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## New insights into the pathogenesis and genetics of psoriatic arthritis

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### Summary

Psoriasis (PS) and psoriatic arthritis (PSA) are inter-related heritable diseases. Psoriatic skin is characterized by hyperproliferative, poorly differentiated keratinocytes and robust mononuclear inflammation. Psoriatic joints are characterized by highly inflamed synovia and entheses with focal erosions of cartilage and bone. Recent genetic analyses have uncovered risk factors shared by both PS and PsA. With respect to common variation, the HLA class I region is the locus that predisposes most strongly to PS and PsA. Other risk factors implicate the IL23 pathway and the induction/regulation of Th17 cells in the pathogenesis of both diseases. Elaboration by cytokines such as IL22 and IL could result in the hyper-proliferative phenotype of keratinocytes and potentially synoviocytes, leading to the vicious cycle of proliferation/inflammation in both the skin and joints. In synovial tissue, disease-related cytokines may also lead to RANK ligand dependent osteoclast formation leading to bone erosion. Genetic risk factors leading specifically to PsA need to be identified. Therapies targeting TNF have frequently been highly successful in the treatment of both diseases, and genetic findings are likely to lead to the development of additional treatments tailored to an individual's genetic profile.

### Introduction

Psoriasis vulgaris (PS) is a chronic inflammatory skin disease affecting 2–3% of the Caucasian population.<sup>1, 2</sup> It frequently develops in early adulthood between the ages of 15 and 30, although individuals of all ages can be affected. The thick scaly skin plaques observed in the psoriatic lesion reflects a number of biological changes including the reduction in the transit time a basal keratinocyte progresses to a desquamated cell (4–6 weeks to only a few days). Moreover, a large number of activated immune cells in the psoriatic dermis elaborate a complex cytokine milieu not found in normal skin.

Up to 30% of PS patients also develop psoriatic arthritis (PsA).<sup>3</sup> These patients complain of chronic joint pain, fatigue, and restriction of mobility, and experience a reduced quality of life compared to normal individuals.<sup>3, 4</sup> Some PsA patients may have an increased prevalence of cardiovascular disease and its associated risk factors than matched controls.<sup>5–8</sup> The same is true for PS patients, and severely affected individuals may have greater risk factors of cardiovascular disease than those with milder disease.<sup>9</sup> Here, we briefly review the clinical features of PsA and the treatment modalities currently available. We also describe the recently identified genetic associations that confer susceptibility to both PS and PsA that begin to

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explain the fundamental basis of the biological alterations found in these diseases and that highlight pathways to be targeted for the development of novel therapies.

## Genetic and environmental contributions

PsA is a highly heritable disease. The recurrence risk ( $\lambda_S$ )<sup>10</sup> (risk to siblings/risk in the general population) of PsA is greater than 27,<sup>11</sup> which is far higher than for PS which is between 4 and 11.<sup>12</sup> Heritability is also greater for PsA than for autoimmune conditions such as rheumatoid arthritis (RA), primary Sjogren's syndrome and thyroid disease.<sup>13</sup> The prevalence of PS is 19 times higher among first degree relatives of probands with PsA compared with the general population.<sup>14</sup>

PS lesions can be triggered by a large number of factors in genetically susceptible individuals, including physical injury to the skin (the "Koebner" response), administration of interferons or other inflammation-inducing stimuli, rapid withdrawal of immunosuppressive drugs, and (systemic) infections with streptococcus or other bacteria.<sup>15</sup> In contrast, the trigger for PsA is not as clear although viral triggers have been suggested.<sup>16</sup>

