In the Literature

Leishmaniasis in Organ Transplant Recipients


Basset and his colleagues in southern France report 11 new cases of visceral leishmaniasis in recipients of organ transplants and review an additional 46 cases reported in the literature. Most reports involved patients from the Mediterranean basin, but also represented were individuals from India, Iran, and Saudi Arabia. Approximately three-fourths of cases occurred in recipients of kidney transplants, but small numbers of recipients of liver, heart, lung, bone marrow, and pancreas transplants were also affected. Most patients (84%) had “irregular” fever, 59% had splenomegaly, and 28% had hepatomegaly; pancytopenia was present in 58%.

Among the 11 new cases, the interval from transplantation to diagnosis of leishmaniasis ranged from 4 months to 12 years.

Amastigotes were detected in bone marrow smears of 46 (85%) of 54 patients and in the livers of 4 patients who had undergone liver transplantation. The organism was identified in samples from an oral lesion and blood in 1 patient each. Serological test results were positive for 30 (91%) of 33 patients tested but negative for the other 3 patients. The results of PCR of blood samples were positive for 10 of 11 patients tested.

Thirty-nine (80%) of 49 patients who received therapy for leishmaniasis were cured, whereas the other 10 patients (20%) died, as did an additional 4 patients who were not treated. Similar cure rates were achieved for therapy with either antimonials and amphotericin B, but the latter was better tolerated. Immunosuppressive therapy was continued for all responders. Fourteen percent of patients had relapse 1 month to 5 years after transplantation.

The means by which infection occurred in these 57 patients is unknown, but possibilities include recrudescence of previously asymptomatic infection, infection via the transplanted organ or by blood transfusion, and naturally acquired infection after transplantation. Basset and colleagues recommend serological testing for blood and organ donors who reside in or who have traveled to areas of endemcity, testing of prospective organ recipients, and annual testing of transplant recipients who live in or travel to areas of endemcity. Serological testing may also be useful as a diagnostic measure in patients with a febrile illness, splenomegaly, and/or cytopenia.

Visceral leishmaniasis is an important problem in some areas of endemcity among patients with AIDS, whose presentation and clinical course is similar to those for transplant recipients, although serological testing may be less sensitive for patients with AIDS [1]. Although visceral leishmaniasis is not endemic to North America, the extensive travel by many of our patients may put some at risk, making it important that clinicians who deal with transplant recipients be aware of this infectious complication.

Reference

Chagas Disease in Bone Marrow Transplant Recipients: Monitoring and Preemption


The World Health Organization estimates that as many as 18 million people in Central and South America are infected with Trypanosoma cruzi, the agent of Chagas disease [1]. Infection is commonly asymptomatic, but clinical manifestations of chronic infection develop after 10–20 years in approximately one-third of infected persons. In previous decades, the prevalence of infection in blood donors was reported to range from 1.7% in Sao Paulo, Brazil, to 53% in Santa Cruz, Bolivia, but this rate has decreased significantly since that time. Nonetheless, because infection can be transmitted by blood transfusion as well as organ transplantation, this disease represents an important problem in areas where it is endemic and is also of some concern in regions to which individuals from areas of endemcity frequently migrate.

Altclas and colleagues have prospectively evaluated the role of preemptive antiparasitic therapy in 25 bone marrow transplant recipients with serological evidence of trypanosomiasis before transplantation, as well as in recipients whose transplant donors were seropositive. Preemptive therapy was instituted when parasitemia was detected, even in the absence of symptoms.

