

Recent advances in the understanding of genetic defects of neutrophil number and function

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Summary

Neutrophils are amongst the first immune cells to arrive at sites of infection and play an important role as the host's first line of defence against invading pathogens. Defects of neutrophil number or function are usually recognized clinically by recurrent infections that often are life-threatening. Over the last few years, a number of genetic mutations have been discovered to be the basis for congenital neutropenia, adding to our understanding of the molecular basis of these diseases. While many genetic mutations that cause severe congenital neutropenia result in a differentiation block at the promyelocyte stage, defects of neutrophil function are more heterogeneous on clinical, genetic and mechanistic levels. In this review we discuss recent advances in our understanding of the genetic and molecular basis of human neutrophil disorders.

Keywords: neutrophils, neutropenia, neutrophil function, immunodeficiency, oxidative burst, adhesion, cell migration.

Polymorphonuclear neutrophils are the most abundant leucocytes in the blood and form the first line of host defence. Within the bone marrow, they differentiate from multipotent myeloid stem cells through several generations of morphologically recognizable cells. In order of maturation these are, the myeloblast, promyelocyte, myelocyte, metamyelocyte, band neutrophil and segmented neutrophil (see Fig 1). After the myelocyte stage, the capacity for significant cell division is lost and maturation from myeloblast to mature segmented neutrophil takes 10–12 d. Mature neutrophils then leave the bone marrow and enter the circulation. The average half life of neutrophils in the blood is about 7 h before they extravasate into peripheral tissues. During an infection and the subsequent inflammatory reaction, neutrophil production and activation is initiated by enhanced proliferation and maturation of precursor cells in the bone marrow, which are then released into the circulation at an accelerated rate (Nathan, 2006).

Circulating neutrophils express specific adhesive receptors, which aid in rolling, tethering and firm adhesion to the vascular endothelium that precedes neutrophil extravasation (see Fig 2). During inflammation, gradients of chemokinetic and chemotactic molecules direct the neutrophils to traverse the vascular endothelial wall and migrate into peripheral tissue towards the site of infection. Interactions between the neutrophil and microbe induce phagocytosis, degranulation and activation of the respiratory burst, which in combination mediate microbial killing primarily within the phagocytic vacuole (see Fig 2) (Nathan, 2006). Microbial killing is further enhanced by formation of neutrophil extracellular traps (NETs), which are fibrous networks composed of chromatin, DNA and proteins from antimicrobial granules, formed by activated neutrophils to assist in killing and prevention of spreading of bacteria (Brinkmann *et al*, 2004). Defects in any part of this complex process manifest as immunodeficiency of neutrophil function with life-threatening infections. Here we describe recent insights into the genetic defects and mechanisms underlying primary neutrophil defects.

Defects of neutrophil differentiation

Severe congenital neutropenia and cyclic neutropenia

Severe congenital neutropenia (SCN) is a heterogeneous disease that results from mutations in a variety of genes (Table I). Although generally seen as a monogenic disorder, a recent report has identified four SCN patients with mutations in multiple genes that are found as monogenic cause for SCN. While it is predicted that in these patients one genetic mutation is dominant disease causative, a second mutation could have a synergistic effect and worsen disease phenotype (Germeshausen *et al*, 2010).

Neutrophil formation in SCN patients is arrested at the promyelocytic stage in bone marrow (Fig 1). Patients are usually diagnosed during the first year of life with very low circulating neutrophil counts, resulting in life-threatening infections (Welte *et al*, 2006). In contrast, patients with cyclic neutropenia usually present later in life and show regular and consistent oscillations (with a mean of 21-d cycles) of their number of circulating neutrophils and have a milder clinical course. At the nadir of the

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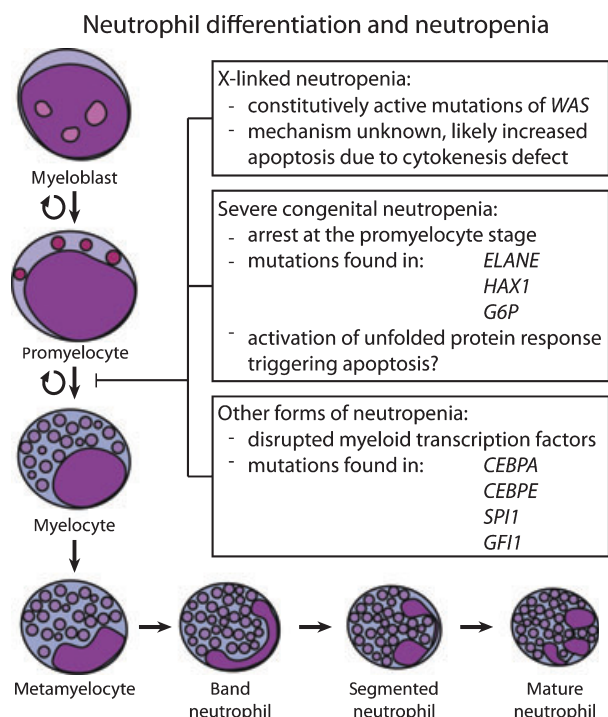


Fig 1. Schematic overview of the stages of neutrophil differentiation. Different forms of neutropenia are shown in the boxes and the associated genes or transcription factors indicated. The majority of congenital neutropenias result in arrest of neutrophil differentiation at the promyelocyte stage. A similar arrest has been reported for some, but not all patients with X-linked neutropenia and other mechanisms may contribute to neutropenia in this disorder. Straight arrows indicate progressive maturation and circular arrows denote stages at which cells division can occur.

