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## Molecular Pathophysiology of Chronic Wounds: Current State and Future Directions

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### Abstract

Venous leg ulcers, diabetic foot ulcers, and pressure ulcers are complex chronic wounds with multifactorial etiologies that are associated with high patient morbidity and mortality. Despite considerable progress in deciphering the pathologies of chronic wounds using “omics” approaches, considerable gaps in knowledge remain, and current therapies are often not efficacious. We provide a comprehensive overview of current understanding of the molecular mechanisms that impair healing and current knowledge on cell-specific dysregulation including keratinocytes, fibroblasts, immune cells, endothelial cells and their contributions to impaired reepithelialization, inflammation, angiogenesis, and tissue remodeling that characterize chronic wounds. We also provide a rationale for further elucidation of ulcer-specific pathologic processes that can be therapeutically targeted to shift chronic nonhealing to acute healing wounds.

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Chronic nonhealing wounds are the result of a failure of the tissue repair process to reestablish structurally and functionally intact cutaneous barrier and are frequently associated with underlying conditions that include vascular disease, diabetes, and aging (Eming et al. 2014). Although differing in etiology, chronic wounds—including venous leg ulcers (VLUs), diabetic foot ulcers (DFUs), and pressure ulcers (PUs)—share an immense negative impact due to high incidences, associated complications, and frequent recurrences (Armstrong et al. 2017; Petersen et al. 2020). In addition, chronic wounds are reaching epidemic proportions worldwide. It has been estimated that up to 2% of the world population will develop a chronic wound, with 6.5 million patients affected in the United States alone (Richmond et al. 2013; Eming et al. 2014; Schneider et al. 2021). Treatment of chronic wounds has become a tremendous economic burden incurring costs of approximately \$20–\$25 billion annually in the United States (Schneider et al. 2021).

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Despite the high mortality rate and severity of chronic wounds, the mechanisms that result in their development remain partially understood, and available treatment options are often not fully efficacious in restoring healing. Several factors have played a role in limiting research on chronic wounds and hindered the development of new therapies, including a lack of animal models that fully recapitulate the human condition and complexity of a heterogeneous patient population with multifactorial ulcer etiologies (Gordillo et al. 2013; Eming et al. 2014; Elliot et al. 2018; Pastar et al. 2018). Recent advances in “omics” approaches using human tissue and various technologies including RNA sequencing (RNA-seq), single-cell RNA-seq, spatial transcriptomics, proteomics, metabolomics, and microbiome/metagenomics have deepened broad understanding of chronic wound pathology at the cellular, molecular, pathway levels, and host–pathogen interfaces (Pastar et al. 2012; Gardner et al. 2013; Fadini et al. 2014; Kalan et al. 2016; Loesche et al. 2017; Stone et al. 2017, 2020b; Ramirez et al. 2018; Cavassan et al. 2019; Kalan et al. 2019; Januszyk et al. 2020; Sawaya et al. 2020; Theocharidis et al. 2020, 2022). These technologies together with accessibility of patients’ biomaterials, including ulcer debridement tissue, wound fluid, and swabs, provide the opportunity to concurrently analyze multiple deregulated targets and thereby identify pathways responsible for impaired healing in patient samples (Fig. 1). Furthermore, comparative “omics” analyses have been successfully employed to elucidate unique features that distinguish chronic from physiologically healing wounds, leading to identification of specific molecular signatures for nonhealing ulcers and identification of novel targets for therapeutic intervention (Ramirez et al. 2018; Sawaya et al. 2020; Stone et al. 2020b; Theocharidis et al. 2022). Here, we outline the current knowledge and the most recent findings focused on deciphering wound healing impairment at the molecular and cellular levels in patients affected with chronic wounds. These mechanisms involve the major structural and resident skin cells: keratinocytes, immune cells, fibroblasts, and endothelial cells. Their roles in healing inhibition are reviewed, providing a rationale for approaching future development of advanced therapeutics.

## **DEREGULATION OF KERATINOCYTE DIFFERENTIATION, MIGRATION, AND PROLIFERATION—HALLMARKS OF THE NONHEALING WOUND PHENOTYPE**

Keratinocytes, a major cellular component of the epidermis, play several critical roles in the wound healing process and are among the first responders to injury (Pastar et al. 2008, 2014). Once the skin is wounded, keratinocytes undergo activation, with the goal to migrate, proliferate, and differentiate within the wound bed and ultimately restore the epidermal barrier (Tomic-Canic et al. 1998; Freedberg et al. 2001; Pastar et al. 2014). Keratinocytes secrete a plethora of cytokines and growth factors; these, in turn, recruit and coordinate other cell types involved in wound healing, stimulate matrix formation, and promote angiogenesis (Pastar et al. 2008; Barrientos et al. 2014). In contrast to tightly controlled keratinocyte activation during physiological wound healing, the reepithelialization process is ineffective in chronic ulcers due to keratinocyte hyperproliferation, poor migration, and deregulated differentiation (Table 1). Contrary to normal skin, where proliferating keratinocytes reside exclusively in the basal layer (Morasso and Tomic-Canic 2005),

hyperproliferative keratinocytes in chronic wounds continue to divide throughout basal and suprabasal layers of the epidermis (Stojadinovic et al. 2005). One of the first studies using gene expression profiling of chronic wound tissue pinpointed incomplete activation and differentiation of keratinocytes and their contribution to parakeratosis and hyper-keratosis (Stojadinovic et al. 2008). Expression of early keratinocyte differentiation markers, keratins 1 and 10 (K1 and K10), was suppressed at the nonhealing edge of VLU, unlike the late differentiation markers involving involucrin, transglutaminase 1, and subset of small proline-rich proteins (SPRR1A, SPRR1B, SPRR2B, SPRR3), which were up-regulated in chronic VLU (Stojadinovic et al. 2008). This dysregulation of the differentiation process points toward impaired barrier, despite the formation of hyper-keratotic cornified layer. Interestingly, keratinocytes at the nonhealing edge of VLU exhibit a gene signature that reflects high mitotic activity, with several crucial checkpoint control proteins down-regulated (such as retinoblastoma [Rb], p107, and p130), and with up-regulation of cell-cycle genes (cyclin B1, cyclin D2, cyclin A2, cyclin F, cyclin M4, and cell division cycle 2). Deregulated expression of cell-cycle-associated genes implies a loss of cell-cycle control, and together with the suppression of genes involved in regulation of an epidermal stem cells niche (Stojadinovic et al. 2014), contributes to the epidermal hyperproliferation evident at the VLU wound edge (Stojadinovic et al. 2008).

