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ABSTRACT BOOK



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Table of Contents

RESPONSE OF MORPHOGENESIS AND CELL PROLIFERATION TO ALLELOPATIC COMPOUNDS (IMPERATA CYLINDRICA) ON RICE GERMPLASM	1
GENETIC STRUCTURE OF JUNIPERUS SERAVSHANICA KOM. FROM KAZAKHSTAN USING POLYMORPHIC MICROSATELLITE MARKERS.....	2
GWAS OF SOYBEAN BREEDING COLLECTION FOR RESISTANCE TO ROOT DISEASES IN CONDITION OF SOUTH-EAST KAZAKHSTAN	3
POPULATION STRUCTURE OF TWO-ROWED BARLEY FROM KAZAKHSTAN USING SNP ILLUMINA ARRAY	4
SEARCH FOR QTL OF AGRONOMIC TRAITS IN BREAD WHEAT USING AVALON × CADENZA MAPPING POPULATION GROWN IN KAZAKHSTAN	5
EVALUATE THE EFFICACY OF HOT RED PEPPER, ROSEMARY AND YARROW POWDER AS A SUPPLEMENTATION TO THE BROILER CHICKEN DIETS ON GROWTH PERFORMANCE AND MEAT CHARACTERISTICS	6
EFFECTS OF FERMENTED SOYBEAN MEAL ON GROWTH PERFORMANCE, CARCASS AND MEAT QUALITY TRAITS, AND INTESTINAL MORPHOLOGY OF TWO COMMERCIAL BROILER STRAINS	7
EFFECT OF CREATINE AND BETAININE FEED ADDITIVES ON THE DIFFERENTIAL GENE EXPRESSION OF HEAT SHOCK PROTEIN 70 AND FACTORS 1 AND 3 IN SOME BROILER CARCASS CUTS	8
SUPPLEMENTAL LYSINE AND METHIONINE HAD NO EFFECTS ON MILK YIELD OF AWASSI EWES FED TWO LEVELS OF DIETARY PROTEIN DURING THE LATE NURSING STAGE.....	9
THE EFFECT OF SALINITY AND PLANT DENSITY ON THE MORPHOLOGICAL AND PHYSIOLOGICAL CHARACTERISTICS IN MAIZE (ZEA MAYS L.)	10
RESPONSES OF HIGHLY LACTATING DAIRY COWS TO SEAWEED EXTRACT FEED INCLUSION	11
THE INCLUSION OF POMEGRANATE SEED PULP IMPROVES GROWTH PERFORMANCE AND CARCASS CHARACTERISTICS OF GROWING AWASSI LAMBS	12
THE EFFECT OF PMCG ON FOLLICULAR DEVELOPMENT AND OVULATION TIME OF PGF2 ALPHA-TREATED AWASSI EWES.....	13

POPULATION STRUCTURE OF TWO-ROWED BARLEY FROM KAZAKHSTAN USING SNP ILLUMINA ARRAY

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Barley (*Hordeum vulgare* L.) is one of the first domesticated cereal crops. In Kazakhstan barley average annual total grain yield is 2 million tons and the country is one of the top barley exporters in the world. Despite the importance of Kazakhstan for the world barley market population structure studies involved Kazakh accessions have not been conducted. The aim of this study was to estimate the population structure of two-rowed barley cultivars from Kazakhstan and accessions from world different regions using 9K single nucleotide polymorphism (SNP) Illumina array. Kazakhstan accessions were compared with barley samples from six different regions around the world. The Neighbor Joining (NJ) tree using accessions from seven different regions around the world separated into three main clusters. The NJ tree showed that the majority of accessions from Kazakhstan were grouped in Subclusters 2.1 (Cluster 2) and 1.2 (Cluster 2). Principal Coordinate analyses of two-rowed barley showed that the majority of the accessions from Kazakhstan are close to samples from Africa and Europe. The two-rowed barley collection was studied using the STRUCTURE package with a range of steps from K=2 to 10. At the K=2 Step, most accessions were in Cluster 1, while Cluster 2 was included 269 samples from the USA, 17 from Kazakhstan, 9 from Europe, and 1 from Africa. At the K=4 Step, the majority of the samples were grouped in Clusters 3 and 4, while Cluster 1 was heavily populated by samples from the USA, and Cluster 2 by samples from Kazakhstan. Thus, the study of the structure of modern barley accessions based on a genome-wide SNP analysis explained the relationship of Kazakh accessions with barley samples from other regions around the world.

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