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Citation for published version:

Digital Object Identifier (DOI):
10.1016/j.dci.2011.08.013

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Developmental and Comparative Immunology

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Chicken interleukin-21 is costimulatory for T cells and blocks maturation of dendritic cells

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1. Introduction

Interleukin-21 is a type I cytokine, belonging to the four α-helical bundle family of cytokines, with structural and functional homology to IL-15, IL-2 and IL-4, and was first described by Parrish-Novak et al. (2000). In mammals it is an immunomodulatory cytokine produced by CD4+ T and natural killer (NKT) cells, and has pleiotropic effects on the proliferation, differentiation and effector functions of T, B, NK and dendritic cells. A cDNA encoding the chicken orthologue of IL-21 (chIL-21) was cloned by RT-PCR from RNA isolated from activated chicken splenocytes and consists of 438 nucleotides, encoding an open reading frame of 145 amino acids (aa). Chicken IL-21 has 20–30% aa identity to its orthologues in mammals, Xenopus and fish, but is more highly conserved within Aves (50–80%). The four α-helical bundle structure of mammalian IL-21 appears to be conserved in the predicted chicken protein, as are the four cysteine residues required for the formation of two disulphide bridges. A glutamine residue in aa position 129, which has been implicated in the binding of IL-21 to the IL-2 receptor γ-chain in mammals, is also conserved. ChIL-21 is expressed in most lymphoid tissues, predominantly by CD4+ TCRβ+ T cells. As in mammals, chIL-21 synergistically enhances T-cell proliferation and inhibits maturation of dendritic cells.

In conjunction with this, IL-21 plays an important role in the generation of Th follicular helper cells (Thf) and germinal centre development (reviewed by Spolski and Leonard, 2008, 2010). IL-21 is also a critical regulator of Th17 development (Monteleone et al., 2008).

Until recently, our understanding of the repertoire of immune mediators, including cytokines, chemokines, toll-like receptors, etc. in the chicken, when compared to mammals, was limited. However, the release of the chicken genome sequence (International Chicken Genome Sequencing Consortium, 2004) has revolutionised our ability to understand both the repertoire and the biology of these and other immune-related molecules (Kaiser et al., 2005; Kaiser, 2007, 2010). Although many apparent homologues of mammalian immune genes have been identified in the chicken genome, many others appear to be absent (Kaiser, 2007, 2010; Kaiser and Stäheli, 2008), and these differences may explain some of the fundamental differences seen between chickens and mammals in their respective immune systems.

We have previously shown that the Th1–Th2 paradigm extends beyond mammalian species, to the chicken (Degen et al., 2005), suggesting evolutionary conservation of at least these two lineages of effector CD4+ T cells. In the last two decades the field of T cell biology has rapidly evolved, and many new effector and regulatory T cell subsets have been described in mammals. Whether equivalent and orthologous populations of cells exist in the chicken remains to be seen, but it is now possible to readily identify, and generate avian-specific reagents to, many of the immune-related molecules necessary to further dissect the immune response in...
the chicken. In this study we describe for the first time the cloning of chicken IL-21 (chl-21) cDNA, and analyse its expression and bioactivity in vitro. This work provides the basis for further studies to investigate if Tfh and Th17 T cell subsets are also present in the chicken.