## Clinical features of PsA

In 1973, Moll and Wright<sup>17</sup> defined PsA as an inflammatory peripheral arthritis and/or spondylitis associated with PS with a negative serology test for rheumatoid factor. Since then, the wide spectrum of clinical presentations for PsA has resulted in classification criteria to help distinguish PsA from other forms of inflammatory arthritis such as rheumatoid arthritis.<sup>18–20</sup> These include equal sex distribution, an asymmetric arthritis particularly involving DIP joints, arthritis mutilans, spondyloarthropathy and a higher incidence of nail involvement than uncomplicated PS.<sup>17, 21</sup> In approximately 80% of patients, arthritis follows the development of PS by a mean of 10 years.<sup>21, 22</sup> In others, joint manifestations may present with or prior to the skin lesions. The arthritis, in most cases, is oligoarticular but may involve more joints over time and result in a symmetric and polyarticular destructive arthritis.<sup>22, 23</sup> A spinal predominant variant may present with asymmetric sacroiliitis and discontinuous spinal involvement that resembles ankylosing spondylitis. Enthesitis can help distinguish PsA from rheumatoid arthritis and osteoarthritis. This is evident in plain radiographs and MRI as periostitis, new bone formation and erosions.<sup>24</sup>

## Current therapies for PsA

The symptoms of mild PsA are often successfully alleviated by non-steroidal anti-inflammatory drugs (NSAIDs), or by local intra-articular injections of corticosteroids.<sup>25</sup> However, neither of these modalities can arrest the development of structural joint damage.<sup>26</sup> Extensive or aggressive disease requires more potent therapy such as traditional disease-modifying anti-rheumatic drugs (DMARDs) like methotrexate and sulfasalazine.<sup>25</sup> Methotrexate has also been widely used to treat severe PS since the 1960s<sup>27</sup>. Its broad anti-inflammatory effect mediated by adenosine can neutralize neutrophils, T cells and macrophages that are all key players in PS and PsA pathogenesis.<sup>28</sup>

Cyclosporine, which potently inhibits T cell activation and cytokine production is effective for the rapid control of both PS and PsA.<sup>27,29</sup> In contrast, biological response modifiers targeting specific T cell co-stimulatory molecules such as Alefacept, a human LFA-3 (CD58)/IgG1 fusion protein, is effective for PS, but not for PsA.<sup>30</sup> Likewise, Efalizumab, a humanized monoclonal antibody against LFA-1 expressed by T cells, is effective for PS<sup>31</sup> but does not differ significantly from placebo in the treatment of PsA.<sup>32</sup> In some cases, treatment with Efalizumab for PS even triggers the onset of, or exacerbates, PsA.<sup>33, 34</sup>

Three TNF $\alpha$  antagonists, adalimumab, etanercept, and infliximab, have been FDA-approved for the treatment of PsA. Significant numbers of patients treated with these agents achieve ACR50 compared to placebo groups.<sup>35,36,37</sup> Multiple clinical trials have also demonstrated the efficacy of TNF $\alpha$  blockade for PS.<sup>38, 39</sup> Etanercept exerts its effect in PS by inhibiting inflammatory myeloid dendritic cell (DC) cytokine production and maturation, thus reducing the activity of the newly described pathogenic lineage of effector CD4<sup>+</sup> T cells, T helper(Th) 17 (T<sub>h</sub>17) cells and the levels of their elaborated cytokines<sup>40</sup>. TNF $\alpha$  antagonists can also regulate differentiation and activation of osteoclasts<sup>41</sup>, thus reducing bone destruction in psoriatic arthritis. Paradoxically, TNF $\alpha$  blockade can also induce or worsen PS, perhaps due to unopposed IFN $\gamma$  production from Th1 cells or to upregulation of plasmacytoid DCs.<sup>42</sup> IL12/23 p40 blockade also results in a dramatic and prolonged clinical response to psoriasis<sup>43, 44</sup>. Collectively, these data imply a pivotal role of DC and T cell interactions via TNF $\alpha$  and IL23/T<sub>h</sub>17 axis in PS and potentially PsA pathogenesis that is discussed further below.

### Pathogenic clues from genetic analyses

The efficacy of immune modulating therapies in the treatment of both PS and PsA implicates shared immunologic mechanisms in the pathogenesis of both diseases. Both skin and synovium are characterized by marked vascularity and robust mononuclear inflammatory infiltration that includes dendritic cells (DC), activated T cells and tissue macrophages<sup>45–47</sup> and multiple genetic risk factors encoded by these immune cells are beginning to be identified.

