açısından önemi. *Arıcılık Araştırma Dergisi* 8(2), 16-19.

Dong, R., Dong, D., Luo, D., Zhou, Q., Chai, X., Zhang, J., ... & Liu, Z. (2017). Transcriptome analyses reveal candidate pod shattering-associated genes involved in the pod ventral sutures of common vetch (*Vicia sativa* L.). *Frontiers in plant science*, 8, 649.

- Dong, R., Shen, S. H., Jahufer, M. Z., Dong, D. K., Luo, D., Zhou, Q., ... & Liu, Z. P. (2019). Effect of genotype and environment on agronomical characters of common vetch (*Vicia sativa* L.). *Genetic Resources and Crop Evolution*, 66, 1587-1599.
- Dubbs, A.L. (1968). Sainfoin as a honey crop. *Montana Agricultural Experiment Station Bulletin*, 627, 108-109.
- Dumlupınar, Z. (2010). Türkiye orjinli yerel yulaf genotiplerinin avenin proteinleri ile morfolojik, fenolojik ve agronomik özellikler yönünden karakterizasyonu. KSÜ Fen Bilimleri Enstitüsü, Tarla Bitkileri Doktora Tezi, 126 s, Kahramanmaraş.
- Er, Ü. (2008). Yonca, korunga ve fiğde tohumla taşınan fungal hastalık etmenlerinin belirlenmesi (Yüksek Lisans Tezi), Ankara Üniversitesi Fen Bilimleri Enstitüsü, Ankara.
- Ergün, A., Tuncer, Ş. D., Çolpan, İ., Yalçın, S., Yıldız, G., Küçükersan, K., Küçükersan, S., & Şehu, A. (2001). Hayvan Besleme ve Beslenme Hastalıkları, Medipres Matbaacılık, Malatya.
- Goenenc, S., & Tanrıvermiş, H. (2008). An overview of the Turkish dairy sector. *International journal of dairy technology*, 61(1), 3-10.

- Goyal, M., & Kaur, A. (2022). Sugar Beet as Cattle Feed: Scope and Prospects. In *Sugar Beet Cultivation, Management and Processing* (pp. 931-953). Singapore: Springer Nature Singapore.
- Govindan, R., Meenakshisundaram, T., Sivaramakumar, N., Naresh, P., Basavan, D., & Palanisamy, D. (2021). Impact of Vitamins and Minerals Enriched Flora in the Management of Calciphytoliths: A Special Focus on Vitamin E.
- Habeeb, A. A. M., Gad, A. E., El-Tarabany, A. A., Mustafa, M. M., & Atta, M. A. A. (2017). Using of sugar beet pulp by-product in farm animals feeding. *Int. J. Sci. Res. Sci. Technol*, 3, 107-120.
- Huang, Y. F., Gao, X. L., Nan, Z. B., & Zhang, Z. X. (2017). Potential value of the common vetch (*Vicia sativa* L.) as an animal feedstuff: a review. *Journal of animal physiology and animal nutrition*, 101(5), 807-823.
- Hoste, H., Martinez-Ortiz-De-Montellano, C., Manolaraki, F., Brunet, S., Ojeda-Robertos, N., Fourquaux, I., ... & Sandoval-Castro, C. A. (2012). Direct and indirect effects of bioactive tannin-rich tropical and temperate legumes against nematode infections. *Veterinary Parasitology*, 186(1-2), 18-27.

- Jilani, M., Ajam Norouzi, H., & Faraji, A. (2018). Effect of bed planting on the quantity and quality of hay in different mixing ratios of vetch and barley in the North of Iran. *Applied Ecology & Environmental Research*, 16(4).
- Kaya, A., & H. Bilgen, 1995. Sığır Yetiştiriciliğinde Kaliteli Kaba Yem Elde Etme Olanakları. Bornova.
- Kupryś-Caruk, M., & Podlaski, S. (2019). Intensification of biogas production in the process of co-fermentation of silages from perennial grasses blended with maize or waste from the agro-food industry. *Pol J Nat Sci*, 34(2), 233-243.
- Kuşvuran, A., Nazlı, R.İ., & Tansı, V., 2011. Türkiye’de ve Batı Karadeniz Bölgesi’nde çayır-mera alanları, hayvan varlığı ve yem bitkileri tarımının bugünkü durumu. *Gaziosmanpaşa Üniversitesi Ziraat Fakültesi Dergisi*, (2): 21-32.
- Lane, L. A., Ayres, J. F., & Lovett, J. V. (2000). The pastoral significance, adaptive characteristics, and grazing value of white clover (*Trifolium repens* L.) in dryland environments in Australia: a review. *Australian Journal of Experimental Agriculture*, 40(7), 1033-1046.

- Manga, İ. (1977). Değişik gün uzunluğu ve sıcaklık derecelerinin korunganın gövde ve kök gelişmesine etkileri. Atatürk Üniversitesi Ziraat Fakültesi Dergisi. 8, 1-21.
- McMahon L.R., Majak W., Mcallister T.A., Hall J.W., Jones G.A., Popp J.D., & Cheng K.J. (1999). Effect of sainfoin on in vitro digestion of fresh alfalfa and bloat in steers. Can. J. Anim. Sci. 79(2): 203–212.
- Muir, B. M. (2022). Sugar Beet Processing to Sugars. In Sugar Beet Cultivation, Management and Processing (pp. 837-862). Singapore: Springer Nature Singapore.
- Mustafa, G., Arshad, M., Bano, I., & Abbas, M. (2020). Biotechnological applications of sugarcane bagasse and sugar beet molasses. Biomass Conversion and Biorefinery, 1-13.
- Mut, Z., Erbaş, Ö. D., & Akay, H. (2017). Farklı yulaf (*Avena sativa* L.) çeşitlerinin kimyasal kalite özellikleri. Yüzüncü Yıl Üniversitesi Tarım Bilimleri Dergisi, 27(3), 347-356.).
- Nan, Z.B., El-Moneim A.M.Abd., Larbi, A., & Nie, B. (2006). Productivity of vetches (*Vicia* spp.) under alpine grassland conditions in China. Tropical Grasslands, 40, 177-182.