2. Materials and methods

2.1. Cloning of chl-21 cDNA

To amplify the full length chl-21 cDNA, nested primers were designed according to the predicted sequence found in Ensembl (http://www.ensembl.org/Gallus_gallus). The first primer pair (chl-21_F1: 5‘-ACTCATGATGAGGATGAGG-3’ and chl-21_R1: 5‘-TACATTGCTTAAAATAGCATA-3’) flanked the predicted cDNA sequence and were used in the first round of PCR. To increase specificity of the PCR, a nested set of primers were designed to the predicted full length cDNA sequence (chl-21_F2: 5‘-ATGAGGATGAGGATGAGGTATTTC-3’ and chl-21_R2: 5‘-TCAAAATAGTACATTTCTGCA-3’) for a second round of PCR. Total RNA was extracted from chicken splenocytes stimulated with 1 μg/ml Concanavalin A (ConA) (Sigma, Poole, UK) for 24 h using a RNaseasy mini kit (Qiagen, Crawley, UK) following the manufacturer’s instructions. First strand synthesis was for 50 min at 42°C in a 20 μl volume containing 4 pmol of oligo dT, 200 U Superscript II (Invitrogen, Paisley, UK) and 500 ng RNA. After denaturation of the reverse transcriptase at 94°C for 3 min, 5 μl of this reaction mix were added as template to a 20 μl PCR reaction, containing 100 pmol each of primers chl-21_F1 and chl-21_R1, 0.4 mM dNTPs and 1 μl Taq polymerase (Invitrogen). Cycling conditions were 1 cycle of 94°C for 3 min, 3 cycles of 94°C for 60 s, 60°C for 30 s and 72°C for 90 s, and then 30 cycles of 94°C for 60 s, 57°C for 30 s and 72°C for 90 s. Five μl of the first PCR product were used in a nested PCR, containing 10 pmol each of primers chl-21_F2 and chl-21_R2, 0.4 mM dNTPs and 1 μl Taq polymerase (Invitrogen) in a 20 μl reaction volume. Cycling conditions were 1 cycle of 94°C for 3 min and 30 cycles of 94°C for 60 s, 57°C for 30 s and 72°C for 90 s. The resulting PCR product was ligated into pGEM-T Easy vector (Promega, Southampton, UK), and the complete sequence of three clones determined on each strand. An EcoRI-fragment containing chl-21 was sub-cloned into the eukaryotic expression vector pcI-neo (Promega), giving rise to pcI-neo-chl-21. The cDNA sequence has been submitted to Ensembl with the accession number AM737357.

2.2. Tissues and cells

Tissues and splenocyte subsets were obtained from three specific-pathogen-free (SPF) 6-week old outbred Rhode Island Red (RIR) chickens. Lymphoid tissues taken were the spleen, bursa, thymus, bone marrow, duodenum, jejunum, ileum, caecal tonsil, Meckel’s diverticulum and Harderian gland. Non-lymphoid tissues taken were the kidney, lung, heart, muscle, liver, brain and skin. Splenocyte subsets were isolated as previously described (Wu et al., 2009a). Briefly, chicken spleens were digested with 556 μg/ml DNase I (Roche Diagnostics Ltd., Burgess Hill, UK) and 2.2 mg/ml collagenase D (Roche Diagnostics Ltd.) in Hank’s Buffered Salt Solution for 1 h. Single cell suspensions were extracted using Histopaque 1077 (Sigma) followed by three washes in PBS. 10^6 cells were labelled with mouse anti-chicken CD4, CD8α, CD8β, TCR1 (TCRγδ), TCR2 (TCRζξ), TCR3 (TCRζξ)1, Bu-1, or KUL01 monoclonal antibodies (mAbs) (Southern Biotech, Birmingham, AL, USA). Polyclonal goat anti-mouse IgG-coated microbeads (Miltenyi Biotec, Bisley, UK) were used to isolate labelled cells by standard positive selection (POSSEL) using an autoMACS™ Pro separator (Miltenyi Biotec).

Splenic T-cell subsets were cultured with or without 1 μg/ml ConA (Sigma), Bu-1+ cells with or without 500 ng/ml PMA (Sigma), and KUL01+ cells with or without 400 ng/ml LPS (Escherichia coli serotype 055:B5) (Sigma). Splenic TCRζξ+ cells were also isolated from four non-SFP 7-week old outbred ISA Brown chickens. They were labelled with TCR2 and TCR3 and positively sorted, as described above, and were then stimulated (in triplicate) by incubation with immobilised anti-TCRζξ mAb AV33 (Parmentier et al., 1995) with or without anti-CD28 mAb AV7 (Young et al., 1994). Incubation was for 15 h at 41°C in 5% CO2, after which cells were harvested and RNA prepared using an RNeasy Mini kit (Qiagen) following the manufacturer’s instructions.

2.3. Production of recombinant chl-21 by COS-7 cells

COS-7 cells were routinely grown and passaged using standard conditions (Tregaskes and Young, 1997). Cells were transfected with either pcI-neo-chl-21 or pcI-neo alone (for a negative control) supernatant) using a DEAE-dextran-based method as previously described (Rothwell et al., 2001, 2004). Growth media were replaced with serum-free media 24 h post-transfection, and cells were then incubated for a further 72 h, prior to harvesting the supernatant containing the recombinant protein. Supernatants were stored at 4°C prior to use.

