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Special Paper

A Bibliometric Portrait of Pakistan Journal of Scientific and Industrial Research (PJSIR) During the Period of 1958-2007

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(received September 17, 2018; revised October 3, 2018; accepted October 5, 2018)

Abstract. Pakistan Journal of Science and Industrial Research (PJSIR) had celebrated its sixtieth anniversary in 2017. Inspired by this occasion, this observational study presents a bibliometric review on the quantity of all published materials under the caption of Physical, Biological and Technological Sciences with Short Communications during the period of 1958-2007 in Pakistan. The data of 340 issues of PJSIR was downloaded and collected to tabulate from the website of electronic journal: (http: www.pjsir.org/arc.php) during January-July, 2018. This study expressed that n=4929; 14.4% articles were published in 340 issues of PJSIR during the period of 1958-2007. Total 4417 (1790; 36.3%, 1651; 33.5%, and 976; 19.8%) articles published under the caption of Physical, Biological, and Technology out of 4929 articles. Remaining 512; 10.3% articles were short communications. Maximum articles n=1375; 28% were published in the fourth decade and n=694; 14% articles in the first decade as a minimum. The short communications n=208; 4.2% related to biological science take a position with the slight margin to other disciplines. PJSIR published regularly from 1958 to this day. It is counted a teamwork of the management of Journal and supported by Pakistan Council of Scientific and Industrial Research (PCSIR) Government-owned body. There are few examples in the world to publish a scientific journal which covers three major disciplines of science.

Keywords: bibliometrics, PJSIR, PCSIR, Ministry of Science and Technology, Pakistan

General and Specific Combining Ability Estimates for Morphological, Yield and its Attributes and Seed Traits in Sunflower (*Helianthus annuus* L.)

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(received October 28, 2016; revised May 25, 2017; accepted May 29, 2017)

Abstract: The improvement in sunflower breeding requires exploitation of combining ability of divergent male and female inbreds. Six cytoplasmic male sterile (CMS) lines and three testers were crossed in line \times tester design, thus 18 F₁ hybrids were developed for evaluation of general combining ability (GCA) and specific combining ability (SCA) of inbred parents for days to 90% maturity, stem girth, head size, achenes/plant, 1000-seed weight, achene yield kg/ha, oil and protein%. The significant variances due to lines and testers both determined GCA variances revealed the predominance of additive genes whilst significance of lines × tester interactions indicated the importance of SCA variances and the involvement of non-additive genes in the expression of traits studied. The foremost role of non-additive genes was apparent when ratio σ^2 SCA/ σ^2 GCA was above 1.0. These results suggested the prevalence of dominant genes and possibility of hybrid crop development. The GCA effects indicated that CMS parents SF-187, 64-A-93 and ARG-0405 and tester RHP-46 were high general combiners, thus may be chosen for crossing and selection programmes, whereas F₁ hybrids SF-187 × RHP-46, 64-A-93 × RHP-46, PAC-ARG-0405 × PAC-ARG-0106, 64-A-93 × RHP-46 and PSF-025 × RHP-64 which used parents with good × good and good × poor GCA estimates revealed higher positive SCA estimates for achene yield, oil and protein traits yet manifested desirable negative effects for 90% maturity. Such results suggested that these hybrids are desirable for the exploitation of hybrid crop development or selection of desirable plants from earlier filial generations.

Keywords: combining ability estimates, line × tester analysis, sunflower

Genetic Variability, Heritability and Correlation Studies in F₂ Populations of Upland Cotton

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(received April 7, 2016; revised June 29, 2017; accepted August 7, 2017)