The hyperproliferative and nonmigratory phenotype of keratinocytes at the nonhealing edge is also characterized by nuclear presence and overexpression of  $\beta$ -catenin and protooncogene c-myc (Waikelet et al. 2001; Stojadinovic et al. 2005, 2014; Lindley et al. 2016; Stone et al. 2017). In contrast to membranous and cytoplasmic localization in normal skin,  $\beta$ -catenin is nuclear in keratinocytes at the nonhealing wound edge, leading to inhibition of keratinocyte migration (Stojadinovic et al. 2005, 2014; Stone et al. 2017).  $\beta$ -Catenin-mediated inhibition of healing is driven by blockade of the epidermal growth factor (EGF) response, inducing c-myc expression and suppression of indispensable cytoskeletal components for epidermal migration K6/K16 through cytoplasmic glucocorticoid receptor (GR) activation (Stojadinovic et al. 2005).

Molecular mechanisms of  $\beta$ -catenin activation in chronic wound keratinocytes also involve membranous glucocorticoid receptor (mbGR) (Jozic et al. 2017). While glucocorticoids are known as potent inhibitors of reepithelialization acting through the phosphorylation and nuclearization of GRs (Vukelic et al. 2010; Jozic et al. 2017), mbGR suppresses keratinocyte migration and wound healing by activating a Wnt-like phospholipase/protein kinase C signaling cascade leading to atypical activation and nuclear localization of  $\beta$ -catenin and c-myc (Jozic et al. 2017). Cumulatively, these findings generated from patients' tissue resulted in the current clinical trial evaluating nuclear c-myc and p-GR as predictive and diagnostic tissue biomarkers for healing outcomes in DFUs (ClinicalTrials.gov 2020). Of note, the inhibitory effects of glucocorticoids can be therapeutically reversed by topically applied statins, which inhibit epidermal cortisol synthesis and subsequent activation of GRs (Sawaya et al. 2018). In addition, topical mevastatin-induced expression of noncoding RNA Gas5 resulted in suppression of c-myc and accelerated wound closure (Sawaya et al. 2018). Recent work has identified an additional mechanism of anti-healing activity of glucocorticoids via interaction of GR with Caveolin 1 (Cav1), a key scaffolding component of plasma membrane caveolae. Cav1 interacts with and sequesters mbGR and EGFR in

keratinocytes to inhibit migration and wound closure in both DFU and VLU (Jozic et al. 2019). Cav1 is significantly up-regulated in nonhealing ulcers, in contrast to physiological healing wounds where it is markedly suppressed (Jozic et al. 2019). The Cav1-mediated sequestration of EGFR together with its mislocalization from membrane to cytoplasm (Brem et al. 2007; Sawaya et al. 2019) can account for diminished EGF signaling in VLUs and DFUs, and lack of response to topically applied EGF (Falanga et al. 1992). Jozic et al. (2021) have also shown that Cav1 induction in keratinocytes at the nonhealing wound edge keeps the cytoskeletal machinery involved in cell migration in the stalled state through deregulation of the cytoskeleton components including members of Rho family of GTPases, Cdc42, and RhoA and their inactivator ArhGAP35, while pharmacological inhibition or genetic depletion of Cav1 accelerated wound closure.

Up-regulation of the pro-oncogene c-myc and activation of WNT/ $\beta$ -catenin signaling is also a common event leading to the development of many cancers and can contribute to the known predisposition of chronic wounds to tumor formation (Gabay et al. 2014; Zhan et al. 2017). Interestingly, a recent study identified up-regulation of specific post-transcriptional gene expression regulator microRNA (miR), miR193b-3p, as a tumor-suppressive mechanism in DFUs via down-regulation of Kirsten rat sarcoma viral oncogene (KRAS) signaling (Marjanovic et al. 2022). While miR193b-3p contributes to low tumor incidence in DFUs, it also acts as a master inhibitor of cellular migration and epithelialization by disrupting stress fiber formation through suppression of RhoA activity. Up-regulation of miR193b-3p was a unique feature of DFUs and not regulated in VLUs, which develop squamous cell carcinomas far more frequently (Trent and Kirsner 2003; Marjanovic et al. 2022).

Another feature of the DFU keratinocytes is their decreased DNA damage repair response. Ramirez et al. showed accumulated DNA breaks in DFU keratinocytes as a result of suppression of the genes involved in DNA repair (MutS Homolog 2-MSH2, Double Strand Break Repair Protein-RAD50, WEE1 G2 Checkpoint Kinase, Tumor Protein P53, and Receptor Tyrosine Kinase-KIT) (Ramirez et al. 2018). The suppression of DNA repair is driven by miR15b-5p, induced by common DFU pathogen *Staphylococcus aureus*, which targets genes involved in the DNA damage response (Ramirez et al. 2018). Additional miRs also contribute to the nonhealing phenotype of chronic wounds (detailed in Li et al. 2022b).

Lack of keratinocyte migration in conjunction with the persistent low-grade inflammation in DFUs may be partially attributed to deregulated expression of immune inhibitory receptor ligand Programmed death-ligand 1 (PDL1) (Kuai et al. 2022). Transmembrane protein PDL1 is suppressed in DFU epidermis when compared to normal skin, contributing to delayed wound closure (Kuai et al. 2022). Moreover, treatment of murine diabetic wounds with PDL1 resulted in improved reepithelialization and modulation of prolonged inflammation (Kuai et al. 2022).

## DEREGULATION OF KERATINOCYTE IMMUNE FUNCTIONS

A less-studied role of keratinocytes in chronic wounds is their immune functions. Keratinocytes communicate with immune cells through numerous cytokines, chemokines,

and extracellular vesicles (Pastar et al. 2014; McBride et al. 2017). Epidermal keratinocytes directly interact with T cells via antigen presentation and produce antimicrobial peptides (AMPs) that inhibit the growth of wound pathogens (Piipponen et al. 2020). However, keratinocyte immune functions are deregulated in chronic wounds. Keratinocytes from VLUs, DFUs, and PUs are characterized by increased levels and nuclear localization of Toll-like receptor 3 (TLR3) (Li et al. 2021). Furthermore, major histocompatibility complex class II (MHC-II)-expressing subgroup of keratinocytes is significantly enriched in PUs when compared to either acute wounds or normal skin (Li et al. 2022a). This is attributed to IFN- $\gamma$  in the wound fluid from PUs, resulting in induction of MHC-II in keratinocytes, which in turn attenuates autologous T cell activation (Li et al. 2022a). AMPs, human  $\beta$  defensin 2 (hBD-2), psoriasin, S100A8, and S100A9 are induced in the epidermis of chronic VLUs compared to skin from healthy individuals (Thorey et al. 2001; Dressel et al. 2010), whereas S100A7 and DEFB4A/DEFB4B are up-regulated in both DFUs and acute human wounds (Sawaya et al. 2020).