2.4. II-21 co-stimulation bioassay and flow cytometric analysis

Spleens and thymuses were removed from 8-week old SPF birds (outbred RIR or inbred line 72) post mortem and immediately placed in DMEM. Tissue was disrupted to release a single cell suspension, the lymphocytes were isolated over Histopaque 1077 (Sigma), washed twice and resuspended at 5 x 10^6 cells/ml in DMEM containing 2 mg/ml BSA, 1% l-glutamine, 1 U/ml penicillin and 1 μg/ml streptomycin. 5 x 10^5 cells were added to round-bottomed 96-well plates containing serial two-fold dilutions of recombinant (r) chl-21 (ex-COS), in a final volume of 200 μl/well, in the presence or absence of 0.2 μg/ml ConA (Sigma), 4 μg/ml PHA (Sigma), 1 μg/ml lipopolysaccharide (LPS) (E. coli serotype 055:B5) (Sigma), or rchl-2 (1/50 ex-COS supernatant; Rothwell et al., 2001). Samples were assayed in triplicate in five replicate assays in total. Cells were pulsed with 3H-thymidine (37 kBq/well, GE Healthcare, Little Chalfont, UK) for the final 6 h of a 48 h incubation at 41°C, 5% CO2. 3H-thymidine uptake was determined by liquid scintillation. Significance (taken as P < 0.05) of II-21-treatment versus the relevant control was determined using Student’s t-test.

2.5. Dendritic cell preparation and culture with IL-21

Chicken bone marrow-derived dendritic cells (chBM-DCs) were generated and expanded in vitro by culturing bone marrow precursors with GM-CSF and IL-4 as described (Wu et al., 2009b). On day 5 of culture, chBM-DCs were primed with different concentrations of rchl-21 (ex-COS) (1/100, 1/250 or 1/500) for 18 h, prior to stimulation with LPS (100 or 500 ng/ml) for a further 8 h. RNA was isolated from the various DC cultures using an RNeasy Mini kit (Qiagen) following manufacturer’s instructions; and expression of genes associated with activation and maturation of DCs analysed by real-time quantitative RT-PCR (qRT-PCR). Details of the qRT-PCR primers and probes are given in Table 1.

2.6. Real-time quantitative RT-PCR analysis

Chl-21 mRNA expression levels in different tissues and lymphoid cells were quantified by TaqMan qRT-PCR, using a
Table 1
Real-time quantitative RT-PCR probes and primers.

<table>
<thead>
<tr>
<th>RNA target</th>
<th>Probe/primer sequence (5′–3′)</th>
<th>Accession number</th>
</tr>
</thead>
<tbody>
<tr>
<td>28S</td>
<td>F GGGGCTGATACGAGGACGAGGAAACT</td>
<td>X59733</td>
</tr>
<tr>
<td></td>
<td>R GCAGGGGAGGATGGGAGGAAACT</td>
<td></td>
</tr>
<tr>
<td>IL-21</td>
<td>(FAM)-TGTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td>AM773577</td>
</tr>
<tr>
<td></td>
<td>R CCGGGAGGATGGGAGGAAACT</td>
<td></td>
</tr>
<tr>
<td>IFN-γ</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>Y09722</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
<tr>
<td>IL-1β</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>AJ24572</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
<tr>
<td>IL-6</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>AJ309540</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
<tr>
<td>IL-12β</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>AV262751</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
<tr>
<td>CCR7</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>HQ269806</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
<tr>
<td>DC-LAMP</td>
<td>F GCAAGAGGGTGAAGAGGAAACT</td>
<td>AM933592</td>
</tr>
<tr>
<td></td>
<td>R GGTTGCTGATTACCGAGGACGAGGAAACT-(TAMRA)</td>
<td></td>
</tr>
</tbody>
</table>

F, forward primer; R, reverse primer.

