# KOMODITAS : KEMIRI

# TEEAL 2007-2008

## PLANT GENETICS AND BREEDING (1 JDL)

Genetic gain prediction by selection index in a UNB-2U popcorn population under recurrent selection

***Bragantia.*** 2007. 66 (3). 389-396

**Author(s):** Santos-F-S. Amaral-Junior-A-T-do. Freitas-Junior-S-de-P. Rangel-R-M. Pereira-M-G

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**Abstract:**

Field studies were conducted in Rio de Janeiro, Brazil, during 2004-05, to select superior progenies for concentration of favourable alleles in a maize population of 192 progenies on the third cycle of intrapopulation half-sib recurrent selection under 2 distinct environments: The selection intensity was 15.6% that kept in touch 30 half-sib families for the continuity of the breeding programme. The utilized selection indices were the SMITH and HAZEL, PESEK and BAKER, WILLIAMS, and MULAMBA and MOCK. The MULAMBA and MOCK index propitiated more elevated magnitudes of the predicted gains for most of the traits, including popping expansion and grain yield, with values of 7.16 and 10.00%, respectively, utilizing arbitrary weight

**Descriptors: crop-yield. genetic-gain. maize. recurrent-selection. seeds**

## PLANT PHYSIOLOGY-GROWTH DAN DEVELOPMENT (1 JDL)

Effects of Corylus cornuta stem density on root suckering and rooting depth of Populus tremuloides ***Canadian Journal of Botany***. 2007. 85 (11). 1041-1045 **Author(s):** Mundell-T-L. Landhausser-S-M. Lieffers-V-J **Author Affiliation:** Centre for Enhanced Forest Management, Department of Renewable Resources, University of Alberta, 4-42 Earth Sciences Building, Edmonton, AB T6G 2E3, Canada

**Abstract:**

Trembling aspen (Populus tremuloides Michx.) is capable of regenerating vegetatively through the formation of adventitious shoots (suckers) from roots. This field study investigated how sucker regeneration following harvest of aspen is affected by understories of beaked hazel (Corylus cornuta Marsh.). Aspen stands with a high density of understory hazel (>45 000 stems per hectare (sph)) or a low density (<5000 sph) were cut in the fall. After one growing season, aspen sucker density and growth were assessed. Soil trenches were excavated to examine the root density and rooting depth of both aspen and hazel. Aspen sucker regeneration was 68 200 sph in areas with low hazel density and 43 600 sph in areas with high hazel density; the cross-sectional surface area of aspen roots in shallow soil layers (0-10 cm) was significantly lower under high densities of hazel. As aspen usually produces most of its root suckers from shallow roots, the reduction of roots in the upper 10 cm of the soil was the likely cause of lower sucker densities. Height growth of the suckers was not influenced by pre-harvest hazel density, possibly owing to high light transmission as a result of the reduced leaf area of the hazel after the harvest

**Descriptors: density; growth; leaf area; natural regeneration; rooting depth; roots; stems; suckering; surface area; understorey Corylus; Betulaceae; Fagales; dicotyledons; angiosperms; Spermatophyta; plants; eukaryotes; Populus; Salicaceae; Salicales**

## PLANT STRUCTURE (2 JDL)

Long-term deer exclusion in yew-wood and oakwood habitats in southwest Ireland: natural regeneration and stand dynamics