neutrophil count, which lasts from 3 to 6 d, patients suffer from fever, mouth ulcers and infections (Dale & Hammond, 1988; Haurie *et al*, 1998). Over 90% of patients with either disorder respond to granulocyte colony-stimulating factor (G-CSF) therapy (Dale *et al*, 1993; Rosenberg *et al*, 2006). In refractory cases, or where SCN is complicated by haematological malignancy, haematopoietic stem cell transplantation is a potentially curative option. Data from the Severe Chronic Neutropenia International Registry (<http://depts.washington.edu/registry/>) indicates a significantly higher than previously recognized cumulative incidence (21%) of developing acute myeloid leukaemia (AML) or myelodysplastic syndrome (MDS) (Freedman & Alter, 2002; Dale *et al*, 2006; Rosenberg *et al*, 2006, 2010). Long term follow up from this registry revealed that the risk of developing AML/MDS was significantly lower than initially thought (2.3%/year compared to 4–12%/year), although the cumulative incidence stays high (22%) after 15 years of follow-up (Rosenberg *et al*, 2010). It has now been demonstrated that the highest risk of AML/MDS is in the cohort of patients that needs greater than the median dose of G-CSF but has less than the median neutrophil response. The most likely explanation of this observation is that G-CSF merely allows those children with the severest disease to live long enough for the full

phenotype to manifest, but it is clearly impossible to totally exclude a leukemogenic effect of exogenous G-CSF. Mutations in the G-CSF receptor are associated with progression in some cases, but may persist for many years without progression and are not an absolute requirement for the development of leukaemia, proving a causative association is confounded by the fact that almost all patients are on G-CSF treatment (Dong *et al*, 1995; Tidow *et al*, 1997; Ancliff *et al*, 2003; Cassinat *et al*, 2004; Rosenberg *et al*, 2006, 2010; Zeidler *et al*, 2009).

ELANE

Several genetic lesions have recently been identified that account for a substantial proportion of cases of SCN or cyclic neutropenia. Mutations in the *ELANE* (previously *ELA2*) gene, encoding neutrophil elastase, were first identified as a cause for cyclic neutropenia (Horwitz *et al*, 1999) and heterozygous *ELANE* mutations were subsequently found to account for around 50% of autosomal dominant SCN cases (Horwitz *et al*, 1999; Dale *et al*, 2000; Ancliff *et al*, 2001; Bellanne-Chantelot *et al*, 2004; Klein, 2009; Xia *et al*, 2009; Zeidler *et al*, 2009). At least 52 different mutations in *ELANE* have been described, including mutations in prodomains and promoter region. The diversity of mutations in SCN appears wider than in cyclic neutropenia, but there is no clear relationship between particular *ELANE* mutations and the clinical form of disease with the exception of the G185R mutation. The G185R mutation introduces a positively charged arginine residue in the immediate proximity of the active site of neutrophil elastase and is likely to alter its biological function. Patients with this mutation appear to have very severe SCN with neutrophil counts close to zero, are refractory to G-CSF or require high G-CSF doses and are more prone to develop leukaemia (Dale *et al*, 2000; Bellanne-Chantelot *et al*, 2004; Horwitz *et al*, 2007).

Neutrophil elastase is a monomeric, 218-amino acid (25 kDa), chymotryptic serine protease, which is synthesized during the early stages of primary granule production in promyelocytes. It is formed as a proenzyme during neutrophil differentiation and stored in azurophilic granules in its active form, ready for release from the granules with full enzymatic activity at sites of inflammation (Bode *et al*, 1989). The mechanism by which elastase defects result in neutropenia remains under investigation. Loss of function is not the primary mechanism as no consistent defects of proteolytic activity, substrate specificity or serpin inhibition were found for elastase mutants (Li & Horwitz, 2001). Furthermore, genetically targeted elastase null mutant mice are not neutropenic (Belaouaj *et al*, 1998), nor more interestingly, were mice targeted with a disease-causing *ELANE* mutant (Grenda *et al*, 2002). Two studies have suggested a role for *ELANE* mutations in activation of the unfolded protein response (UPR) and apoptosis in SCN pathogenesis. The UPR is triggered by accumulation of misfolded proteins in the endoplasmic reticulum (ER) and may lead to apoptosis of the cell. UPR involves three major mechanisms: attenuation of global protein synthe-

Table I. Disorders of neutrophil differentiation.

Disease	Inheritance	Genetic defect	Phenotypic defect
Severe congenital neutropenia	Autosomal dominant, autosomal recessive or sporadic	<i>ELANE</i> mutation <i>HAX1</i> mutation <i>GFI1</i> mutation	Severe neutropenia, developmental arrest of neutrophil precursors and maturational arrest at promyelocytic stage
Cyclic neutropenia	Autosomal dominant or sporadic	<i>ELANE</i> mutation	Fluctuations between normal granulocyte counts and severe neutropenia with 21-d periodicity. Increased apoptosis in myeloid precursors
Glucose-6-phosphatase deficiency	Autosomal recessive	<i>G6PC3</i> mutation	Loss of glucose-6-phosphatase activity and increased susceptibility to apoptosis
X-linked neutropenia	X-linked	Activating <i>WAS</i> mutation	Neutropenia and monocytopenia
Neutrophil specific granule deficiency	Autosomal recessive	<i>CEBPE</i> mutation	Absent secondary and tertiary granule proteins. Primary granules lack defensins
p14 deficiency	Autosomal recessive	<i>ROBLD3</i> (<i>p14</i> , <i>MAPBPIP</i>) mutation	Defective lysosome function, neutropenia, hypogammaglobulinaemia, short stature and hypopigmentation
Hermansky-Pudlak syndrome type 2	Autosomal recessive	<i>AP3B1</i> mutation	Neutropenia, hypopigmentation and defective platelet function
Griscelli syndrome type 2	Autosomal recessive	<i>RAB27A</i> mutation	Variable hypopigmentation, neutropenia and frequent pyogenic infections
Chediak-Higashi syndrome	Autosomal recessive	<i>LYST</i> (<i>CHS1</i>) mutation	Hypopigmentation, recurrent infections, defective bacterial killing and enlarged and irregular azurophilic granules

AP3B1, adaptor-related protein complex 3, beta 1 subunit; *CEBPE*, CCAAT/enhancer binding protein (C/EBP), epsilon; *LYST*, Lysosomal Trafficking Regulator (*CHS1*, Chediak-Higashi Syndrome 1); *ELANE*, neutrophil elastase; *G6PC3*, glucose-6-phosphate catalytic subunit 3; *GFI1*, growth factor independent-1 transcription repressor; *HAX1*, HCLS1 associated protein X-1; *RAB27A*, RAB27A, member RAS oncogene family; *ROBLD3*, roadblock domain containing 3 (MAPBPIP, mitogen-activated protein-binding protein-interacting protein).

