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EXPOSURE PATHWAYS AND HUMAN HEALTH RISK ASSESSMENT FROM ARSENIC EXPOSURE IN BANGLADESH

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High arsenic exposures, prevalent through dietary and non-dietary sources in Bangladesh, present a major health risk to the public. Groundwater, the most important source of water for drinking, cooking, and irrigation in Bangladesh, is a significant contributor to the daily human intake of arsenic. Other arsenic intake pathways, established as relevant for Bangladeshi adults through this study, include consumption of contaminated edible plant parts and animal-origin food, inhalation of contaminated air, soil ingestion, betel quid chewing, and tobacco smoking. A quantitative human health risk assessment is described as a result of arsenic exposure through food and water intake, tea intake, accidental soil ingestion, and chewing of betel quid, while people meet their desirable dietary intake requirements throughout their lifetime. This study qualifies and quantifies these arsenic intake pathways through analysis of the range of arsenic levels observed in different food types, water, soil, and air in Bangladesh, and highlights the contributions of dietary intake variation and cooking method in influencing arsenic exposures. In evaluating the contribution of each intake pathway to average daily arsenic intake, the results show that food and water intake combined, make up approximately 98% of the daily arsenic intake with the balance contributed to by intake pathways such as tea consumption, soil ingestion, and quid consumption. Under an exposure scenario where the arsenic concentration in water is in the WHO guideline (0.01mg/L), food intake is the major arsenic intake pathway ranging from 67% to 80% of the average daily arsenic intake. However, the contribution from food drops to a range of 29% to 45% for an exposure scenario where arsenic in water is at the Bangladesh standard (0.05mg/L). The lifetime excess risk of cancer occurrence from chronic arsenic exposure, considering a population of 160 million people, based on an exposure scenario with 85 million people on the WHO guideline value and 75 million people at the Bangladesh standard, and assuming 35 million people associated with a heavy activity level, is estimated as 1.15 million cases. This study also highlights the potential of desirable dietary patterns and intakes in increasing arsenic exposure which is relevant to Bangladesh where nutritional deficiencies and lower-than-desirable dietary intakes continue to be a major concern.

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PHENOTYPIC VARIABILITY CONFIRMED BY NUCLEAR RIBOSOMAL DNA SUGGESTS A POSSIBLE NATURAL HYBRID ZONE OF TRIATOMA BRASILIENSIS SPECIES COMPLEX

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Triatoma brasiliensis macromelasoma occurs in Pernambuco state, Brazil, which is situated between the distribution areas of *Triatoma brasiliensis brasiliensis* (north) and *Triatoma juazeirensis* (south). *T. b. macromelasoma* displays greater variations in its chromatic phenotype than either *T. b. brasiliensis* or *T. juazeirensis* and patterns reminiscent of one or the other. Experimental crosses from each of these members of the *T. brasiliensis* species complex generated fertile offspring suggesting that viable hybrids could be present in nature, despite their significant genetic distances. Considering the geographical position of occurrence of the *T. b. macromelasoma* (in Pernambuco) it was proposed to be an area capable of supporting natural hybridization between *T. b. brasiliensis* and *T. juazeirensis.* Since phenotypic variability is expected, this study investigated the existence of intermediate chromatic phenotypes for *T. b. macromelasoma* in various locations in areas between the *T. b. brasiliensis* and *T. juazeirensis* occurrences. Thirteen different color patterns were for the first time characterized and nine of those displayed intermediate phenotypes. Molecular analysis performed using ribosomal DNA intergenic region, grouped all within the *T. brasiliensis* complex. The intermediate chromatic phenotypes, molecular analysis and experimental crosses all support the distinction of a zone of hybridization that gave rise to the *T. b. macromelasoma* through homoploidal evolution.

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