Genetic approaches for finding disease genes depend on whether they are rare mutations or common variation. The identification of rare variants responsible for Mendelian traits can be accomplished by linkage analysis followed by positional cloning as long as sufficient affected members/families are available for statistical analyses. The identification of common variation for common diseases such as PS and PsA is performed with genetic association studies. While association studies have been performed for highly plausible candidate genes (i.e those for the major histocompatibility locus antigen cluster (MHC) and IL12p40)<sup>48, 49</sup>, recently improved technologies for genome wide association studies (GWAS) have facilitated a genome-wide and unbiased approach (see BOX).

Below we present genes/loci associated with PsA. Most were originally described to be associated with PS, and were then tested for their association with PsA. Their likely contributions to immunopathology and disease pathogenesis, particularly in the context of joint inflammation, are discussed and illustrated in Figure 1.

### PSORS1 and other HLA antigens

Psoriasis susceptibility locus 1 (PSORS1) was the first PS susceptibility locus to be localized and maps to the MHC class I region. The strong association between PSORS1 and HLA-Cw6<sup>50,51–58</sup> is estimated to account for one-third to one-half of the genetic liability to PS<sup>59</sup>. HLA-Cw\*0602 is also increased among patients with PsA compared to controls<sup>48</sup> (Table 1) and leads to earlier mean age of onset of PS in PsA patients ( $p = 0.003$ ).<sup>48</sup>

GWAs studies also indicate that alleles from the HLA class I region are more highly associated with PsA than any other loci in the genome are<sup>60</sup>. The SNPs most highly associated with PsA tag HLA-Cw\*0602, but also the rarer and closely-related HLA-Cw\*1203 allele.<sup>56,57</sup> Interestingly, and as described elsewhere, HLA-Cw\*0602 and HLA-Cw\*1203 may recognize the same antigen since they are identical in their alpha-2 domains and peptide binding pockets C, D, and E.<sup>56</sup> However, they differ by five amino acids in their alpha-1 domain, placing them in different killer cell immunoglobulin-like receptor (KIR) ligand groups. As other independent studies point to HLA-Cw\*0602 alone as being the PSORS1 risk allele,<sup>52</sup> functional studies

may be needed to resolve this discrepancy and to conclusively rule out SNPs affecting expression of HLA-C alleles or other skin specific genes in this region such as corneodesmosin and alpha-helix coiled-coil rod homolog gene (HCR).<sup>53, 54, 58, 61–63</sup>

Earlier studies on PsA associations with MHC alleles were generally performed with small numbers of patients but deserve some discussion. HLA-B27 is associated with spinal involvement, whereas HLA-B38 and B39 are associated with peripheral polyarthritis.<sup>64</sup> These latter two alleles are highly correlated with HLA-Cw\*1203, hence, this earlier finding may be due to the HLA-Cw\*1203 association with PsA. The presence of the RA “shared epitope” HLA-DRB1 from the HLA class II region is reported to be associated with radiological erosions in PsA.<sup>65</sup> Moreover, HLA-B39 alone, HLA-B27 in the presence of HLA-DR7, and HLA-DQw3 in the absence of HLA-DR7, are reported to confer an increased risk for disease progression. Conversely, HLA-B22 is reported to be protective for disease progression.<sup>64</sup> Patients with both HLA-Cw6 and HLA-DRB1\*07 alleles are reported to have a less severe course of arthritis than patients with HLA-C26 or HLA-DRB1\*07 alone.<sup>66</sup> It is not clear if some of these associations are due to “linkage disequilibrium” within the MHC, reflecting a predisposing haplotype harboring a different risk factor, or are truly causative themselves.

