Αγαπητές και αγαπητοί υποψήφιοι για το ΠΜΣ Γενετική, Βελτίωση Φυτών και Παραγωγή Πολλαπλασιαστικού Υλικού,

Έχετε υποβάλει επιτυχώς την υποψηφιότητά σας και καλείστε στην εξέταση των Αγγλικών τη Δευτέρα 26/9/2022 στις 10:30 στην αίθουσα 52 της Γεωπονικής Σχολής στην Πανεπιστημιούπολη (Campus) του ΑΠΘ. Στην εξέταση θα κληθείτε να μεταφράσετε 4 μικρά κείμενα από τη διεθνή βιβλιογραφία που περιέχουν όρους σχετικούς με την ειδίκευση. Για διευκόλυνσή σας ακολουθεί ένα δείγμα θεμάτων. Επίσης για ορολογία μπορείτε να ανατρέξετε στο λεξικό όρων Γενετικής και Βελτίωσης της Ελληνικής Επιστημονικής Εταιρείας Γενετικής και Βελτίωσης των Φυτών στον ακόλουθο σύνδεσμο:

http://www.plantbreeding.gr/ (μετακινηθείτε προς τα κάτω και βρείτε το λεξικό στα ΧΡΗΣΙΜΑ ΑΡΧΕΙΑ)

Την επόμενη μέρα Τρίτη 27/9/2022 θα πραγματοποιηθεί στον ίδιο χώρο (αίθουσα 52) η συνέντευξη όπου, εφόσον επιτύχετε στην εξέταση στα Αγγλικά, θα κληθείτε να υποστηρίξετε την υποψηφιότητά σας και θα παρουσιάσετε συνοπτικά την ερευνητική σας πρόταση. Καθώς η συνέντευξη θα διαρκεί περίπου 10-15 λεπτά για τον καθένα θα κληθείτε με αλφαβητική σειρά στις 9:30 για όσων το επώνυμο αρχίζει από Α-Μ και στις 12:00 για Ν-Ω.

Η διαδικασία της επιλογής θα ολοκληρωθεί και τα αποτελέσματα θα ανακοινωθούν έως τις 10 Οκτωβρίου. Τα μαθήματα αρχίζουν στις 17 Οκτωβρίου.

Ευχόμαστε σε όλους καλή επιτυχία και σας περιμένουμε στις εξετάσεις και τη συνέντευξη.

Για τη ΣΕ

Αλέξης Πολύδωρος

ΥΠΟΔΕΙΓΜΑΤΑ ΘΕΜΑΤΩΝ

*Hybrid varieties* are the first-generation offspring of a cross between parents with contrasting genotypes. A *hybrid variety* differs from a variety produced by hybridization for self-pollinated crops. With the _hybrid variety, the F 1 generation is grown and the hybrid genotype is reproduced faithfully in every plant if the parents are homozygous *(pure lines* or *inbred lines).* With *hybridization* in self-pollinated crops, a line combining genes from the parents is selected following several generations of inbreeding.

Hybrid breeding began in 1909 when G. H. Shull suggested a method for producing hybrid seed corn. The previous year Shull had reported that *an ordinary field of maize is composed of many complex hybrids, which decline in vigor with inbreeding, and that the breeder should strive to maintain the best*

*hybrid combinations.* As a result of his inbreeding and crossing studies, Shull outlined a plan for inbreeding to establish pure lines and crossing the pure (inbred) lines to produce uniformly productive single-cross hybrid combinations. These steps completely revolutionized corn breeding, and hybrid breeding has since been extended to many field and vegetable crops.

Maize and its closest wild relatives, the teosintes, differ strikingly in the morphology of their female inflorescences or ears. Despite their divergent morphologies, several studies indicate that some varieties of teosinte are cytologically indistinguishable from maize and capable of forming fully fertile hybrids with maize. Molecular analyses identified one form of teosinte (*Zea mays* ssp. *parviglumis*) as the progenitor of maize. Analyses of the inheritance of the morphological traits that distinguish maize and teosinte indicates that they are under the control of multiple genes and exhibit quantitative inheritance. Nevertheless, these analyses have also identified a few loci of large effect that appear to represent key innovations during maize domestication. Remaining challenges are to identify additional major and minor effect genes, the polymorphisms within these genes that control the phenotypes, and how the combination of the individual and epistatic effects of these genes transformed teosinte into maize.

The concept of whole genome amplification is something that has arisen in the past few years as the polymerase chain reaction (PCR) has been adapted to replicate regions of genomes that are of biological interest. The applications are many — forensic science, embryonic disease diagnosis, bioterrorism genome detection, ‘immortalization’ of clinical samples, microbial diversity, and genotyping. Several recent papers suggest that whole genomes can be replicated without bias or non-random distribution of the target, these findings open up a new avenue to molecular biology.

The transition from vegetative to reproductive growth is an essential process in the life cycle of plants. Plant floral induction pathways respond to both environmental and endogenous cues and much has been learnt about these genetic pathways by studying mutants of Arabidopsis. Gibberellins (GAs) are plant growth regulators important in many aspects of plant growth and in Arabidopsis they promote flowering. Here we provide genetic evidence that GAs inhibit flowering in grapevine. A grapevine dwarf mutant derived from the L1 cell layer of the champagne cultivar Pinot Meunier produces inflorescences along the length of the shoot where tendrils are normally formed. The mutated gene associated with the phenotype is a homologue of the wheat 'green revolution' gene Reduced height-1 and the Arabidopsis gene GA-insensitive. The conversion of tendrils to inflorescences in the mutant demonstrates that the grapevine tendril is a modified inflorescence inhibited from completing floral development by GAs.

Holliday (1994), describing in molecular terms DNA methylation as an epigenetic mechanism, defined epigenetics as the study of the changes in gene expression, which occur in organisms with differentiated cells, and the mitotic inheritance of given patterns of gene expression. Following the proof that epigenetic mechanisms, leading to changes of gene functions, are not only mitotically stable during development but are also meiotically heritable led to the definition of epigenetics as the study of mitotically and meiotically heritable changes in gene expression that do not entail a change inDNAsequence