Health Bits & Pieces Winter 2015 (HFN 33:4)
Written by Dan Kenner

Toxic Shock

Every day millions of women are exposing themselves to a dangerous carcinogen found in feminine hygiene products. According to a study at a university in Argentina, 85% of tampons, cotton and other hygiene products contain traces of glyphosate, the World's most widely used weed killer, also known as Roundup®. It is already established that traces of glyphosate can be found in food products. Some countries restrict its use to protect public health and the environment; but most countries, including the U.S., permit it. There is evidence that glyphosate exposure is a potential cause of human breast cancer in quantities so miniscule they are measured in parts per trillion.

Guyton K, Loomis D, Grosse Y, et al., "Carcinogenicity of tetrachlorvinphos, parathion, malathion, diazinon, and glyphosate," The Lancet, *Volume 16, No. 5, p490–491, May 2015; Thiantanawat A, Rangkadilok N, Suriyo T, Satayavivad J, Thongprakaisang S, "Glyphosate induces human breast cancer cells growth via estrogen receptors,"* Food and Chemical Toxicology, *2013 Sep;59:129-36. doi: 10.1016/j.fct.2013.05.057. Epub 2013 Jun 10.*

The Chemical Feast

Exposure to toxic chemicals is almost unavoidable in today's world. Most exposures are small enough that we don't immediately notice ill effects. On the other hand, the cumulative effects of chemicals are coming into focus as an area of increasing concern. We are exposed to pesticides, herbicides, chemical solvents, and industrial chemicals of all kinds through the food we eat, the water we drink, and the air we breathe. More than 80,000 chemicals are introduced into the World each year. It is possible that our indoor environment is as toxic as our outdoor environment and perhaps even more so. Despite the rising incidence of many types of cancer, very little research has been conducted into the potential impact of these environmental newcomers or the thousands of mostly unresearched chemical agents to which we have already been exposed.

In response to this a taskforce of over 170 scientists from leading research centers in 28 countries set out to study the link between the development of cancer and 85 chemicals that people are frequently exposed to but that are not considered carcinogenic. They found that 50 of them promoted key pathological mechanisms that are considered cancer-related at exposure levels commonly found in the environment. According to cancer biologist Dr. Hemad Yasaei, "This research backs up the idea that chemicals not considered harmful by themselves are combining and accumulating in our bodies to trigger cancer and might lie behind the global cancer epidemic we are witnessing." The researchers have estimated that chemicals could be responsible for as many as 20% of all cancers. The cumulative effects of chemicals need to be researched more thoroughly because all humans are exposed to toxic chemicals on a daily basis. The impact of reducing cancer incidence through lessened exposure could be significant.

Goodson W, Lowe L, et al., "Assessing the carcinogenic potential of low-dose exposures to chemical mixtures in the environment: the challenge ahead," Carcinogenesis, *2015; 36 (Suppl 1): S254 DOI:10.1093/carcin/bgv039.*

Antibiotics and Gut Flora

The overuse of antibiotics has been a matter of concern for many years now. Many doctors routinely overprescribe antibiotics, which has contributed to the proliferation of antibiotic-resistant bacteria. Antibiotic-resistant bacteria cause at least two million cases of disease and over 20,000 fatalities every year. Nonessential use of antibiotics, such as for treatment of viral infections and antibiotic prophylaxis to prevent infection after surgery, is the subject of debate since it enhances the spread of antibiotic resistance and may actually contribute to development of future infections. Recent research on the effects of antibiotics on microbial diversity in the gut flora have disturbing implications with respect to the role antibiotic treatment might play in the development of chronic disease.

Microbial diversity was adversely affected for months following the use of various antibiotics in healthy adults. Researchers measured microbial diversity, quantity of butyrate-producing bacteria, and antibiotic-resistant genes. The researchers noticed a decrease in butyrate-producing bacteria. Butyrate plays an important role in colon health and the bacteria that produce it are considered to be among the friendliest. Clindamycin significantly reduced gut flora for up to 4 months and ciprofloxacin up to 12 months. Amoxicillin did not affect microbiome diversity but had the greatest effect on antibiotic-resistant genes. The salivary microbiome recovered quickly from antibiotic exposure but the fecal microbiome showed long-lasting changes with butyrate-producing bacterial species severely underrepresented and an increase of genes associated with antibiotic resistance.