Tumor necrosis factor alpha (*TNFA*) polymorphisms are of interest given the success of anti-TNF agents in PS and PsA. The polymorphisms that are associated with PS and PsA, such as those in the *TNFA* promoter at positions –238 and –308, have been demonstrated to be due to linkage disequilibrium with HLA-Cw\*0602.<sup>67</sup> However, TNF\*-857T, may represent a risk factor for PsA that is independent of the PSORS1 allele.<sup>67</sup>

In the case of PsA susceptibility, there are also important interactions with certain HLA-class I alleles and killer inhibitory receptors (KIRs) that are located on chromosome 19. Susceptibility to PsA is strongly associated with the presence of KIR2DS1 and/or KIR2DS2 plus HLA-Cw ligand group homozygosity (so that an inhibitory signal is diminished).<sup>68,69,70</sup> Certain combinations of natural killer receptors and HLA-B alleles are also associated with slower time to develop AIDS, and lower risk of HIV infection in exposed uninfected individuals<sup>71</sup>. These include the combined genotype of *KIR3DL1* high expressing alleles and HLA-B\*57 which is associated with PsA. Certain combinations of HLA and KIR are also reported to affect outcome to infection by other viruses such as hepatitis B virus, hepatitis C virus and human papilloma virus<sup>72</sup>. It is tempting to speculate that selection of alleles in the past that protected against viral infection lead to susceptibility to diseases such as psoriatic arthritis.

## Other susceptibility genes

With the exception of the MHC, linkages and associations have not been replicated in all cohorts. This can be due to low effect size of individual genetic variation, ascertainment bias and gene-environment interactions. The following are genes that have recently been implicated in PS and PsA from genetic analyses (also summarized in Table 1).

### Genes influencing the IL-23/Th17 pathway

Susceptibility to both PS and PsA is associated with alleles of the *IL12B* and IL23 receptor (*IL23R*) genes (Table 1).<sup>49, 60, 73–75</sup> The same *IL23R* alleles are risk factors for other inflammatory or autoimmune diseases such as Crohn’s disease and ankylosing spondylitis<sup>76, 77</sup>. This implicates a shared inflammatory pathway mediated by IL23R in all of these diseases.<sup>76, 78–80</sup> A variant near *IL23A* (encoding IL-23p19) also confer PS susceptibility.<sup>81</sup> IL-23 is composed of two sub-units, IL-23p19 (encoded by *IL23A*) and IL-12p40 (encoded by *IL12B*), and is recognized by the heterodimeric receptor encoded by *IL23R* and *IL12RB1*. IL-12 is a heterodimer of IL12p40 and IL12p35 and binds to the heterodimeric receptor complex of

IL12R $\beta$ 2 and IL12R $\beta$ 1. These cytokines play key roles in regulating both innate and adaptive immunity. IL-12, elaborated by activated dendritic cells and macrophages during inflammation can regulate the differentiation of naïve T<sub>h</sub> cells into IFN- $\gamma$  producing T<sub>h</sub>1 cells. IL-23 is also elaborated by dendritic cells and macrophages, and is a survival factor for T<sub>h</sub>17 cells. The level of IL23p19 and p40 sub-units, but not IL12p35, are significantly increased in lesional compared to non-lesional skin,<sup>82</sup> which could be due to the direct effect of genetic risk factors such as an increased affinity for transcription factors in enhancers of these genes. Serum levels of IL12/23 p40 sub-unit is also one of the proteins that can maximally discriminate PsA patients from controls.<sup>83</sup>

T<sub>h</sub>17 cells are developmentally and functionally distinct from classical T<sub>h</sub>1 and T<sub>h</sub>2 lineages and are characterized by the production of IL-17 and IL-22 cytokines.<sup>84</sup> Like the traditional T<sub>h</sub>1 and T<sub>h</sub>2 cells, they are proposed to have evolved to provide adaptive immunity to specific classes of pathogens, such as extracellular bacteria. Aberrant T<sub>h</sub>17 responses are implicated in a growing list of autoimmune disorders<sup>85</sup> and both IL-17 and IL-22 cytokines are increased in PS lesions<sup>40, 86</sup>. They induce pro-inflammatory chemokines, and promote epidermal acanthosis and parakeratosis.<sup>87–90</sup> However, it is still unclear if this axis is similarly relevant in triggering joint disease in PsA. While activated T cells infiltrate PSA joints with similar distribution patterns as in lesional skin: CD4+ T cells predominate over CD8+ in the dermis<sup>37</sup> and synovial membrane<sup>91</sup>, and the reverse in both epidermis and synovial fluid,<sup>92, 93</sup> the joint levels of T<sub>h</sub>17 associated cytokines have yet to be established. These activated T cells from PsA joints can induce osteoclastogenesis and trigger bone resorption and articular damage in PsA via RANK/RANKL interactions.<sup>94, 95</sup> Osteoclastogenesis can be triggered by TNF $\alpha$ , and there is *in vitro* evidence that IL-23 can induce this as well, by a mechanism that is IL-17, TNF $\alpha$  and RANKL dependent<sup>96, 97</sup>. IL-17 has also been shown *in vitro* to induce the expression of RANKL in osteoblasts.<sup>96, 97</sup> Treatment with human IL12/23 p40 monoclonal antibody can reduce the signs and symptoms of psoriatic arthritis, supporting an important pathogenic role for IL23 and potentially T<sub>h</sub>17 cytokines in potentiating osteoclastogenesis and exerting a pro-erosive influence in PsA.<sup>98</sup>