- Özkan, U. (2020). Türkiye yem bitkileri tarımına karşılaştırmalı genel bakış ve değerlendirme. *Turkish Journal of Agricultural Engineering Research*, 1(1), 29-43.
- Peterson, D.M., & Brinegar, A.C. (1986). 'Oat storage proteins', in Webster F H, *Oats: Chemistry and Technology*, St. Paul, MN, American Association of Cereal Chemists.
- Potter, N. N., & Hotchkiss, J. H. (2012). *Food science*. Springer Science & Business Media.
- Reese, J. (2018). *The end of animal farming: How scientists, entrepreneurs, and activists are building an animal-free food system*. Beacon Press.
- Robards, K., Prenzler, P., Ryan, D., & Kamal-Eldin, A. (2009). Oat Oil. In *Gourmet and Health-Promoting Specialty Oils* (pp. 433-454). AOCS Press.
- Shaeffer, C. C., Wells, M. S., Nelson, C. J., Collins, M., Nelson, C. J., Moore, K. J., & Barnes, R. F. (2017). Legumes for northern areas. *Forages: An Introduction to Grassland Agriculture*. Hoboken: Wiley-Blackwell, 117-131.
- Singh, R., De, S., & Belkheir, A. (2013). *Avena sativa* (Oat), a potential nutraceutical and therapeutic agent: an overview. *Critical reviews in food science and nutrition*, 53(2), 126-144.

- Soya, H., Avcıoğlu, R., & Geren, H. (2004). Yembitkileri. Hasad Yayıncılık.
- Sungur, Z. (2016). Demokrat Parti Döneminde (1950-1960) Tarım Politikaları ve Etkileri. Journal of Mehmet Akif Ersoy University Social Science Institute, 8(14).
- Tan, M., & Sancak, C. (2009). Korunga (*Onobrychis viciifolia* Scop.). Baklagil Yembitkileri, Tarım ve Köyişleri Bakanlığı, Tarımsal Üretim ve Geliştirme Genel Müdürlüğü, İzmir, 2, 337-352.
- Tucak, M., Ravlić, M., Horvat, D., & Čupić, T. (2021). Improvement of forage nutritive quality of alfalfa and red clover through plant breeding. Agronomy, 11(11), 2176.
- Thornton, P. K., & Gerber, P. J. (2010). Climate change and the growth of the livestock sector in developing countries. Mitigation and adaptation strategies for global change, 15, 169-184.
- TÜİK, 2023a. Adrese Dayalı Nüfus Kayıt Sistemi Sonuçları. (<https://biruni.tuik.gov.tr/medas/?kn=110&locale=tr>). Erişim Tarihi: 12.11.2023.
- TÜİK, 2023b. Bitkisel Üretim İstatistikleri. (<https://biruni.tuik.gov.tr/medas/?kn=110&locale=tr>). Erişim Tarihi: 13.11.2023.

TÜİK, 2023c. Hayvancılık İstatistikleri. (<https://biruni.tuik.gov.tr/medas/?locale=tr>). Erişim Tarihi: 16.11.2023.

Upton, M. (2004). The role of livestock in economic development and poverty reduction.

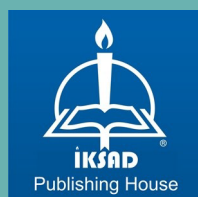
Vladu, M., Tudor, V. C., Mărcuță, L., Mihai, D., & Tudor, A. D. (2021). Study on the production and valorization of sugar beet in the European Union. *Romanian Agricultural Research*, 38, 447-455.

Wang Y., Berg B.P., Barbieri L.R., Veira D.M., & McAllister T.A. (2006). Comparison of alfalfa and mixed alfalfa-sainfoin pastures for grazing cattle: effects on incidence of bloat, ruminal fermentation, and feed intake. *Can. J. Anim. Sci.* 86(3): 383–392.

Wu, M. T., Salunkhe, D. K., & Dull, G. G. (1976). Effects of environmental factors and agronomic and storage practices on quality of sugarbeet. *Critical Reviews in Food Science & Nutrition*, 7(3), 281-296.

Yolcu, H., & Tan, M. (2008). Ülkemiz yem bitkileri tarımına genel bir bakış. *Tarım Bilimleri Dergisi*, 14(3): 303-312.

- Youngs, V. L., & Püskülcü, H. (1976). Variation in Fatty Acid Composition of Oat Groats from Different Cultivars 1. Crop Science, 16(6), 881-883.
- Zhao, S., Yang, F., Wang, Y., Fan, X., Feng, C., & Wang, Y. (2021). Dynamics of fermentation parameters and bacterial community in high-moisture alfalfa silage with or without lactic acid bacteria. Microorganisms, 9(6), 1225.



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