In contrast to up-regulation of AMPs targeting extracellular bacteria in chronic wounds, recent studies have identified suppression of a unique antimicrobial effector Perforin 2 (P-2), targeting intracellular pathogens in chronic DFUs (Pastar et al. 2021c). While the intracellular life cycle of *S. aureus* is not completely understood, P-2 is shown to be essential for control and elimination of intracellular bacteria in both professional and nonprofessional phagocytic skin cells and is induced during physiological wound healing (Strbo et al. 2019). Moreover, pathogenic *S. aureus* can invade and persist inside the keratinocytes to contribute to wound chronicity (Pastar et al. 2021c). P-2 was found suppressed in DFU epidermis, which was associated with accumulation of intracellular *S. aureus*, induction of AIM-2 inflammasome, and pyroptosis that collectively contributed to healing inhibition and unresolved inflammation in DFUs (Pastar et al. 2021c). Unlike pathogenic *S. aureus* responsible for P-2 suppression (Strbo et al. 2019), commensal *Staphylococcus epidermidis* was able to induce P-2 in keratinocytes and  $\gamma\delta$  T cells (Pastar et al. 2020), suggesting potential of therapeutic targeting of P-2 to prevent or reverse persistent intracellular chronic wound infections. Taken together, these studies underscore the importance of intracellular bacterial niche in chronic wound keratinocytes and their contribution to inhibition of wound healing in addition to the well described role of the extracellular microbiome (see White and Grice 2022).

While specific processes of hyperproliferation and impaired migration and differentiation, together with dysregulation of associated pathways and regulators are characteristics of all types of chronic wounds, the recent findings on up-regulation of tumor suppressor miR-193b-3p unique for DFUs, also suggest that pathology of keratinocytes is ulcer-type specific (Marjanovic et al. 2022). Future use of single-cell and spatial “omics” methods is required to shed more light on pathways and therapeutic approaches targeting keratinocytes and reepithelialization in specific types of chronic wounds.

## **INFLAMMATION IN CHRONIC WOUNDS—A FRIEND, A FOE AND MORE**

One key characteristic of chronic nonhealing wounds is unresolved inflammation. It has been postulated that the chronic wound is “stuck in a chronic inflammatory

state” that does not progress. Recent studies, however, contributed to a paradigm shift, showing that imbalance of proinflammatory and anti-inflammatory responses along with impaired function, and signaling of inflammatory cells traps the wound in a dysregulated inflammatory state that fails to reach levels seen in acute wounds. In turn, this ineffective inflammatory state fails to stimulate progression of healing to reepithelization and remodeling phases and promote successful closure (Eming et al. 2014; Stone et al. 2017; Ramirez et al. 2018; Theocharidis et al. 2022). Comparative transcriptomic analyses of chronic wounds and acute physiological wounds have demonstrated suboptimal levels of inflammatory signaling in nonhealing VLU and DFUs (Stone et al. 2017; Sawaya et al. 2019, 2020). Promoting inflammatory profile to the one resembling an acute wound has been demonstrated to clinically correlate with reversal from a nonhealing to healing phenotype in VLUs as a response to treatment with a bioengineered human skin equivalent (Stone et al. 2017). Below we review current knowledge of this dysregulated inflammatory process by delineating the role of each immune cell and their contribution to the overall chronic wound pathogenesis (Table 2).

One of the first responders to the injury site are mast cells. Mast cell recruitment is facilitated by keratinocyte-released mediators (Trautmann et al. 2000), and once present, they contribute to clot stabilization, endothelial permeability, vasodilation, neoangiogenesis, and fibrogenesis. Mast cells degranulate and release vasoactive and proinflammatory mediators including histamine, tumor necrosis factor  $\alpha$  (TNF- $\alpha$ ), interleukin 8 (IL-8), and proteases that facilitate the influx of neutrophils and other immune cells to the wound site. They also stimulate proinflammatory mediator production by keratinocytes and fibroblasts (Kohda et al. 2002; Giustizieri et al. 2004; Nishida et al. 2019), and are essential to bacterial killing in infected wounds (Zimmermann et al. 2019).

However, studies have observed differential mast cell mediators and location in chronic VLUs as compared with normal skin and acute wounds, suggesting that their altered function contributes to impaired wound healing. Immunohistochemistry of perilesional VLU skin identified increased mast cells and TNF- $\alpha$  and tryptase expression, and identified increased chymase expression, a protease that degrades the extracellular matrix and damages tissue in the VLU bed (Huttunen et al. 2000; Abd-El-Aleem et al. 2005). At elevated concentrations in vitro, mast cells and their mediators inhibit keratinocyte activity and epithelial outgrowth (Huttunen et al. 2001), which may also contribute to delayed wound healing in vivo. Increased degranulation of mast cells also contributes to abnormal wound healing in DFUs (Theocharidis et al. 2022). Patients with diabetes have increased numbers of degranulated mast cells even in unwounded skin (Dong et al. 2020; Tellechea et al. 2020). Pretreatment with a mast cell degranulation inhibitor attenuated wound-healing impairment in a diabetic mouse model and shifted macrophages to a regenerative M2 phenotype (Tellechea et al. 2016, 2020). Further studies are needed to more specifically define mast cell contributions to prolonged inflammation and impaired wound healing in VLUs and PUs.

A specialized subset of epidermal dendritic cells, Langerhans cells (LCs), represents a potent group of antigen-presenting cells known as the first-line defenders in skin (Gallo and Gallucci 2013). LCs are an important immune component during the early phase of physiological acute wound healing (Gallo and Gallucci 2013; Stojadinovic et al. 2013).



Decreased numbers of LCs are associated with nonhealing DFUs, while the epidermis of healing DFUs has been shown to be repopulated with higher numbers of LCs (Stojadinovic et al. 2013).

During the early inflammatory phase, neutrophils play an important role in the first-line defense of clearing foreign debris, necrotic wound tissue, and bacteria, and promote inflammation via cytokines and chemokines including TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and C-X-C motif chemokine ligand (CXCL8) (Pittman and Kubes 2013). The levels of neutrophils in chronic wounds are previously thought to be elevated compared to acute wounds, as demonstrated by increased neutrophil infiltration and its marker myeloperoxidase (MPO) in chronic VLU and PUs (Diegelmann 2003; Eming et al. 2010). However, further studies showed that neutrophil presence varies based on wound etiology and location, with elevated levels in the wound bed due to prolonged inflammation attenuating neutrophil apoptosis or phagocytosis (Theocharidis et al. 2022) and decreased levels at the wound edge reflecting impaired migratory ability of immune cells (Sawaya et al. 2020), or increased cell death from release of neutrophil extracellular traps (NETs) (Wong et al. 2015; Sawaya et al. 2022). NETs, which are web-like matrices lined with neutrophil-produced cytotoxic proteins, function to either directly kill or facilitate phagocytosis of extracellular pathogens. However, NET release, known as NETosis, can damage the surrounding tissue and contribute to prolonged inflammation (Fadini et al. 2016). At the DFU ulcer edge, decreased neutrophil recruitment has been linked to deregulation of transcriptional networks involving Forkhead Box M1 (FOXM1) and Signal Transducer and Activator of Transcription 3 (STAT3), which activate and promote survival of immune cells (Sawaya et al. 2020). Suppression of triggering receptor expressed on myeloid cells 1 (TREM1), an upstream regulator of FOXM1 and negative regulator of NET formation, was found to be responsible for dysfunctional neutrophils, accumulated NETs, and increased reactive oxygen species (ROS) in DFUs (AP Sawaya et al. in prep.). *S. aureus* biofilms have been shown to evade neutrophil-mediated killing by eliciting NETosis that is ineffective at clearing biofilm (Bhattacharya et al. 2018), suggesting that wound infection modulates NET function, and increased NETosis does not necessarily translate to antimicrobial benefits. In diabetes, neutrophils are primed to undergo NETosis (Wong et al. 2015), and NET overproduction has been reported in DFU patients as correlating with infection and wound severity (Liu et al. 2019; Yang et al. 2020). While the deregulation of neutrophils and the role of NETosis have been characterized in DFUs, they have not yet been well-studied in other types of chronic ulcers.