A region of chromosome 4q27 encoding IL-2 and/or IL-21 and associated with celiac disease<sup>99</sup>, type 1 diabetes<sup>100</sup>, RA<sup>101</sup> and systemic lupus erythematosus (SLE)<sup>102</sup> is associated with PsA susceptibility in one study (Table 1)<sup>60</sup>. IL-2 is a pathogenic cytokine for PS, and blockade of the IL-2 receptor with therapeutic antibodies has led to disease resolution in some cases.<sup>103</sup> Together with TGF $\beta$ , IL-2 is also essential for expansion of regulatory T cells (T<sub>reg</sub>).<sup>104</sup> IL-21 is produced by activated T cells and influences the proliferation of T and B cells, and the cytolytic activity of natural killer cells.<sup>105</sup> Importantly, IL-21 is produced by T<sub>h</sub>17 cells<sup>106</sup> and is thought to promote and sustain T<sub>h</sub>17 differentiation and IL-17 production in an autocrine fashion.<sup>107–109</sup> IL-21 can also up-regulate IL-23R<sup>109</sup> that, as previously mentioned, has been implicated in PS and PsA pathogenesis. However, the presence of IL-21 has yet to be demonstrated in psoriatic skin or synovium.

It is of interest that the genetic associations described above converge on cellular pathways involved in a decision of antigen-stimulated cells to differentiate into either a T<sub>h</sub>17 or T<sub>reg</sub> cell. In mice, when TGF $\beta$  is at low concentrations it synergizes with IL-6 and IL-21 to relieve FOXP3 mediated inhibition of ROR $\gamma$ t promoting IL-23R expression and favoring T<sub>h</sub>17 cell development<sup>110</sup>; a process that is dependent on histone/protein deacetylase activity<sup>111</sup>. Conversely, high concentrations of TGF $\beta$  repress IL-23R expression and favor the development of T<sub>regs</sub>. The role of T<sub>regs</sub> in PsA has not been described, but it is known that they can suppress RANKL-dependent osteoclast formation<sup>112</sup>.

### The 5q31 locus and Ps/PsA

The 5q31 region harbors genes encoding IL4, IL13 and IL5 that are upregulated in T cells committed to the Th2 lineage<sup>104</sup> and certain alleles confer susceptibility to a number of inflammatory diseases including Crohn's disease (CD), asthma and PS<sup>113–116,117</sup> PS associated variants upstream from IL13 and within *SLC22A4/OCTN1* may both be causative<sup>118</sup> and independent of CD variants. However, an independent study indicated that the same OCTN1 variant is associated with both CD and PsA.<sup>119</sup>

The role the 5q31 locus plays in the development of PS and potentially PsA is not clear. IL-4 prevents the development of arthritis in an animal model induced by Ags or infections agents, inducing a switch from a Th1-type to a Th2-type response.<sup>120</sup> IL-4 and IL-13 also negatively regulate TNF $\alpha$  and IFN $\gamma$  induced pathways in keratinocytes via activation of STAT6, suppressor of cytokine signaling (SOCS)-1 and SOCS-3. This interferes with STAT-1 and NF-kappaB signaling and activation of the beta-defensins HBD-2 and HBD-3.<sup>121</sup> IL4 and IL13 also play a role in the induction of T<sub>regs</sub> from peripheral naïve CD4<sup>+</sup> T cells.<sup>122</sup> This induction is independent of the presence of TGF $\beta$  or IL-10, but is dependent on antigen-specific stimulation and B7 co-stimulation.

