recipients based on medical urgency. This new method of organ allocation bases recipient selection on parameters tied to patient mortality instead of absolute waiting time. In addition to patient evaluation by the UNOS MELD score, patients are also evaluated for potential contraindications to transplantation such as limited cardiovascular/respiratory function, advanced malignancy, or active infection such as HIV.

Once a liver recipient has been identified, procurement is completed via one of several surgical methods depending on the type of donation and the specific donor's anatomy. All cadaveric liver procurements involve a long midline incision necessary to expose both the thoracic and abdominal cavities and rule out malignant pathologies.

The majority of hepatic surgical dissection is then performed before or after a systemic flush of the donor's blood with cold preservation solution. To ensure the organ is perfused with preservation solution, the main blood vessels to and from the liver are the last to be transected. In contrast, living donor transplantation involves a less invasive donor incision which exposes only enough of the liver as is necessary for procurement. Additionally, extra care must be taken to ensure that dissection of the donated portion of the liver does not interfere with the normal perfusion and function of the remaining part.

Since the inception of liver transplantation, advancements in organ preservation, better immunosuppressant therapies, and effective management of complications have led to a five-year allograft survival rate of 71 percent and a patient survival rate of 80 percent in the United States. Complications include infection, acute or chronic rejection, vascular occlusion, and renal dysfunction secondary to liver transplantation. In a study of 181 liver transplants performed between 1998 and 2000, researchers found one-week acute renal dysfunction rates of approximately 39 percent and chronic renal dysfunction was discovered in about 6 percent of patients during long-term follow-up.

Renal dysfunction may indicate a necessary change in immunosuppressant therapy to include less nephrotoxic therapeutics. Of increasing interest is the long-term incidence of malignancy related to solid organ transplantation. Studies agree that the development of malignancy is multifactorial and related to the type of transplant, the preexistence of any diseased states, the serological status of the recipient, and immunosuppressant use. Vigilant identification of long-term liver transplantation risks aids in treatment and reduces transplant-related morbidity and mortality.

SEE ALSO: Allograft; Immunosupression; Organ Donation; Organ Transplantation; United Network for Organ Sharing (UNOS).

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Locus

In genetics, a locus is the position of a gene on a chromosome. Genes are located on chromosomes in a linear fashion, and each gene, or one of its alleles, have precise locations or loci on chromosomes. The exact chromosomal address of a gene may look something like "1p34.2", where "1" designates the chromosome number, "p" designates the long arm or the short arm, and "34.2" is the exact location of the gene on that chromosomal arm. These numerical positions can be seen using a microscopically viewable ideogram of chromosomes that have been stained using one of several staining techniques like Giemsa Banding (G banding). By G-Banding chromosomes in metaphase, individual areas of chromosome absorb chemicals differently, giving chromosomes their banded appearance; then numbers and letters are used to pinpoint

exact locations of genes. If a higher-resolution banding is used, sub-bands and sub-sub-bands become visible. Sometimes, groups of genes occupy larger areas on chromosomes, and their location may be given as "11q14-q21" which is the OCA1 gene. This means that the genes extend from band q14 to band q21.

The distance between two loci is a very important parameter in clinical genetics. It gives us critical information on linkage between two or more genes, where linkage is the probability for neighboring alleles on a common chromosome to be transmitted together, as an intact unit, through meiosis. Linkage is the only method that allows us to create gene maps and trace disease genes along family generations. The distance between loci is the only predictor of genetic linkage.

Genetic distance is measured in units called centiMorgans (cM), which is defined as the genetic length over which, on average, one observes recombination 1 percent of the time. To measure distance between two loci, we need to know two variables: the recombination fraction between the two loci, and whether this recombination fraction deviates from 0.5. From these two variables, we can compute the lod score (Z) for "logarithmic of the odds." Positive values of Z (odds>1) suggest the loci are linked, and negative values (odds<1) suggest loci are unlinked.

Genes located on a chromosome are not necessarily linked. These are called syntenic loci regardless of how far apart they are from each other, or how close together they lie on the chromosome. If two syntenic loci are so far apart that there is going to be at least one crossover between them with every meiosis, recombinant and nonrecombinant genotypes will occur in the offspring in equal proportions and the two loci will appear to be unlinked just as if the loci were on separate chromosomes. Locus heterogeneity is a situation in which identical clinical symptoms are caused by abnormalities at two or more genetic loci. If locus heterogeneity is unrecognized, it can confound genetic linkage analysis and give the false impression that a marker is unlinked to a disease locus when in fact it may be linked, but only in a subgroup of all families analyzed.

SEE ALSO: Chromosome, Cytogenetics, Genetic Disorders, Genetic Testing/Counseling, Genetics.

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Longitudinal Study

A longitudinal study involves the repeated collection of data over time. When the data are collected over time from the same cases, this can also be described as a panel study. Longitudinal studies can also be retrospective if they involve the tracing of archived records over time (e.g., medical records for a group of patients). In contrast, a cross-sectional study involves the collection of data at only one point in time. Longitudinal designs offer unique advantages; by being able to track changes to cases over time, researchers can develop a more nuanced view of dynamic effects and can begin to develop more powerful tests of causality. Longitudinal designs can also incorporate other methodological dimensions, such as a hierarchical (or multilevel) structure. This enables the differentiation of effects of compositional factors (i.e., characteristics of cases or individuals) and contextual factors (i.e., characteristics of groups or areas) over time.

For example, the British Household Panel Survey has collected data on a representative sample of the United Kingdom since 1991. The study's sample consists of more than 5,000 households, and includes over 10,000 individual interviews per year. The same individuals are interviewed year after year, and if a member of a household forms a new household, the new household is incorporated into the survey as well. It includes measures of physical and psychological well-being, as well as measurements of income, employment status, individual demographics, and household composition.

The Longitudinal Survey of Immigrants to Canada offers an example of a longitudinal study of shorter duration. It consists of a sample of 20,000; participants are interviewed at three different times: at six months (wave 1), two years (wave 2), and four years after landing in Canada (wave 3). Data from this survey can be used to examine how new immigrants adjust to life in Canada over time; more specifically, this survey offers data on how the health of new immigrants changes