sis, enhanced transcription of normal ER-resident chaperone proteins involved in normal protein folding and degradation of misfolded proteins. Upon severe ER stress, the UPR triggers apoptosis (Ron & Walter, 2007). It has been suggested that elastase mutants induce the unfolded protein response. One study has shown that expression of several elastase mutants in a myeloid cell line resulted in disrupted intracellular trafficking and accumulation of cytoplasmic elastase. Furthermore, apoptosis was increased, which was associated with upregulated expression of the ER chaperone binding immunoglobulin protein (BiP) (Kollner *et al*, 2006). The second study confirmed increased BiP expression in the same myeloid cell line using additional elastase mutants, but importantly also observed increased BiP expression in granulocytic precursors isolated from patients with SCN (Grenda *et al*, 2007).

HAX1

While *ELANE* mutations account for around 50% of SCN cases, they appear not to be the cause of SCN in the original pedigree described by Kostmann (1956) as only one patient of this family was found to carry a mutation in the *ELANE* gene (Carlsson *et al*, 2006; Melin *et al*, 2007). Instead, three of the original kindred were found to have homozygous *HAX1* mutations (Klein *et al*, 2007). A small number of SCN patients have now been found to carry *HAX1* mutations with the W44X

mutation being the most common (72% of cases) (Klein *et al*, 2007; Germeshausen *et al*, 2008; Smith *et al*, 2009). *HAX1* deficient neutrophils showed enhanced spontaneous as well as induced apoptosis and while normal neutrophils maintain the inner mitochondrial membrane potential, *HAX1* deficient neutrophils failed to do so, suggesting *HAX1* is involved in stabilizing the mitochondrial membrane potential (Klein *et al*, 2007). Studies in *HAX1*-deficient mice have shown that *HAX1* is required for processing of the mitochondrial protease high-temperature-regulated A2 (HtrA2), which is then activated and released into the mitochondrial intermembrane space and prevents accumulation of other pro-apoptotic factors (Chao *et al*, 2008). Loss of HtrA2 was shown to lead to an accumulation of unfolded proteins in mitochondria and enhanced mitochondrial stress in HtrA2-deficient mice (Moi-soi *et al*, 2009). Defects of *HAX1* or HtrA2 may result in failure to maintain normal mitochondria function and consequently induce apoptosis, but further investigations are required to determine if such mechanism is indeed involved in enhanced apoptosis of neutrophils in SCN caused by *HAX1* deficiency.

Glucose-6-phosphatase (G6P) deficiency

Recently, mutations in the *G6PC3* gene, encoding glucose-6-phosphatase, catalytic subunit 3, were found to give rise to SCN. To date, a total of 15 SCN patients have been identified

to have mutations in *G6PC3* resulting in impaired enzymatic activity and an increased susceptibility to apoptosis (Arostegui *et al*, 2009; Boztug *et al*, 2009; Xia *et al*, 2009). Additional features include variable cardiac, urogenital and vascular anomalies. Analysis of neutrophil progenitor cells showed enlarged rough ER and increased BiP expression (Boztug *et al*, 2009), suggesting involvement of UPR as has been hypothesized for *ELANE* mutations causing SCN and cyclic neutropenia. Moreover, G6P-deficient mice display a SCN phenotype including neutropenia, increased susceptibility to bacterial infection, increased apoptosis and defects in neutrophil respiratory burst and chemotaxis (Cheung *et al*, 2007). Peritoneal and bone marrow neutrophils were found to exhibit enhanced expression of ER chaperones, suggesting *G6PC3*^{-/-} neutrophils undergo ER stress and UPR leading to increased neutrophil apoptosis (Cheung *et al*, 2007).

X-linked neutropenia

Although loss of function mutations in *WAS*, the gene encoding the Wiskott–Aldrich syndrome (WAS) protein (WASp), normally result in classical WAS or X-linked thrombocytopenia, to date four different constitutively activating mutations have been described to cause a distinct clinical disease, X-linked neutropenia (XLN). XLN does not resemble WAS but is instead characterized by moderate-severe neutropenia, recurrent infections and in some cases myelodysplasia (Devriendt *et al*, 2001; Ancliff *et al*, 2006; Beel *et al*, 2009; Xia *et al*, 2009; Thrasher & Burns, 2010). It appears that mutations in the conserved GTPase-binding domain of WASp disrupt the autoinhibitory molecular confirmation of the cytosolic protein, resulting in mutant protein with enhanced Arp2/3-mediated actin polymerization activity (Devriendt *et al*, 2001; Ancliff *et al*, 2006; Moulding *et al*, 2007; Beel *et al*, 2009). The mechanism by which hyperactive WASp causes neutropenia remains to be fully elucidated, but recent data suggest that enhanced and delocalized actin polymerization disrupts normal mitosis and leads to genomic instability and increased apoptosis of neutrophil precursors (Moulding *et al*, 2007). Despite clinical heterogeneity, infection susceptibility is generally relatively mild given the degree of neutropenia and patients can usually be managed with antibiotic prophylaxis. Concern regarding myelodysplasia and an increased risk of malignant transformation associated with G-CSFR mutations and monosomy 7, has led to a recommendation that G-CSF is used with caution and ideally reserved for management of acute infections (Beel & Vandenberghe, 2009; Beel *et al*, 2009). A fifth mutation in *WAS* (P460S) has recently been described to be linked with neutropenia, but it is not known whether this mutation affects the ability of WASp to induce Arp2/3-mediated actin polymerization (Xia *et al*, 2009).

