in four distinct regions (superficial, middle, deep, and calcified cartilage zones)—chondrocytes constitute the unique cellular component in these layers. Originally, cartilage was considered to be an inert tissue, but it is now known to be a highly responsive tissue that reacts to inflammatory mediators and mechanical factors, which in turn, alter the balance between cartilage anabolism and catabolism. In RA, the initial areas of cartilage degradation are juxtaposed to the synovial pannus. The cartilage matrix is characterized by a generalized loss of proteoglycan, most evident in the superficial zones adjacent to the synovial fluid. Degradation of cartilage may also take place in the perichondrocytic zone and in regions adjacent to the subchondral bone.

PATHOGENESIS

The pathogenic mechanisms of synovial inflammation are likely to result from a complex interplay of genetic, environmental, and immunologic factors that produces dysregulation of the immune system and a breakdown in self-tolerance **(Fig. 380-4)**. Precisely what triggers these initiating events and what genetic and environmental factors disrupt the immune system remains a mystery. However, a detailed molecular picture is emerging of the mechanisms underlying the chronic inflammatory response and the destruction of the articular cartilage and bone.

In RA, the preclinical stage appears to be characterized by a breakdown in self-tolerance. This idea is supported by the finding that autoantibodies, such as RF and anti-CCP antibodies, may be found in sera from patients many years before clinical disease can be detected. However, the antigenic targets of anti-CCP antibodies and RF are not restricted to the joint, and their role in disease pathogenesis remains speculative. Anti-CCP antibodies are directed against deaminated peptides, which result from posttranslational modification by the enzyme PADI4. They recognize citrulline-containing regions of several different matrix proteins, including filaggrin, keratin, fibrinogen, and vimentin, and are present at higher levels in the joint fluid compared to the serum. Other autoantibodies have been found in a minority of patients with RA, but they also occur in the setting of other types of arthritis. They bind to a diverse array of autoantigens, including type II collagen, human cartilage gp-39, aggrecan, calpastatin, BiP (immunoglobulin binding protein), and glucose-6-phosphate isomerase.

In theory, environmental stimulants may synergize with other factors to bring about inflammation in RA. People who smoke display higher citrullination of proteins in bronchoalveolar fluid than those who do not smoke. Thus, it has been speculated that long-term exposure to tobacco smoke might induce citrullination of cellular proteins in the lung and stimulate the expression of a neoepitope capable of inducing self-reactivity, which in turns, leads to formation of immune complexes and joint inflammation. Exposure to silicone dust and mineral oil, which has adjuvant effects, has also been linked to an increased risk for anti-CCP antibody-positive RA.

How might microbes or their products be involved in the initiating events of RA? The immune system is alerted to the presence of microbial infections through Toll-like receptors (TLRs). There are 10 TLRs in humans that recognize a variety of microbial products, including bacterial cell-surface lipopolysaccharides and heat-shock proteins (TLR4), lipoproteins (TLR2), double-strand RNA viruses (TLR3), and unmethylated CpG DNA from bacteria (TLR9). TLR2, -3, and -4 are abundantly expressed by synovial fibroblasts in early RA and, when bound by their ligands, upregulate production of proinflammatory cytokines. Although such events could amplify inflammatory pathways in RA, a specific role for TLRs in disease pathogenesis has not been elucidated.

The pathogenesis of RA is built upon the concept that self-reactive T cells drive the chronic inflammatory response. In theory, self-reactive T cells might arise in RA from abnormal central (thymic) selection due to defects in DNA repair leading to an imbalance of T cell death and life, or defects in the cell signaling apparatus lowering the threshold for T cell activation. Similarly, abnormal selection of the T cell repertoire in the periphery might lead to a breakdown in T cell tolerance. The support for these theories comes mainly from studies of arthritis in mouse models. It has not been shown that patients with RA have abnormal thymic selection of T cells or defective apoptotic pathways regulating cell death. At least some antigen stimulation inside the joint seems likely, owing to the fact that T cells in the synovium express a cell-surface phenotype indicating prior antigen exposure and show evidence of clonal expansion. Of interest, peripheral blood T cells from patients with RA have been shown to display a fingerprint of premature aging that mostly affects inexperienced naïve T cells. In these studies, the most glaring findings have been the loss of telomeric sequences and a decrease in the thymic output of new T cells. Although intriguing, it is not clear how generalized T cell abnormalities might provoke a systemic disease dominated by synovitis.