Zaura E, Brandt B, Mattos M, et al., "Same exposure but two radically different responses to antibiotics: Resilience of the salivary microbiome versus long term microbial shifts in feces," mBio *6:6 ; Published 10 November 2015, doi:10.1128/mBio.01693-15.*

Baby Guts

Antibiotics account for about 25% of all medications prescribed to children. One-third of these prescriptions are considered unnecessary. Recent research has shown that antibiotic use in infants causes changes in gut bacteria that lead to disease later in life including resistance to infection, allergies, autoimmune disease, and even obesity. This could be a partial explanation for the sharp rise in allergies and autoimmune disease in recent years. One study showed that changes in the gut microbiota can be connected with autoimmunity. This large study carried out by researchers at MIT, Harvard, and Massachusetts General Hospital identified a correlation between changes in gut microbiota and the onset of Type-1 diabetes. The study followed which changes in the microbiome would shift the balance toward Type-1 diabetes in children at high risk of developing the disease.

Antibiotic use may wipe out key gut bacteria that support the maturity of immune cells. Changes in the intestinal bacteria of infants can predict future development of food allergies or asthma. Researchers found that infants with a lower diversity of gut bacteria at three months of age are more likely to develop sensitivities to foods like milk, eggs, or peanuts by the age of 12 months. Researchers stated that patterns of gut bacteria during infancy could possibly serve as a biomarker of future disease. Antibiotics can affect the balance of the two predominant bacterial groups in the gut, which can significantly affect the accumulation of fat stores in the body. Past research has shown a relationship between the balance of these two groups, the Bacteriodetes and the Firmicutes, and obesity. A decrease in Bacteriodetes relative to Firmicutes in the gut has been associated with significant accumulation of body fat.

Vangay P, Ward T, Gerber J, Knights D, "Antibiotics, Pediatric Dysbiosis, and Disease," Cell Host & Microbe*, Volume 17, Issue 5, p553–564, 13 May 2015; Kostic A, Gevers D, Siljander H, et al., "The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes,"* Cell Host & Microbe*, 11 February 2015; Volume 17, Issue 2, p260–273, DOI: http://dx.doi.org/10.1016/j.chom.2015.01.001; Azad M, Konya T, Guttman D, et al., "Infant gut microbiota and food sensitization: associations in the first year of life,"* Clinical & Experimental Allergy, *March 2015; Volume 45, Issue 3 p632–643 DOI: 10.1111/cea.12487.*

Sleep that Knits up the Ravel'd Protein ...

Researchers at University of California, Berkeley found evidence that a deficiency of deep sleep is associated with a buildup of the beta-amyloid protein. Beta-amyloid protein accumulating in brain tissue is implicated in the development of Alzheimer's disease. This toxic protein appears to attack the brain's ability to retain long-term memory. This finding indicates a relationship among sleep, memory, and the incidence of Alzheimer's disease.

Accumulation of beta-amyloid protein has been found in Alzheimer's patients as well as in patients with sleep disorders. Deep sleep appears to prevent beta-amyloid proteins from accumulating and destroying brain cells. A study found that brain cells shrink during deep sleep, which allows more efficient irrigation of the brain cells by the cerebrospinal fluid and consequently enhanced removal and drainage of toxic materials that could potentially accumulate. One of the mysteries of why we need sleep may be that the body needs to detoxify the brain.

Past research has shown a positive correlation between lack of memory and the build-up of beta-amyloid protein. This research opens a new avenue toward prevention and treatment of Alzheimer's since there are numerous therapeutic approaches to sleep disorders. There are many natural approaches including the use of supplements and herbal medications, avoiding caffeine, and even use of electronic devices late at night.

Walker M, et al., "β-amyloid disrupts human NREM slow waves and related hippocampus-dependent memory consolidation," Nature Neuroscience*, June 2015 DOI:10.1038/nn.4035; Xie L, Kang H, Xu Q, et al., "Sleep initiated fluid flux drives metabolite clearance from the adult brain,"* Science*, October 18, 2013 Oct 18;342(6156):373-7. doi: 10.1126/science.1241224.*