Myeloid transcription factors

During haematopoiesis transcription factors determine the regulation of gene expression required for cellular prolifera-

tion, differentiation and survival. Myeloid transcription factors, such as the alpha and epsilon members of the CCAAT/enhancer binding protein (C/EBP) family and PU.1 (encoded by the *CEBP* and *SPI1* genes respectively), are key regulators of granulocytic-macrophage progenitor cells and were, prior to the above discoveries, a key area of investigation. Germline mutations the *CEBPA* gene do not seem to give rise to SCN, but rather are associated with leukaemia (Smith *et al*, 2004). In contrast, mice lacking C/EBP α are unable to respond to G-CSF and as a result have a selective loss of granulocytes (Zhang *et al*, 1997). It has been proposed that the transcription factor lymphoid enhancer factor-1 (LEF-1) plays a key role in regulating neutrophil granulopoiesis by regulating C/EBP α (Skokowa & Welte, 2009). LEF-1 expression was found to be reduced in SCN patients carrying either *ELANE* or *HAX1* mutations, resulting in reduced expression of C/EBP α and neutrophil elastase (Skokowa *et al*, 2006, 2009). Reconstitution of LEF-1 in cells from SCN patients corrected their defective myelopoiesis and restored differentiation of mature neutrophils, while inhibition of LEF-1 in progenitor cells from healthy individuals inhibited their proliferation and induced apoptosis (Skokowa *et al*, 2006). However, no mutations in *LEF1* have yet been found in SCN patients.

C/EBP ϵ consists of four isoforms and is expressed exclusively in cells of myeloid and T-cell lineages (Antonson *et al*, 1996). Targeted disruption of the *Cebpe* gene in mice results in failed terminal differentiation of neutrophils and eosinophils (Yamanaka *et al*, 1997). C/EBP ϵ ^{-/-} neutrophils are defective in phagocytosis, bacterial killing and migration, and show impaired cytokine production after an inflammatory challenge (Yamanaka *et al*, 1997; Lekstrom-Himes & Xanthopoulos, 1999; Hock *et al*, 2003). In addition, there is accelerated apoptosis in maturing granulocytic cells (Verbeek *et al*, 2001). The phenotype of C/EBP ϵ ^{-/-} mice is strikingly similar to a rare congenital neutrophil disorder neutrophil-specific granule deficiency (SGD). Five cases with this disease have been reported worldwide who suffer from frequent and severe bacterial infections and their neutrophils are characterized by bilobed nuclei and insufficient neutrophil function including lack of secondary granule proteins and defensins, impaired chemotaxis and impaired bactericidal activity (Gallin, 1985; Gombart & Koeffler, 2002). In two of these patients mutations in *CEBPE* have been found, resulting in loss of two or all four of the C/EBP ϵ isoforms (Lekstrom-Himes *et al*, 1999; Gombart *et al*, 2001). A third patient was found to exhibit elevated expression of C/EBP ϵ , caused by a heterozygous *CEBPE* mutation (Khanna-Gupta *et al*, 2007). While this mutation did not seem to affect C/EBP ϵ function, expression of both C/EBP ϵ and PU.1 was increased. Both transcription factors are targets for repression by the transcriptional repressor transcription factor growth factor independence-1 (Gfi-1) and its expression was found to be reduced in this SGD patient (Khanna-Gupta *et al*, 2007).

Gfi-1 is a zinc-fingered transcription factor, which regulates multiple target genes for neutrophil differentiation, including

CEBPE and *SPI1* (*PU.1*). Gene targeted *GFI1*^{-/-} mice lack mature circulating neutrophils and are highly susceptible to bacterial infection (Hock *et al*, 2003). Two individuals were reported with mutations in the human *GFI1* gene and neutropenia. Such mutations result in loss of repression of *ELANE* and *CEBPE* expression, which may induce the UPR or directly impair the proliferation and survival of immature granulocytes (Person *et al*, 2003; Zhuang *et al*, 2006). Three other mutations in *GFI1* were detected in a large screen of SCN patients, although it is not known whether these are disease-causing and two of them were found in addition to mutations in *ELANE* (Xia *et al*, 2009). Targeted gene disruption of the transcription factor PU.1 in mice also resulted in neutropenia (amongst other haematopoietic abnormalities) and abnormal neutrophil development with production of only a few cells with neutrophil characteristics, which failed to differentiate into mature, functional neutrophils (McKercher *et al*, 1996; Anderson *et al*, 1998).

Other forms of neutropenia

For many SCN patients no underlying molecular cause has been identified and there are several disorders that exhibit neutropenia as part of a broader spectrum of symptoms (Table I). A mutation in the gene encoding endosomal adaptor protein 14 (p14), encoded by the *ROBLD3* gene, was found to cause neutropenia, while neutrophil maturation in the bone marrow was intact. To date, four patients from one family have been described with this mutation, who suffered from recurrent *Streptococcus pneumoniae* infection, hypogammaglobulinaemia, short stature and hypopigmented skin (Bohn *et al*, 2007). Patients showed substantially reduced protein expression, which resulted in defective lysosome function and delayed bacterial killing by neutrophils (Bohn *et al*, 2007). Other diseases that include neutropenia in their clinical presentation include Hermansky-Pudlak syndrome type 2, which is caused by mutations in *AP3B1* (Jung *et al*, 2006), Griscelli syndrome type 2, caused by mutations in the *RAB27A* gene, which encodes the GTPase Rab27 (Meeths *et al*, 2009) and the Chediak-Higashi syndrome, caused by mutations in the *LYST* (*CHS1*) gene (Introne *et al*, 1999). Patients with X-linked hyper IgM syndrome, which is characterized by CD40L deficiency, also frequently develop neutropenia and the mechanism may be related to reduced cytokine production from bone marrow stromal cells secondary to lack of CD40L stimulation (Solanilla *et al*, 2000).