Abstract. A field experiment was conducted at the experimental area of the Department of Plant Breeding & Genetics, Sindh Agriculture University Tandojam, during the year 2014-2015 in order to carry-out genetic analysis in F₂ populations of upland cotton. The trial was laid-out in a Randomized Complete Block Design with four replications. The material was consisted of eight parents and ten F_2 populations. The analysis of variance revealed significant differences among the parents and F_2 populations for all the traits studied except that fibre length was non-significant in parents. The results further suggested that maximum heritability, higher genetic variances coupled with more genetic gains were expressed by the F₂ populations CRIS-134 × CRIS-508 and CRIS-134 × CIM-598 for 1st sympodial node number; CRIS-134 × Neelum-121 and CRIS-134 × CRIS-508 for sympodial branches/plant; CRIS-342 × FH-113 for boll weight; CRIS-342 × Neelum-121 for bolls/plant, seed cotton yield/plant, lint % and micronaire value and progenies CRIS-342 × MNH-886 followed by CRIS-342 × Neelum-121 for staple length. These results also suggested that a number of F₂ populations indicated their potential for various seed cotton yield and fibre traits. The phenotypic correlations revealed that most of the traits were significantly and positively associated with seed cotton yield/plant. However, higher correlations of sympodial branches/plant ($r = 0.69^{**}$) and bolls/ plant ($r = 0.82^{**}$) with seed cotton yield indicated that both the traits are more reliable as compared to other traits for selection of higher seed cotton yields. Very interestingly, fibre traits like lint%, fibre length and micronaire were also significantly correlated with seed cotton yield, suggesting that fibre quality traits can be improved without compromising on seed cotton yield. Thus, the material under study is very promising and worthy of selection to improve many traits simultaneously.

Keywords: genetic variability, heritability, F2 populations, correlations, cotton genotypes

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Fortification and Stability of Iodine in Bread to Mitigate Iodine Deficiency Disorder

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(received January 2, 2017; revised October 3, 2017; accepted October 23, 2017)

Abstract. The core objective of this study was to prepare iodized bread by using iodized salt and potassium iodide (KI) to fulfill Recommended Daily Intake (RDI) of iodine. Triplicate level of each fortificant was added in separate treatments in different concentrations with an aim that 2 slices of bread provide RDI of iodine. The prepared samples were analyzed for stability of iodine by spectrophotometric method and for sensory attributes by panel of judges. Results showed good retention of iodine in bread with 15-20% loss of iodine in final product after processing. A slight level of potassium was increased in treatments in which KI was used while other minerals profile was not affected by fortificants and showed no significant behaviour after examining the results statistically.

Keywords: fortification, stability iodized bread, iodine deficiency

Pak. j. sci. ind. res. Ser. B: biol. sci. 2018 61B(3) 151-157

Spatial Patterns and Trends of *Escherichia coli* in Public Water Supply System of Lahore, Pakistan

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(received May 30, 2017; revised November 11, 2017; accepted December 29, 2017)

Abstract. Most of the Northern and Central part of Lahore district is supplied with ground water by Water and Sanitation Government Authority. The quality of public water supply is getting deteriorating due to increasing population of Lahore city. Moreover, the effects of microbial water pollutants on health of population of study area have been addressed. In this research, presence of *Escherichia coli* in pre & post monsoon seasons has been focused. The water samples were taken from tube wells as well as adjacent houses. A questionnaire survey was also conducted to find out the responses of people in study area. It was clear from the results of the study that *E. coli* were detected in all the water samples of public water supply system. An increase in growth of pathogens was also noticed in post monsoon season. It was also proved from study that many people were suffering from diarrhoea at sample places where *E. coli* were identified. The mixing of sewage with drinking water was the major cause of presence of pathogens in water samples of houses although they were less or absent in water samples of tube wells.

Keywords: spatial patterns, Escherichia coli, water supply system, sewage contamination

Population Status and Distribution of Himalayan Brown Bear (Ursus arctos isabellinus) in Musk Deer National Park Neelum, Azad Jammu and Kashmir (Pakistan)

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(received October 3, 2016; revised May 19, 2017; accepted June 22, 2017)

Abstract. The Himalayan brown bear (*Ursus arctos isabellinus*) is considered as 'Endangered' in Pakistan. However, a small population of this species still exists in northern Pakistan including Azad Jammu and Kashmir (AJK). A study was conducted to determine population status and distribution of Himalayan brown bear in Musk Deer National Park (MDNP), from April 2011 to September 2012. MDNP, covering an area of 528.16 km², is situated in the extreme north of AJ&K (upper Neelum Valley) about 155 km away from Muzaffarabad. Study area was divided into three zones (Phulawai, Sardari and Loser) and searched for brown bear signs and evidences. A total of 17 transect surveys were carried out to collect the data on current population status and distribution of Himalayan brown bear in the study area. In addition, questionnaires based surveys were carried out in the area to gather maximum information about this species. Based on direct and indirect signs collected, a total population of about 12 individuals with a population density of 0.42 bear/km² was estimated in the MDNP with maximum (0.45 bear/km²) in Loser and minimum (0.37 bear/km²) in Phulawai zone. Altitudinal preference was recorded highest (0.46 bear/km²) at the elevation level of >3000 m asl. For the proper management and conservation of Himalayan brown bear, more comprehensive study should be carried out throughout its potential habitat.