### Other Genetic Associations

Psoriasis is also associated with allele/s of tumor necrosis factor, alpha-induced protein 3 (*TNFAIP3*), a zinc finger/ubiquitin editing enzyme, A20, and with SNPs upstream from the gene encoding its partner TNFAIP3 interacting protein 1 (TNIP1). Their encoded proteins play a role in restricting NF- $\kappa$ B dependent signaling and preventing inflammation. Independent polymorphisms in *TNFAIP3* are associated with rheumatoid arthritis, and systemic lupus erythematosus.<sup>123–126,81</sup> TNIP1 is upregulated in psoriasis lesions and uninvolved versus normal skin from controls<sup>81</sup> and the association of TNFAIP3 and TNIP1 with PsA needs to be examined.

Another potential avenue to explore in the genetics of PsA is the overlap between Ankylosing Spondylitis (AS) and PsA since at least some genetic risk factors are shared (e.g. HLA-B27, IL23R<sup>77</sup>, IL-1<sup>127</sup>). Two regions of chromosome 2q12-13 harboring the interleukin-1 (IL-1) cytokine cluster contributed independently to risk of PsA; a region in IL1A, and a region near the end of IL1B, through IL1F7, IL1F8, and into IL1F10<sup>127</sup>. *ARTS1*, *TSHR* and *FCRL3* are also associated with AS<sup>77</sup>. Since over forty percent of patients with PsA have spondyloarthritis, patients with combinations of genetic risk factors also found in AS patients may belong to a particular subset.

Other similarities in skin and joints are worth exploring. The activated osteoclast is a CD68<sup>+</sup> blood-derived, macrophage-like cell that lives normally in an unactivated state on the bone cortex or outer surface.<sup>128</sup> CD68<sup>+</sup>/CD11c<sup>+</sup> dendritic cells are also present in the dermal-epidermal junction of lesional psoriatic skin and are the main producers of IL-20.<sup>129</sup> IL-20 production can be stimulated by TNF $\alpha$ <sup>95</sup> that is produced by myeloid leukocytes including DCs and macrophages. Hence, genetic factors that contribute to the differentiation, activation, or down-regulation of myeloid cells may be important for the CD68<sup>+</sup> osteoclasts in PSA and also for the CD68<sup>+</sup>/CD11c<sup>+</sup> dendritic cells in PS.

### Conclusion

The immune system is a tightly regulated network of cells and cytokines, and genetic factors that lead to immune alterations may likely tip the balance towards inflammation in the skin and synovium of PS and PsA, respectively. Noteworthy shared associations in PS and PsA involve components of the IL-23/Th17 pathway, namely, *IL23R*, *IL12B*, and potentially

*IL23A* and *IL21*. As it is known that the different  $T_h$  subsets can counter-regulate each other, <sup>130, 131</sup> further dissection of the contribution and interaction of different  $T_h$  subsets in PsA is of extreme interest. It will also be of interest to determine if they also play a role in osteoclastogenesis. It is also important to identify specific genetic factors that differentiate PsA from PS.

Genetic risk factors generally have odds ratios below 2 and frequently between 1.1 and 1.5. Even for the MHC, the OR is < 4.0. Hence, multiple genes of low risk effect may be involved in susceptibility to PS and PsA. This is similar to CD where ~30 genes with low risk effects (generally <1.3) have been identified, and where there are predicted to be possibly 100 risk factors with even lower risk effects (<1.1).<sup>132</sup>

Many questions are left unanswered that, we hope, genetics can further elucidate. Can we stratify patients into different subpopulations based on genetic risk factors and tailor therapy? Which genetic risk factors can predict response to treatment? What role does the environment play in triggering disease? Answering these questions will require much larger patient populations, and well-annotated clinical databases, than those studied so far.