Defects of migration and cytoskeletal function

Leucocyte adhesion disorders

Leucocyte adhesion disorders arise from defects in cell adhesion to extracellular matrix and vascular endothelium (Table II). These functions are normally mediated by leuco-

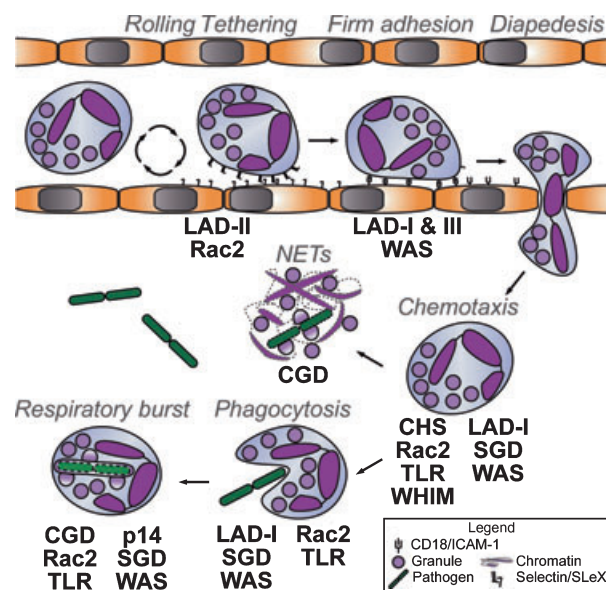


Fig 2. Schematic overview of normal neutrophil function and its defects. In response to inflammatory signals, e.g. caused by bacteria, neutrophils leave the blood stream and enter tissue via the multistep paradigm of rolling, tethering, adhesion and diapedesis. Inside the tissue neutrophils chemotax towards the source of inflammation and phagocytose and kill the bacteria using respiratory burst machinery and formation of neutrophil extracellular traps (NETs). One or more of these cellular processes can be disrupted by an inherited neutrophil defect. The genetic diseases associated with impairment of each functional stage are indicated in bold font. Abbreviations as in the main text.

cyte adhesion molecules including integrins and selectins (Fig 2). Integrins are classified in families where each member shares a common β chain that is non-covalently linked to a unique α chain. The β_2 integrins share CD18 as the β chain and are confined primarily to leucocytes. Depending on which α chain is utilized, they are known as lymphocyte-function-associated antigen (LFA-1 or CD11a/CD18), complement receptor-3 (CR3, Mac-1 or CD11b/CD18), p150,95 (or CD11c/CD18) and $\alpha_v\beta_2$ (or CD11d/CD18). All β_2 integrins are expressed constitutively at the cell surface but are quantitatively and functionally upregulated by activation of the cell, to achieve optimal ligand binding. The ligands for β_2 integrins are members of the immunoglobulin gene superfamily, intercellular adhesion molecule-1 (ICAM-1) and ICAM-2, which are expressed on endothelial cells and upregulated during inflammation. Three distinct human disorders of leucocyte adhesion have been recognized: leucocyte adhesion deficiency type 1 (LAD-I) of which hundreds of cases are described, and the rarer LAD type 2 (LAD-II) and LAD type 3 (LAD-III).

LAD-I

LAD-I is characterized in its severe form by delayed separation of the umbilical cord with omphalitis, recurrent life-threatening

Table II. Disorders of neutrophil function.

Disease	Inheritance	Genetic defect	Phenotypic defect
Defects of migration and cytoskeletal function			
LAD-I	Autosomal recessive	<i>ITGB2</i> mutation	Neutrophilia, inability to make pus and lack or reduction of CD18 expression
LAD-II	Autosomal recessive	<i>SLC35C1</i> mutation	Granulocytes unable to bind to selectins on endothelium. Congenital disorder of fucosylation
LAD-III	Autosomal recessive	<i>RASGRP2</i> mutation <i>FERMT3</i> mutation	Neutrophilia, severe bleeding tendency and defective integrin activation
WHIM	Autosomal dominant or autosomal recessive	<i>CXCR4</i> mutation	Warts, hypogammaglobulinaemia, infections and myelokathexis
WAS	X-linked	<i>WAS</i> mutation	Dysfunctional actin polymerization and defects of adhesion, migration and phagocytosis
Rac2 deficiency	Autosomal dominant	<i>RAC2</i> mutation	Abnormal chemotaxis, defective respiratory burst, impaired degranulation and neutrophillia
Defects of the respiratory burst			
CGD	X-linked autosomal recessive	<i>CYBB</i> mutation <i>NCF1</i> , <i>NCF2</i> , <i>NCF4</i> and <i>CYBA</i> mutations	Neutrophils unable to produce superoxide
G6PD deficiency	X-linked	<i>G6PD</i> mutation	Neutrophils unable to produce superoxide
MPO deficiency	Multigenic?	<i>MPO</i> and other genetic mutations?	Impaired respiratory burst from defective hypochlorous acid production
Defects of TLR signalling			
IRAK-4 deficiency	Autosomal recessive	<i>IRAK4</i> mutation	Increased susceptibility to invasive bacterial disease, defective L-selectin shedding, migration and respiratory burst
MyD88 deficiency	Autosomal recessive	<i>MYD88</i> mutation	Increased susceptibility to invasive bacterial disease
NEMO deficiency	X-linked	<i>IKBK</i> mutation	Increased susceptibility to invasive bacterial disease and impaired respiratory burst

CGD, chronic granulomatous disease; *CXCR4*, CXC-containing chemokine receptor-4; *CYBA*, cytochrome b-245 alpha polypeptide; *CYBB*, cytochrome b-245 beta polypeptide; *FERMT3*, fermitin family homolog 3; *G6PD/G6PD*, glucose-6-phosphate dehydrogenase; *IRAK-4/IRAK4*, interleukin-1 receptor-associated kinase 4; *IKBK*, inhibitor of nuclear factor kappa-B kinase subunit gamma; *ITGB2*, integrin beta-2; LAD, leucocyte adhesion deficiency; *MPO/MPO*, myeloperoxidase; *MyD88/MYD88*, myeloid differentiation primary response gene 88; *NCF*, neutrophil cytosolic factor; *NEMO*, nuclear factor kB modulator; *RASGRP2*, RAS guanyl releasing protein-2; *SLC35C1*, solute carrier family 35 member C1; *WAS/WAS*, Wiskott–Aldrich syndrome; *WHIM*, warts, hypogammaglobulinaemia, infections and myelokathexis.