Keywords: population, distribution, Himalayan brown bear, Musk Deer National Park, Azad Jammu and Kashmir

Repellent Responses of Maize Weevil, *Sitophilus zeamais* Motsch (Coleoptera:Curculionidae) towards Entomocidal Plant Products

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(received August 31, 2016; revised. March 30, 2017; accepted August 24, 2017)

Abstract. Laboratory studies were conducted to investigate the repellency effect of six plant species (*Azadirachta indica, Caralluma fimbriata, Allium sativum, Curcuma longa, Citrullus colocynthis* and *Calotropis procera*) against *Sitophilus zeamais* reared on maize grains (Cv. Azam White) in the Laboratory of Entomology Department, Gomal University, Dera Ismail Khan, Pakistan. Six concentrations viz. 5000, 10000, 15000, 20000, 25000 and 30000 ppm of each plant powder were applied to 20 g of sterilized maize grains under constant conditions of $27 \pm 1^{\circ}$ C and $65 \pm 5\%$ relative humidity. Twenty newly emerged adult maize weevil were introduced into glass petri dishes and percent repellency of plant powders was determined. *A. indica* seed powder at 30,000 concentration showed 100% repellency against maize weevil followed by *C. longa* (76%) after 72 h exposure period whereas *C. procera* was found least effective showing only 39% repellency of the test insects compared to control. The powders of *A. sativum, C. fimbriata* were found moderately repellent against the test insects. During the observations, it was also noted that repellency of the tested plant powders was dose dependent, the higher the concentration of the tested plant products could be used for a safer control of maize weevil.

Keywords: plant powders, insect repellency, Sitophilus zeamais, maize grain

Review

Epigenetic Alterations and their Dietary Backgrounds

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(received June 27, 2016; revised April 25, 2017; accepted May 10, 2017)

Abstract. The key intention of this review is to summarize the different studies which relate the genomediet interactions with future perspectives of exploring an insight into the well defined functions of diverse micronutrients and other dietary components that play a vital task in defining the early developmental patterns of an organism. Human fetus development is a complex process that is totally dependent on the dietary components which interact with the genes to regulate the different proliferation and differentiation stages. We want to explore those complex interactions that lay hidden between micro-nutrients and gene expressions but are means of the apparent changes of a phenotype of an individual. Along with this the review will also perceive some basics of development of certain diseases as well, due to these complex genome-diet interactions thus leading to refine the dietary outlines for maternal and prenatal developmental stages in future. Research has also shown that genome-diet interactions are very complex as without proper nutrients the end result is the genome instability which may lead to chronic diseases, developmental defects and certain types of cancer.

Keywords: epigenetics, genome diet, methylation, DNA sequence, eukaryotes

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Review

Probable Ingredients for *Trans* Free Margarine with Omega-3 Fatty Acids

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(received October 20, 2015; revised July 25, 2017; accepted July 31, 2017)

Abstract. Margarine is widely used as table spread, in cooking and bakery products. Awareness of consumers regarding the intake of omega fatty acids has led the food industry to develop foods which are rich sources of omega fatty acids. Harmful effects of *trans* on the development of cardiovascular diseases have steered the researchers to find out wide range of *trans* free options, without compromising on functional and physical properties of fats. Nutritionists recommend margarine for the growing and school going babies, it is usually manufactured from the combination of hard and soft fats, followed by the addition of vitamins A, D and E. However, little is known regarding the supplementation of margarines with omega fatty acids of chia oil. This paper summarizes the physical and chemical characteristics of few ingredients that may be used in the formulation of *trans* free margarine with higher magnitude of omega fatty acids.

Keywords: margarine, omega fatty acids, trans free, chia oil

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