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Is the role of *Chlamydia trachomatis* underestimated in reactive arthritis patients in India

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Background: Although *Chlamydia trachomatis*-induced Reactive Arthritis (ReA) constitutes a significant disease burden in various countries, however it remains largely unrecognized and probably underestimated in India. Due to availability of multiple serovars, biphasic lifecycle and asymptomatic infection, diagnosis of this pathogen is difficult, thereby leading to chronic, persistent chlamydial infection in the synovium. The aim of the present prospective study was to find the presence of intra-articular *C. trachomatis* infection by nucleic acid amplification tests and secretory IgA determination in patients with ReA and in *forme fruste* of ReA, *viz.:* Undifferentiated Spondyloarthropathy (uSpA) attending a major tertiary Army hospital inNew Delhi (India).

Methods & Materials: Synovial fluid was aspirated from the knee joints of age and sex-matched 30 arthritic patients, *viz.*: ReA/uSpA (n = 15) and Osteoarthritis controls (OA) (n = 15) following the European Spondyloarthropathy Study Group criteria for ReA while clinical and radiological diagnosis was done for OA patients. The clinical details were recorded in all patients. Both *C. trachomatis*-specific surface Major Outer Membrane Protein (MOMP) and endogenous plasmid genes were targeted using semi-nested Polymerase Chain Reaction (snPCR) and nested PCR (nPCR), while anti-*C. trachomatis* IgA antibodies were estimated by commercial enzyme-linked immunosorbent assay kit (*Savyon Diagnostics, Israel*). Statistical evaluation of data was done by using trial version of Graph Prism Pad software (version 5.0; *GraphPad Software, Inc., San Diego, California, USA*).

Results: Overall, 33.3% (5/15) ReA/uSpA patients were found to be *C. trachomatis*-positive for either MOMP/plasmid gene in the joint fluid. 20% (3/15) were positive for plasmid gene while MOMP gene was present in 13.3% (2/15) patients in the study group (ReA/uSpA). Intra-articular anti-*C. trachomatis* IgA antibodies were detected in 26.6% (4/15) patients in the synovial fluid. Significant correlation ('p' value < 0.05) was found between PCR and serologic findings. None of OA controls was found positive for either chlamydial antibody/MOMP gene/plasmid gene.

Conclusion: The observations in the present study indicate that intra-articular *C. trachomatis* infection in ReA/uSpA patients is both underestimated as well as underdiagnosed inIndia. It also suggests the usefulness of serology for better clinical management of such patients.

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Relative prevalence of STI pathogens, vaginal conditions and HIV co-infection among STI patients attending Alexandra Health Centre, Gauteng Province, South Africa (2011-2013)

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Background: To determine the aetiology of urethral discharge (MUS), vaginal discharge (VDS) and genital ulcer (GUS) syndromes as well as the prevalence of HIV co-infections in Gauteng between January and April 2011-2013.

Methods & Materials: A total of 1180 consecutive patients were recruited at Alexandra Health Clinic, Johannesburg. From this total, 402 presented with MUS, 620 presented with VDS and 203 presented with GUS including mixed syndromes. Urethral swabs/smears (MUS), endocervical swabs/vaginal smears (VDS), genital ulcer swabs/smears (GUS) and sera (all) were collected with written informed consent. A real-time multiplex PCR assay was used to detect *Neisseria gonorrhoeae* (NG), *Chlamydia trachomatis* (CT), *Trichomonas vaginalis* (TV) and *Mycoplasma genitalium* (MG) from MUS/VDS swabs, and herpes simplex virus (HSV), *Treponema pallidum* (TP) *Haemophilus ducreyi* (HD) and *C. trachomatis* L1-3 (LGV) from ulcer swabs. Vaginal smears (VDS) were examined for bacterial vaginosis (BV) and candidiasis (CA) and genital ulcer smears (GUS) for granuloma inguinale (GI). Sera were tested for HIV.

Results: *N. gonorrhoeae* was the most common aetiological agent (309/402; 76.9%) for MUS cases; BV the most common non-STI cause of VDS (346/620; 55.8%) and HSV accounted for the majority of ulcers (127/203; 62.6%). *Chlamydia trachomatis* accounted for 27.6% (111/402) MUS and 16.6% (103/620) VDS cases, *Mycoplasma genitalium* accounted for 8.2% (33/402) MUS and 9.7% (60/620) VDS cases whereas *Trichomonas vaginalis* accounted for 4.2% (17/402) and 22.9% (142/620) of MUS and VDS cases respectively. *T. pallidum* accounted for 1.5% (3/203) of GUS cases. There was only 1 case of LGV. There were no cases of *H. ducreyi* and GI. The seroprevalence of HIV was 31.0% (130/402) among MUS, 45.2% (280/620) among VDS and 57.1% (116/203) among GUS patients.

Conclusion: Gonorrhoea, BV and HSV are the leading causes of MUS, VDS and GUS respectively. The HIV co-infection data emphasize the importance of STI patients as a focus for HIV HCT initiatives.

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