### BOX

These approaches search for association of a disease with single nucleotide polymorphisms (SNPs); variations in DNA sequence that exists in two forms (alleles) in a population. Such markers (~500,000 or more) have been selected throughout the genome by the International HapMap project<sup>134</sup> as representatives of the sequence that surround them. When an “association” between a SNP and a disease exists, the frequency of the alleles differs in cases compared to healthy controls. The marker is usually not the “cause” of the trait, but identifies the general locale of the offending alteration.

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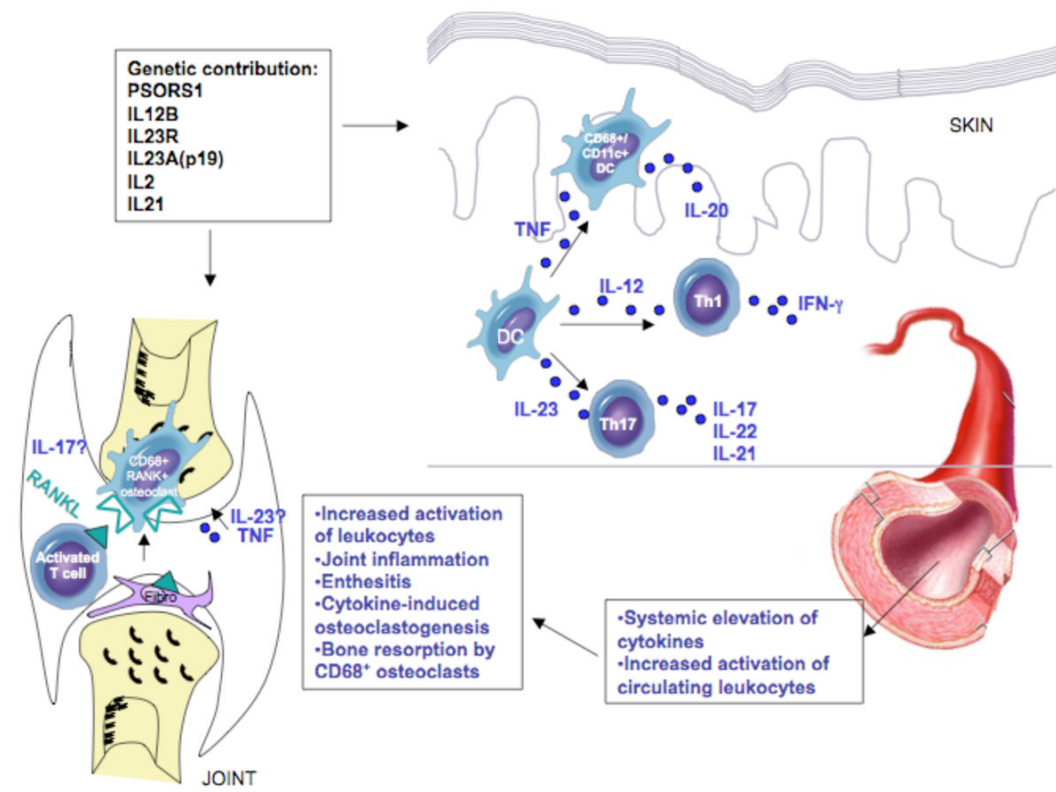
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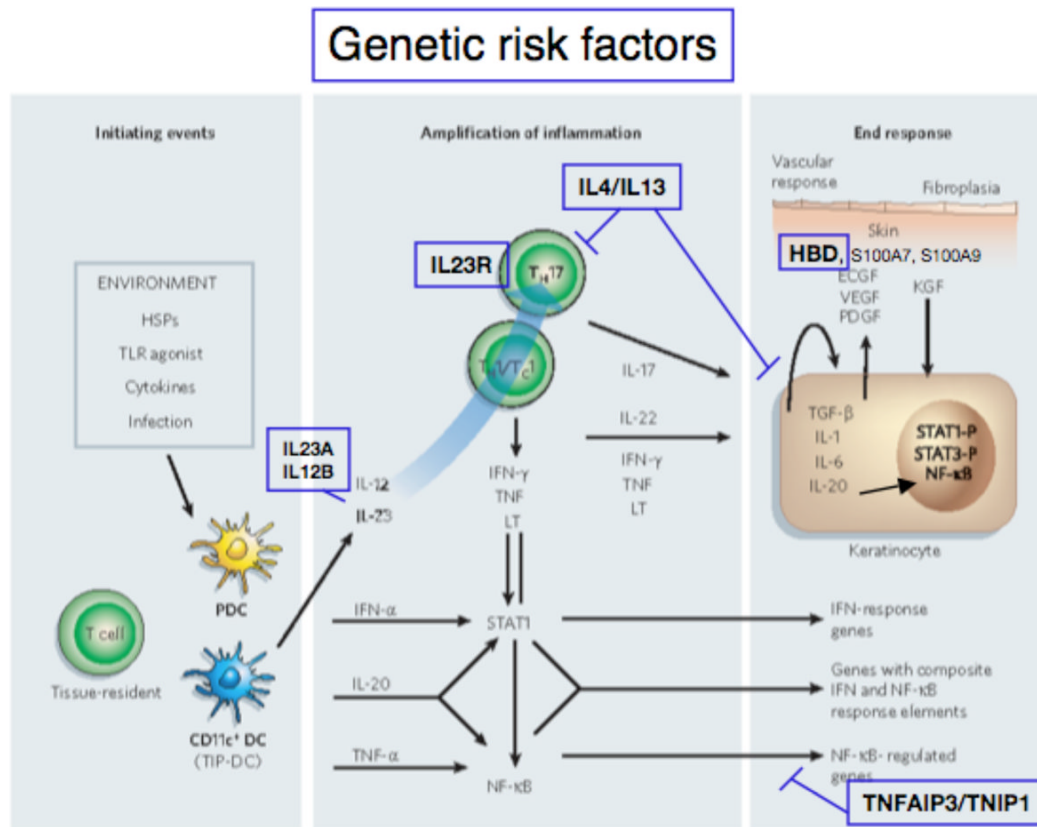
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Adapted from Lowes, MA et al. Nature 2007