There is substantial evidence supporting a role for CD4+ T cells in the pathogenesis of RA. First, the co-receptor CD4 on the surface of T cells binds to invariant sites on MHC class II molecules, stabilizing the MHC-peptide–T cell receptor complex during T cell activation. Because the SE on MHC class II molecules is a risk factor for RA, it follows that CD4+ T cell activation may play a role in the pathogenesis of this disease. Second, CD4+ memory T cells are enriched in the synovial tissue from patients with RA and can be implicated through "guilt by association." Third, CD4+ T cells have been shown to be important in the initiation of arthritis in animal models. Fourth, some, but not all, T cell–directed therapies have shown clinical efficacy in this disease. Taken together, these lines of evidence suggest that CD4+ T cells play an important role in orchestrating the chronic inflammatory response in RA. However, other cell types, such as CD8+ T cells, natural killer (NK) cells, and B cells are present in synovial tissue and may also influence pathogenic responses.

In the rheumatoid joint, by mechanisms of cell-cell contact and release of soluble mediators, activated T cells stimulate macrophages and fibroblast-like synoviocytes to generate proinflammatory mediators and proteases that drive the synovial inflammatory response and destroy the cartilage and bone. CD4+ T cell activation is dependent on two signals: (1) T cell receptor binding to peptide-MHC on antigen-presenting cells; and (2) CD28 binding to CD80/86 on antigen-presenting cells. CD4+ T cells also provide help to B cells, which in turn, produce antibodies that may promote further inflammation in the joint. The previous T cell–centric model for the pathogenesis of RA was based on a T_H1-driven paradigm, which came from studies indicating that CD4+ T helper (T_H) cells differentiated into T_H1 and T_H2 subsets, each with their distinctive cytokine profiles. T_H1 cells were found to mainly produce interferon γ (IFN-γ), lymphotoxin β, and TNF-α, whereas T_H2 cells predominately secreted interleukin (IL)-4, IL-5, IL-6, IL-10, and IL-13. The recent discovery of another subset of T_H cells, namely the T_H17 lineage, has revolutionized our concepts concerning the pathogenesis of RA. In humans, naïve T cells are induced to differentiate into T_H17 cells by exposure to transforming growth factor β (TGF-β), IL-1, IL-6, and IL-23. Upon activation, T_H17 cells secrete a variety of proinflammatory mediators such as IL-17, IL-21, IL-22, TNF-α, IL-26, IL-6, and granulocyte-macrophage colony-stimulating factor (GM-CSF). Substantial evidence now exists from both animal models and humans that IL-17 plays an important role not only in promoting joint inflammation, but also in destroying cartilage and subchondral bone

The immune system has evolved mechanisms to counterbalance the potential harmful immune-mediated inflammatory responses provoked by infectious agents and other triggers. Among these negative regulators are regulatory T (T_{reg}) cells, which are produced in the thymus and induced in the periphery to suppress immune-mediated inflammation. They are characterized by the surface expression of CD25 and the transcription factor forkhead box P3 (FOXP3) and orchestrate dominant tolerance through contact with other immune cells and secretion of inhibitory cytokines, such as TGF-β, IL-10, and IL-35. T_{reg} cells appear to be heterogeneous and capable of suppressing distinct classes (T_H1, T_H2, T_H17) of the immune response. In RA, the data that T_{reg} numbers are deficient compared to normal healthy controls are contradictory and inconclusive. Although some experimental evidence suggests that T_{reg} suppressive activity is lost due to dysfunctional expression of cytotoxic T lymphocyte antigen 4