3. Results and discussion

3.1. Characterisation of chicken IL-21 cDNA

The chIL-21 cDNA consists of 438 nucleotides, encoding an open reading frame of 145 amino acids (aa), with the predicted signal sequence (SignalP 3.0) comprising the first 19 aa. Comparison of the predicted aa sequence of chIL-21 with orthologous proteins from mammals, amphibia and fish (Fig. 1) (Parrish-Novak et al., 2000), birds (Fig. 1A) (53% aa identity to the zebra finch, 71% to the duck and 78% to the turkey) than between the chicken and other classes of organisms. Alignment of the predicted avian IL-21 aa sequences with the chicken orthologue shows significant sequence differences at the 3′ end of the gene, with both the zebra finch and turkey sequences 8 aa shorter than those of chicken and duck. For example, the current version of the zebra finch genome has two apparent isoforms of IL-21, one encoded by four exons and the other five. The first four exons of each splice variant are aa identical in sequence, yet only the first exon is in common between the two splice variants in the genome sequence.

There is conserved synteny of the IL-2 and IL-21 genes in mammals (human, mouse, cow, pig) (Parrish-Novak et al., 2000), birds (chicken, turkey and zebra finch) and Fugu (Bird et al., 2005), with these two genes lying close to each other on the same chromosome in each of these species.

3.2. Tissue distribution and cellular expression of chicken IL-21

Expression of chIL-21 mRNA in various tissues and cell subsets was analysed by qRT-PCR. As shown in Fig. 2A, chIL-21 is widely expressed, albeit at low levels, in most lymphoid tissues, including the gut; it is also detected in the lung, liver and skin. Highest expression was in Meckel’s diverticulum, the lung, spleen and Harderian gland. The spleen, Meckel’s diverticulum, the Harderian gland, and to a lesser extent the lung, are lymphoid tissues which are rich in plasma cells. In mammals, IL-21 plays a role in B cell differentiation into plasma cells (Ozaki et al., 2004; Ettinger et al., 2005) and one could postulate that the relatively high levels of IL-21 in these tissues could be driving the differentiation of B cells to plasma cells. Despite the fact that these tissues were isolated from specific-pathogen-free chickens, it is perfectly reasonable to suppose that these birds will be making antibodies to other pathogens or molecules. At the cellular level, IL-21 is expressed in CD4+ and TCRγ+ (TCR2 and 3) cells, but not in CD8+ or TCRγ+ (TCR1) cells, and is up-regulated following mitogenic stimulation of CD4+ and TCR3+ cells (Fig. 2B). Specific stimulation of TCRγ+ cells by TCR-cross-linking induced significantly greater levels of IL-21 expression (P < 0.05) (Fig. 2C) than non-specific mitogenic stimulation, but the addition of anti-CD28 did not enhance IL-21 expression. A very low level of IL-21 expression...
(40-Ct = 2.4) was detected in the ConA-stimulated CD8+ population, which could be attributed to contaminating CD4+ cells in the preparation, since the purity of cell sorting using the autoMACS Pro was approximately 90–95%. Similarly, a low level of IL-21 expression (40-Ct = 3.7) was also detected in the stimulated Bu-1+ cell subset, and this may also be due to contaminating CD4+ cells. However, although unlikely, in both cases it could represent induction of IL-21 expression in these two cell types. Overall, our data closely reflect what is seen in mammalian systems, where IL-21 is expressed by CD4+ T and NKT cells (Parrish-Novak et al., 2000; Muneta et al., 2003; Coquet et al., 2007). It is not yet possible to determine whether IL-21 is expressed in chicken NKT cells, as these cells have yet to be described in the bird.

### 3.3. Biological activity of chicken IL-21

Recombinant chicken IL-21 was expressed in COS-7 cells and its effect on the proliferation of mitogen-stimulated splenocytes and

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**Fig. 1.** Alignment of the predicted chIL-21 amino acid sequence with (A) mammalian, amphibian and fish IL-21, and (B) other avian species, with reference to secondary structural features and functionally important residues. Shaded areas represent conservation of aa similarity – the darker the shading, the more conserved the residue across species. Dashes indicate gaps in the alignment. The predicted amino terminus of the mature chicken protein is indicated with an arrow. The four a-helices determined for huIL-21 are over-lined (A) and as predicted for chIL-21 (using Psipred; Jones, 1999) are underlined (B). Potential N-linked glycosylation sites are double-underlined. Four cysteines are conserved in all species and are indicated by asterisks, and the glutamine (Q) residue implicated in the interaction with the common g chain receptor is also conserved (indicated by a solid triangle). The accession numbers of the sequences used are as follows: human, DQ645417; bovine, AB070302; porcine, AB070302; murine, DQ645418; Xenopus, EF533945; Fugu, AJ844554; zebrafish, EF143579; chicken, AM773757; zebra finch, XM_002188250; turkey, Pre-ensembl: ENSMGAT00000011849; duck, Pre-ensembl: ENSAPLT00000007179.
thymocytes was investigated. Fig. 3 shows that rchIL-21 significantly enhances the proliferation of splenocytes (Fig. 3A) and thymocytes (Fig. 3B) sub-optimally stimulated with mitogens (ConA or PHA) or LPS (splenocytes only) in a dose-dependent manner, at all dilutions shown, when compared to mitogen alone ($P < 0.05$). Recombinant chIL-21 alone also induced significant levels of proliferation in splenocytes ($P < 0.05$), but generally not in thymocytes. It also synergised with IL-2 to augment proliferation of splenocytes (Fig. 3C), but not thymocytes (data not shown). Similarly in mammals, IL-21 is a co-stimulatory factor for T cells.