bacterial (usually with *Staphylococcus aureus* and Gram-negative enteric organisms) and fungal infections, gingivitis, and delayed wound healing. Patients are neutrophilic in the absence of infection with marked granulocytosis during acute infection. The absence of pus formation at sites of infection is one of the hallmarks of LAD-I, indicating a defect of neutrophil recruitment from the vasculature to sites of infection (Anderson & Springer, 1987; Etzioni *et al*, 1999). LAD-I is caused by recessively inherited mutations in *ITGB2*, encoding CD18, and is located on chromosome 21. All leucocytes are consequently deficient in CD18 cell-surface expression resulting in defects of neutrophil adhesion, transendothelial migration and chemotaxis (Anderson & Springer, 1987; Hogg & Bates, 2000; Tsai *et al*, 2008). The degree of CD18 deficiency correlates well with the severity of the clinical condition. Patients suffering from the severe form of the disease (<2% normal cell surface expression of CD18) are likely to die in childhood as a result of infection unless treated by haematopoietic stem cell transplantation, whereas those

with moderate disease (2–10% expression) can survive into adulthood. Periodontitis, skin ulcerations and poor wound healing are common problems for those surviving past infancy. Although neutrophil defects appear to be the major clinical problem in LAD, the function of other immune cells is likely to be impaired given the universal expression of CD18 in leucocyte populations. Spontaneous reversion mutations, resulting in corrected copy of the gene have been described in a few patients (Uzel *et al*, 2008) but correction has so far been restricted to cytotoxic T-cells with no beneficial effect on host protection. Bone marrow transplantation is currently the only curative therapy available. In contrast with haploidentical procedures, which have a poor survival rate of about 50%, longterm survival is above 80% if a suitable human leucocyte antigen (HLA)-matched donor can be used (Qasim *et al*, 2009). Gene therapy has successfully corrected a natural model of LAD-I in dogs (Bauer *et al*, 2008), and may in the future provide an alternative to stem cell transplantation for patients for whom no suitable donor can be found.

LAD-II

LAD-II has been described in only a few patients and results from an autosomal recessively inherited general defect in fucose metabolism leading to an absence of sialyl-Lewis X (SLeX, also called CD15s) and other fucosylated ligands for selectins (Etzioni *et al*, 1992; Marquardt *et al*, 1999a; Hidalgo *et al*, 2003). SLeX-containing glycoproteins on the endothelium normally bind the L-selectin cell-adhesion molecule on neutrophils, slowing them from the blood stream to establish rolling along endothelium. In LAD-II, this interaction is impaired abrogating firm integrin-mediated attachment and subsequent diapedesis (see Fig 2) and resulting in an immunodeficiency of LAD-II that is similar to that of LAD-I, but less severe. In addition to recurrent bacterial infections, other features include moderate-severe mental retardation, dysmorphism short stature and a Bombay blood phenotype. With advancing age, bacterial infections reduce in frequency and severity but periodontitis and mental retardation with epilepsy become more prominent. Missense mutations have been identified in *SLC35C1*, encoding a highly conserved GDP-fucose transporter, which explains the observed defect of GDP-fucose import into the Golgi apparatus where fucosylation takes place (Lubke *et al*, 1999, 2001; Luhn *et al*, 2001). *In vitro* fucosylation defects of cultured fibroblasts from LAD-II patients can be corrected by the addition of fucose (Marquardt *et al*, 1999b), suggesting that the defective transporter may have partial activity, or that other pathways for fucosylation exist. The clinical usefulness of this is unclear however as oral fucose treatment restored expression of fucosylated selectin ligands and improved immunodeficiency in only one out of three LAD-II patients reported (Marquardt *et al*, 1999b; Etzioni & Tonetti, 2000; Luhn *et al*, 2001).

LAD-III

LAD-III was initially described as a variant of LAD-I, and presents a similar clinical phenotype including severe recurrent bacterial and fungal infections, leucocytosis, lack of pus formation and poor wound healing. In addition, however, affected individuals demonstrate a severe bleeding tendency, which is similar to Glanzmann thrombasthenia. Bleeding can be the presenting symptom and results in an ongoing requirement for red cell and platelet transfusions (Kuijpers *et al*, 1997). Hepatosplenomegaly, possibly resulting from extra-medullary haematopoiesis, and an increase in bone density resembling osteopetrosis have also been reported (Kuijpers *et al*, 2007; Kilic & Etzioni, 2009). Patients have normal β_1 , β_2 and β_3 -integrin expression, but defective integrin activation through 'inside-out' signalling pathways, which results in failure to establish high affinity ligand binding (McDowall *et al*, 2003; Kinashi *et al*, 2004). Although mutations in *RASGRP2*, which encodes for calcium- and diacylglycerol-regulated guanine exchange factor (CalDAG-GEFI), were initially identified and implicated in LAD-III (Pavolsky

et al, 2007), further analysis has shown that these mutations are probably not disease-causing (Kuijpers *et al*, 2009; Svensson *et al*, 2009). Instead, separate recessively inherited mutations in *FERMT3*, which encodes the haematopoietic-restricted Kindlin-3 protein, were identified in LAD-III patients (Mory *et al*, 2008; Kuijpers *et al*, 2009; Svensson *et al*, 2009). All mutations described abrogate expression of Kindlin-3 protein, which normally functions to activate leucocyte integrins for optimal function. Restoring Kindlin-3 protein expression in affected cells of patients with LAD-III restored integrin-mediated adhesion and migration defects, directly implicating Kindlin-3 mutations in this disease (Svensson *et al*, 2009). Bone marrow transplantation (BMT) can be curative in LAD-III although it remains to be clarified whether engraftment failure and post BMT mortality are specifically problematic (Kuijpers *et al*, 2009; Elhasid *et al*, 2010; Jurk *et al*, 2010; Sabnis *et al*, 2010).

WHIM

WHIM syndrome is classically characterized by the clinical features of warts, hypogammaglobulinaemia, recurrent respiratory tract infections and myelokathexis, although affected individuals may not present all features (Tassone *et al*, 2009). Almost all patients carry dominant mutations in *CXCR4*, which encodes the chemokine receptor CXCR4, typically resulting in expression of a truncated form of CXCR4 that lacks its intracellular tail (Hernandez *et al*, 2003; Balabanian *et al*, 2005; Tassone *et al*, 2009). This causes alterations of CXCR4 signalling, and possibly receptor internalization, resulting in augmented responses to CXCL12, the functional ligand of CXCR4 (Gulino *et al*, 2004; Balabanian *et al*, 2005; Lagane *et al*, 2008). This is thought to attenuate neutrophil migration causing retention of mature neutrophils in the bone marrow (myelokathexis) and enhanced bone marrow homing of senescent neutrophils (Martin *et al*, 2003). In general, WHIM syndrome is not considered to be a severe immunodeficiency and can be managed with G-CSF, prophylactic antibiotics and immunoglobulin replacement. However, respiratory infections can lead to chronic lung disease and there is a significant malignancy susceptibility, particularly to human papillomavirus (HPV) related carcinomas (Kawai & Malech, 2009).