***Forest Ecology and Management***. 2006. 236 (2-3). 356-367

**Author(s):** Perrin-P-M. Kelly-D-L. Mitchell-F-J-G

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**Abstract:**

Woodland dominated by Taxus baccata is one of the rarest of European woodland types and has priority habitat status under Annex I of the EU Habitats Directive, yet little is known about its stand dynamics or the effects of long-term grazing. The abundance of naturally regenerating seedlings and saplings was monitored over a 32-year period in exclosures in a yew-wood and a neighbouring oakwood in the Killarney National Park, southwest Ireland. Both woods are heavily grazed by introduced sika deer (Cervus nippon). Mortality, recruitment and growth of adult trees were monitored over a 20-year period. Comparison was made with unfenced plots adjacent to each of the exclosures. Regeneration in the yew-wood exclosures was chiefly by Ilex aquifolium, Sorbus aucuparia and Fraxinus excelsior. No T. baccata saplings were recorded and seedlings of this species were very rare throughout the duration of the experiment. Taxus baccata trees which died during the 20-year monitoring period were significantly smaller than those which survived, indicating that self-thinning is occurring and the wood in its present form may be of relatively recent origins. Changes in adult tree species composition suggest that yew woodland in Ireland may develop from a yew-hazel scrub woodland sere. A variety of species regenerated in the oakwood exclosures, including T. baccata, and dense holly thickets formed in several areas. Quercus petraea failed to regenerate beneath the oak canopy. We conclude that chronic heavy grazing in the Killarney woodlands strongly influences the natural regeneration of several tree species. Research into the scientific manipulation of grazing levels in temperate woodlands is required. However, grazing intensity is not the only factor affecting regeneration, canopy conditions in particular are also likely to be of high significance, and this should be reflected in management plans

**Descriptors: forest-management. forests. growth. habitats. mortality. national-parks. natural-regeneration. population-density. recruitment. seedlings. stand-characteristics. stand-structure. survival. woodlands**

Home range and habitat selection of hazel grouse Bonasa bonasia in a temperate forest of South Korea

***Forest Ecology and Management***. 2006. 226 (1-3). 22-25

**Author(s):** Rhim-ShinJae

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**Abstract:**

Home range and habitat selection of hazel grouse Bonasa bonasia (five males and three females) were assessed by radio-tracking in a temperate forest of South Korea during January 2002-September 2004. The home range consisted of 4 types of forests: natural deciduous forest (dominated by Quercus mongolica, Ulmus davidiana and Fraxinus rhynchophylla); mixed forest (comprising Q. mongolica and Pinus densiflora); and deciduous and coniferous plantations (both dominated by Betula platyphylla, Larix kaempferi and P. koraiensis). Ninety-five percent minimum convex polygon home range size based on three to five times location per week ranged from 36.2 to 73.6 ha, with a median of 53.8 ha. Hazel grouse' habitat use differed from random use of available habitats within the home range. In this home range scale of habitat selection, natural deciduous forest and coniferous plantation ranked highest, followed by mixed forest, deciduous plantation and others (rock and bare areas). Declines in amount of natural deciduous forest may be harmful to hazel grouse populations, but also beneficial by creating more dense understorey coverage in coniferous plantations. For the conservation and management of hazel grouse populations, natural deciduous forest and coniferous plantation should be maintained and protected in Korea

**Descriptors: deciduous-forests. forest-plantations. forests. habitat-selection. habitats. mixed-forests. nature-conservation. resting-places. wildlife-conservation. wildlife-management**

## PLANT TAXONOMY AND GEOGRAPHY ( 1 JDL)

Hamawilsonia boglei gen. et sp nov (hamamelidaceae) from the late paleocene almont flora of central North Dakota

***International Journal of Plant Sciences***. 2008. 169 (5). 687-700

**Author(s):** Benedict-John-C. Pigg-Kathleen-B. (kpigg@asu.edu). DeVore-Melanie-L

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**Abstract:**

Hamawilsonia boglei Benedict, Pigg & DeVore gen. et sp. nov. ( Hamamelidaceae) is described from the Late Paleocene Almont flora of central North Dakota. The infructescence is an anatomically preserved spike with up to 20 sessile, robust, cuboidal to ovoid capsules borne on an elongate, thick axis up to 9: 2 cm long 3 0: 5 cm wide. Individual fruits are 10 - 12 mm across and bilocular, with paired persistent, recurved styles borne on the distal carpel face. One locule is often larger than the other. Anatomically, the fruit wall is composed of a sclerified endocarp and a poorly preserved exocarp. Seeds are elliptical to slightly obovate with a sclerotic seed

coat. Hamawilsonia is an extinct Late Paleocene genus with a combination of characters not seen in any extant hamamelid genus. Hamawilsonia is similar to the Asian endemic genus Sinowilsonia in its elongate spikelike infructescence, resembles the witch hazel Hamamelis in fruit and seed morphology, and has seed anatomy that combines features found in several extant genera. Affinities with Sinowilsonia are further supported by the c-ooccurrence of associated pollen catkins and in situ tricolpate pollen with a distinctive reticulate sculpturing. Like several other Almont taxa (Amersinia, Beringiaphyllum, Davidia, and Palaeocarpinus), Hamawilsonia is a genus with strong North American - Asian affinities

