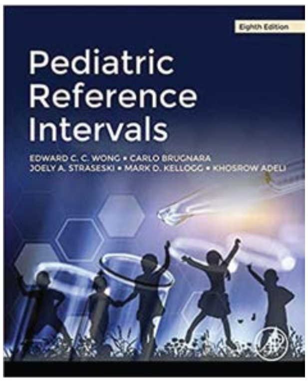
BOOK REVIEWS



Pediatric Reference Intervals, Eighth Edition. Edward C. C. Wong, Carlo Brugnara, Joely Straseski, Mark D. Kellogg and Khosrow Adeli. Academic Press, an imprint of Elsevier, 125 London Wall, London EC2Y 5AS, United Kingdom. 2021. xxvi + 361 pages. Price: US$ 150. ISBN: 978-0-12-817939-0.

A new edition of this book is being released after 10 years and has a lot of additions and broader coverage than the previous ones. The layout of the book is simple, the formatting is uniform and referring to it for any particular test reference interval (RI) is easy.

Children undergo a significant transformation from birth to adolescence in terms of physiological and physical development and are influenced by genetic, environmental, nutritional and cultural factors. Therefore, deriving a RI in this population is challenging. It is easy to derive RI in the adult population from samples collected for health check-ups. We are aware that studies in the pediatric population are difficult to conduct and hence the data for many parameters are limited due to ethical and logistic issues. The authors of this book have attempted to cover the entire pediatric age group for most parameters in biochemistry and hematology. The references are fairly recent. The population size (*n*) has been mentioned against each RI, so that the reader can gauge the reliability of the values. The intervals are available in both conventional and SI units for most parameters.

RIs for biochemistry tests have been stated instrument-wise, since some perhaps most parameter values can vary between instruments. One needs to be aware that RI for most tests performed by methods based on the immunoassay principle will vary significantly across different equipment used. The best example of such a test is the commonly used parameter vitamin B12, which varies widely between the Abbott and Beckman Coulter equipment. The book covers 2–3 instrument manufacturers for most tests. This can be expanded in the future editions to other instruments as well, when reliable studies for these equipment become available. For example, lipase values vary based on the method and equipment. In this book, RI is mentioned for lipase in just one equipment. A significant variation in RI is seen for other enzymes too, across different instruments. RI for parameters for in-born errors of metabolism are available. This is advantageous since it is difficult to find the literature on this important component of laboratory medicine. The study group strength for these is also reliable. Values of parameters such as NT-proBNP, CRP, ferritin, D-dimer and procalcitonin are useful, especially during the present COVID-19 pandemic. Random urine RI for calcium is particularly useful because a 24 h collection is difficult in children. RI for sex hormones is available age-wise and Tanner stage-wise. Detailed RI for 17-OHP and immunoglobulins is handy. We note that cortisol RI mentioned in this book is for a random sample, though a diurnal variation is known even in children after about two years of age. This is probably due to a high inter-individual variation in the pediatric population.

In hematology, RIs are given not only in term babies, but also in pre-term (wherever clinically relevant), e.g. haemoglobin in case of neonatal anaemia and immature granulocyte count for sepsis. Most 'cytoses' and 'cytopenias' in the WHO classification of hemato-lymphoid malignancies are defined by an absolute number of a type of leucocyte. The international guidelines (College of American Pathologists as well as International Council for Standardization in Hematology) also recommend reporting results of the white blood cell (WBC) differential in absolute numbers rather than in percentages. Thus RI for each absolute WBC count is beneficial.

This book provides RIs for coagulation parameters such as prothrombin time and activated partial thromboplastin time. However, readers should be aware that laboratorians must establish biological RIs for these tests, which vary with the analyser and the reagent used in the laboratory. Similarly, there is a need to have ethno-geographical considerations for parameters such as mean platelet volume in Harris platelet syndrome (also called Bengal macrothrombocytopenia) and neutrophil count in benign ethnic neutropenia in the Nigerian population. A more detailed RI for total bilirubin would be helpful for newborns. Bicarbonate is a labile parameter; hence RI may not be totally reliable in the pediatric population given the challenges of sample collection. The references state that stored, frozen samples were processed for bicarbonate, but there is not much clarity on the sample collection procedure. RIs are mentioned for osmolality urine but not for osmolality of serum. There is a typographical error in the units of measurement for TSH RI, which needs to be corrected from mg/l to mIU/l. Further editions should include RI for bone marrow myelogram, as this is one more area where there is a drastic difference between pediatric and adult values, which can completely change the final diagnosis, e.g. lymphocyte count. There is also scope to include newer hematological parameters like platelet large cell ratio, cell population data (volume, conductivity and scatter in various leucocytes), etc. to adapt to the progress in science.