Wiskott–Aldrich syndrome

Dynamic reorganization of the actin cytoskeleton is a key process during many neutrophil functions including diapedesis, migration and phagocytosis. In haematopoietic cells, WASp is an important regulator of cytoskeletal function, transducing signals from cell surface receptors to the actin cytoskeleton. Loss of function mutations in the WAS gene give rise to the rare inherited X-linked Wiskott–Aldrich syndrome (WAS), which is characterized in its classic form by recurrent infections, eczema and microthrombocytopenia (Bouma *et al*,

2009a; Thrasher & Burns, 2010). The immunodeficiency seen in severe WAS is broad, affecting cells of both the innate and adaptive immune systems and this is reflected in the range of infections seen which include bacterial, viral, fungal and occasionally opportunistic pathogens. Although WAS is not considered to be a neutrophil disorder and indeed clinical features of neutrophil dysfunction are not prominent, specific defects have been reported *in vitro*. WASp-deficient neutrophils are impaired in their ability to cluster $\beta 2$ integrins, which results in defective adhesion and transendothelial migration under conditions of physiological shear flow (Zicha *et al*, 1998; Zhang *et al*, 2006). In addition, phagocytosis and respiratory burst are impaired in neutrophils from patients and the murine WASp knockout model (Zhang *et al*, 1999, 2006).

Rac2

The GTPase Rac2 is another important regulator of leucocyte cytoskeletal rearrangement but is also critical for activity of the nicotinamide adenine dinucleotide phosphate (NADPH) oxidase, through interaction with $p67^{phox}$ (see below) (Segal & Abo, 1993). Human Rac2 deficiency has been described in one patient presenting in infancy with a picture similar to LAD: severe bacterial infections, neutrophilia, absent pus formation and wound healing. A point mutation was found in the *RAC2* gene (Ambruso *et al*, 2000; Williams *et al*, 2000) which resulted in loss of GTP binding and dominant inhibition of Rac2 protein function (Gu *et al*, 2001). In keeping with dual roles in cytoskeletal regulation and respiratory burst, the patient's neutrophils exhibited decreased chemotaxis, polarization, azurophilic granule secretion and superoxide anion production. This patient underwent successful bone marrow transplantation (Williams *et al*, 2000).

Defects of the respiratory burst

Chronic granulomatous disease

Although still rare, chronic granulomatous disease (CGD) is the most common of the neutrophil function disorders with an estimated prevalence of approximately 4–8 per million (Winkelstein *et al*, 2000; Jones *et al*, 2008). CGD is caused by defects in any component of NADPH oxidase, the enzyme responsible for the oxidative or 'respiratory' burst in neutrophils (Goldblatt & Thrasher, 2000; Segal, 2005). The NADPH oxidase is a membrane-bound complex that is assembled in phagosomes or at the plasma membrane upon neutrophil activation by receptor binding or soluble factors. The main redox component is membrane-bound flavocytochrome b_{558} , a heterodimer of two proteins: the α subunit, $p22^{phox}$ and the β subunit, $gp91^{phox}$. Both $p22^{phox}$ and $gp91^{phox}$ are missing in cells derived from most CGD patients with a molecular lesion of either subunit, indicating that mutual interaction is required for the assembly of the mature flavocytochrome b_{558} complex (Parkos *et al*, 1989). The other subunits of the NADPH

oxidase complex are four factors recruited from the cytosol, $p47^{phox}$, $p67^{phox}$, $p40^{phox}$ and $p21rac2$ (Segal, 2005), inducing conformational changes in flavocytochrome b_{558} , that permit binding of the substrate NADPH and energetically favour electron transport (Bedard & Krause, 2007). Once assembled, NADPH-oxidase catalyses the transfer of electrons across the phagosome membrane from NADPH to molecular oxygen, resulting in the formation of free radical superoxide (O_2^-) and subsequently hydrogen peroxide (H_2O_2), hypochlorous acid (HOCl) and hydroxyl radical ($\cdot OH$). Although reactive oxygen species have been supposed to have significant intrinsic microbicidal activity it appears more likely that the process of electron transport ultimately regulates pH and ionic composition within the phagosome, which is crucial for activation of proteolytic enzymes as they are discharged into the phagocytic vacuole (Segal, 2005).

Patients affected by CGD lack specific components of the NADPH oxidase complex as a result of mutations in corresponding genes. X-linked CGD affecting $gp91^{phox}$ (*CYBB* gene) is the most common and accounts for about 70% of cases. Mutations affecting the other components demonstrate autosomal recessive inheritance: approximately 25% of cases result from mutations in $p47^{phox}$ (*NCF1* gene), while loss of $p67^{phox}$ (*NCF2* gene) or $p22^{phox}$ (*CYBA* gene) account for only a small number of cases (each around 5%) (van den Berg *et al*, 2009). In all these forms of CGD, failure to produce a respiratory burst results in susceptibility to severe and recurrent infections predominantly by catalase-positive bacteria and fungi, particularly *Aspergillus* species, *S. aureus* and *Salmonella* species. In addition to defective respiratory burst, CGD neutrophils also fail to form NETs (Fuchs *et al*, 2007), which were recently found to provide an important additional antimicrobial mechanism for neutrophils to bind and kill bacteria. Lymphadenitis, osteomyelitis, abscesses and septicaemia are common but pulmonary infections are most frequent and result in chronic lung disease in a high proportion of patients (Winkelstein *et al*, 2000; Jones *et al*, 2008; van den Berg *et al*, 2009). Granulomatous inflammation is the other major feature of CGD, particularly affecting hollow organs, such as the gastrointestinal and genitourinary tracts. This can result in obstruction or more commonly Crohn's-like inflammatory bowel disease, which may occur early in life and be the sole presenting feature (Freudenberg *et al*, 2010). There is an increased incidence of autoinflammatory manifestations including chorio-retinitis and discoid lupus, which can also be seen in carriers of X-linked CGD (De Ravin *et al*, 2008; van den Berg *et al*, 2009). In general, autosomal recessive forms of CGD have a milder disease course than X-linked CGD, although this is more difficult to establish for the rare $p67^{phox}$ or $p22^{phox}$ forms. Within each subtype, there is significant clinical heterogeneity which, to date, has not been correlated with the specific type of mutation. Recently, the first patient bearing a mutation in $p40^{phox}$ (*NCF4* gene) was described presenting with granulomatous colitis (Matute *et al*, 2009). Loss of $p40^{phox}$ function differs from other forms of CGD as