Four groups of patients were evaluated.
1. Two (16.6%) of 12 T. cruzi-seropositive autologous transplant recipients who developed asymptomatic parasitemia, both of whom were successfully treated with benznidazole without subsequent relapse.
2. Four (44.4%) of 9 patients who were seropositive and received allogeneic transplants from seronegative donors and who subsequently had organisms visualized in peripheral blood specimens by a sensitive method; only 1 patient, who had panniculitis in which T. cruzi was seen on examination of a biopsy specimen, was symptomatic. Parasitemia cleared after a course of benznidazole, without subsequent relapse, in all 4 patients.
3. One seropositive recipient of an allogeneic transplantation from a seropositive donor with no evidence of infection.
4. Three seronegative, parasitemia-negative recipients of allogeneic transplants from seropositive donors, none of whom developed infection (although, in 2 cases, donors were given benznidazole in the pretransplantation period).

Knowledge of the risk of Chagas disease is increasingly important in the United States, where it has been estimated that as many as 370,000 emigrants from regions of endemicity are infected with T. cruzi. The limited data from this study suggest that patients who undergo bone marrow transplantation and who are at risk of developing Chagas disease should be closely monitored and that preemptive therapy should be instituted for those with evidence of active infection, even in the absence of symptoms.

Reference


African Trypanosomes: Will the Twain Meet?


Human African trypanosomiasis comes in 2 flavors. Infection in western and central Africa is caused by Trypanosoma brucei subspecies gambiense, whereas T. brucei subspecies rhodesiense is endemic in areas of southern and eastern Africa, where it is zoonotic and affects livestock. Infection caused by the former subspecies usually has a slowly progressive course, whereas the latter is associated with more-acute and rapidly progressive disease. Uganda is the only country where both forms of the disease exists, albeit in geographically discrete regions. The area affected by T. brucei subspecies rhodesiense in southeastern Uganda has, however, increased by a factor of 2.5 since 1985, extending toward the northwestern part of the country, where T. brucei subspecies gambiense is present. This migration suggests that the 2 subspecies are in danger of becoming sympatric, an occurrence that would significantly complicate control of the disease as well as the treatment of individual patients.

Piccozzi and colleagues examined blood specimens from patients with known or suspected sleeping sickness by PCR testing specific for each subspecies. The results indicated that the areas in which these 2 subspecies are causing disease do not overlap yet. However, T. brucei subspecies rhodesiense has expanded northward into 3 newly affected districts as the result of movement of livestock and has thus extended its focus to within 150 km of the area affected by T. brucei subspecies gambiense.

The 2 subspecies are morphologically indistinguishable, and more-sophisticated testing, such as the molecular method used here, is not generally available in areas of endemicity. At present, the infecting species is inferred from knowledge of the geographic area in which the infection was acquired. Because the appropriate choice of treatment (all parenteral and all toxic) depends on the subspecies causing the infection (as well as the stage of infection), the commingling of subspecies within a geographic area will significantly complicate patient treatment. The most effective means by which this commingling can be prevented is by effective control of the disease in livestock.

The Complexity of Defining a Bacterial Species


The common practice of characterizing bacterial species by sequencing a few strains may be inadequate to fully understand the pathogenic potential and virulence mechanisms for certain species. Tettelin and colleagues examined the entire genome (the “pan-genome”) of 8 strains of group B Streptococcus, representing each of the 5 serotypes commonly associated with disease in humans. They found that the strains shared a “core genome,” representing ~80% of the total genome, but differed in parts of the remaining genome, termed the “dispensable genome.” Many of the virulence mechanisms lie within the dispensable genome, and some of the variations are thought to have been acquired by horizontal transfer from other species. The variability of the dispensable genome was such that even the sequencing of hundreds of genomes might be insufficient to completely identify all genes present in the species.

The authors found similar results with Streptococcus pyogenes. By contrast, examination of 8 strains of Bacillus anthracis found that sequencing of only 4 strains was required before no additional new genes were found. This is consistent with other evidence indicating that strains of B. anthracis are primarily derived from a single clone.

The authors conclude that, although sequencing of the genome of only a few isolates may be sufficient for some species, for others, there is sufficient variability in parts of the genome that make it necessary to sequence many isolates to determine the full range of genetic variations and pathogenicity factors.