This book takes all the pre-analytical, analytical and post-analytical variables into account, viz. sample type and age, method of testing and all units of measurement. The test list is exhaustive, which makes it convenient for paediatricians, laboratorians and researchers alike to refer to and obtain RIs for any parameter.

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Annual Review of Phytopathology, 2021. Jan E. Leach and Steven E. Lindow (eds). Annual Reviews, 4139 E1 Camino Way, P.O. Box 10139, Palo Alto, California 94303-0139, USA. Vol. 59. xii + 445 pages. Price: US$ 118.00. ISSN: 0066-4286; ISBN: 978-0-8243-1359-3.

This volume, with a collection of 18 chapters, is well balanced and organized, accommodating pathogen profile, epidemiology and host–pathogen interactions covering pathogenesis, host adaptation and immunity.

Reliable, sensitive and precise detection of infectious plant diseases, and their microbial pathogens with accurate quantification is a primary need for managing them, and for experimental purposes in greenhouses, laboratories, field conditions and political borders. Plant diagnostic laboratories (PDLs) of the United States have become persuasive models in the march for preserving plant health for sustainable food security. The financial support and continuous competence-building framework pave the way for this success. PDLs are funded and supported by Land-Grant Universities (also called Land-Grant Colleges or Land-Grant Institutions) of the US, purposed to receive the benefits of the Morrill Acts through a Bill signed by Abraham Lincoln. The prefix 'Land-Grant' is derived from a Bill facilitating raising funds using the distributed, federally controlled land to the states for establishing institutions of higher education offering a wide spectrum of educational opportunities. PDLs, also called plant clinics, connect the plant-associated professionals and general public at the state level with research-based information through their extension services. Better infrastructure, including the latest instrumentation, enables the use of essential genomic tools. Linkage established between the diagnosticians and the education system involving them in teaching undergraduate and graduate courses, and collaboration in the research mission of the faculty adds value. Iles *et al*. make a practical assessment of the performance of PDLs at the level of their administrators, diagnosticians, and the methods and techniques used per se with factors influencing their use and adoption along with pronouncements about the futuristic necessities of equipping the next-generation plant health specialists. The availability of genomic information on plants and pathogens has intensified studies on the natural variations in biology. However, the complexity of plant–pathogen relationships remains challenging for mechanical and functional understanding. Weinberg *et al*. explore the use of an evolutionary framework for advancing genomic approaches in pathogen diagnostics and disease epidemiology both at the national and local levels. Chen *et al*. deal with the biology of root-infecting pathogens causing the serious Verticillium wilts with emphasis on population genomics in relation to population divergence revealing the virulence traits.

Describing the pathogen and disease profiles is required for bringing them to the forefront of research. Potyviruses infecting a large number of crops worldwide have been responsible for several epidemics in the past, causing heavy yield losses. Besides documenting the profile of a set of top 10 potyviruses, Yang *et al*. delve into the genomics and proteomics-generated information, projecting the possible targets for intervention through new plant breeding technologies for enhancing disease resistance. The genus *Fusarium* has a large number of species that are plant pathogenic. Many of them being toxigenic, are harmful to humans and animals. The taxonomy of this genus derived from many earlier attempts based on morphological, sexual compatibility and phylogenetic relationships has a complicated structure at the species and subspecies level. Munkvold *et al*. stress the need for a precise understanding of mycotoxin potential of individual species for dealing with the toxicological risks associated with *Fusarium* diseases, and analyse how this trait aligns with the present-day phylogenetic reasoning of the species concept. Variations in toxin production exist among species possessing similar gene clusters, collectively governing specific toxin biosynthetic pathways. This indicates the need for deeper insights into the regulatory aspects of the associated gene functionalities for determining the discriminating factors in species characterization.

Successful pathogens have evolved complex infection processes involving developmental changes along with the generation/formation of biochemical ammunitions to enter and spread in the plant tissues to complete their life cycle. Proteins being the biological workhorses, participate in virtually every process within the cells. Following their biosynthesis, proteins undergo post-translational changes resulting in chemical alterations. These modifications drive the signalling within a cell, enabling the biological functions of proteins. Liu *et al*. explore the post-translational modification involved in the fungal and bacterial pathogens during pathogenesis, forming the initial step in the interaction with the host plant. Management of bacterial diseases is difficult due to the availability of only a few bactericidal chemicals/antibiotics, and their use poses problems due to the natural development of resistance, lessening their relevance. Fire blight of apple and pear is a complex disease and the pathogen *Erwinia amylovora* has both epiphytic and endophytic phases of host colonization in the blossom infection. Kharadi *et al*. consider the genetics involved in pathogenesis together with the influence of floral microbiome during the initial stage of the pathogen establishing an internal relationship with the host, and its response. Joshi *et al*. describe the involvement of quorum sensing (QS), a population density-dependent communication mechanism between bacteria for managing bacterial diseases. Many plant-associated bacteria interact with their hosts through QS, which regulates specific bacterial processes, including the expression of bacterial virulence genes. A variety of small-molecule plant constituents target this bacterial communication system characterizing inter-kingdom signalling. As genetic manipulation of the synthesis and production of these plant metabolites is easy, the review opens up novel approaches for disease management.