As monocytes migrate to the wound and mature into macrophages, they play a key role in both initiation and resolution of the inflammatory response by clearing apoptotic neutrophils and restoring tissue integrity for wound closure. In physiological wound healing, the transition from the inflammatory to proliferative phase is facilitated by a shift in macrophage polarization from classically activated M1 phenotype, characterized by proinflammatory cytokines, to alternatively activated M2 phenotype, characterized by markers of inflammatory resolution and initiation of tissue repair (Lawrence and Natoli 2011; Murray et al. 2014; Nassiri et al. 2015). However, in-depth transcriptomic studies identified multiple unique subtypes of macrophages confirming a broad spectrum of macrophage activation programs beyond the initial concept of polarization (M1 versus

M2) (Xue et al. 2014), indicating complexity of macrophage phenotypes in wound healing. Studies focusing on M1-M2 polarization have shown that transition to the M2 phenotype can be induced by efferocytosis, a process in which macrophages phagocytose apoptotic neutrophils (Elliott et al. 2017), as well as by various signals from regulatory T cells and epigenetic modifications (Nosbaum et al. 2016; Pastar et al. 2021b). Until recently, the accepted paradigm proposed that in nonhealing wounds, overexpression of proinflammatory cytokines and impaired clearance of apoptotic neutrophils led to deregulated polarization and activation of wound macrophages with a predominant M1 phenotype (Nassiri et al. 2015). However, more recent studies employing single-cell transcriptomics in tissue from clinically monitored DFU patients identified increased numbers and M1 macrophage polarization in the healing DFUs, in contrast to decreased M1 macrophages in nonhealing DFUs (Theocharidis et al. 2022). It is important to note that excessive activity of M2 macrophages in wound healing may lead to fibrotic scarring via activation of the Wnt/ $\beta$ -catenin pathway (Gay et al. 2020). Taken together, balanced regulation of M1-M2 polarization is indispensable for proper wound healing, although what constitutes a successful macrophage wound healing response likely varies by ulcer subtype.

The role of adaptive immunity in chronic wounds has not been extensively investigated; however, preliminary evidence suggests T cells also take part in maintaining a dysfunctional proinflammatory profile for nonhealing ulcers (Theocharidis et al. 2022). Processes of T cell differentiation and migration are diminished at the wound edge of nonhealing VLU (Stone et al. 2017), resulting in fewer numbers of T cells in chronic wounds in an impaired or unresponsive state, unable to secrete factors such as insulin growth factor 1 (IGF-1) and IL-2 that are produced in a normal wound healing response (Toulon et al. 2009; Xu et al. 2017). Studies have also demonstrated that infection can induce strong T cell stimulation that reduces T cell receptor (TCR) repertoire diversity, thereby affecting the immune response to subsequent infections by different pathogens. Patients with diabetes have decreased serum levels of naive T cells and increased levels of effector T cells, and effector T cells accumulate and display a significantly reduced TCR- $\beta$  repertoire diversity in the serum (Moura et al. 2017, 2019) and tissue (Loots et al. 1998) of patients affected with DFUs and VLUs, respectively. Effector T cells are major producers of interferon  $\gamma$  (IFN- $\gamma$ ) and TNF- $\alpha$  inflammatory cytokines that in turn promote naive T cell activation and differentiation (Moura et al. 2017; Mehta et al. 2018). The ratio of T cell phenotype (effector/naive) and level of TCR repertoire diversity in serum have been proposed as predictive biomarkers of DFU healing outcome (Moura et al. 2019). A recent study using single-cell transcriptomics identified higher proportions of naive and early differentiated progenitor T-lymphocytes in healing DFUs, while nonhealing DFUs had higher proportions of cytotoxic natural killer T (NKT) cells, indicating a shift in T cell subpopulations that correlates with healing outcomes (Theocharidis et al. 2022). Whereas the “omics” technologies have deepened understanding of specific inflammatory cell subtypes in chronic DFU pathology, future longitudinal studies that profile tissues from expanded cohorts of all types of chronic wounds are required to elucidate dynamic changes in the inflammatory cell milieu and their contributions to clinical outcomes and response to therapies in patients.



## ALTERED FIBROBLAST FUNCTION IN CHRONIC WOUNDS

Fibroblasts are the main manufacturers of the extracellular matrix (ECM) and granulation tissue during physiological wound healing. The transformation from quiescent dermal fibroblast to activated myofibroblast is crucial for successful wound healing and contraction, recruitment of immune cells, and angiogenesis (Li and Wang 2011; Hinz 2016; Arif et al. 2021). Acute wound fibroblasts are astoundingly heterogeneous in terms of their developmental origin, location in tissue, gene expression, and ECM secretion as also detailed in this collection (please see Ganier et al. 2022 and Jiang et al. 2022), and the most recent findings identified fibroblast heterogeneity in chronic wounds as well (Theocharidis et al. 2022).

Although VLUs, DFUs, and PUs differ by etiology, fibroblast dysfunction and phenotypic cellular aging remain unifying themes (Table 3; Brem et al. 2008; Eming et al. 2014). Fibroblasts isolated from nonhealing ulcers demonstrate severely attenuated migratory capacity, mitogenic response, ECM deposition and proliferation, and increased apoptosis (Ågren et al. 1999; Brem et al. 2008; Liang et al. 2016; Maione et al. 2016). Aged wound fibroblasts divide and migrate less, produce less ECM, and demonstrate up-regulated MMP activity compared to their younger counterparts, which leads to insufficient tension and granulation tissue formation in the wound bed (Ashcroft et al. 1997; Fujiwara et al. 2019; Mahmoudi et al. 2019; Ding et al. 2021). Premature aging of PU fibroblasts is attributed to high oxidative stress caused by a deficiency of the chemokines necessary to overcome the persistent inflammation (Wall et al. 2008; Fujiwara et al. 2019).