**Descriptors: Paleobiology; Systematics and Taxonomy**

## SOIL BIOLOGY (1 JDL)

Changes in chemical and biological soil properties as induced by anthropogenic disturbance: a case study of an agricultural soil under recurrent flooding by wastewaters

***Soil Biology & Biochemistry.*** 2006. 38 (8). 2069-2080

**Author(s):** Gelsomino-A. Badalucco-L. Ambrosoli-R. Crecchio-C. Puglisi-E. Meli-S-M

**Author Affiliation:** Dipartimento di Biotecnologie per il Monitoraggio Agroalimentare ed Ambientale, Universita Mediterranea di Reggio Calabria, Feo di Vito, I-89060 Reggio Calabria, Italy

**Abstract:**

Monitoring the environmental impact of anthropogenic disturbance on soil ecosystem is of great importance for optimizing strategies for soil use, conservation and remediation. The aim of this study was to assess whether and to what extent a long-term, human-induced disturbance could have affected main chemical and biological properties in an agricultural soil. The study site was a hazel (Corylus avellana L.) orchard located in the area surrounding the volcanic apparatus of Somma-Vesuvius (Southern Italy). For the last two decades, the site has been repeatedly subjected to floodings by wastewaters containing not only alluvial sediments but also potentially hazardous compounds from illegally disposed wastes. Soil disturbance was assessed by a multitechnique approach, which combined chemical, biochemical and physiological (Biolog(R)) methods together with community fingerprinting by denaturing gradient gel electrophoresis (DGGE) and amplified ribosomal DNA restriction analysis (ARDRA). A hazel site never subjected to flooding provided the control soil. Soil sampling was repeated three times over a 1-year period. The effect of flooding by wastewaters, sampling time and their interaction were statistically evaluated. Under wastewater flooding, soil pH and most organic matter-related pools, i.e. total organic C, total N, and active soil C-resources such as basal (SBR) and substrate-induced respiration (SIR) and microbial biomass C (MBC) were all increased; whereas sampling time mostly affected two active-N pools, namely K2SO4-extractable N (Extr-N) and potentially mineralizable N that varied unconcurrently in tested soils. Also the electrical conductivity varied across samplings. Parameters related to microbial maintenance energy (ATP and qCO2) were higher in the flooded soil, even though they were not statistically affected by wastewater flooding or by sampling time. The Biolog(R) method evidenced that under recurrent flooding, soil microbial populations became functionally more uniform when compared to the control soil. Molecular fingerprinting of PCR-amplified 16S rDNA targets revealed that, along with seasonal shifts, a marked change in the genetic structure of total bacterial community occurred in the flooded soil. Furthermore, compositional shifts in the actinomycete community were less marked and mostly influenced by seasonal effects. Yet, a decreased genetic diversity in the ammonia-oxidizing bacteria community was evidenced in the flooded soil by ARDRA. Thus both the genetic and the functional structure of native soil bacterial populations were changed under repeated flooding by wastewaters. Repeated sampling over a 1-year period allowed us to reveal soil disturbance effects beyond seasonal variations

**Descriptors: agricultural-soils. alluvium. ATP. biological-activity-in-soil. DNA-fingerprinting. flooding. hazelnuts. microbial-flora. ribosomal-DNA. seasonal-variation. soil-bacteria. soil-biology. soil-chemical-properties. soil-types. volcanic-soils. waste-water**

## FOOD COMPOSITION (1 JDL)

Hazel (Corylus avellana L.) leaves as source of antimicrobial and antioxidative compounds

***Food Chemistry.*** 2007. 105 (3). 1018-1025

**Author(s):** Oliveira-I. Sousa-A. Valentao-P. Andrade-P-B. Ferreira-I-C-F-R. Ferreres-F. Bento-A. Seabra-R. Estevinho-L. Pereira-J-A