Small RNAs (sRNAs) comprising microRNAs and small interfering RNAs have become an important class of signalling molecules in the regulation of plant development, and in abiotic and biotic stress responses. The machinery for RNA silencing is known as RNA interference. With cell-to-cell and systemic mobility implicated in inter-species and inter-kingdom systems, the plant sRNAs directly affect target RNAs during both viral and non-viral infections resulting in transcription reprogramming through host-induced gene silencing (HIGS) involving trans-species sRNA trafficking. In turn, sRNAs of eukaryotic pathogens regulate their virulence in host tissues. These effects result in the regulation of host receptor gene expression and HIGS in the pathogens interfering with their virulence. Qiao *et al*. enumerate these activities at the interface between the host and the pathogen (restricted to filamentous and oomycetes), exhibiting the citadel of layered immunity responses. Xu *et al*. examine the virus–host (vector and plant) interactions with the insect-vectored rice stripe virus (RSV), transmitted in a persistent circulating manner, which has become a growing concern in East Asia for rice production. This article raises the need for identifying RSV-resistant genotypes, the role of virulence factors in the plant–virus interactions, development of cell lines of the insect vector for understanding the differential levels of virus replication in the insect vector and the plant, and adoption of reverse genetics approach. The information on functional aspects of virus-encoded proteins would help in gaining deeper insights on the biology of the virus in relation to its vector and the host plant.

The obligate biotrophic fungal pathogens causing rust diseases being highly specialized, possess the most complex life cycle with alternation of generations. This involves infection of two different host plants known as heteroecism, giving rise to distinctly different spore-producing structures to complete their life cycle. The process of pathogenesis and expression of virulence are modulated successfully with two different unrelated host species at the genetic level. Selection for this delicate balancing of host–pathogen interactions has been shaped during the course of evolution, reflecting differential host adaptation. Duplessis *et al*. scrutinize the genomic-based advancements using a set of type species of the pathogen with an evolutionary view. Breakdown of resistance is a major challenge for preventing epidemics. Deployment of disease resistance genes based on their effectiveness and usefulness against the contemporary pathogen strains needs phenotyping of disease resistance under controlled conditions at large spatio-temporal scales. Even though the multilocational disease nursery concept eases this to a certain extent, its relevance becomes meaningful only with knowledge of pathogen population structure prevailing in the target area(s). Mathematical models developed in the past as an alternative tool for resistance deployment strategies are examined by Rimbaud *et al*. to improve future modelling approaches with relevance to resistance durability and epidemiological control. Pyramiding resistance genes appear to be the most epidemiologically efficient and evolutionarily durable strategy in the absence of pre-adapted pathogen genotypes, despite the limitations of pyramiding. Bacterial spot of pepper and tomato caused independently by four different *Xanthomonas* species is a seed-borne endemic disease of serious concern worldwide. Even though host resistance is available in pepper, pathogens overcome the same, and resistance is not available in tomatoes. This is confounded by the development of resistance to bactericides used for disease management. Considering the ecological and evolutionary aspects influencing pathogen population dynamics in relation to disease incidence, Potnis has synthesized a more refined disease pyramid and emphasizes the need for new research approaches for sustainable management practices.