Related to aging, fibroblast senescence is also implicated in wound chronicity (Liang et al. 2016; Berlanga-Acosta et al. 2020; Wang and Shi 2020). Fibroblast senescence is beneficial in early phases of acute wound healing and in curbing fibrosis at healing resolution (Brockman et al. 1970; Jun and Lau 2010a,b; Pauty et al. 2021). However, inappropriate fibroblast senescence in VLUs and DFUs is associated with inability to heal (Stanley and Osler 2001; Harding et al. 2005; Wilkinson et al. 2019). Fibroblasts isolated from PUs also demonstrate increased replicative senescence with elevated expressions of plasmin, plasminogen activator inhibitor-1 (PAI-1), and TGF- $\beta$  (Vande Berg et al. 2005), which is in line with findings that fibroblast senescence is induced by the deposition of a “senescence-promoting” ECM, including PAI-1 (Hiebert et al. 2018).

Chronic hypoxia is a known contributor to wound chronicity (Sheffield 1998; Eisenbud 2012). Hypoxia in the early stages of wound healing is beneficial in that it induces myofibroblast expression of genes such as transforming growth factor  $\beta$  (TGF- $\beta$ ) and collagen A1 (COLA1) (Falanga et al. 2002) and stimulates recruitment of peripheral stem cells to the wound (Brem and Tomic-Canic 2007; Gallagher et al. 2007). Increased levels of blood-borne stem cells and their intracellular hypoxia inducible factors (HIFs) are positively correlated with healing status (Thom et al. 2016). However, hypoxia impairs hydroxylation of proline and lysine during collagen synthesis, and consequently the maturation of procollagen and prolyl hydroxylase activity (Gordillo and Sen 2003; Tandara and Mustoe 2004; Thackham et al. 2008; Sen 2009; Chambers and Leaper 2011). As such, chronic hypoxia negatively affects fibroblast growth, activity, and TGF- $\beta$  and EGF receptor

expression (Falanga et al. 1994; Tandara and Mustoe 2004; Mustoe et al. 2006; Eisenbud 2012). However, restoring oxygen levels with hyperbaric therapy can result in increased growth and activation of myofibroblasts and increased granulation tissue deposition (Zhao et al. 1994; Kranke et al. 2015).

An altered wound microenvironment acts as another driver of fibroblast dysfunction and chronic wound formation. Hyperglycemia impairs proliferation, migration, and differentiation of DFU fibroblasts (DFUFs) and accelerates their senescence (Bian et al. 2020; Wan et al. 2021). Fibroblasts isolated from nonulcerated diabetic skin are strikingly similar to fibroblasts isolated from healthy foot skin in terms of their function and gene expression profiles, implying that hyperglycemia itself does not negatively impact fibroblasts prior to wounding (Ramirez et al. 2015). However, hyperglycemia induces a metabolic epigenetic memory in fibroblasts that is maintained even when reexposed to normal glucose levels and may prime diabetic skin to ulcer formation (Park et al. 2014a). A unique population of fibroblasts has been identified in the ulcer beds of the DFU patients with healing wounds and is characterized by overexpression of matrix remodeling and inflammatory response genes (Theocharidis et al. 2022). In addition, fibroblast plasticity is dysregulated in chronic wounds due to aberrant activation of Notch1 signaling, suggesting that different subpopulations of fibroblasts may be responsible for the failure to achieve healing (Shao et al. 2020). Proteomic analyses of chronic wound fibroblasts identified two major groups of dysregulated processes. First, dysfunctional lysosomal capacity and protein turnover, which is commonly dysregulated in age-associated diseases, contributes to impaired cell motility and proliferation (Cellerino and Ori 2017; Berberich et al. 2020). Second, altered TGF- $\beta$  activity causes aberrant myofibroblast contraction (Berberich et al. 2020). Dysregulation of TGF- $\beta$  pathway and unresponsiveness of its receptor has been documented in all types of chronic wounds (Kim et al. 2003; Dalton et al. 2007; Pastar et al. 2010; Zhang et al. 2016; Brunner et al. 2021). Additionally, chronic wound fibroblasts have a diminished mitogenic response to growth factors found in the wound bed including platelet-derived growth factor BB (PDGF-BB), fibroblast growth factor (FGF), and EGF (Stanley et al. 1997; Ågren et al. 1999). Improper gap junction formation and subsequent pathologic spread of various apoptotic and inflammatory signals in chronic wounds is attributed to dermal up-regulation of connexins (Sutcliffe et al. 2015).

Reprogramming DFUFs has been explored as a promising therapeutic option for chronic wounds. In a series of studies, DFUFs from non-healing DFUs were first reprogrammed into induced pluripotent stem cells (iPSCs) to reacquire wound healing function and then reprogrammed back into fibroblasts (Takahashi et al. 2007; Gerami-Naini et al. 2016; Kashpur et al. 2019). Post-reprogrammed DFUFs reversed the impaired healing capacity seen in the original DFUFs, which was attributed to miR-mediated epigenetic mechanisms (Kashpur et al. 2019; Pastar et al. 2021a) revealing potential of iPSC-based therapeutic approach for chronic wounds.

## IMPAIRED ANGIOGENESIS IN CHRONIC WOUNDS

Angiogenesis and vasculogenesis are integral components of wound healing, which function to increase immune cell recruitment, supply oxygen, and nutrients to the hypermetabolic

regenerating wound, as well as dispose of toxic metabolites and waste products (Eming et al. 2007). Impaired angiogenesis is associated with a poor nutritional supply state and tissue hypoxia that ultimately induces cellular death in chronic wounds (Table 3; Biswas et al. 2010; Eming et al. 2010; Krisp et al. 2013). Dysregulation of these pathways is implicated in chronic wound formation and in their failure to heal (Brem and Tomic-Canic 2007; Costa and Soares 2013; Okonkwo and DiPietro 2017).

Antiangiogenic proteins, such as myeloperoxidase, are expressed at higher levels in DFU versus acute physiological wounds. Conversely, angiogenic stimulators, including superoxide dismutase and angiogenin, exhibit decreased expression in DFUs (Krisp et al. 2013; Singh et al. 2022). Ischemia-induced microvascular endothelial cell damage contributes to slowed angiogenesis in VLU, and hyperglycemia causes alterations in structure and function of both micro and macro vessels, in part through miR-200b induction (Leu et al. 1995; Chan et al. 2012; Singh et al. 2017; Haspula et al. 2019). Additionally, chronic wounds display an aberrant cleavage and destruction of growth factors and their receptors by increased protease activity, major factors include VEGF in DFUs and chemokine ligand 9 in Pus (Lauer et al. 2000; Romagnani et al. 2004; Edsberg et al. 2012; Singh et al. 2017).

