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70. Synthesis of wood-silica sol-acrylate hybrid composites

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To enhance the properties of wood, a hybrid system including silica sol and acrylate emulsion were introduced into poplar wood by impregnation treatment under vacuum condition. The status of hybrid component within wood pores were observed by SEM, which showed that the hybrid substances were deposited in the woody fibers and vessels of the cellulose clearances and distributed along the cell wall. FT-IR indicated that the -OH group of wood cellulose were partially bonded with the hybrid components. TG and DTG curves of the hybrid wood composites showed a less weight loss with temperature than the untreated wood. The weight loss of the composite was only 31.5% at 630°C, while that of the untreated wood was 67.88% at 360°C. Thus the hybrid composite endowed the wood with better fire resistance. The properties of the hybrid wood composites were improved, compared with that of poplar wood. The hardness index values of organic/inorganic-wood composite are 9.051, 5.602 and 5.170 along longitudinal direction, radial direction and tangential direction, 2.88 times, 2.10 times and 2.07 times than the untreated wood, respectively. Compression strength is 80.2 Mpa along longitudinal direction, 18.1 Mpa along radial direction, and 11.0 Mpa along tangential direction.

71. Composite wood by infiltration silica sol/styrene-acrylic emulsion system

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To improve some performance of poplar wood, such as low hardness, bad dimension stability, bad abrasion performance, silica sol and styrene-acrylic latex mixture system were introduced into pores of poplar wood. The factors affecting weight percent gains (WPG) and dimensional stability as well as mechanical properties of the composite wood were investigated. The results showed that WPG increased with the amount of precursors and the times of impregnation. And the dimensional stability and the mechanical performance and water resistant were enhanced.

72. Dissipation of the herbicide isoxaflutole in agricultural soils

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Isoxaflutole is a relatively new pre-emergence herbicide used in corn production. Isoxaflutole's phytotoxic metabolite (DKN) has a low sorption coefficient and may be persistent in soil, indicating that this herbicide may have a tendency to contaminate water resources through leaching and runoff. Two-year field dissipation studies were conducted in three soil types (sandy loam, loam, and clay loam) in west central Minnesota to indicate the rate at which isoxaflutole/DKN dissipates under the relatively cool, wet soil conditions typical of the northern Corn Belt. Separate plots were treated with isoxaflutole and potassium bromide, a non-sorbed, non-degraded tracer. Soil cores were collected to 1 m depth and sectioned into 0-10, 10-20, 20-40, 40-60, and 60-100 cm increments; bromide or herbicide concentration was measured at each depth. Leaching of both tracer and herbicide beyond 40 cm was observed. These results will provide information for the development of best management practices for this herbicide.

73. Genomics and biochemistry of atrazine biodegradation by soil bacteria

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Atrazine [6-chloro-N²-ethyl-N⁴-isopropylamino-1,3,5-triazine-2,4-diamine] is one of the most widely used herbicides in the United States for control of broadleaf weeds in corn, sorghum, and sugarcane. We have shown that hydroxyatrazine is the first intermediate in the atrazine mineralization pathway of atrazine-degrading bacteria. *Pseudomonas* strain ADP metabolizes atrazine as its sole source of nitrogen for growth and this bacterium initiates atrazine catabolism via three enzymatic steps encoded by *atzA*, *B* and *C*. These genes are present in different genera of atrazine-degrading bacteria isolated from geographically diverse locations in the World. The *atzA*, *B* and *C* genes were localized to a self-transmissible, plasmid, pADP-1 and the complete nucleotide sequence of pADP-1 revealed the relative locations of these genes. Computational and functional analyses indicated that three new catabolic genes, *atzD*, *atzE*, and *atzF*, hydrolyzing urea, biuret, and allophanate, respectively, were located on pADP-1. More recently, we have finished the complete genomic sequence of the gram positive, atrazine-degrading microorganism, *Arthrobacter aureescens* TC1. We have found that atrazine degradation genes are located on a large plasmid, and that catabolism is initiated by the *trzN* gene. This bacterium can degrade a large number of triazine herbicides, by funneling plasmid derived degradation products to chromosome-encoded enzymes. In this presentation, I will discuss how the genomics and genetics of soil bacteria can provide insight into how plasmid-borne pathways evolve to encode the catabolism of compounds recently added to the biosphere.

74. Isolation and metabolic and proteomic characterization of aromatic degrading bacteria from contaminated soil

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Bacterial species recently isolated from a contaminated soil can degrade a wide range of pesticides and polycyclic aromatic hydrocarbons (PAHs). Analysis of the soil showed 13 PAHs in a range from 0.6 to 30 mg/kg each dry weight and 12 PAH metabolites. Nineteen bacterial strains were isolated from the soil and characterized by two different spray plated methods, turbidity test, and 16S rRNA gene sequencing. Strains C3, C4, P1-1, and JS19b1 were most close to *Burkholderia* sp. 56 (AY177370), *Sinorhizobium* sp. HF6 (AB195269), *Arthrobacter* sp. BS20 (AY452081), and *Mycobacterium* sp. RJGII.135 (U30661), respectively. Strains C3, C4, and P1-1 degraded phenanthrene (40 mg/l) completely after 7-day incubation. Strain C3 also decomposed nine carbamate pesticides (40 mg/l each) from 20% (pirimicarb) to 100% (aminocarb, carbaryl, and xylylcarb) in 14 days. Strain JS19b1 degraded 40% of 2,4-D (40 mg/l) and 100% of pyrene (40 mg/l) in 14 days. Metabolite and protein profiling showed comprehensive metabolism networks of the pesticides and PAHs.