The concept of plant immunity (Jones and Dangl), a highly complex, multilayered defence system (zig-zag model), has been developed with an ecological perspective accommodating natural selection among individuals. This has arisen from the self–non-self innate immunity model discriminating infectious non-self from non-infectious self (Janeway), and a subsequent danger model (Matzinger) stressing the importance of endogenous danger signals (damage-associated molecular patterns, DAMPs) arising from injured or wounded cells, which are of self in nature. In other words, the danger model is concerned with ‘danger’ rather than non-self. The self–non-self and danger models are centred around responses to infections in animals. With only a limited number of plant DAMPs and their receptors characterized, Tanaka and Heil apply the danger model considering both exogenous and endogenous (damaging non-self or the damaged self) as danger signals of plant innate immunity and compare it with the mammalian innate immunity system, wherever possible. Further, the identification and characterization of DAMPs and their receptors are stressed for a holistic understanding of DAMP signalling in the plant immune system. Chloroplast is a double membrane-bound endosymbiotic organelle possessing its own DNA, considered to be inherited from its ancestor – a photosynthetic cyanobacterium engulfed by an early eukaryotic cell. Besides conducting photosynthesis in plant and algal cells, chloroplasts also carry out fatty acid and much of the amino acid syntheses, generate defence hormones, reactive oxygen species (ROS) and nitrogen species, and participate in the antimicrobial response. Consequent to pathogen recognition by the plant through pattern recognition receptors or resistance proteins, chloroplast-generated ROS initiates the local hypersensitive response leading to downstream signalling for immune responses in the multilayered host defence strategy. This process is distinguished as chloroplast immunity. By moving around in plant cells, chloroplasts interact with other organelles in response to environmental and developmental perturbations. The chloroplast-generated signals are involved in retrograde signalling (organelle-to-nucleus communication) to impact gene expression and influence cellular metabolism. Pointing out the deficiency in understanding these implications in the interphase between the pathogen and host plant relationship, Kachroo *et al*. examine chloroplast immunity in plant defence.

Immune responses to necrotrophic pathogens do not match those of biotrophic pathogens. Interaction between the pathogen-secreted effectors and their host targets (receptors) determines the recognition of the pathogen by the host plant, resulting in either triggering the defence responses or defeating this process by evasion or suppression. Choosing a model consisting of wheat and its three different necrotrophic foliar pathogens, Friesen and Farris dissect the components of compatibility in both the asymptomatic (latent) and necrotrophic phases of the disease syndrome. Conceivably, each of these necrotrophic pathogens has evolved independently with the host. However, they share similar modulation of host-cell features by partly seizing the host defence pathway to cause cellular disruption (necrosis) for deriving nutrients during the latter phase of pathogenesis for completing their life cycle.

Despite a century-old discovery of the phenomenon of hybrid necrosis, described as a hybrid autoimmune syndrome, its relevance to plant immunity is of interest. This deleterious effect of hybrid necrosis is caused by inappropriate activation of genes expressed in the progeny resulting from the cross between two incompatible parental plants. These genes encode for nucleotide-binding domain, leucine-rich repeat (NLR) receptor proteins, and play roles in pathogen detection. Activation of NLR genes draws parallels between hybrid necrosis and tissue necrosis (hypersensitive response/programmed cell death) as an immune response to pathogen infection in plants. This cellular scenario results in the formation of NLR complexes known as resistosome in plants comparable to inflammasome in animals constituting autoimmunity. Molecular aspects of hybrid necrosis have already benefitted in a mechanistic understanding of certain features of plant immunity. Li and Weigel indicate that the utility of functional genomics of hybrid necrosis has helped advance our knowledge on the evolution of the plant immune system and would lead to uncovering new modes of immune signalling. Bi and Zhou further delve into the signalling aspects of cell death from the viewpoint of regulated cell death (RCD), which is well defined in animals. RCD is essential for tissue homeostasis or to restore biological equilibrium under stress conditions, featuring the elimination of useless or potentially dangerous cells. This process is triggered by DAMPs and executed through multiple cell-death pathways involving pore-forming proteins with the ability to punch holes in the cell membrane to alter its permeability. The wheel-like NLR resistosome with a funnel-shaped structure accommodates the signalling domain of NLR at the centre stage to initiate immune signalling and RCD. This article raises important issues related to the recently established link between the two layers (pattern-triggered immunity and effector-triggered immunity) of plant immunity, invigorating new thinking in immune signalling.

Each chapter in this volume includes future issues, which opens up new opportunities/directions for research with possibilities for developing novel strategies for disease management. These will positively impact modern crop breeding for sustainable agriculture. To sum up, this volume is laudable for the breadth and depth of its content, and its ability to remain up-to-date. It serves the needs not only of plant pathologists, but all those interested in the science of plant life, as probing diseases makes known the unknowns.

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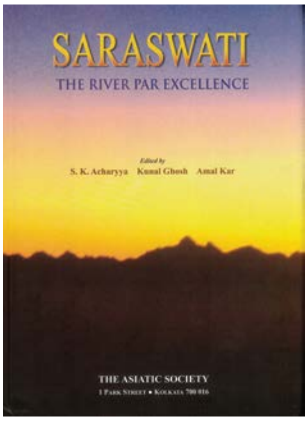

Saraswati: The River Par Excellence. S. K. Acharyya, Kunal Ghosh and Amal Kar (eds). The Asiatic Society, 1 Park Street, Kolkata 700 016. 2020. xiv + 249 pp. Price: Rs 2500.