A major consequence of impaired angiogenesis in chronic wounds is inability to recruit pro-healing stem cells, including bone marrow-derived cells and endothelial progenitor cells (EPCs), to the site of injury (Gallagher et al. 2007; Thom et al. 2016; Singh et al. 2022). This recruitment must be synchronized by a repertoire of chemokines, which are exhausted in conditions that have compromised healing responses including human aging and diabetes (Gallagher et al. 2007; Barrientos et al. 2008; Pastar et al. 2010; Thom et al. 2016; Singh et al. 2022). Aberrant EPC behavior, cell numbers, recruitment, and transition to a proinflammatory state have been well documented in diabetic patients (Gallagher et al. 2007; Liu and Velazquez 2008). Common causes of EPC dysfunction include hyperglycemia, increased oxidative stress, chronic inflammation, and activation of NADPH oxidase (Drela et al. 2012; Kim et al. 2012; Yu et al. 2016), and similar themes of EPC dysfunction have been confirmed in murine models of diabetic wound healing (Gallagher et al. 2007; Albiero et al. 2011; Singh et al. 2022). Genetic studies have highlighted a nitric oxide synthase 1 adaptor protein (NOS1AP) variation in the population that is associated with impaired wound healing and attenuated stem cell mobilization in DFU patients (Margolis et al. 2017). Consequently, hyperbaric oxygen therapy is beneficial to wound healing by promoting EPC mobilization and recruitment in addition to its benefits in reversing hypoxia, as discussed above (Thom et al. 2011; Huang et al. 2020). A better understanding of the mechanisms that result in dysfunction of angiogenesis is of vital importance in the wound healing field especially with an increase in microvascular complications that accompanies the aging population affected with wound healing disorders.

## IMBALANCE OF EXTRACELLULAR MATRIX (ECM) COMPONENTS IN CHRONIC WOUNDS

Chronic wounds are characterized by a dysfunctional ECM and altered protease activity (Monika et al. 2021). Matrix metalloproteinases (MMPs), and their regulators, tissue inhibitor of matrix metalloproteinase (TIMP), are enzymes that play an integral role in all stages of wound healing (McCarty and Percival 2013; Michopoulou and Rousselle 2015). While the tight control of MMP dynamics is crucial for proper wound healing, their perturbed activities including chronically elevated levels of MMPs, reduced levels of TIMPs, or altered ratios of the two, lead to impaired remodeling response and failure of wounds to heal (Cook et al. 2000; Lindley et al. 2016). Elevated MMP9 and a high MMP9/TIMP1 ratio has been proposed as a predictor of nonhealing ulcers (Liu et al. 2009; Singh et al. 2014; Jindatanmanusan et al. 2018; Trøstrup et al. 2018; Jones et al. 2019), whereas a high MMP1/TIMP1 ratio is associated with improved healing outcomes (Muller et al. 2008). MMP13 and granulocyte-macrophage colony-stimulating factor (GM-CSF) levels in wound fluid may be an important healing status biomarker specific for VLU (Stacey et al. 2019). Interestingly, adding MMP inhibitors to chronic wound fluid only partially inhibits proteolytic activity, demonstrating that non-MMP proteinases also contribute to ECM destruction in chronic wounds (Trøstrup et al. 2018). In addition to increased collagen-matrix degradation, the chronic wound environment is characterized by up-regulated serine proteases that degrade important components of the ECM including fibronectin, dermatopontin, and important growth factors and receptors necessary for ECM remodeling and cell growth (Rao et al. 1995; Wlaschek et al. 1997; Lobmann et al. 2002; Barrientos et al. 2008; Buchstein et al. 2009; Eming et al. 2014; Krishnaswamy et al. 2014). For example, fibronectin (FN) mRNA expressed by fibroblasts is increased in chronic wounds; however, FN-rich ECMs are thin, defective, and unstable, which is likely due to increased ECM turnover caused by increased levels of elastase serine protease present in chronic wounds (Grinnell and Zhu 1996; Yager et al. 1997; Maione et al. 2016). In addition, lack of FN cell-surface receptor on keratinocytes prevents migration of epidermal keratinocytes in chronic wounds despite higher levels of FN expressed by fibroblasts (Ongenaes et al. 2000). Human neutrophil elastase is increased in chronic wound tissue including chronic VLUs, PUs, and DFUs (Rogers et al. 1995; Eming et al. 2010; Wiegand et al. 2010). Increased neutrophil elastase in DFUs is also associated with infection and worsening wound severity (Fadini et al. 2016).

Chronic wounds, specifically VLUs, have also shown evidence of marked tissue fibrosis (Blumberg et al. 2012; Stone et al. 2020a,b). In nonhealing VLUs, prolonged ineffective inflammation has been associated with a sustained remodeling response and the development of a fibrotic ulcer (Stone et al. 2020b). Gene expression profiling of chronic nonhealing VLUs revealed enrichment of collagens and secreted matricellular proteins in combination with up-regulation of tenascin (TNC), osteopontin (SPP1), FN1, connective tissue and hepatocyte growth factors (CTGFs, HGFs), and plasminogen activator inhibitor 1 PAI-1 (Stone et al. 2020b). Profibrotic TGF- $\beta$  signaling was also found enriched and activated in the ulcer bed, thus confirming the chronic VLU as a fibrotic condition. Further studies showed bioengineered bilayered cellular construct (BLCC) application decreased

TGF- $\beta$ 1-induced gene expression with a concurrent increase in expression of the TGF- $\beta$  inhibitor decorin. BLCC application also resulted in increased expression of MMP-8 and levels of MMP-activating zinc, which stimulated antifibrotic remodeling. Ultimately, these studies indicated a novel treatment approach of chronic wounds, preventing fibrosis as well as a new classification of VLU as a fibrotic disease (Stone et al. 2020a,b).

Together, these reports underscore the complex, temporospatial nature of ECM turnover within the wound microenvironment. They highlight the need for continued exploration into ECM dynamics in chronic wounds, reversal of fibrosis, the inhibition of proteases, and pathways that lead to their activation to develop effective therapies (McCarty and Percival 2013).

## CONCLUSIONS AND FUTURE DIRECTIONS

Despite major recent advances in understanding pathophysiology of chronic wounds and molecular mechanisms of wound healing impairment, treatment options remain limited with only a handful of products FDA approved for efficacy. However, over 50% of DFUs and over 70% of VLUs fail to heal with standard of care therapies (Eming et al. 2014), and there is no efficacious therapy approved for PU treatment, emphasizing the urgent need for the development of novel therapeutic modalities.

A lack of validated preclinical models is one of the major challenges in the chronic wound healing field that hinders translation of therapies to clinical practice (Gordillo et al. 2013; Eming et al. 2014; Elliot et al. 2018; Pastar et al. 2018). Preclinical animal testing is required for preclinical evaluation and regulatory approval of novel therapeutics; their low concordance rate with complex human chronic wounds represents a significant impediment to development of products with clinical efficacies. For example, numerous studies using various growth factors as chronic wound therapeutics were considered promising based on the preclinical data but have failed to show efficacy in clinical trials (Falanga et al. 1992; Barrientos et al. 2008; Yamakawa and Hayashida 2019). Intrinsic suppression of EGF signaling, including mislocalization of the EGF receptor (Brem et al. 2007; Jozic et al. 2019; Sawaya et al. 2019), and suppression of TGF- $\beta$  receptors (Pastar et al. 2010) found only in human tissue but not in animal models, together with a harsh proteolytic chronic wound environment, have been identified as major factors responsible for inadequate translation of EGF and TGF- $\beta$  to clinical practice (Eming et al. 2014; Eming and Tomic-Canic 2017). Further to the point, even when tested post-FDA approval, topical PDGF showed that its effect was dependent on the animal model used (Park et al. 2014b).