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**Abstract:**

Aqueous extracts of leaves of different hazel (Corylus avellana L.) cultivars (Cv. M. Bollwiller, Fertille de Coutard and Daviana), were analysed by reversed-phase HPLC/DAD for the definition of their phenolic composition. Antioxidant potential was assessed by the reducing power assay, and the scavenging effect on DPPH (2,2-diphenyl-1-picrylhydrazyl) radicals and beta -carotene linoleate model system. Their antimicrobial capacity was also tested against Gram positive (Bacillus cereus, Bacillus subtilis, Staphylococcus aureus) and Gram negative bacteria (Pseudomonas aeruginosa, Escherichia coli, Klebsiella pneumoniae) and fungi (Candida albicans, Cryptococcus neoformans). Eight phenolic compounds were identified: 3-, 4- and 5-caffeoylquinic acids, caffeoyltartaric acid, p-coumaroyltartaric acid, myricetin-rhamnoside, quercetin 3-rhamnoside and kaempferol 3-rhamnoside. A p-coumaric acid, three myricetin and one quercetin derivatives were also detected. The hazel leaves extract presented high antioxidant activity in a concentration-dependent way, in general with similar behaviour of all cultivars. Gram positive bacteria revealed to be very sensitive to hazel leaf extract (MIC 0.1 mg/ml for B. cereus and S. aureus and 1 mg/ml for B. subtilis). However, Gram negative and the fungi displayed much lower sensitivity, being P. aeruginosa and C. albicans resistant at 100 mg/ml. Cv. M. Bollwiller exhibited the most potent antimicrobial activity

**Descriptors:** **antimicrobial-properties. antioxidant-properties. chemical-composition. cultivars. hazelnuts. leaves. phenolic-compounds. plant-extracts. quercetin**

## PHYSIOLOGY OF HUMAN NUTRITION (1 JDL)

Disassociation between the effects of amino acids and insulin on signaling, ubiquitin ligases, and protein turnover in human muscle

***American Journal of Physiology: Endocrinology and Metabolism***. 2008. 295 (3). E595-E604

**Author(s):** Greenhaff-PL. Karagounis-LG. Peirce-N. Simpson-EJ. Hazell-M. Layfield-R. Wackerhage-H. Smith-K. Atherton-P. Selby-A. Rennie-MJ

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**Abstract:**

We determined the effects of intravenous infusion of amino acids (AA) at serum insulin of 5, 30, 72, and 167 mU/l on anabolic signaling, expression of ubiquitin-proteasome components, and protein turnover in muscles of healthy young men. Tripling AA availability at 5 mU/l insulin doubled incorporation of [1-(13)C]leucine [i.e., muscle protein synthesis (MPS), $P < 0.01$] without affecting the rate of leg protein breakdown (LPB; appearance of d(5)-phenylalanine). While keeping AA availability constant, increasing insulin to 30 mU/l halved LPB ($P < 0.05$) without further inhibition at higher doses, whereas rates of MPS were identical to that at 5 mU/l insulin. The phosphorylation of PKB Ser(473) and p70(S6k) Thr(389) increased concomitantly with insulin, but whereas raising insulin to 30 mU/l increased the phosphorylation of mTOR Ser(2448), 4E-BP1 Thr(37/46), or GSK3beta Ser(9) and decreased that of eEF2 Thr(56), higher insulin doses to 72 and 167 mU/l did not augment these latter responses. MAFbx and proteasome C2 subunit proteins declined as insulin increased, with MuRF-1 expression largely unchanged. Thus increasing AA and insulin availability causes changes in anabolic signaling and amounts of enzymes of the ubiquitin-proteasome pathway, which cannot be easily reconciled with observed effects on MPS or LPB

**Descriptors:** **Adult. Amino Acids. Blood Glucose. Blotting, Western. Dose-Response Relationship, Drug. Gene Expression. Humans. Hypoglycemic Agents. Insulin. Male. Muscle Proteins. Muscle, Skeletal. Phosphorylation. Proteasome Endopeptidase Complex. Protein Kinases. RNA. RNA, Messenger. Regional Blood Flow. Reverse Transcriptase Polymerase Chain Reaction. Ribosomal Protein S6 Kinases, 70-kDa. Signal Transduction. Ubiquitin-Protein Ligase Complexes**