In mammals, IL-21 has an inhibitory effect on DC activation and maturation (Brandt et al., 2003; Strengell et al., 2006). The effects of rchIL-21 on DC maturation were investigated by priming chBM-DCs (derived after culturing bone marrow cells for 5 days with GM-CSF and IL-4; Wu et al., 2009b) with rchIL-21, prior to activation with LPS. The mRNA expression levels of CCR7 (Wu et al., 2011) and DC-LAMP (Wu et al., 2010), typical markers of DC maturation, as well as the mRNA expression of the cytokines IL-12α, IFN-γ, IL-1β and IL-6, were analysed by qRT-PCR (Fig. 4). All of these genes, with the exception of IL-12α which was not expressed, were expressed at low levels in unstimulated chBM-DCs, and the addition of rchIL-21 to the culture media for the final 18 h made little difference to their expression levels (Fig. 4A). Upon LPS-stimulation of immature chBM-DCs, expression of the four cytokines was significantly up-regulated, as previously shown (Wu et al., 2009b, 2010), as was expression of DC-LAMP and CCR7 (Fig. 4B), indicating these are markers of DC maturation. In chBM-DC cultures that were primed with rchIL-21 and then stimulated with LPS, expression of all six genes was significantly down-regulated when compared to LPS-stimulated chBM-DCs in the absence of rchIL-21 (Fig. 4C). These data suggest that chIL-21 therefore has an immunosuppressive effect on the function of avian DCs, as it does in mammals.

Our data presented here on the cloning and initial characterisation of chIL-21 bioactivity indicate that, as with other chicken cytokines described to date, despite limited aa identity with their
mammalian orthologues, there is conservation of bioactivity between the Mammalia and Aves. We have demonstrated that, as in mammals, chIL-21 is expressed by CD4+ TCRαβ+ cells, acts as a co-stimulator of T cells, and has a negative regulatory effect on DCs. Further work is required to clarify if it plays a role in avian B cell differentiation. With the rapidly increasing number of characterised avian immune genes, including cytokines and cell surface markers, we are now able to further dissect the avian immune response, and determine whether important new paradigms, to date only described in mammals, extend to the chicken. For example, identification of IL-21 and the preliminary bioactivity data presented herein provide additional and important new tools to begin to investigate whether the Th17 and Tfh cell lineages are present in the chicken.

Fig. 3. Effect of IL-21 on the proliferation of (A) mitogen-stimulated splenocytes; (B) mitogen-stimulated thymocytes; (C) splenocytes co-stimulated with IL-2. Cells were unstimulated or stimulated with sub-optimal levels of mitogen (ConA or PHA) or LPS, or recombinant chIL-2 (ex-COS) at different dilutions, and co-cultured with two-fold dilutions of recombinant chIL-21 (ex-COS) for 48 h. Cell proliferation is expressed as counts per minute (cpm) by measuring incorporation of 3H-thymidine. Error bars represent standard error of the mean (SEM) cpm of triplicate samples. Student’s t-test was used to determine significance (P < 0.05) of IL-21 treatment, when compared to the relevant control. The # symbol indicates where IL-21 treatment did not significantly enhance proliferation. Data shown are representative of five separate experiments.
This work was supported by the Biotechnology and Biological Sciences Research Council [Grant number BB/E008941/1] and Institute Strategic Programme Grants to IAH and The Roslin Institute. We thank Victoria Waters for providing the panel of splenocyte cell subset RNAs.

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