Another impediment to more approved therapies is limitation of a single primary end point, complete closure. Current ongoing initiatives identified multiple new measurable wound care end points and supporting evidence from both clinical practice and patient-reported outcomes (Driver et al. 2017, 2019; Gould et al. 2021). These findings provide new insights and a potential roadmap for future acceptance of multiple end points that would accelerate the process of approval and potentially bring more therapies to patients who desperately need them.

The most recent “omics” work including current and future data resources generated from the human biomaterials combined with new bioinformatics tools provide better insights and “higher resolution” understanding of pathophysiology for disease target-based repositioning methods (Sawaya et al. 2018, 2019). Expanded analyses of existing transcriptional profiling or single-cell expression data can highlight the relationships between chronic wound signatures and gene expression profiles associated with existing drugs, identifying new therapeutic strategies (Subramanian et al. 2017). Whereas computational drug methods using expression data sets have already been applied to repurpose existing FDA-approved drugs in a limited number of cutaneous diseases (Nyström et al. 2015; Mirza et al. 2017; Lee et al. 2022), similar approaches have not been fully explored for chronic wounds.

The following recent series of studies can be extrapolated in future investigations to elucidate the mechanisms of existing or new therapies. The bilayered human skin equivalent (BLCC) is the only FDA-approved therapy that has demonstrated efficacy in healing chronic VLU (Falanga et al. 1998; ClinicalTrials.gov 2011; Stone et al. 2017) and a clinical trial was designed to understand the mechanisms of action of the BLCC in promoting healing of chronic wounds by exploring the transcriptional profiles of ulcer tissue from patients that were treated with BLCC versus those who were treated with standard of care. The findings unveiled specific biologic processes through which BLCC application converts chronic non-healing VLUs into an acute healing phenotype, including the role of stimulated inflammatory response and reversal of fibrosis (Stone et al. 2017, 2020b). Importantly, these processes can serve as the basis for future studies to find much needed novel therapies for chronic ulcers. Similar approaches can be integrated into clinical trials to elucidate the mechanisms of the chronic wound healing response and most importantly to ultimately improve the lives of patients suffering from chronic wounds.

Complexity of pathophysiology of chronic wounds mandates multifaceted approach coupling diagnostics and monitoring tools with combinatorial targeted therapies. One can envision treatment that targets multiple cellular dysfunctions (described above in detail) in a precise timely manner only to wounds that would benefit from such combinatorial treatment. Future longitudinal studies using “omics” approaches will yield identification of biomarkers or predictors of healing outcomes, monitors of progression during the treatments, predictors of infection, or detection of a biofilm, all of which could help steer clinical decision making (Lindley et al. 2016). Adapting precision medicine strategies to this complex clinical problem, including development of biomarkers, will facilitate better personalized treatment approach allowing for targeting clinical interventions and therapies to individual wound and patient with maximum efficacy.

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## COMPETING INTEREST STATEMENT

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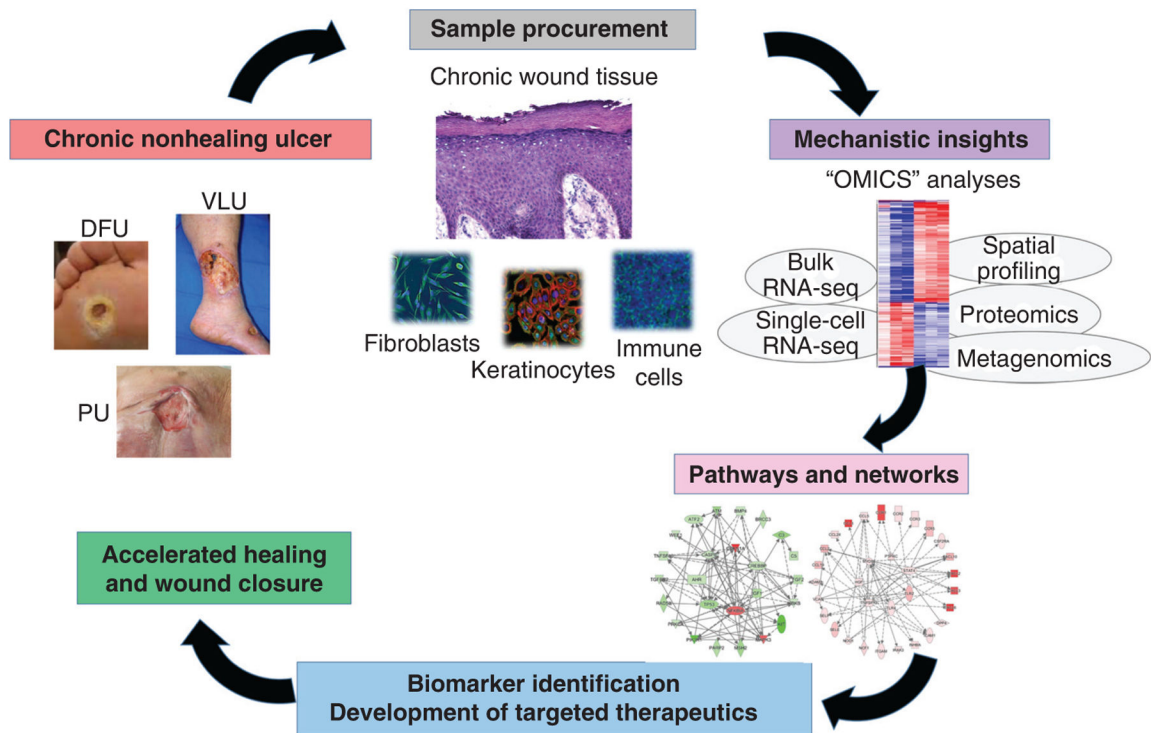
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**Figure 1.** “Omics” approaches to therapeutic targeting of chronic ulcers. Comparative “omics” and bioinformatics analyses can be used to decipher pathophysiologic mechanisms that drive chronic wound pathology and to identify biomarkers and novel therapies likely to heal chronic wounds. (DFU) Diabetic foot ulcer, (VLU) venous leg ulcer, (PU) pressure ulcer.

Table 1.