superoxide production in response to phorbol ester is normal and the substantial defect in superoxide release is seen only during phagocytosis (Matute *et al*, 2009).

The diagnosis of CGD and the detection of carrier status are based on measurement of superoxide release in response to neutrophil activation by one of a variety of tests including nitroblue tetrazolium reduction, dihydrorhodamine (DHR) oxidation or chemiluminescence. Particular consideration needs to be given to myeloperoxidase (MPO) deficiency which also results in an abnormal DHR response but normal NBT test and to p40^{phox} CGD in which superoxide release is only abnormal when phagocytosis is used as an activation stimulus.

Treatment for CGD is dependent on prophylaxis against both bacterial and fungal infection with antimicrobials. In general in Europe, interferon gamma does not form part of the prophylactic arsenal but is reserved for treatment of acute infection. Despite prophylaxis, longterm survival is significantly reduced to approximately 50–60% in the fourth decade of life for X-linked disease and around 80% for autosomal recessive forms (Jones *et al*, 2008; van den Berg *et al*, 2009). Haematopoietic stem cell transplantation is potentially curative and may be considered for patients who have had life threatening infections or severe inflammatory complications, particularly if an HLA-matched sibling donor is available. Clinical trials of gene therapy of X-linked CGD have been in progress for some years and although long-term cure has not yet been achieved, significant clinical benefit in terms of clearing life-threatening infection has been reported (Ott *et al*, 2006; Stein *et al*, 2010). Challenges for the future include establishing long term gene correction and designing new vectors to avoid complications such as retrovirus-induced insertional mutagenesis which has induced myelodysplasia in one trial (Ott *et al*, 2006; Stein *et al*, 2010).

Other defects of oxidative metabolism

Glucose-6-phosphate dehydrogenase (G6PD) deficiency causes defects in oxidative metabolism as G6PD is required for the reduction of NADP⁺ to NADPH. Better known for causing haemolysis, G6PD deficiency can also result in an increased susceptibility to infection. However, as G6PD activity needs to be <5% to cause such symptoms, only a tiny proportion of individuals have this complication (Baehner *et al*, 1971). MPO is a component of neutrophil granules and normally functions to generate antimicrobial hypochlorous acid. This is lacking in MPO deficiency and although the majority of affected individuals are asymptomatic, a small proportion suffer from recurrent mucosal, skin or invasive *Candida* infections (Lanza, 1998).

Defects of TLR signalling

Toll-like receptors (TLRs) have been recognized as key leucocyte receptors for recognition of pathogen-associated molecules. Their ligation, with the exception of TLR3, results in signalling through the MyD88 adapter molecule and

recruitment of the IL-1R-associated kinase (IRAK) complex to regulate activation of nuclear factor- κ B (NF- κ B) and mitogen-activated protein kinase (MAPKs) signalling leading to release of pro-inflammatory cytokines and initiation of antimicrobial effector functions. Defects of TLR signalling, as seen in human deficiency of the IRAK-4 subunit, cause susceptibility to invasive bacterial disease, although curiously this improves with age (Ku *et al*, 2005, 2007). Several leucocyte subtypes demonstrate impaired inflammatory responses and neutrophils of patients with IRAK-4 deficiency show defective shedding of the rolling/tethering receptor L-selectin, defective migration, variable defects of phagocytosis and impaired priming of formyl-methionyl-leucyl-phenylalanine (fMLP)-induced respiratory burst in response to a variety of TLR ligands (Medvedev *et al*, 2003; Picard *et al*, 2003; von Bernuth *et al*, 2006; Ku *et al*, 2007; Bouma *et al*, 2009b; Singh *et al*, 2009; van Bruggen *et al*, 2010). Patients with MyD88 deficiency have been reported with an indistinguishable cellular phenotype from IRAK-4 deficiency and it is likely that neutrophil function will be similarly defective, but this was not investigated (von Bernuth *et al*, 2008). Additionally, patients with NF- κ B essential modulator (NEMO) deficiency, who exhibit mutations in the regulatory complex that controls degradation of I κ B and thus NF- κ B activation, show impaired priming of the neutrophil respiratory burst, although not as severe as IRAK-4 deficient neutrophils (Singh *et al*, 2009).

Concluding remarks

Recent advances in defining the molecular basis of neutrophil defects have significantly enhanced our understanding of these disorders and will enable improved studies of disease outcome and the effect of current therapies. In contrast with congenital neutropenias, in which many different underlying mutations result in similar final effects on neutrophil differentiation and production, defects of neutrophil function are disparate genetically, biochemically and clinically. While G-CSF is the mainstay of treatment for genetic neutropenias, a variety of treatment modalities from prophylactic antimicrobials to stem cell transplantation are appropriate for functional disorders. In addition to the defined disorders discussed here, a significant proportion of individuals with infection susceptibility and demonstrable neutrophil dysfunction remain undefined. This group presents a significant challenge for the future, both to determine underlying molecular mechanisms and optimum treatment. Future challenges, which need to be addressed, are improved diagnostic testing for neutrophil function and novel therapeutic options, such as gene therapy, for patients for whom no suitable donor is available for stem cell transplantation.

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