**Figure 1. Model of the relationship between skin and joint inflammation**

Genes with variants (box) contributing to psoriasis and/or psoriatic arthritis susceptibility. While infiltrating leukocytes and their cytokine products are currently better characterized in the skin than in the inflamed joint, they may be similar in both sites. Leukocytes and cytokines originating in the skin may play a direct or indirect role in the development of arthritis. Alternatively, they may originate in the synovium in a similar manner to their development in the skin. Gene variants (blue boxes) that predispose to psoriasis influence pro-inflammatory pathways, notably the Th1 and Th17 pathways. Model of cytokine networks in psoriasis adapted from Lowes, MA et al, 2007. The role of the 5q31 region harboring IL4/IL13 is speculative at this stage. HBD (beta defensin) is upregulated in keratinocytes as a result of stimulation by IL20 and other cytokines. An increase in the number of copies of gene family members is also associated with psoriasis.

Genes/SNPs associated with PsA. Numbers of cases/controls used for each study along with corresponding odds ratios (ORs) and P values are shown.

Table 1

Gene	Chs	SNP	Case	Control	OR	P	Ref
IL12B	5q33	rs6887695	576	480	1.1	0.0013	60
			748	937	1.5	$4.72 \times 10^{-7}$	133
			748	937	1.48	$2.1 \times 10^{-5}$	133
IL23R	1p31	rs11209026	576	480	1.70	$8 \times 10^{-4}$	60
			748	937	1.59	0.002	133
IL2/IL21	4q27	rs13151961	576	480	1.37	0.002	60
IL-1 gene cluster	2q13	rs3811047	212	159	1.82	0.0025	127
TNF-alpha	6p21	-857	375	376	1.96	$6.9 \times 10^{-11}$	67
HLA class I6p21 rs10484554			576	480	2.4		60
		HLA-Cw6	94				48
HLA class I - HCP5	6p21	rs2395029	576	480	3.2	$1.9 \times 10^{-10}$	60
Killer inhibitory receptor	19q/6p21		366/75				68
(2DS1 and/or 2DS2) + HLA-Cw ligand group homozygosity							70