Overview of representative findings focused on understanding cellular responses involved in reepithelialization in acute and chronic wounds (CWs)

Processes and cells	Acute wound	Chronic wound	Type of CWs	References
Epithelialization	Keratinocyte activation, regulated migration, proliferation, and differentiation	Deregulation of proliferation, differentiation, and migration	VLU DFU PU	Ening et al. 2014; Pastar et al. 2014
Keratinocyte proliferation	Tightly regulated during acute wound healing; proliferating keratinocytes reside in the basal layer	Hyperproliferative keratinocytes in the upper epidermal layers due to nuclear presence of $\beta$ -catenin and c-myc	DFU VLU	Morasso and Tomic-Canic 2005; Stojadinovic et al. 2005, 2008, 2014; Jozic et al. 2017; Stone et al. 2017
Keratinocyte migration	Stimulated epidermal migration and K6/16 activation	Inhibition of keratinocyte migration through multiple signaling pathways including GR and WNT/ $\beta$ -catenin	DFU VLU	Stojadinovic et al. 2005; Vukelic et al. 2010; Jozic et al. 2017, 2019, 2021; Sawaya et al. 2018; Marjanovic et al. 2022
Keratinocyte differentiation	Activated during barrier restoration	Suppression of keratinocyte differentiation markers (KI and K10)	VLU	Stojadinovic et al. 2008
Epidermal stem cells (ESCs)	ESCs contribute to epidermal homeostasis and wound closure	Deregulation and deprivation of ESC niche	VLU	Morasso and Tomic-Canic 2005; Stojadinovic et al. 2014
Growth factors signaling	Coordinated action of growth factors and receptors	Dysfunctional EGF and TGF- $\beta$ signaling	DFU VLU PU	Brem et al. 2007; Barrientos et al. 2008; Pastar et al. 2010; Jozic et al. 2019
Keratinocyte immunity	Tightly regulated TLR response and production of proinflammatory cytokines and chemokines	Deregulation due to nuclear TLR3, suppression of PDL1, accumulated DNA breaks, and enriched MHC-II	DFU VLU PU	Pastar et al. 2014; Ramirez et al. 2018; Li et al. 2021, 2022a; Kuai et al. 2022
Antimicrobial response	Increased levels of AMP contribute to response against extracellular and intracellular pathogens	Increased levels of AMPs against extracellular bacteria, suppression of P-2 against intracellular pathogens	DFU	Thorey et al. 2001; Dressel et al. 2010; Sawaya et al. 2020; Pastar et al. 2021c

(VLU) Venous leg ulcer, (DFU) diabetic foot ulcer, (PU) pressure ulcer, (GR) glucocorticoid receptor, (EGF) epidermal growth factor,

(TGF- $\beta$ ) transforming growth factor  $\beta$ , (TLR) Toll-like receptor, (MHC-II) major histocompatibility complex class II, (AMP) antimicrobial peptide.

**Table 2.** Summary of representative findings from studies focusing on understanding the role of inflammation and its cellular components in acute and chronic wounds (CWs)

Processes and cells	Acute wound	Chronic wound	Type of CW	References
Inflammation	High levels of controlled inflammatory cell activity	Low, persistent level not reaching levels of acute wounds	DFU VLU	Stone et al. 2017, 2020b; Sawaya et al. 2020; Theocharidis et al. 2022
Neutrophils	Present during early inflammatory phase; low levels of controlled NETosis	Increased NETosis, neutrophil numbers decreased at ulcer edge and increased in ulcer bed	DFU VLU PU	Diegelmann 2003; Liu et al. 2019; Sawaya et al. 2020, 2022; Yang et al. 2020; Theocharidis et al. 2022
Macrophages	Controlled M1-M2 transition assures resolution of inflammation	Increased level of M1 macrophages associated with healing ulcers	DFU	Theocharidis et al. 2022
Mast cells	Controlled degranulation in early phases; low numbers	Increased numbers at the wound edge and degranulation promoting ECM degradation	VLU DFU	Huttunen et al. 2000; Abd-El-Aleem et al. 2005; Theocharidis et al. 2022
T cells	T cell recruitment with high CD4 <sup>+</sup> proportion; epidermal T cell activation	Shift in T cell populations; increased naive T cell proportion correlates with healing DFUs; higher levels of natural killer T (NKT) cells in nonhealing DFUs; decreased epidermal T cell activation	DFU VLU	Toutou et al. 2009, Stone et al. 2017; Moura et al. 2019; Theocharidis et al. 2022
Langerhans cells	Increased number during early inflammatory phase	Decreased number associated with nonhealing outcomes	DFU	Stojadinovic et al. 2013

(DFU) Diabetic foot ulcer, (VLU) venous leg ulcer, (PU) pressure ulcer.

**Table 3.**

Overview of representative findings from studies focused on understanding cellular responses involved in extracellular matrix (ECM) formation and angiogenesis in acute and chronic wounds (CWs)

Processes and cells	Acute wound	Chronic wound	Type of CW	References
<b>ECM formation and fibroblasts</b>				
Fibroblast proliferation and migration	Similar replicative capacity as fibroblasts isolated from healthy intact skin	Decreased proliferation, migration, decreased mitogenic response, increased senescence	DFU VLU	Ågren et al. 1999; Brem et al. 2008; Berberich et al. 2020
MMPs and TIMPs	Small initial increase, with resolution of ECM remodeling	Significantly greater number of proteases in chronic wounds, low levels of TIMPs	DFU VLU PU	Grinnell and Zhu 1996; Cook et al. 2000; Liu et al. 2009; Singh et al. 2014; Lindley et al. 2016; Jindatanmanusan et al. 2018; Trostrup et al. 2018; Stacey et al. 2019
Growth factors	Coordinated action of growth factors and receptors	Increased TGF-β and IGF; EGF degradation; dysfunctional TGF-β	DFU VLU PU	Barrientos et al. 2008; Brem et al. 2008; Berberich et al. 2020
Lysosomes	N/A	Accumulation of lysosomal proteins	VLU	Berberich et al. 2020
Fibrosis	Minimal, tightly regulated ECM remodeling	Enriched fibrotic and fibrogenic pathways and associated gene networks	VLU	Stone et al. 2020a,b
Fibronectin (FN), chondroitin sulfate (CS), and tenascin (TN)	Abundant expression early in healing process, return to nonwounded levels by 12 mo, stable FN	Prolonged (>12 mo) presence of FN, CS, and TN, increased degradation of FN	DFU VLU	Rao et al. 1995; Loots et al. 1998; Stone et al. 2020b
<b>Angiogenesis</b>				
Angiogenesis stimulators/inhibitors	Increased angiogenic stimulators and decreased antiangiogenic proteins	Increased antiangiogenic proteins (annexin V) in chronic wounds and decreased or rapidly degraded angiogenic stimulators (VEGF)	DFU	Lauer et al. 2000; Romagnani et al. 2004; Edsberg et al. 2012; Krisp et al. 2013; Singh et al. 2017, 2022
Bone marrow-derived stem cells and endothelial progenitors	Recruitment of stem cells and progenitors in response to wounding	Impaired recruitment of bone marrow-derived stem cells and endothelial progenitors	DFU VLU	Gallagher et al. 2007; Liu and Velazquez 2008; Thom et al. 2016; Singh et al. 2022
Pericapillary fibrin cuffs	Tortuous capillaries and fibrin cuffs absent	Extravasation of macromolecules and possible trapping of TGF-β	VLU	Leu et al. 1995

(DFU) Diabetic foot ulcer, (VLU) venous leg ulcer, (PU) pressure ulcer, (TIMP) tissue inhibitor of matrix metalloproteinase.