The Saraswati River, labelled as ‘The River Par Excellence’ in this edited volume, has also been previously referred to as ‘The Lost River’ and ‘The Prehistoric River Saraswati’ but more of that later in this review. What then is the Saraswati River? Is it an active river system in the present geography of northwestern India or is it a fluvial palaeodrainage of the distant past that supported the Harappan Civilization almost four millennia ago and left behind archives of its geologic records? Is it a mythical entity or was it a real large river with ample discharge that supported the Harappans for about a millennium? And then, there is also the most unresolved question of how and when the decline of this large river took place and how that decline was related to the collapse of the Harappan/Saraswati Civilization? Such are the intriguing questions that have continued to engage for over a century, the scholars from the disciplinary diversity of archaeology, climate science and palaeoclimate, geology and palaeohydrology, geomorphology and remote sensing, as well as ancient Indian history and cultures. The scientific study of this palaeodrainage system alongside the archaeological studies of the excavations of the Harappan cities and settlements in the region has led to considerable cross-disciplinary exchanges resulting in continuous and ongoing dialogue, debate, and controversy in the past few decades.

As noted by the Editors of this volume, several epithets were bestowed on this river in the Rig Veda, such as *Nadinam asurya* (the most powerful among the rivers), *Nadinam suchi* (the purest among the rivers) and *Naditame* (best among the rivers). Lost rivers and their lost civilizations do not fade away, even though millennia may go by, because they arouse the curiosity and imagination of those societies and civilizations that follow them. The present is but a fleeting moment in the continuum between the past and the future. The future is not for us to see, but glimpses of the past are there for us to see, and the exploration of the past is ingrained in us so that we may enlarge the envelop of variability of natural processes that the study of the present allows us.

The exploration of the Saraswati River is an ongoing endeavour in unravelling the geography and history of northwestern India and as noted earlier, it has drawn in several other disciplines. In the past two decades, three other books have preceded the present edited volume. A comprehensive account of two centuries of work on this river system and its linked civilization was synthesized in a book by Michel Danino in 2010 under the title of ‘*The Lost River – On the trail of the Sarasvati*’. Two other books ‘*Saraswati: the river that disappeared*’ (2002) and ‘*Prehistoric River Saraswati, western India*’ (2017), both authored by late K. S. Valdiya together bear testimony to the interest that persists in demystifying this ‘lost river’ through multi-disciplinary studies both on the landscape and the lives of those who populated those riverscapes. Incidentally, the present volume includes contributions by the late K. S. Valdiya (chapter 1) and Michel Danino (chapter 8) as well as those who bring a multi-disciplinary perspective to this subject from the aspects of geology and tectonics; geography, remote sensing and mapping; rivers and cultural linkages; geohydrology, geoarchaeology and bioarchaeology.

As has been the case with many other disciplines, the exploration of the Saraswati River was also impacted by the use of satellite technologies in the seventies of the previous century. Two influential studies – the first by Ghose *et al*. on ‘The lost courses of the Saraswati River in the Great Indian Desert – new evidence from Landsat Imagery’ published in the *Geographical Journal* in 1979, and the second by Yashpal *et al*. in 1980 on ‘Remote Sensing of the lost Saraswati River’ published in the *Proceedings of the Indian Academy of Sciences* were the pioneering works that led to a renewal of interest on the drainage reorganization of a part of northwestern India (Haryana Plains, Rajasthan and Kutch). Much has transpired since then and the literature on the Saraswati River has grown manifold. The last decade or so has witnessed new directions of study that include, besides remote sensing aided palaeochannel studies, the recognition and reconstruction of buried channel networks that have a distinctive Higher Himalayan provenance for the deposited sands. The fingerprinting of the provenance of the sands that were deposited in the palaeochannels related to the Sutlej system was based on U–Pb geochronology of detrital zircon grains; and that has settled the question of whether the provenance of the Saraswati palaeochannel was in the Higher Himalaya or not in favour of the former.

Despite several recent published studies, there is still debate as to whether the river had avulsed from the wide valley of the Ghaggar basin before the Harappans or whether the river had a substantial flow during the Early and Mature phases of the Harappan Civilization. The questions of how and when the river avulsed to the present valley of the Sutlej remain open.

Although reference was made to the possible existence of a large river system (following the earlier references in the Rig Veda) as early as the second half of the nineteenth century in 1855, questions remain to be answered. Hence this edited volume is a welcome addition to our developing knowledge base on the subject.